Full Length Research Paper

Inheritance of some spike related polygenic traits in spring wheat (*Triticum aestivum* L)

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Five quantitative spike related traits were studied in wheat genotypes by analyzing F1 data derived from a 5 × 5 diallel cross to assess the magnitude of gene action. The experiment was conducted at experimental area of Plant Breeding and Genetics, University of Agriculture Faisalabad. Analysis of variance proved to be significant for all characters and absence of epistasis for all traits which in turn attested fitness of the data for additive dominance model for genetic analysis. Number of grains spike^{-1} and grain yield plant^{-1} were found to be advocated by over-dominance type of gene action while preponderance of additive with partial dominance was observed for spike length, number of spikelets spike^{-1}and spike density. It was observed that varieties Pasban-90, line 9267, Pak-81 and Chakwal-86 possessed most of the dominant genes for spike length, number of spikelets spike^{-1}, number of grains spike^{-1}, grain yield plant^{-1} and spike density. The operation of additive type of gene action with partial dominance for spike length, number of spikelets spike^{-1} and spike density entails pedigree method of breeding for significant genetic improvement of   these traits while heterosis can be exploited for number of grains spike^{-1} and grain yield plant^{-1}.

Key words: Wheat, gene action, inheritance, genetic parameters, spike characters.

INTRODUCTION

Wheat covers more of the earth's surface than any other cereal crop. (Anon, 2005) and feeds about two thirds of the world population (Rahman et al., 2008). Being the main staple food item, it covers 40% of the total cultivated area and 65% of the food crops area in the country. Globally, it is the second largest cereal crop after maize. Owing to 14.4% contribution to the value added in agriculture and 3.1% to GDP, it occupies a central position in formulation of agricultural policies (Govt. of Pakistan, Finance Department, 2011). Southern Punjab, although cotton zone, contributes about 44% of the total

wheat production of the province. Due to long stay of cotton crop in the field, 80% wheat is being planted under late conditions. In order to fulfill the rapid demand of increasing population, we need to increase grain production per unit area by using available resources. Therefore it is necessary to evolve new wheat cultivars having wider genetic base capable of producing better yield under wide range of agro climatic conditions (Chowdhry et al., 2002). This situation necessitates the development of medium to late maturing wheat varieties that can be successfully grown after the harvest of cotton (Ahmad et al., 2005). Availability of diversified germplasm is the basic requirement for the success of any breeding program (Akram et al., 1997). Genetic variability present

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Table 1. Mean squares of some spike related traits in 5 × 5 diallel cross.

SOV	DF	Spike length	Number of spikelets spike^{-1}	Spike density	Number of grains spike^{-1}	Grain yield plant^{-1}
Replication	2	0.22$^{n.s.}$	0.23$^{n.s.}$	0.01$^{n.s.}$	0.17$^{n.s.}$	0.004$^{n.s.}$
Genotypes	24	2.25**	0.93**	0.03**	49.09**	5.85**
Error	48	0.39	0.41	0.01	5.03	1.88
C.V. percentage		5.25	3.41	6.53	3.34	5.79
S.E		0.51	0.52	0.08	1.83	1.12

P*<0.01; n.s., not significant.

in collected and preserved germplasms are important source in generating new plant ideotypes having desired traits that help to increase crop production and thus improve the level of human nutrition (Singh, 1991).

MATERIALS AND METHODS

The plant material comprised of 5 wheat varieties/lines viz., Pasban-90, Chakwal-86, Pak-81, 9250 and 9267, having wide genetic stand and varied by date of release, pedigree and yield components and were crossed in a full diallel fashion at experimental farm area of University of Agriculture, Faisalabad, Pakistan. During the next cropping season, seeds of F1 hybrids along with their parents were sown in the field in a randomized complete block design with three replications. The entries were assigned randomly to experimental units in each block having row to row and plant to plant distance of 30 and 15 cm respectively. Two seeds per hole were sown with the help of a dibbler and later thinned to one seedling per hole after germination. All recommended cultural practices and inputs like, manuring and irrigation etc. were kept uniform for all entries from sowing till harvesting and experiment was conducted under uniform conditions to minimize environmental variation to the maximum extent. For data collection ten guarded plants for each parent and cross were tagged at random for each replication and data was recorded for spike length of mother shoot of selected plants in centimeters from base to the tip of spike excluding awns. Finally average spike length was obtained. The spike of wheat consists of smaller units called spikelets which bear 3 to 5 florets. Spikelets were counted from the mother spike of selected plants and were averaged spike density was calculated by dividing the number of spikelets spike^{-1} with its respective spike length. Similarly, the spike of the mother shoot was thrashed manually and numbers of grains spike^{-1} were counted for each genotype and for grain yields all spikes of individual selected plants were threshed manually and weighed using electric balance (Compax- Cx-600).

Statistical analysis

The data collected for all above-mentioned characters were subjected to analysis of variance as proposed by Steel and Torrie (1997). In case, where significant differences were found, the data were subjected to regression covariance/variance (Wr/Vr) analysis and analysis of variance of Wr +Vr and Wr-Vr arrays. The diallel crossing system as suggested by Hayman (1957, 1958) and Jinks (1954, 1955), modified by Mather and Jinks (1982) and adopted by Singh and Chaudhry (1995), was used for analysis of genetic parameters.

## RESULTS AND DISCUSSION

Spike length (cm)

This particular character hold great value for plant breeders as it determines the yield of wheat. The analysis of variance for spike length revealed that differences among the genotypes were highly significant (Table 1). The Vr/Wr graph shows that regression line cuts the Wr-axis above the origin indicating additive type of gene action with partial dominance (Figure 1A). The deviation of regression line was not significant from unit slop, thus indicating the absence of non-allelic interactions. Similar results were reported by researchers like Walia et al. (1995), Aziz et al. (1999), Chowdhry et al. (2002) and Kashif and Khaliq (2003). On the other hand Ali et al. (1999) and Nazeer (2011) found non-additive type of gene action for this trait. Array points (Figure 1A) indicated that genotype Pak-81 has maximum dominant genes which is nearest to the origin while 9250 was farthest from the origin, so it possessed most of the recessive genes. Besides Pak-81, Chakwal-86 and Pasban-90 also had maximum number of dominant genes having proximity to the origin. The expression of character for spike length ranges between 10.72 and 13.90 cm (Table 2). The genotype 9250 having maximum array means (12.42 cm) exhibited the best general combining ability effects while genotype Pak-81 having minimum array mean (11.19 cm) indicated poor general combining ability effects (Table 2). As a whole, array table showed that cross 9250 × 9250 possessed the highest value (13.90) exhibiting the best specific combining ability effect and cross Pak-81 × 9267 having the lowest value (10.72) represented the poor specific combining ability effect. The present study showed the additive type of gene action for spike length so selection in early generations would be fruitful.
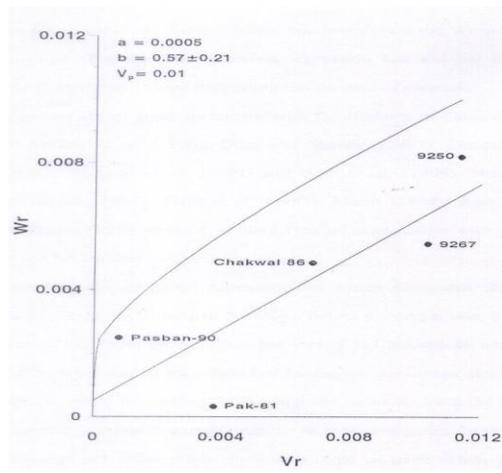
Number of spikelets spike^{-1}

The analysis of variance revealed that differences among the genotypes were highly significant for number of spikelets spike^{-1} (Table 1). Vr/Wr graph shows that
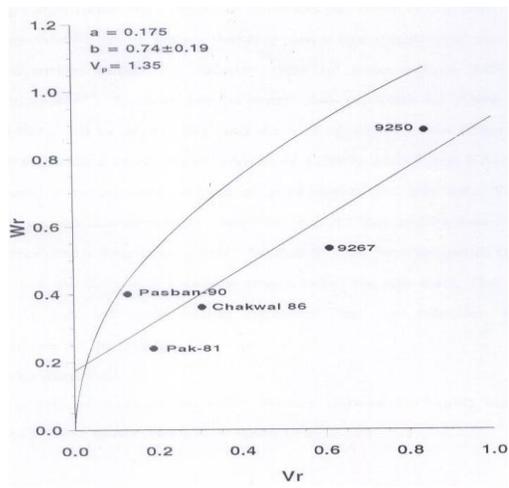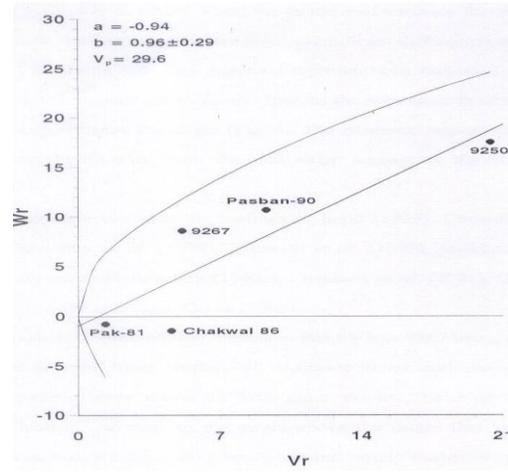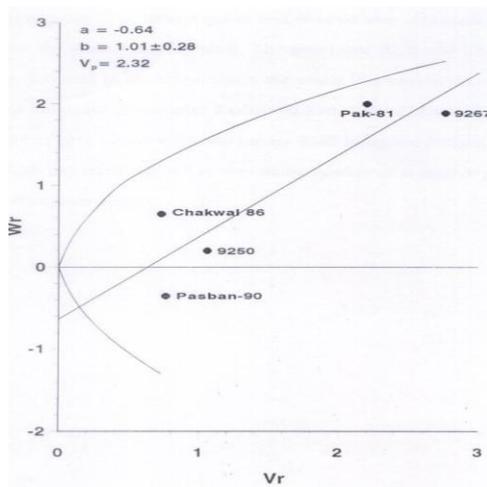
(A)
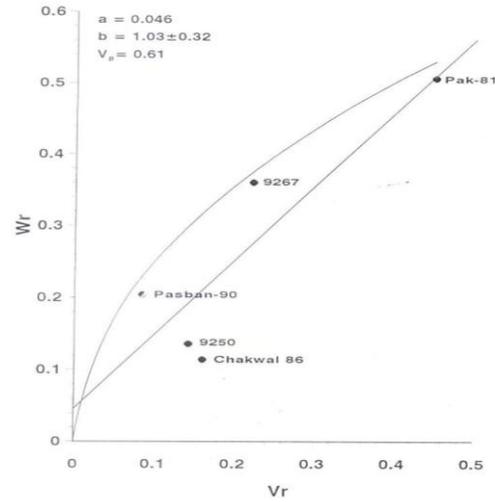
(B)

(C)

(D)

(E)

Figure 1.   (A) Spike length; (B) number of spikelets spike^{-1} (C); spike density; (D) number of grains spike^{-1}; (E) grain yield plant^{-1}.

Table 2. Array means of mean spike length (cm) in a 5 × 5 diallel cross.

Genotypes	Pasban-90	Chakwal-86	9250	9267	Pak-81
Pasban-90	1210	12.34	12.54	12.45	11.65
Chakwal-86	12.34	12.82	12.21	11.74	11.41
9250	12.54	12.21	13.9	11.98	11.46
9267	12.45	11.74	11.98	12.76	10.72
Pak-81	11.65	11.39	11.5	10.73	10.73
Total	61.1	60.5	62.1	59.65	55.97
Mean	12.22	12.1	12.42	11.93	11.19

Table 3. Array means of mean number of spikelets per spike in a 5 × 6.

Genotypes	Pasban-90	Chakwal-86	9250	9267	Pak-81
Pasban-90	18.23	18.51	18.88	18.6	18.17
Chakwal-86	18.51	19.56	19.08	19.14	19.38
9250	18.88	19.08	19.85	19.51	19.41
9267	18.6	19.14	19.51	18.83	18.3
Pak-81	18.17	19.38	19.42	18.3	18.08
Total	92.39	95.68	96.75	94.38	93.35
Mean	18.48	19.14	19.35	18.87	18.67

regression line intercepted the Wr-axis above the origin indicating additive type of gene action with partial dominance (Figure 1B). The regression line is of unit slope, suggesting the absence of epiststis for number of spikelets spike^{-1}. Similar results were also reported by Ali et al. (1999), Asif et al.(1999), Aziz et al. (1999), Kashif and Khaliq (2003) and Nazeer et al. (2011) but Pandey et al. (1999), Habib and Khan (2003) and Rehman et al. (2003) demonstrated over dominance type of gene action for this trait. From the Vr/Wr graph (Figure 1B), it is shown that genotype Chakwal-86 and 9250 have maximum dominant genes being closer to the origin whereas as Pak-81 has the maximum recessive genes so it is the far away from the origin point for this trait. The expression of character for number of spikelets spike^{-1} ranges between 18.17 and 19.56 (Table 3). The genotype 9250 having maximum array means (19.35) indicated the best general combining ability effects while genotype Chakwal-86 having minimum array means (19.14) indicated poor general combining ability effect (Table 3). As a whole, array table showed that cross Chakwal-85 × Chakwal-85 possessed the highest value (19.56) so it revealed the best specific combining ability effect and cross 9267 × Chakwal-86 having the lowest value (19.14) represented the poor specific combining ability effect. The absence of non-allelic interaction and presence of additive type of gene action with partial dominance suggests that selection would be very fruitful in early segregating generation.

Spike density

The analysis of variance for spike density showed the highly significant differences among genotypes under study (Table 1). Graphic representation of Vr/Wr variances for spike density shows that regression line intercepted the Wr-axis on positive side above the point of origin, indicating partial dominance with additive type of gene action (Figure 1C). Altinbas and Bilgen (1996) revealed additive effects and dominance effects while Hussain et al. (1990) reported over dominance type of gene action for spike density. As the regression line did not deviate significantly from unit slope, it shows absence of non-allelic interaction. From the graph, it is shown that genotype Pak-81 have maximum dominant genes being nearest to the origin followed by Pasban-90 which has also partial dominance with additive type of gene action and contain maximum dominant genes. As 9250 has the maximum recessive genes so it is the farthest from the origin point for spike density. The expression of character ranges between 1.70 to 1.42 g (Table 4). The genotype Pak-81 having maximum array means (1.67 g) indicated the best general combining ability effects while genotype Pasban-90 having minimum array means (1.51 g) showed poor general combining ability effects (Table 4). As a whole, array table depicted that cross Chakwal-86 × Pak-81 possessed the highest value (1.70) revealing the best specific combining ability effect and cross between genotype

Table 4. Array means of mean spike density in a 5 × 5 diallel cross.

Genotypes	Pasban-90	Chakwal-86	9250	9267	Pak-81
Pasban-90	1.51	1.5	1.5	1.49	1.56
Chakwal-86	1.51	1.52	1.57	1.64	1.7
9250	1.51	1.57	1.42	1.64	1.69
9267	1.49	1.64	1.64	1.47	1.7
Pak-81	1.56	1.7	1.69	1.7	1.69
Total	7.58	7.95	7.85	7.96	8.36
Mean	1.51	1.59	1.57	1.59	1.67

Table 5. Array means of mean number of grains per spike in a 5 × 5.

Genotypes	Pasban-90	Chakwal-86	9250	9267	Pak-81
Pasban-90	62.33	70	68.66	67.33	65
Chakwal-86	70	68.33	67.66	65.16	65
9250	68.66	67.66	77	70.66	65
9267	67.33	65.16	70.66	65.66	65.66
Pak-81	65	65	65	65.66	67.66
Total	333.33	336.16	349	334.5	328.33
Mean	66.66	67.23	69.8	66.9	65.66

9250 have lowest value (1.42) representing the poor specific combining ability effect. The additive with partial type of gene action indicates that the selection in early generations would be fruitful.

Number of grains spike^{-1}

One of the most important yield components is number of grains per spike. From (Table 1) analysis of variance for the number of grains spike^{-1} showed that there are highly significant differences among the genotypes. The graphical representation indicated the over dominance type of gene action for this trait, as the regression line intercepted the Wr-axis just below the origin (Figure 1D). The estimated regression line did not deviate significantly from the unit slope suggesting the absence of epistasis. The results are in good agreement with the findings of Mishra et al. (1996), Uma and Sharma (1997), Dhaduk and Shukla (1998), Shahzad et al. (1998) and Asif et al. (1999). However, Awaad (1996), Ali and Khan (1998), Aziz et al. (1999), Tahir (1999), Riaz and Chowdhry (2003) and Nazeer (2011) reported additive type of gene action with partial dominance for the number of grains per spike. By viewing the graphical representation which illustrated that the variety Pak-81, being the closest to the origin below the origin line, has the most number of dominant genes. The other variety is Chakwal-86 which is also near to the origin below the origin line having the maximum number of dominant genes, while the variety 9250 being the far away from the origin, which indicated that it has maximum number of recessive genes for the trait number of grains per spike. The expression of character for grain yield plant^{-1} ranges between 62.33 and 77.0 (Table 5). The genotype 9250 having maximum array means (69.8 g) indicated the best general combining ability effects while genotype Pak-81 having minimum array means (65.66) revealed poor general combining ability effects (Table 5). The absence of non-allelic interaction and presence of over dominance type of gene action suggests that selection for this trait should be differed until later generations.

Grain yield plant^{-1} (g)

There were highly significant differences among the genotypes as shown form the analysis of variance for grain yield plant^{-1} (Table 1). The inheritance pattern for grain yield appeared to be non additive type of gene action as the regression line intercepted the Wr-axis below the origin (Figure 1E). Deviation of the estimated regression line from the unity was not significant thus indicating the absence of non-allelic interaction. The results derived from the present study are in accordance with those of the earlier findings of Mishra et al. (1996),Flintham (1997), Asif et al. (1999), Aziz and Chowdhry (1999),Sheikh et al. (2000), Chowdhry et al. (2002) and Kashif and Khaliq (2003) while Chowdhry et al. (1995), Ali and Khan (1998) and Ali et al. (1999) found additive with partial dominance type of gene action for this trait. The graphical representation of array points revealed that the genotype

Table 6. Array means of mean grain yield per plant (gm) in a 5 × 5.

Genotypes	Pasban-90	Chakwal-86	9250	9267	Pak-81
Pasban-90	22.65	23.92	23.67	21.76	23.32
Chakwal-86	23.92	23.01	22.52	22.81	24.57
9250	23.67	22.52	23.01	25.06	22.71
9267	21.76	22.81	25.06	24.85	25.67
Pak-81	23.32	24.57	22.71	25.67	26.19
Total	115.34	116.845	116.98	120.16	122.47
Mean	23.06	23.36	23.39	24.03	24.49

Pasban-90 is closest to the origin below the origin line, having the maximum number of dominant genes and showed over-dominance type of gene action for grain yield plant^{-1}. The genotypes 9250 and Chakwal-86 which are also near to the origin above the origin line having the maximum number of dominant genes after Pasban-90 and showed that additive with partial type of gene action while the variety 9267 being the farthest from the origin which indicated that it has maximum number of recessive genes for this trait. The expression of character for grain yield plant^{-1} ranges between 21.76 to 26.19 g (Table 6). The genotype Pak-81 having maximum array means (24.49 g) indicated the best general combining ability effects while genotype Pasban-90 having minimum array means (23.06 g) revealed poor general combining ability effects (Table 6). As a whole, array table showed that cross Pasban-90 × 9267 showed the highest value exhibiting the best specific combining ability effect and selfing cross of Pak-81 with lowest value representing the poor specific combining ability effect. The over dominance type of gene action and absence of non-allelic interaction suggests that selection would be ineffective in early segregating generation.

Conclusion

The results from this study determined that all genotypes had considerable genetic diversity among themselves. Characters such as spike length, number of spikelets spike^{-1} and spike density that are in command of additive gene action. Since, additive genes are directly inherited from parents to offspring and resemblance among parents and progenies is the result of additive genes (Falconer, 1989); moreover, additive genes determine the breeding value of plant material therefore these traits could significantly be improved by pursuing pedigree method right in early segregating generation (Ali et al., 2008). Pervasiveness of dominance phenomenon as depict by Wr/Vr graphs which demonstrate over dominance for number of grains spike^{-1} and grain yield plant^{-1}called for prudent and more vigilant selection exercise for exploitation of these attributes and suggested that manipulation of the parents might be useful through heterosis.

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