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# Genetic Performance of Bread Wheat Genotypes For Spike Parameters Under Normal and Late Planting

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**Abstract:** Diallel analysis revealed that both additive and dominant effects were significant for spike length, spikelets per spike, grains per spike, seed set and grain weight per spike under normal planting. Under late planting additive effects were significant for all the traits studied. However, dominant effects were also significant for grains per spike and seed set. Graphical analysis indicated that gene action for spikelets per spike under normal planting changed to overdominant under late planting and overdominant gene action for spike length changed to additive. However, additive gene action for spike density and grain weight per spike and overdominant gene action for seed set remained unchanged. Spike length, grains per spike and seed set were controlled by dominant genes while spike density and grain weight per spike *were* under recessive gene control under both plantings. However, dominant gene control for spikelets per spike changed to recessive under late planting. It was also noticed that parental genotypes shifted their positions from recessive to dominant or midway or from dominant to midway or most recessive or the other way, in the graphical presentation.

**Key words:** Spike density, spikelets, gene action, additive, dominance, heritability, wheat

## Introduction

Earlier genetic studies have yielded useful information which can aid towards planning/developing new breeding strategies. Genetic control and action of genes provide information about the patterns of inheritance. Lonc (1986) reported a recessive gene control for spike length and grains per spike and dominant gene control for spikelets per spike. Similarly, Lonc (1988) observed additive gene action for spike length, overdominance for grains per spike and dominant gene control for spikelets per spike and grains per spike in wheat. Additive gene action for spike length and grains per spike in wheat was also reported by Li *et al*. (1991). In another study Lonc *et al*. (1993) observed partial dominance for spike density, grains per spike and seed set in wheat. They also observed recessive gene control for spike density. Prodanovic (1993) reported high heritability estimates for spike length and overdominance gene action for grains per spike.

Genotype x environment interaction is the most influential factor for the expression of any trait. Thus, keeping the importance of spike parameters the present study was planned to investigate their inheritance pattern in six wheat genotypes under normal as well as late planting conditions.

## Materials and Methods

The experiment was conducted in the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material comprised six wheat genotypes viz., Pak.81, LU26S, Faisalabad 85 (Fsd.85), Pasban 90 (Psbn.90), 4943 and 4072, crossed in a $6 \times 6$ diallel fashion during the crop season 1995-96. The experimental material consisting of all $F_1$s along with their parents, was planted in the next crop season in lines (under normal planting conditions) using a triplicated randomized complete block design. Plant to plant and row to row spacings were 15 and 25 cm, respectively. Seeds were sown in holes (made with the help of dibble) at the rate of 2 seeds per site which were later thinned to single healthy seedling per site after germination. Each treatment was a single line of 5 meter length comprising of approximately 30 plants. All the other cultural operations including hoeing, weeding, irrigation, fertilizers, etc. were carried out identically to reduce experimental error. The same material was also planted in December (under late planting conditions) using same methodology.

At maturity data for various spike parameters including spike length, spikelets per spike, spike density, grains per spike, seed set and grain weight per spike were collected separately from each of the normal and late sown experiments and were analyzed separately. Analysis of variance according to Steel and Torrie (1984) was used to sort out significant differences among genotypes. Formal diallel analysis as suggested by Mather and Jinks (1982) was conducted to investigate gene action and degree of dominance. Graphical analysis and computation of genetic components of variation were also carried out according to Hayman (1957). To fulfill the assumptions of Hayman for the adequacy of additive-dominance model two tests were employed. The first test was an analysis of regression coefficient. Variances (of each array) and covariances (array with its parental values) were estimated from the mean diallel table. Then the regression of covariance on the variances was computed. According to Mather and Jinks (1982) the regression coefficient is expected to be significantly different from zero but not from unity. Failure of this test indicate presence of non-allelic interaction (epistasis) or genes are not independent in their action, or show non-random association among parents. The second test was the analysis of variance of the Wr + Vr and Wr-Vr. If dominance (or certain types of non-allelic interaction) is present Wr + Vr must change from array to array. Similarly, if there exists epistasis, Wr-Vr will vary between arrays.

## Results and Discussion

Data subjected to analysis of variance revealed significant differences for all the six spike parameters studied. Thus basic diallel analysis according to Mather and Jinks (1982) was employed for further investigation.

**Spike length:** Diallel analysis (Table 1) revealed significant additive (a) and dominant (b) genetic effects for spike length under normal planting. Directional dominance deviation (b,) was, however, absent. Gene distribution was found symmetrical ($b_2$) and the role of specific genes ($b_3$) was observed as significant. Maternal (c) and reciprocal (d) effects were absent thus, retesting of a and b items was not needed. Formal diallel analysis under late planting showed that only the additive genetic effects (a) were highly significant. Dominant effects (b) were non-significant. Significant $b_2$ item displayed different gene distribution among the parents. Role of specific genes ($b_3$) was non-significant. Maternal (c) and reciprocal effects (d) were also found absent. Both scaling tests indicated that data were fully adequate for further analysis under both plantings.

Computation of genetic components (Table 2) showed that both additive and dominant variation were significant under normal planting. However, only additive (D) variation was observed as

significant under late planting. Distribution of positive and negative alleles among the parents under normal planting was almost equal as indicated by necessarily equal H and H2 values and $H_2/4H$, ratio (0.257) while under late planting H and H2 values and $H_2/4H$, ratio (0.145) indicated the unequal distribution of these alleles among the parents. F was negative and non-significant in both plantings. An influential role of environment was also observed in both plantings. Average degree of dominance under normal planting was 1.363 presenting an overdominance gene action. Graphical representation (Fig. 1 a) also showed the same result. Overdominance gene action for spike length was also reported by Khan *et al*. (1984) and Iqbal *et al*. (1991).

Narrow sense heritability estimate (0.3575) was about 50 percent of the broad sense heritability. High broad and narrow sense heritability estimates for spike length have also been reported by Sharma *et al*. (1986), Ma (1988) and Prodanovic (1993). This indicated an equal proportion of additive and dominant variation in the total heritable genetic variation.

Under late planting average degree of dominance (0.603) indicated partial dominance. A very high estimate of narrow sense heritability (0.7095) indicated that almost whole of the inherited genetic variation was additive. This fact was also evident in Wr/Vr graph (Fig. 1 c) which presented a positive intercept showing absence of dominance. These results are in agreement with those of Sharma *et al*. (1986), Lonc (1988), Chowdhry and Ahmad (1990) and Li *et al*. (1991) who also reported additive gene action with partial dominance for this trait.

Wr/Vr graph under normal planting displayed that Psbn. 90 and LU26S were located nearest to the origin with most dominant genes while Pak.81 being farthest from the origin had the most recessive genes. However, under late planting Fsd. 85, LU26S and 4943 were the most dominant parents while Pak.81 was the most recessive parent.

Negative correlation (-0.393 and -0.106) between Wr + Vr and parental values and the graph (Fig. 1 b & d) under both plantings indicted that dominant genes were responsible for increase in spike length as parents with greater spike length have smaller Wr + Vr values and vice versa. However, Lonc (1986) reported a recessive gene control for the trait.

**Spikelets per spike:** Additive (a) genetic effects were highly significant while significant dominant gene effects (b) were revealed for spikelets per spike under normal planting. Directional dominance. deviations ($b_1$) were, also found highly significant. Distribution of genes among the parents was symmetrical with important specific gene effects. No maternal (c) or reciprocal effects (d) were detected. Analysis of variance for this character under late planting revealed highly significant genetic effects of only additive (a) nature. While dominant gene effects (b) were nonsignificant. Symmetrical gene distribution was also indicated by non-significant $b_2$ item. Significant maternal (c) effects required retesting of a item. After re-testing highly significant a reduced to non-significant indicating that maternal effects suppressed the additive genetic effects. Reciprocal effects (d) were found nonsignificant.

Regression coefficient b differed significantly from zero with line of unit slope under both plantings . Similarly, analysis of variance of arrays also revealed non-significant differences indicating the absence of non-allelic interaction. The data were thus, considered adequate for the additive-dominance model.

Genetic components of variation (Table 2) revealed significant additive as well as dominant variation under both plantings. Values of H and H2 were necessarily equal under normal planting. Similarly, ratio of $H_2/4H$, (0.232) also depicted the equal frequency of positive and negative alleles among the parents. While unequal values of H and H2 under late planting and ratio of $H_2/4H$, (0.158) indicated the unequal distribution of positive and negative alleles among the parents. F was significant and positive under normal planting indicating that dominant genes were more frequent. However, under late planting F was non-significant and negative.

Environmental variation was found significant under both plantings. Average degree of dominance for the trait under normal planting was less than 1. Similarly, graphical presentation of the data (Fig. 2a) also depicted a positive intercept showing additive gene action with partial dominance. While under late planting average degree of dominance (1.180) indicated an overdominance type of gene action. The Wr/Vr graph (Fig. 2c) also depicted a similar type of gene action. Similar results have also been reported by Lonc and Zalewski (1991) and Khan *et al*. (1992). High broad sense (0.7417 and 0.6887, respectively)- and narrow sense (0.5454 and 0.5630, respectively) heritability estimates under both plantings were also recorded which are in conformity with those of Ma (1988), Jedynski (1988) _and Mandal *et al*. (1991). The location of array points indicated that parents Pak.81 and 4943 were the most dominant while Fsd. 85 was having the least dominant genes under normal planting while Psbn. 90 and Pak.81 were the most dominant parents and Fsd. 85 was the most recessive parent under late planting.

The negative correlation $1, -0.716i$ and the trend line of Wr + Vr/P graph (Fig. 2b) indicated that the dominant genes were responsible for increased spikelets per spike under normal planting. While positive correlation (0.767) and graph (Fig. 2d) depicted that the recessive genes were responsible for the increase in spikelets per spike under late planting. Lonc (1986) also reported recessive gene control for spikelets per spike while Lonc (1988) reported a dominant gene control for this trait.

**Spike density:** Diallel analysis (Table 1) under normal planting depicted highly significant additive (a) genetic effects while dominance effects (d) were non-significant. Gene distribution among the parents was similar (non-significant ($b_2$) with a significant role of specific genes ($b_3$). Maternal (c) and reciprocal (d) effects were not detected. In case of late planting additive (a) effects were highly significant while dominant (b) effects and directional dominant deviations ($b_1$) were non-significant. Gene distribution among the parents was also similar with absence of specific gene effects. Maternal (c) and reciprocal (d) effects were also not observed rendering re-testing of a and b components needless.

Test of the regression coefficient under normal planting (b =0.615 ± 0.283) revealed that it differed non-significantly both from zero and unity indicating the presence of non-allelic interaction. But analysis of variance of Wr + Vr and Wr-Vr displayed non-significant differences showing absence of non-allelic interaction. Data were thus, considered partially adequate due to the failure of regression test under normal planting.

Under late planting regression coefficient (b =0.952 ± 0.258) was significantly different from zero but not from unity showing absence of non-allelic interaction. Similarly, analysis of variance of arrays depicted non-significant differences for Wr + Vr and Wr-Vr displaying absence of dominance and non-allelic interaction. Thus, the adequacy of the data for additive-dominance model was fulfilled under late planting.

Table 2 presented the genetic components of variation which revealed significant additive (0) genetic effects under both plantings while dominance was absent. Unequal values of $H_1$ and $H_2$ and $H_2/4H$ ,ratios (0.323 and 0.375) depicted dissimilar distribution of negative and positive genes among the parents. F was negative and non-significant under both plantings. Average degrees of dominance (0.976 and 0.329) revealed the absence of dominance under both plantings. Lonc *et al.* (1993) had also reported absence of dominance but partial dominance for this trait. The Wr/Vr graphs (Fig. 3a and c) also revealed that the intercept of the regression line on the Wr axis was positive displaying an additive type of gene action with partial dominance under both plantings. Narrow sense heritability under normal planting was about 60 percent of the broad sense heritability indicating that greater portion of the inherited variation was of additive nature. Similarly, a very high estimate of narrow sense heritability under late planting clearly indicated that additive genetic variation out of

the total inherited genetic variation was of greater magnitude than the dominant variation.

The location of array points along the regression line under normal planting depicted that LU26S and 4072 possessed the most dominant genes while Fsd. 85 possessed the most recessive genes. Under late planting Psbn. 90, 4943 and Pak.81 were the most dominant parents while Fsd. 85 was again the most recessive parent.

When Wr + Vr values were plotted against parental values (Fig. 3b and d) and the correlation was computed (0.498 and 0.236) it became evident that spike density was controlled by the recessive genes under both plantings. Presence of more dominant genes reduced the spike density.. Therefore, Fsd. 85 with more recessive genes had greater spike density. Lonc *et al.* (1993) also reported a recessive gene control for this trait.

**Grains per spike:** Formal diallel analysis of variance for grains per spike under normal planting (Table 1) revealed highly significant additive (a) and dominant (b) gene effects, the former being greater in magnitude. Significant $b_2$ value indicated the different distribution of genes among the parents while non-significant $b_3$ value displayed the unimportant effects of specific genes. Maternal (c) and reciprocal effects (d) were found absent. Under late planting, diallel analysis of variance revealed highly significant additive and dominant gene effects. Item b, represented that dominant directional deviation was non-significant. Symmetrical distribution of genes was indicated by non-significant $b_2$. Important contribution of specific genes for the control of the characters was also indicated (significant $b_3$). Maternal and reciprocal effects were absent.

Scaling test of regression coefficient (1) = 0.701 t 0.189) under normal planting displayed that it was significantly different from zero but not from unity. The other test i.e., analysis of variance of Wr + Vr and Wr-Vr indicated significant differences for the both displaying presence of dominance and non-allelic interaction. Thus, it made the data partially adequate for the additive-dominance model under normal planting. Test of regression coefficient (b = 0.792 ±0.359) under late planting depicted that it differed non-significantly from zero and unity indicating the presence of non-allelic interaction. But the analysis of variance of Wr + Vr and Wr-Vr indicated the absence of non-allelic interaction and thus, made the data partially adequate for the additive-dominance model under late planting. Evidence of non-allelic interaction for grains per spike was also reported by Jedynski (1988).

Genetic components of variations are presented in Table 2 which revealed that both additive and dominant variations were significant under both plantings. However, additive component (D) was greater under normal planting and that of dominance under late planting. Dominant gene distribution among the parents under both plantings was, however, unequal ($H_1 < H_2$) which was also evident from $H_2/4H_1$ ratios (0.187 and 0.221). Similarly, F was non-significant and positive under both plantings. Average degree of dominance for the trait under normal planting was less than 1 (0.953) suggesting partial dominance. The graphical presentation (Fig. 4a) of the data also revealed partial dominance with additive gene action. Yadav *et al.* (1988), Li *et al.* (1991) and Asad *et al.* (1992) have also reported an additive gene action for grains per spike. A high narrow-sense heritability estimate (about 70% of the broad sense estimate) also indicated the greater portion of additive variance in the total inherited genetic variation. High heritability estimates for this trait were also reported by Sharma *et al.* (1986) and Ma (1988). Average degree of dominance under late planting (1.166) suggested an overdorninant type of gene action. Similarly, the Wr/Vr graph (Fig. 4c) also depicted an overdominance gene action. These results are in accordance with those of Lonc (1988), Lonc and Zalewski (1991) and Prodanovic (1993) who reported overdominance gene action while differ from Lonc *et al.* (1993) who reported partial dominance for grains per spike.

The position of the array points (Fig. 4a) indicated that Pak.81 and

4943 were the most dominant parents under normal planting while Fsd. 85, located farthest from the origin, was the most recessive parent. The array points in the graph under late planting (Fig. 4c) indicated that Pak.81 was the parent with most dominant genes while 4943 was the most recessive parent. LU26S was located midway. The correlated response of Wr + Vr and parental values under both plantings was negative (-0.794 and -0.384). Further when these values were plotted (Fig. 4b and d), it was observed that parents with larger phenotypic values also had lesser Wr + Vr values and vice versa. Thus, it was inferred that dominant genes increased grains per spike under both plantings. Similarly, dominant gene control for the trait was also reported by Lonc and Zalewski (1991) and Bebyakin and Starichkova (1992) while Lonc (1986) reported recessive gene control for this trait.

**Seed set:** The analysis of variance (Table 1) revealed highly significant genetic effects of both additive (a) and dominant (b) nature under normal planting. The directional deviation of the dominant genes ($b_1$) was alto significant. Asymmetry of gene distribution was indicated by significant value of $b_2$. Highly significant $b_3$ indicated the effective role of specific genes for the control of this character. Maternal (c) and reciprocal (d) effects were absent. Presence of both additive and dominance gene effects was also indicated by the significant a and b items under late planting. Absence of directional dominance and symmetrical gene distribution was shown by non-significant b and $b_2$ items, respectively. However, significant $b_3$ indicated the involvement of specific gene effects for the trait. Maternal and reciprocal effects were found absent. Scaling tests used to test the adequacy of the data for the additive-dominance model indicated that regression coefficient b under both plantings differed significantly from zero but not from unity. While analysis of variance of Wr + Vr and WrVr presented significant differences for arrays indicating the involvement of non-allelic interaction under normal planting. But absence of non-allelic interaction was indicated by the analysis of variance test of arrays under late planting.

Both D and H components were found significant (Table 2) showing the presence of additive as well as dominant variation under both plantings. Unequal values of H and H2 suggested the dissimilar distribution of positive and negative genes among the parents. The ratios of $H_2 14H_1$ (0.198 and 0.200) also supported these results. F was positive and significant under normal planting but non-significant under late planting. Average degree of dominance (1.620 and 1.417) suggested an overdominance type of gene action for this trait under both plantings. This was also conformed by WrNr graphs (Fig. 5a and c) where the intercept of the regression line was negative. Very small narrow sense heritability estimates, 0.1886 under normal planting and 0.2975 under late planting, also indicated that dominant variation was more profound than the additive one in the inheritance of seed set percentage under both plantings. The position of the array points indicated that genotypes 4072 and LU26S were the most dominant parents while Fsd. 85 Was the most recessive one under normal planting. Psbn. 90 was located midway. However, under late planting Fsd. 85 possessed the maximum number of dominant genes followed by 4943 while 4072 had the lowest dominant genes. LU26S showed the equal distribution of dominant and recessive genes. The correlated response of the dominant gene distribution with the phenotype of the common parent of the array was negative (-0.868 and -0.661). Similarly, the graphs (Fig. 5b and d) also, indicated that parents with greater mean values had a smaller Wr + Vr value. Thus, it was inferred that seed set percentage was increased due to dominant genes under both plantings. The close location of the parental values along the graph line also supported this fact.

**Grain weight per spike:** Diallel analysis (Table 1) under normal planting showed highly significant a and b items indicating the presence of both additive and dominant gene effects. Directional dominance effects ($b_1$) were, however, non-significant.

Table 1: Analysis of variance for spike parameters of wheat under normal and late plantings (Mean Squares)

| Items | df | Spike length | | Spikelets per spike | | Spike density | | Grains per spike | | Seed set | | Grain weight per spike | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Normal | Late | Normal | Late | Normal | Late | Normal | Late | Normal | Late | Normal | Late | Normal |
| a | 5 | 3.4997** | 5.1250** | 8.4368** | 11.699*$ | 0.05567* | 0.2303** | 65.514*4 | 54.618** | 18.914** | 38.721** | 0.9183** | 0.1710** |
| b | 15 | 1.4189** | 0.3964 | 1.5556* | 1.785 | 0.0212 | 0.0182 | 11.554 | 16.065 | 21.605** | 19.917** | 0.0820** | 0.0023 |
| $b_1$ | 9 | 2.1952 | 1.4841 | 7.5851** | 1.504 | 0.0001 | 0.0879 | 55.488 | 23.650 | 124.020 | 17.101 | 0.0296 | 0.0001 |
| $b_2$ | 5 | 0.3430 | 0.5494* | 0.8405 | 2.371 | 0.0051 | 0.0058 | 11.629* | 8.214 | 17.319 | 16.499 | 0.1369** | 0.0019 |
| $b_3$ | 1 | 1.9304** | 0.1906 | 1.2829** | 1.490 | 0.0326* | 0.0173 | 6.632 | 19.584" | 12.606" | 22.128 | 0.0574 | 0.0028 |
| c | 5 | 0.4052 | 0.4307 | 0.3925 | 2.869* | 0.0058 | 0.0070 | 0.379 | 1.086 | 1.439 | 4.280 | 0.0160 | 0.0023 |
| d | 10 | 0.4183 | 0.1962 | 0.2995 | 0.609 | 0.0108 | 0.0104 | 0.823 | 2.551 | 1.878 | 7.538 | 0.0205 | 0.0018 |
| Blocks | 2 | 0.0550 | 0.2170 | 1.5210 | 1.976 | 0.0060 | 0.0305 | 0.872 | 6.250 | 4.242 | 1.796 | 0.0800 | 0.0005 |
| B x a | 10 | 0.5771 | 0.3154 | 0.6622 | 0.865 | 0.0120 | 0.0118 | 0.637 | 2.488 | 2.0101 | 5.684 | 0.0253 | 0.0020 |
| B x b | 30 | 0.3752 | 0.2212 | 0.6181 | 1.104 | 0.0110 | 0.0124 | 2.986 | 3.921 | 2.399 | 5.264 | 0.0381 | 0.0043 |
| B x $b_1$ | 2 | 0.1364 | 0.1989 | 0.1592 | 0.803 | 0.0003 | 0.0172 | 3.693 | 2.878 | 6.015 | 1.055 | 0.0833 | 0.0008 |
| B x $b_2$ | 10 | 0.3569 | 0.1528 | 0.9187 | 1.003 | 0.0139 | 0.0103 | 3.076 | 3.153 | 3.221 | 6.703 | 0.0164 | 0.0017 |
| B x $b_3$ | 18 | 0.4119 | 0.2612 | 0.4854 | 1.194 | 0.0106 | 0.0131 | 2.857 | 4.464 | 1.541 | 4.933 | 0.0452 | 0.0062 |
| B x c | 10 | 0.3994 | 0.3961 | 0.7383 | 0.842 | 0.0117 | 0.0132 | 1.915 | 2.621 | 2.867 | 4.960 | 0.0683 | 0.0037 |
| B x d | 20 | 0.4670 | 0.2507 | 0.4566 | 0.847 | 0.0130 | 0.0089 | 1.409 | 2.350 | 1.639 | 7.902 | 0.0778 | 0.0054 |
| Block interaction | 70 | 0.4337 | 0.2681 | 0.5912 | 0.959 | 0.0118 | 0.0114 | 2.047 | 3.082 | 2.206 | 6.034 | 0.0520 | 0.0042 |

$ = reduced to non-significant after re-testing with B x c mean squares *, ** = significant at 0.05 and 0.01 probability levels, respectively.

Table 2: Genetic components of variation for 6 spike parameters under normal and late plantings.

| | Components | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | D | $H_1$ | $H_2$ | F | E | $H_2/4H_1$ | $(H_1/D)^{0.5}$ | $h^2_{(NS)}$ | $h^2_{(NS)}$ |
| Spike length Normal | 0.35±0.07 | 0.65±0.18 | 0.66±0.16 | -0.01±0.03 | 0.14±0.03 | 0.257 | 1.363 | 0.3575 | 0.7047 |
| Spike length Late | 0.41±0.05 | 0.15±0.13 | 0.09±0.12 | -0.07±0.13 | 0.09±0.02 | 0.145 | 0.603 | 0.7095 | 0.7664 |
| Spielets per spike Normal | 1.27±0.07 | 0.67±0.18 | 0.62±0.16 | 0.45±0.17 | 0.21±0.03 | 0.232 | 0.730 | 0.5454 | 0.7417 |
| Spielets per spike Late | 0.60±0.11 | 0.84±0.29 | 0.53±0.26 | -0.28±0.27 | 0.33±0.04 | 0.158 | 1.180 | 0.5630 | 0.6887 |
| Spike density Normal | 0.005±0.002 | 0.005±0.005 | 0.006±0.005 | -0.001±0.005 | 0.004±0.001 | 0.323 | 0.976 | 0.3122 | 0.5126 |
| Spike density Late | 0.026±0.001 | 0.003±0.004 | 0.004±0.003 | -0.00001±0.003 | 0.004±0.001 | 0.375 | 0.329 | 0.7062 | 0.7666 |
| Grains per spike Normal | 9.35±1.53 | 8.50±3.89 | 6.36±3.48 | 3.99±3.74 | 0.67±0.58 | 0.187 | 0.953 | 0.6238 | 0.8883 |
| Grains per spike Late | 7.15±0.77 | 9.72±1.96 | 8.60±1.75 | 2.55±1.89 | 1.0610.29 | 0.221 | 1.166 | 0.4713 | 0.8257 |
| Seed set Normal | 6.19±1.04 | 16.24±2.63 | 12.89±2.35 | 7.68±2.53 | 0.75±0.40 | 0.198 | 1.620 | 0.1886 | 0.8461 |
| Seed set Late | 5.81±1.69 | 11.6814.30 | 9.33±3.84 | 5.42±4.14 | 1.97±0.65 | 0.200 | 1.417 | 0.2975 | 0.6781 |
| Grain weight *per* spike Normal | 0.052±0.006 | 0.038±0.015 | 0.020±0.014 | -0.026±0.015 | 0.018±0.002 | 0.128 | 0.861 | 0.6814 | 0.7504 |
| Grain weight per spike Late | 0.015±0.0003 | -0.002±0.0006 | -0.001±0.0006 | -0.004±0.0006 | 0.001±0.0001 | 0.176 | | 0.8950 | 0.8667 |
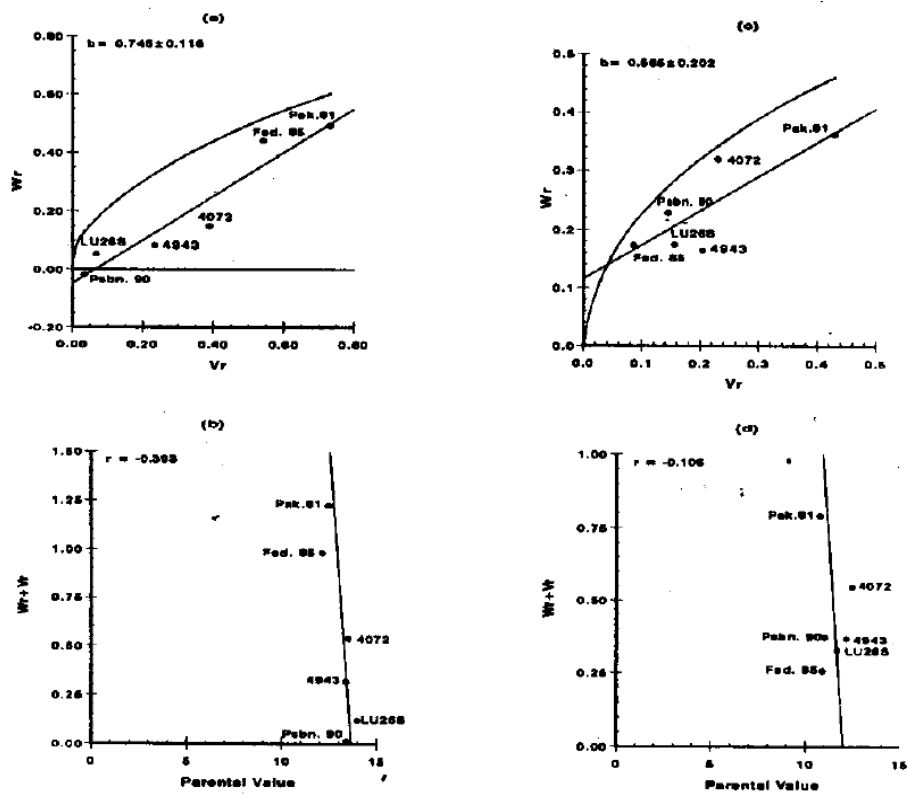
Fig. 1: WrIVr and Wr + Vr/P graphs for spike length under normal (a,b) and late planting (c, d)


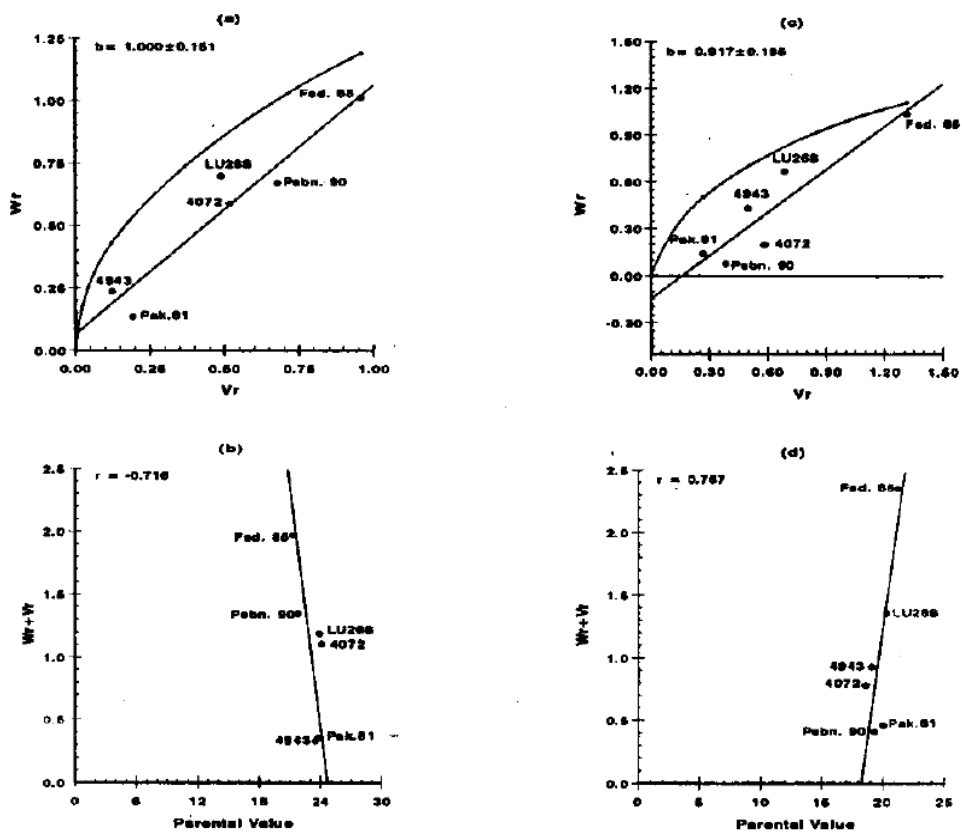
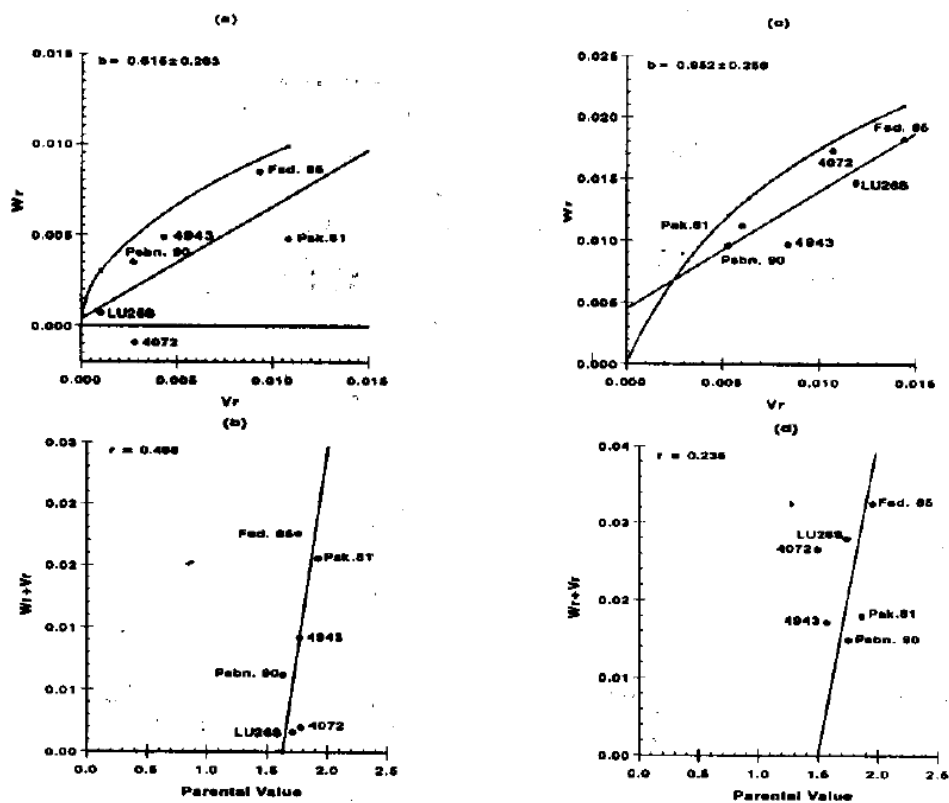Fig. 2: Wr/Vr and Wr +Vr/P graphs for spikelets per spike under normal (a, b) and late planting (c, d)

Fig. 3: Wr,Vr and Wr + Vr/P graphs for spike density under normal (a, b) and late planting (c, d)



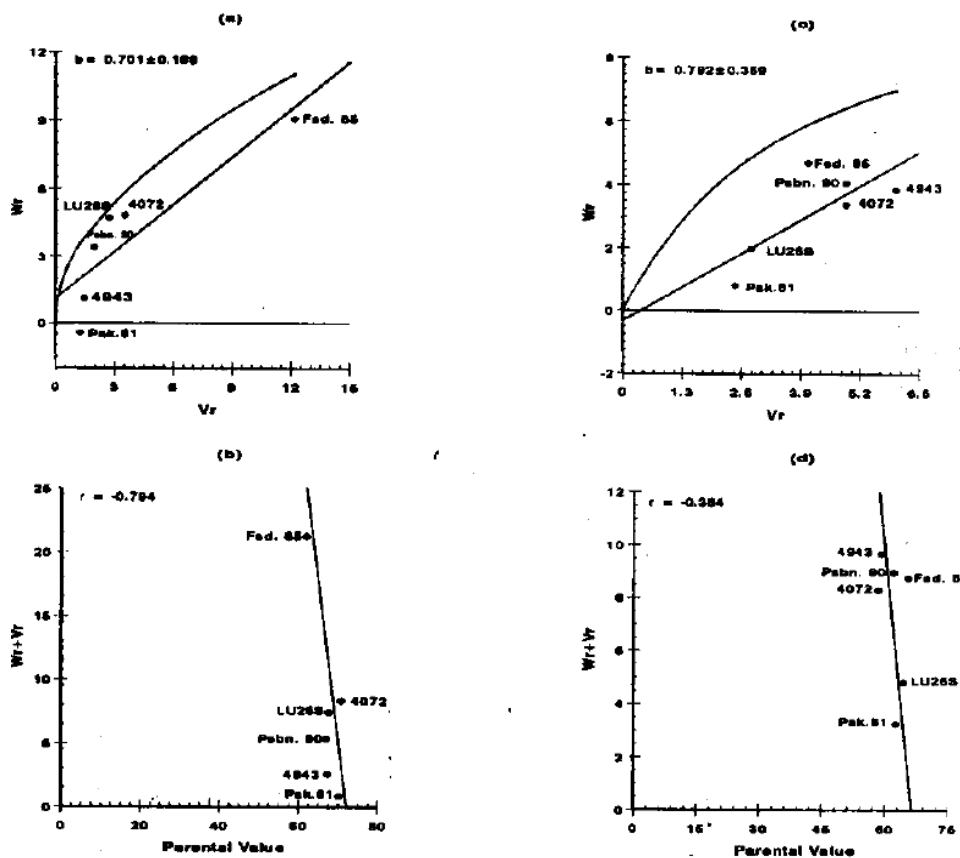Fig. 4: Wr/Vr and Wr +Vr/P graphs for grains per spike under normal la,b) and late planting (c, d)

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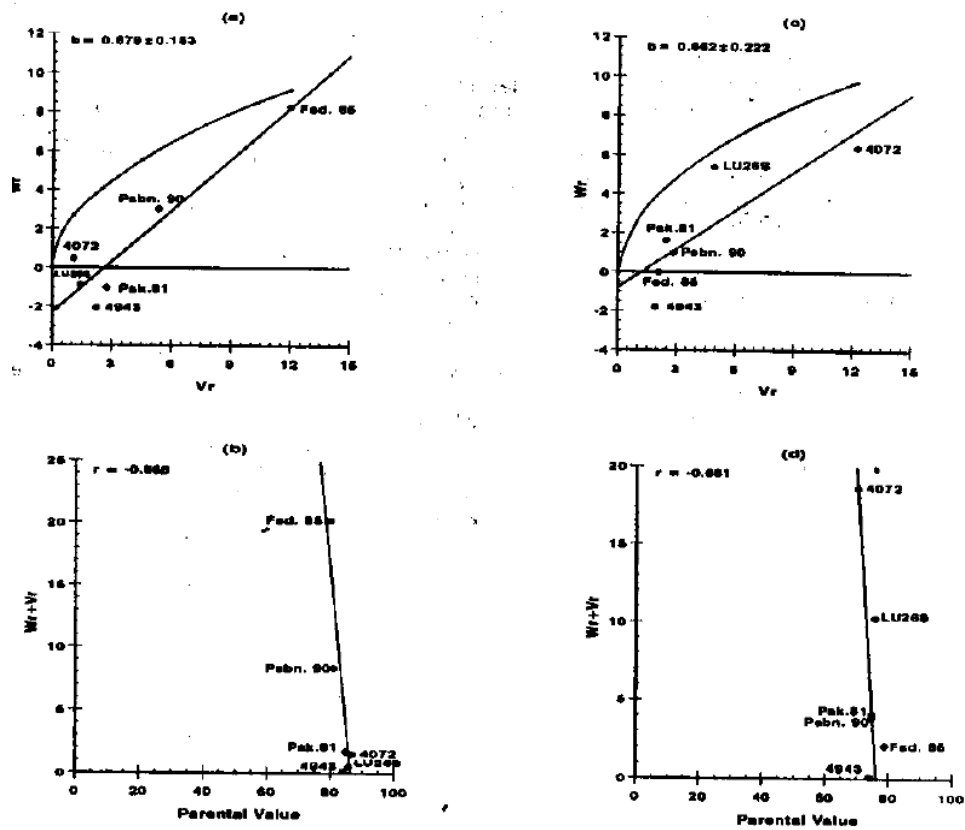
Fig. 5: Wr/Vr and Wr +Vr/P graphs for seed set under normal (a,b) and late planting (c,d)
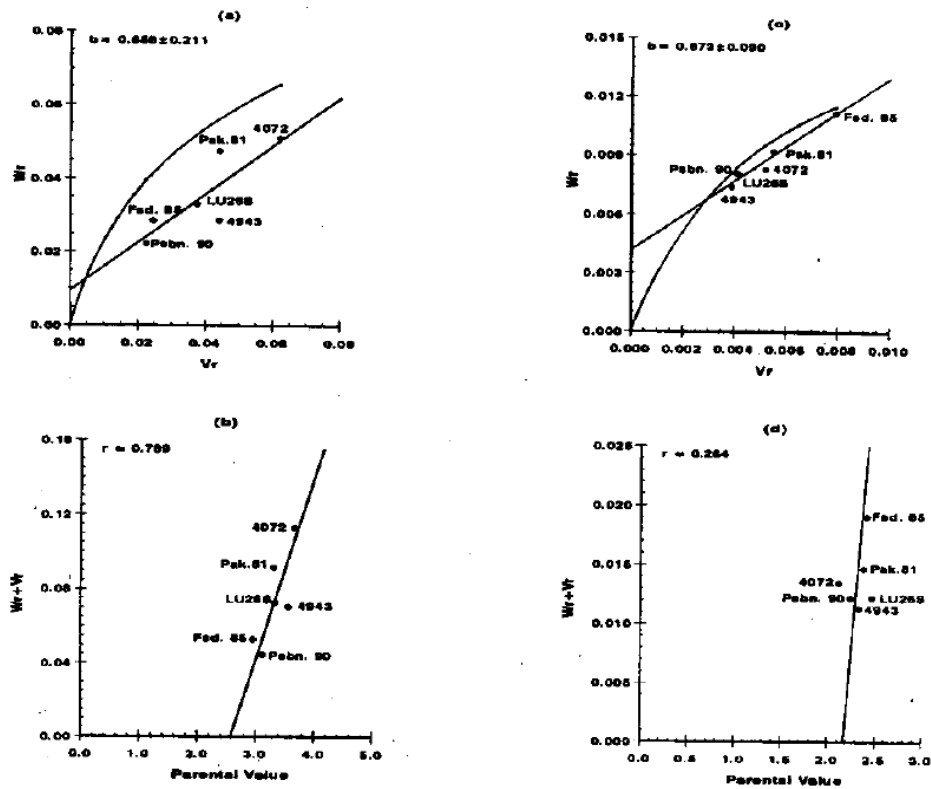


Fig. 6: Wr/Vr and Wr + Vr/P graphs for seed set under normal (a,b) and late planting (c,d)

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Asymmetry of gene distribution among the parents was evident by significant $b_2$. Non-significant $b_3$, c and d items displayed the absence of specific gene effects, maternal and reciprocal effects. Retesting of a and b items was thus, not required. Under late planting, analysis of variance indicated that only a item was significant showing the presence of additive gene effects. Nonsignificant $b_2$ and $b_3$ items indicated the symmetry of gene distribution among the parents and unimportant effect of specific genes. Maternal and reciprocal effects were found absent. Data subjected to both of the scaling tests indicated the adequacy for the additive-dominance model for both plantings.

The genetic components of variation (Table 2) indicated significant amount of both additive and dominance genetic variation under normal planting. Unequal H and H2 components and $H_2/4H$, ratio (0.128) indicated the different distribution of positive and negative genes. F was negative and non-significant. Environmental variation was found significant. Genetic components of variation under late planting revealed that additive variation (D) was significant. The estimate of dominant variation was negative. According to Singh and Chaudhry (1985) the negative estimates of variance are not expected. However, the possibility of such estimates cannot be ruled out unless the experiments are so conducted that sampling errors are minimized and diallel assumptions for interpretation of genetic components are properly fulfilled.

F was negative and significant suggesting that recessive genes were more frequent under late planting. Significant environmental effect was also indicated. Average degree of dominance under normal planting (0.861) suggested the absence of dominance which was also supported by Wr/Vr graph (Fig. 6a) giving the same results; intercept of the regression line was positive showing partial dominance with additive gene action. Partial dominance for the trait has also been reported by Lonc et al. (1993). However, Knezevic and Kraljevic-Balalic (1993) reported both additive and non-additive gene action for this trait. Narrow sense heritability under normal planting was about 91 percent of the broad sense one, indicating the preponderance of additive variation than the dominant variation in the total genetic variation inherited. Narrow sense heritability estimate under late planting was greater as compared with broad sense one and was not reliable due to the negative estimates of the dominance components. Because of the same, value of average degree of dominance could not be computed. However, graphical analysis (Fig. 6c) showed that the intercept of the regression line was positive displaying an additive gene action. The arrangement of array points in Wr/Vr graph for normal planting revealed that Psbn. 90 had the highest number of dominant genes while 4072 had the lowest number. Under late planting genotype 4943 secured the maximum dominant genes and Fsd. 85 being farthest from the origin, had the lowest dominant genes.

Fig. 6b and d revealed positive correlation (0.789 and 0.264) between Wr + Vr and parental values under both plantings where increasing parental values had greater Wr + Vr values. Thus, it was thought that grain weight per spike was conditioned by recessive genes under both plantings. A similar recessive gene control for the trait was reported by Jedynski (1988) while Lonc (1988), Lonc and Zalewski (1991) and Knezevic and Kraljevic-Balalic (1993) reported dominance gene control for grain weight per spike. The overall perusal of results indicated that genetic behaviour for most of the spike characters was influenced by the change in the environments; their gene action changed in response of environmental change. Similarly, heritability of most of the characters also showed an increase or decrease with the change of planting time. It was also noticed that parental genotypes shifted their positions from recessive to dominant or midway or from dominant to midway or most recessive or the other way, in the graphical presentation.

These facts signified the element of genotype × environment effect in the expression and performance of genetic parameters. This G × E interaction may cause selections from one environment to perform poorly in the other. Therefore, it is necessary for the breeders to test their material at various sites and locations for better and stable performance before going for final decision to overcome such problems. Special emphasis should be placed on these quantitative spike traits which are more likely to be altered by the environmental change.

## References

Asad, M.N., K. Alam and M.A. Chowdhry, 1992. Combining ability computation from diallel crosses comprising five bread wheat cultivars. J. Agric. Res., 30: 307-314.

Bebyakin, V.M. and N.I. Starichkova, 1992. Genetic control of characters determining yield in spring durum wheat. Tsitologlya i Genetica, 26: 60-64.

Chowdhry, M.A. and B. Ahmad, 1990. Combining ability in a seven parent diallel cross of spring wheat. Pak. J. Scient. Res., 42: 18-24.

Hayman, B.I., 1957. Interaction, heterosis and diallel crosses. Genetics, 42: 336-355.

Iqbal, M., K. Alam and M.A. Chowdhry, 1991. Genetic analysis of plant height and the traits above flag leaf node in bread wheat. Sarhad J. Agric., 7: 131-134.

Jedynski, S., 1988. Heritability and diallel cross analysis of several agronomic characters in winter wheat hybrids. Zeszyty Naukowe Akademir Roimczej we Wroclaiu Rolnrctwo, 47: 27-43.

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: 211-215.

Khan, N.I., M.A. Bajwa, M.S. Qari and S. Muhammad, 1984. Genetic architecture of some agronomic characters and resistance to leaf rust in spring wheat. Pak. J. Agric. Res., 22: 101-111.

Knezevic, D. and M. Kraljevic-Balalic, 1993. Genetic analysis for weight of kernels per spike in wheat. Genetika, 25: 71-75.

Li, L.Z., D.B. Lu and D.Q. Cui, 1991. Study on the combining ability for yield and quality characters in winter wheat. Acta Agric. Univ. Henanensis, 25: 372-378.

Lonc, W. and D. Zalewski, 1991. Diallel analysis of quantitative characters in F, hybrids of winter wheat. Hodowla Roslin, Aklirnatyzacja i Nasiennictwo, 35: 101-113.

Lonc, W., 1886. Gene action for agronomic characters in winter wheat. Tez. T. I. Sekts Masco USSR., 425: 1-19.

Lonc, W., 1988. A diallel analysis of useful traits of spring wheat (Triticum aestivum L. ssp. vulgare) hybrids. Genet. Polonica, 29: 365-373.

Lonc, W., W. Kadlubiec and J. Strugala, 1993. Genetic determination of agronomic characters in F$_2$ hybrids of winter wheat. Proceedings of the Symposium on Quantitative Genetics of Crops, May 24-25, 1993, Kudowa-Zdroj, Poland, pp: 229-247.

Ma, S.F., 1988. An analysis of combining ability and heritability for agronomic characters in spring wheat parents. Ningxia J. Agra For. Sci. Technol., 5: 22-24.

Mandal, A.S., S. Choudhary and K.K. Ghosac, 1991. Genotypic and phenotypic variability in wheat. Environ. Ecol., 9: 926-928.

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

Prodanovic, S., 1993. Genetic values of F$_1$ wheat crosses obtained in diallel crosses. Rev. Res. Work Fac. Agric. Belgrade, 38: 25-37.

Sharma, J.K., H.B. Singh and G.S. Sethi, 1986. Gene action and selection parameters in bread wheat. Himachal J. Agric. Res., 12: 1-5.

Singh, R.K. and B.D. Chaudhry, 1985. Methods in Quantitative Genetic Analysis. 1st Edn., Kalyani Publ., Ludhiana, New Delhi, pp: 102-118.

Steel, R.G.D. and J.H. Torrie, 1984. Principles and Procedures of Statistics. McGraw Hill Book Co. Inc., New York, USA.

Yadav, M.S., I. Singh, S.K. Sharma and K.P. Singh, 1988. Combining ability analysis over environments in spring wheat. Int. J. Trop. Agric., 6: 102-105.