 band with marker Vp-1B3 associated with PHS resistance (Fig. 2, p. 68). These results give an indication of the resistance associated with these markers.

One interesting observation to come out of this study is that the combination of $D u P w 004$ and $V p-1 B 3$ markers associated with resistance showed a GI range of $0-0.25$. However, the results will be confirmed when more resistant type genotypes are included. Three genotypes, lines 203 (FOW1) and 214 (CHIL/CHUM18//ARA90) from the 15th HRWYT and line 2070 (CHAPIO/FRET2) from the 18th HRWSN 2070, showed this combination.

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## JANTA VEDIC COLLEGE Department of Genetics and Plant Breeding, Baraut Baghpat (UP), India.

## Gene action for quantitative traits in bread wheat.

Sarvan Kumar and Dhirendra Singh.


#### Abstract

An experiment during rabi 2005-06 and 2006-07 estimated gene action in bread wheat. Seven wheat cultivars (DBW 14, HUW 468, HUW 533, GW 273, PBW 443, PBW 502, and DL788-2) were used for five straight crosses (DBW14/HUW468, DL788-2/PBW502, DBW14/HUW533, GW273/HUW468, and PBW443/HUW533) and six generations $\mathrm{P}_{1}, \mathrm{P}_{2}, \mathrm{~F}_{1}, \mathrm{~F}_{2}, \mathrm{BC}_{1}$, and $\mathrm{BC}_{2}$ were obatined for each cross. A generation mean analysis was made on days-to- $75 \%$ heading, days-to-maturity, plant height, effective tillers/plant, spike length, spikelets/spike, grains/spike, grain weight/ spike, seeds/plant, 1,000-kernel weight, grain yield/plant, and at three different stages during Helminthosporium leaf blight infection (dough, soft dough, and hard dough). A majority most of the exhibited significant additive and dominance gene effects in scaling test on different characters in all the crosses indicating the presence of nonallelic interaction.


Joint scaling tests revealed that the simple additive-dominance model was adequate for spike length, grain weight/spike in all five crosses; for days-to-75\% heading, days-to-maturity in cross PBW443/HUW533; for spikelets/ spike in crosses DBW14/HUW468, DBW14/HUW533, and GW273/HUW468; and for 1,000-kernel weight and grain yield/plant in cross 'PBW443/HUW533'. For the remaining crosses, the model was not adequate. The six-parameter model was used for those crosses where simple additive-dominance model was inadequate. The classification of epistasis revealed the predominance of duplicate type of epistasis in a majority of the crosses for all the traits, whereas complementary type epistasis was present for seeds/plant in crosses 'DBW14/HUW468', 'DBW14/HUW533', and 'PBW443/ HUW533'; days-to-maturity and effective tillers/plant in cross 'DBW14/HUW468'; spikelets/spike in cross 'DL788-2/ PBW502'; and grains/spike and HLB-3 in cross 'DBW14/HUW533'. Based on the above findings, we concluded that attributes such as spike length and grain weight/spike are controlled by fixable genes and may be improved by adopting simple selection or any other breeding approach that can exploit additive effects. Attributes such as days-to-75\% heading, days-to-maturity, plant height, tillers/plant, effective tillers/plant, and other related traits included in the study were controlled by both additive and nonadditive type of gene effects. Therefore, a breeding plan that can exploit both types of gene effects, such as intermating in early segregating generations followed by selection or reciprocal recurrent selection, might be useful. Heterosis breeding might be a useful tool for improvement of grain yield in wheat because it showed a complementary type of epistasis in most of the crosses in this study.

Introduction. Wheat is one of the main food crops of India and contributes significantly to the central pool. The cultivation of wheat in India started very early during prehistoric times and, thus, the origin of wheat is still a matter of speculation. Wheat research for development of high-yielding cultivars and improving management techniques started in India long ago. A large number of valuable cultivars were bred and released for commercial cultivation. These cultivars were tall and mainly suited to low-input management with low yield potential. However, a turning point in the history

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of wheat breeding came during mid 1960s with the introduction of semidwarf, photoinsensitive, high-yielding Mexican wheat breeding material developed at CIMMYT with the guidance of Nobel under the All India Coordinated Wheat Improvement Project. Three genotypes, Lerma Roja, S 308, and Sonara-64, that out yielded the old, tall wheat cultivars were released for general cultivation in major wheat-growing areas of India.

The improvement of quantitative traits through selection depends upon the nature and magnitude of the gene effect involved in the inheritance of that particular trait. Generation mean analysis, a first-degree statistic, is a simple but useful technique for characterizing gene effects for quantitative traits (Hayman 1958; Jinks and Jones 1958; Gamble 1962). Generation mean analysis estimates the epistatic effects. Both additive and nonadditive gene effects have been found to be important in wheat (Paroda and Joshi 1970; Singh and Singh 1992), however, both vary with the materials involved. The greatest merit of generation mean analysis lies in the estimate of epistatic gene effects, additive x additive (i), additive x dominance ( j ), and dominance x dominance ( 1 ), which is the most commonly used design. We have estimated the gene effects for yield and yield components using generation mean analysis.

Material and Methods. Seven diverse cultivars of bread wheat, DBW 14, HUW 468, HUW 533, GW 273, PBW 443, PBW 502, and DL788-2, were used in five cross combinations (DBW14/HUW468, DL788-2/PBW502, DBW14/ HUW533, GW273/HUW468, and PBW443/HUW533), each with six basic generations $\mathrm{P}_{1}, \mathrm{P}_{2}, \mathrm{~F}_{1}, \mathrm{~F}_{2}, \mathrm{BC}_{1}$, and $\mathrm{BC}_{2}$. The material of five crosses was evaluated in a randomized block design with three replications in a plot size with $2.5-\mathrm{m}$ rows spaced 23 cm apart with a plant-to-plant distance of 10 cm during rabi season 2006-07 at the Research Farm of Janta Vedic College, Baraut Baghpat. Data were recorded on ten randomly selected competitive plants from each replication of parental lines and 30 plants from each of the $\mathrm{F}_{1}, \mathrm{~F}_{2}, \mathrm{BC}_{1}$, and $\mathrm{BC}_{2}$ populations for 15 characters (days-to- $75 \%$ heading, days-to-maturity, plant height, effective tillers/plant, spike length, spikelets/spike, grains/spike, grain weight/spike, seeds/ plant, 1,000-kernel weight, grain yield/plant, and at three different stages during Helminthosporium leaf blight infection, i.e., HLB-1 (77-80 d, dough stage), HLB-2 (83-86 d, soft dough stage), and HLB-3 (87-89 d, hard dough stage). Mather's scaling test was used to identify the interacting crosses and a joint scaling test was used to test the adequacy of a simple additive dominance model (m, d, h; Mather 1949; Cavalla 1952). The genetic effects in the interacting crosses were estimated using a six-parameter model (m, d, h, i, j, l; Hayman 1958).

Results and Discussion. The mean performance for the different characters of each of the five crosses in different generations are given in Table 1 (pp. 71-72). The $\mathrm{F}_{1}$ and $\mathrm{F}_{2}$ populations were higher than the respective parents in cross 'DBW14/HUW468' for all the characters except days-to-maturity, 1,000 -kernel weight, and all stages of HLB. Similarly, the high mean value of the $\mathrm{F}_{1}$ and $\mathrm{F}_{2}$ populations from their parents was observed in cross 'DL788-2/PBW502' for plant height, effective tillers/plant, spike length, spikelets/spike, seeds/plant, and grain yield/plant. In cross 'DBW14/ HUW533', we observed high mean values in the $\mathrm{F}_{1}$ and $\mathrm{F}_{2}$ generations for days-to-maturity, plant height, effective tillers/ plant, spike length, spikelets/spike, HLB-2, and HLB-3. High performance of the $F_{1}$ and $F_{2}$ populations were recorded for effective tillers/plant, spike length, and HLB-1 in cross 'GW273/HUW468'. In cross 'PBW443/HUW533', the higher value of the $F_{1}$ and $F_{2}$ population to their respective parents was observed for spike length and all three stages of HLB score.

The performance of $\mathrm{F}_{2}$ generation higher than the $\mathrm{F}_{1}$ generation was observed for days to $75 \%$ heading, plant height, effective tillers/plant, spike length, spikelets/spike, grains/spike, seeds/plant, 1,000-kernel weight, grain yield/ plant, HLB-2, and HLB-3 in the cross 'DBW14/HUW468'. Cross 'DL788-2/PBW502' had a higher value in the $\mathrm{F}_{2}$ population than in the $F_{1}$ population for plant height, effective tillers/plant, spike length, spikelets/spike, seeds/plant, and all three HLB stage scores. Higher mean values in the $\mathrm{F}_{2}$ population over their $\mathrm{F}_{1}$ were observed for days-to-maturity, plant height, grains/spike, grain weight/spike, seeds/plant, grain yield/plant, and all HLB stages in cross 'DBW14/HUW533'. In the cross 'GW 273/HUW 468', days-to-maturity and all three stages of HLB had higher mean values in the $\mathrm{F}_{2}$ than in the $F_{1}$ population, however, in cross 'PBW443/HUW533', the higher mean values were for plant height, spike length, spikelets/spike, grains/spike, grain weight/spike, HLB-1, HLB-2, and HLB-3. These results revealed no inbreeding depression for 'genotype $x$ environment' interactions or epistasic gene effects; the later effects were invariably noted in the present investigation.

The scaling test parameters ( $\mathrm{A}, \mathrm{B}, \mathrm{C}$, and D ) from the data on different traits in all the crosses showed at least one parameter that was significantly different from 0 , indicating the presence of a nonallelic interaction (Table 2, p. 73). An additive, dominance model in the analysis of data and the presence of nonallelic interaction (epistasis) in all characters in all crosses were observed. A simple, additive-dominance model was found to be adequate for spike length and grain weight/spike in all five crosses (Table 3, p. 74); for days-to- $75 \%$ heading and days-to-maturity in cross 'PBW443/ HUW533'; for effective tillers/plant in crosses 'DBW14/HUW533', 'GW273/HUW468', and 'PBW443/HUW533';

$\vee O$ L. 56. for spikelets/spike in crosses 'DBW14/HUW468', 'DBW14/HUW533', and 'GW273/HUW468'; for 1,000-kernel weight and grain yield/plant in cross 'PBW443/ HUW533' (Singh et al. 1998; Dhillon et al. 2002; Shekhawat et al. 2006). The Chi-square ( $\mathrm{c}^{2}$ ) value was significant for rest of the characters and indicated the complexity of the genetic control of these traits in bread wheat, which may be attributed to epistasis between interacting genes in bread wheat (Singh et al. 1984; Simon et al. 1994; Mostafavi et al. 2005). Differences among the results may be due to differences in the genetic backgrounds. We emphasize that the inferences drawn from the generation mean analysis in crops were specific to the population under study and can not be correlated to other crops.

A six-parameter model was applied to all traits in all crosses (Mohammad et.al. 1991). The m, d, and h components also were estimates that revealed that additive (d) and dominance (h) both components were significant in all five crosses for seeds/plant. For days-to- $75 \%$ heading in cross 'DBW14/HUW468' and 'DBW14/HUW533'; for days-to- maturity in cross 'DBW14/HUW533'; for plant height in all the crosses except 'DBW14/HUW468'; for grains/spike in crosses ‘DBW14/HUW533', 'GW273/ HUW468', and 'PBW443/ HUW533'; for 1,000-kernel weight in crosses 'DL788-2/ PBW502' and 'DBW14/ HUW533'; for grain yield/ plant in cross 'DBW14/ HUW533'; for all the three stages of HLB in crosses 'DBW14/HUW533' and



VOL. 56. fects d and h are important in the inheritance of these traits in wheat (Vimal et al. 1999; Sharma et al. 2003).

The analysis of gene effects revealed that interactions played a major role in the inheritance of grain yield and its related components (Table 4, p. 75-76). Additive gene effects were observed for days-to-75\% heading in all the crosses except 'PBW443/HUW533'; for days-to-maturity in crosses 'DBW14/HUW468' and 'DL788-2/PBW502'; for plant height in cross 'PBW443/HUW533'; for effective tillers/plant in crosses 'DBW14/HUW468' and 'DL788-2/PBW502; for grains/spike in crosses 'DBW14/HUW468' and 'DL788-2/PBW502'; and for seeds/plant in crosses 'GW 273/ HUW468' and 'PBW443/HUW533'. Dominance effects were significant for days-to-75\% heading in all crosses except 'PBW443/HUW533'; for days-to-maturity in cross 'DL788-2/PBW502'; for plant height in all crosses except 'DBW14/ HUW468'; for effective tillers/plant in cross 'DL788-2/PBW502'; for spikelets/spike in cross 'PBW443/HUW533'; for grains/spike in crosses 'DBW14/HUW468', 'DL788-2/PBW502', and 'PBW443/HUW533'; for seeds per plant in
Table 4. Estimation of the components of generation mean analysis using six-parameter model of Hayman (1958) for 16 traits in five crosses of bread wheat ( $\mathrm{m}=$ mean effect, $\mathrm{d}=$ additive effect, $\mathrm{h}=$ dominance effect, $\mathrm{i}=$ 'additive x additive' interaction, $\mathrm{j}=$ 'additive x dominant' interaction, $1=$ 'dominant x dominant' interaction; * and $* *$ equal significance at $5 \%$ and $1 \%$, respectively; $\mathrm{D}=$ duplicate and $\mathrm{C}=$ complimentary).

| Cross/ character | Gene effect |  |  |  |  |  | Type of epistasis |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | m | d | h | i | j | 1 |  |
| DBW14/HUW 468 (I) |  |  |  |  |  |  |  |
| Days-to-75\% heading | $81.66 * * \pm 1.85$ | $-17.66 * * \pm 2.49$ | $-26.49 * * \pm 9.05$ | $-36.66 * * \pm 8.94$ | $-6.16 * \pm 2.71$ | $40.99 * * \pm 12.74$ | D |
| Days-to-maturity | $120.66 * * \pm 0.88$ | $-10.33 * * \pm 1.76$ | $7.00 \pm 5.03$ | $2.00 \pm 4.98$ | $-7.33 * * \pm 1.81$ | $3.33 \pm 8.01$ | C |
| Plant height (cm) | $89.00 * * \pm 3.05$ | $-1.67 \pm 1.59$ | $-29.16 \pm 12.76$ | $-30.00 * \pm 12.63$ | $1.16 \pm 2.12$ | $34.33 * \pm 14.25$ | D |
| Effective tillers/plant | $11.67 * * \pm 0.88$ | $1.33 * \pm 0.67$ | $-2.67 \pm 3.84$ | $-5.33 \pm 3.77$ | $1.33 \pm 0.81$ | $-1.33 \pm 4.67$ | C |
| Grains/spike | $47.67 * * \pm 0.33$ | $-4.33 * \pm 1.97$ | $9.49 * \pm 4.53$ | $11.33 * * \pm 4.16$ | $-6.83 * * \pm 2.40$ | $-29.67 * * \pm 8.76$ | D |
| Seeds/plant | $56.53 * * \pm 37.12$ | $27.00 \pm 45.32$ | $-14.83 \pm 174.10$ | $-131.33 \pm 173.97$ | $6.50 \pm 45.56$ | $-442.33 * * \pm 234.74$ | C |
| 1,000-kernel weight (gm) | $31.00 * * \pm 0.58$ | $-0.33 \pm 1.05$ | $-7.33 * \pm 3.39$ | $4.67 \pm 3.12$ | $-1.33 \pm 1.58$ | $2.67 \pm 5.48$ | D |
| Grain yield/plant (gm) | $14.19 * * \pm 0.53$ | $-3.67 * * \pm 0.40$ | $6.19 * * \pm 2.27$ | $6.24 * * \pm 2.26$ | $-4.69 * * \pm 0.47$ | $-18.83 * * \pm 2.70$ | D |
| HLB -1 | $12.33 * * \pm 0.33$ | $3.33 \pm 4.71$ | $-21.16 * \pm 9.53$ | $-21.33 * \pm 9.52$ | $3.16 \pm 4.72$ | $42.33 * \pm 18.92$ | D |
| HLB -2 | $45.33 * * \pm 0.33$ | $6.67 * \pm 3.33$ | $-121.33 * * \pm 7.32$ | $-116.00 * * \pm 6.79$ | $4.99 \pm 4.29$ | $154.67 * * \pm 14.47$ | D |
| HLB -3 | $56.33 * * \pm 0.33$ | $-4.00 \pm 4.96$ | $-78.17 * * \pm 10.62$ | $-65.33 * * \pm 10.02$ | $1.50 \pm 4.97$ | $82.99 * * \pm 21.12$ | D |
| DL788-2/PBW502 (II) |  |  |  |  |  |  |  |
| Days-to-75\% heading | $76.00 * * \pm 0.57$ | $-7.67 * * \pm 2.05$ | $25.17 * * \pm 4.88$ | $26.00 * * \pm 4.71$ | $-5.17 * \pm 2.09$ | $-31.67 * * \pm 8.90$ | D |
| Days-to-maturity | $125.00 * * \pm 0.58$ | $4.33 * * \pm 1.05$ | $18.67 * * \pm 3.41$ | $15.33 * * \pm 3.12$ | $4.67 * * \pm 1.40$ | $-25.33 * * \pm 5.53$ | D |
| Plant height (cm) | $94.00 * * \pm 1.52$ | $-4.00 \pm 3.91$ | $-31.50 * * \pm 10.53$ | $-32.00 * * \pm 9.93$ | $-1.83 \pm 4.14$ | $11.00 \pm 18.20$ | D |
| Effective tillers/plant | $14.00 * * \pm 0.58$ | $2.00 * \pm 0.82$ | $-13.83 * * \pm 2.87$ | $-16.00 * * \pm 2.82$ | $1.83 * \pm 0.89$ | $18.33 * * \pm 4.12$ | D |
| Grains/spike | $22.00 * * \pm 1.15$ | $-1.33 \pm 0.67$ | $-5.33 \pm 5.01$ | $-5.33 \pm 4.81$ | $-1.33 \pm 1.05$ | $-5.33 \pm 6.03$ | C |
| Spikelets/spike | $35.00 * * \pm 1.15$ | $-7.00 * \pm 3.26$ | $45.33 * * \pm 8.18$ | $46.00 * * \pm 8.00$ | $-8.00 * * \pm 3.50$ | $-65.33 * * \pm 14.29$ | D |
| Seeds/plant | $488.33 * * \pm 3.52$ | $-11.87 \pm 21.51$ | $-40.27 \pm 45.56$ | $-108.27 * \pm 45.27$ | $-30.19 \pm 21.97$ | $16.53 \pm 87.78$ | D |
| 1,000-kernel weight (gm) | $28.66{ }^{* *} \pm 0.67$ | $-1.00 \pm 1.24$ | $7.00 \pm 3.76$ | $10.00 * * \pm 3.65$ | $0.67 \pm 1.25$ | $-3.33 \pm 5.93$ | D |
| Grain yield/plant (gm) | $13.69 * * \pm 0.12$ | $-0.53 \pm 0.74$ | $-7.27 * * \pm 1.61$ | $-8.38 * * \pm 1.56$ | $-0.52 \pm 0.76$ | $18.68 * * \pm 3.12$ | D |
| HLB-1 | $16.00 * * \pm 3.51$ | $3.33 \pm 3.33$ | $-49.50 * * \pm 15.76$ | $-49.33 * * \pm 15.54$ | $-3.50 \pm 4.22$ | $84.33 * * \pm 20.06$ | D |
| HLB -2 | $56.67 * * \pm 6.06$ | $0.33 \pm 0.33$ | $-137.17 * * \pm 24.64$ | $-134.00 * * \pm 24.26$ | $-3.83 * \pm 1.95$ | $157.00 * * \pm 25.77$ | D |
| HLB -3 | $74.00 * * \pm 4.00$ | $7.33 \pm 9.26$ | $-100.33 * * \pm 25.05$ | $-98.67 * * \pm 24.47$ | $1.99 \pm 10.15$ | $115.33 * * \pm 41.74$ | D |


| Days-to-75\% heading | $76.00 * * \pm 0.57$ | $-9.67 * * \pm 1.05$ | $31.67 * * \pm 3.32$ | $24.67 * * \pm 3.12$ | $3.00 * \pm 1.28$ | $-54.00 * * \pm 5.32$ | D |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Days-to-maturity | $128.33 * * \pm 0.88$ | $0.33 \pm 1.05$ | $-2.50 \pm 4.26$ | $-8.67 * \pm 4.10$ | $3.83 * * \pm 1.29$ | $0.99 \pm 5.96$ | D |
| Plant height (cm) | $111.33 * * \pm 1.20$ | $2.67 \pm 2.40$ | $-62.83 * * \pm 6.98$ | $-68.00 * * \pm 6.79$ | $14.50 * * \pm 2.65$ | $76.33 * * \pm 11.22$ | D |
| Grains/spike | $41.66 * * \pm 1.45$ | $5.00 \pm 4.88$ | $-7.83 \pm 11.44$ | $-2.00 \pm 11.37$ | $3.17 \pm 4.91$ | $-4.33 \pm 20.55$ | C |
| Seeds/plant | $468.33 * * \pm 9.35$ | $-2.00 \pm 9.97$ | $-20.00 * * \pm 44.59$ | $-12.00 \pm 42.39$ | $-33.33 * \pm 15.74$ | $-121.33 * \pm 61.30$ | C |
| 1,000-kernel weight (gm) | $31.66 * * \pm 0.33$ | $-1.67 \pm 1.56$ | $-1.83 \pm 3.44$ | $0.67 \pm 3.39$ | $-6.17 * * \pm 1.63$ | $3.67 \pm 6.49$ | D |
| Grain yield/plant (gm) | $11.74 * * \pm 0.34$ | $-0.67 * \pm 0.31$ | $-2.59 \pm 1.51$ | $1.15 \pm 1.48$ | $-4.21 * * \pm 0.38$ | $2.80 \pm 1.93$ | D |
| HLB -1 | $5.33 * * \pm 3.33$ | $-3.67 \pm 3.34$ | $-9.33 \pm 15.52$ | $-7.33 \pm 14.92$ | $-1.67 \pm 4.16$ | $17.33 \pm 20.76$ | D |
| HLB -2 | $34.67 * * \pm 0.33$ | $-0.33 \pm 4.48$ | $-81.17 * * \pm 9.97$ | $-74.00 * * \pm 9.06$ | $3.16 \pm 5.12$ | $89.00 * * \pm 19.81$ | D |
| HLB -3 | $56.67 * * \pm 0.33$ | $13.33 * * \pm 3.84$ | $-30.83 * * \pm 9.01$ | $-29.33 * * \pm 7.80$ | $18.83 * * \pm 5.00$ | $-10.33 \pm 17.87$ | C |

A N N U A L W H $\mathcal{L}$ A $\tau \quad N \in W T L \in \tau \tau \in R$ V O L. 56. crosses 'DBW14/HUW533' and 'GW273/HUW468'; for HLB-1 in all the crosses except 'DBW14/HUW533'; and for HLB-2and HLB-3 in all five crosses.

The digenic interactions 'additive $x$ additive' (i) and 'dominant $x$ dominant' (l) had an important role in controlling the inheritance of yield and its related components. 'Additive x additive', 'additive x dominant', and 'dominant x dominant' interactions were significant for days-to-75\% heading in the 'DBW14/HUW468', 'DL788-2/PBW502', and 'DBW14/HUW533' crosses; whereas, 'additive $x$ additive' and 'dominant $x$ dominant' components were significant for days-to- $75 \%$ heading in the 'GW273/HUW468' cross. The 'dominant $x$ dominant' component was predominant for days-to- $75 \%$ heading in all crosses except 'PBW443/HUW533'. For days-to-maturity, 'additive x dominant' effects were significant in crosses 'DBW14/HUW468', 'DL788-2/PBW502', and 'DBW14/HUW533'; however, 'additive x additive' effects were more important in crosses 'DL788-2/PBW502' and 'DBW14/HUW533' and a 'dominant $x$ dominant' gene interaction was significant in crosses 'DL788-2/PBW502' and 'GW273/HUW468'. For plant height, all

| Cross/ character | Gene effect |  |  |  |  |  | Type of epistasis |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | m | d | h | i | j | 1 |  |
| GW273/HUW 468 (IV) |  |  |  |  |  |  |  |
| Days-to-75\% heading | $76.0 * * \pm 0.58$ | $-2.33 * \pm 1.33$ | $29.33 * * \pm 3.87$ | $28.67 * * \pm 3.52$ | $-1.67 \pm 1.88$ | $-37.33 * * \pm 6.63$ | D |
| Days-to-maturity | $125.33 * * \pm 1.20$ | $-1.33 \pm 1.05$ | $5.99 \pm 5.30$ | $7.99 \pm 5.24$ | $-2.67 \pm 1.15$ | $-17.33 * * \pm 6.56$ | D |
| Plant height (cm) | $89.33 * * \pm 1.20$ | $1.33 \pm 1.49$ | $-10.50 * \pm 5.28$ | $-13.33 * \pm 5.65$ | $-0.16 \pm 1.94$ | $27.67 * * \pm 8.13$ | D |
| Grains/spike | $38.00 * * \pm 1.15$ | $2.67 \pm 2.90$ | $-8.00 \pm 7.49$ | $-5.33 \pm 7.42$ | $6.00 * \pm 3.02$ | $20.00 * \pm 12.67$ | D |
| Seeds/plant | $430.67 * * 20.85$ | $67.00 * * \pm 8.28$ | $-168.17 * * \pm 91.29$ | $-236.67 * * \pm 85.03$ |  | $495.00 * * \pm 111.67$ | D |
| 1,000-kernel weight (gm) | $29.00 * * \pm 0.33$ | $-3.67 * * \pm 1.45$ | $10.00 * * \pm 2.99$ | $11.33 * * \pm 2.90$ | $-0.67 \pm 1.58$ | $-18.67 * * \pm 5.98$ | D |
| Grain yield/plant (gm) | $12.16 * * \pm 0.40$ | $-1.62 * * \pm 0.17$ | $-5.06 * * \pm 1.77$ | $-6.67 * * \pm 1.64$ | $1.61 * * \pm 0.20$ | $16.43 * * \pm 2.21$ | D |
| HLB -1 | $20.33 * * \pm 3.67$ | $6.33 \pm 3.67$ | $-55.33 * * \pm 16.86$ | $-60.67 * * \pm 16.39$ | $4.33 \pm 5.36$ | $78.67 * * 22.18$ | D |
| HLB -2 | $49.67 * * \pm 3.71$ | $0.00 \pm 4.96$ | $-114.33 * * \pm 18.62$ | $-118.67 \pm 17.86$ | $-7.33 \pm 6.43$ | $139.33 * * \pm 26.95$ | D |
| HLB -3 | $70.33 * * \pm 2.84$ | $4.33 \pm 7.08$ | $-56.50 * * \pm 18.29$ | $-63.33 * * \pm 18.18$ | $-2.50 \pm 7.35$ | $57.00 * \pm 30.80$ | D |
| PBW443/HUW 533 (V) |  |  |  |  |  |  |  |
| Plant height (cm) | $94.33 * * \pm 2.90$ | $-36.67 * * \pm 1.10$ | $-41.17 * * \pm 11.92$ | $-29.33 * * \pm 11.83$ | $-23.50 * * \pm 1.47$ | $29.00 * * \pm 12.79$ | D |
| Spikelets/spike | $20.00 * * \pm 1.15$ | $2.00 \pm 1.63$ | $-11.67 * \pm 5.86$ | $-12.00 * * \pm 5.65$ | $2.33 \pm 1.94$ | $15.33 * \pm 8.58$ | D |
| Grains/spike | $37.00 * * \pm 2.08$ | $-2.99 \pm 1.88$ | $-18.50 * \pm 9.45$ | $-16.67 * \pm 9.14$ | $-0.50 \pm 2.31$ | $33.00 * * \pm 12.22$ | D |
| Seeds/plant | $361.33 * * \pm 12.87$ | $-67.66 * * \pm 26.41$ | $43.83 \pm 74.67$ | $53.33 \pm 73.77$ | $-20.17 \pm 28.59$ | $12.33 \pm 119.76$ | C |
| HLB - 1 | $16.67 * * \pm 3.67$ | $7.00 * \pm 3.34$ | $-47.50 * * \pm 16.74$ | $-46.00 * * \pm 16.12$ | $1.50 \pm 4.52$ | $49.67 * * \pm 21.81$ | D |
| HLB -2 | $53.33 * * \pm 3.67$ | $14.33 * \pm 7.34$ | $-80.17 * * \pm 21.14$ | $-91.33 * * \pm 20.75$ | $6.83 \pm 8.37$ | $84.33 * * \pm 33.80$ | D |
| HLB -3 | $63.33 * * \pm 3.17$ | $10.33 * \pm 4.95$ | $-35.16 * \pm 18.26$ | $-35.33 * \pm 16.12$ | $3.50 \pm 6.82$ | $27.68 \pm 29.13$ | D | types of gene effects were found significant in cross 'DBW14/ HUW533', 'additive $x$ additive' and 'dominant $x$ dominant' effects were noticed in crosses 'DBW14/HUW468' and 'GW273/ HUW468', and an 'additive $x$ additive' gene interaction was found significant in cross DL7882/PBW502 (Amawate et al. 1995). Effective tillers/plant had all types of gene effects were found significant only in cross 'DL788-2/PBW502' and 'dominant X dominant' predominanted in cross 'DL788-2/PBW502'. Spikelets/spike were nonsignificant for all types of gene effect in all the crosses except 'PBW443/ HUW533'. For grains/spike, 'additive x additive', 'additive x dominant' and dominant components were significant in crosses 'DBW14/HUW468' and 'DL7882/PBW502', 'additive $x$ dominant' and 'dominant $\mathbf{x}$ dominant' effects were significant in cross ‘GW273/HUW468', 'additive x additive' and 'dominant $\mathbf{x}$ dominant' components were significant in cross PBW443/HUW533, and a 'dominant X dominant' component was predominant in all other crosses except 'DBW14/ HUW533'. All types of epistasis were significant for seeds/plant in cross 'GW273/HUW468' and 'additive $x$ additive' and 'dominant x dominant' components were predominant in crosses 'DBW14/ HUW468', ‘DBW14/HUW533', and 'GW273/HUW468'. For 1,000-kernel weight, the 'additive x additive' components was significant in crosses 'DL788-2/

 PBW502' and 'GW273/HUW468' and 'additive $x$ dominant' and 'dominant $x$ dominant' interactions were more important in crosses 'DBW14/HUW533' and 'GW273/HUW468', respectively. Grain yield/plant in crosses 'DBW14/ HUW468' and 'GW273/HUW468' had significance for all gene interactions, whereas 'additive X additive' and 'dominant X dominant' components were significant in 'DL788-2/PBW502', and 'additive x dominant' effects were important in all crosses except 'DBW14/HUW533'. For HLB-1 and HLB-2, 'additive $x$ additive' and 'dominant $x$ dominant' were more important in all crosses except 'DBW14/HUW533', which had a nonsignificant interaction, but 'additive x additive' and 'dominant X dominant' effects were significant for HLB-2 in crosses 'DBW14/HUW533' and 'GW273/HUW468', and an 'additive x dominant' effect was significant in cross 'DL788-2/PBW502'. HLB-3 had significant 'additive x additive' and 'dominant $x$ dominant' gene effects in crosses 'DBW14/HUW468', 'DL788-2/PBW502', and 'GW273/HUW468', but only an 'additive x additive' effect were significant in cross 'PBW443/HUW533', and 'additive x additive' and dominant components were important in the 'DBW14/HUW533' cross.

Dominant (h) and 'dominant $\mathbf{x}$ dominant' (l), for their negative and positive gene effects, revealed a preponderance of duplicate types of epistasis, which will hinder improvement of populations where dominant-type gene actions also exist; thus, heterosis can not be exploited in such a situation. The complementary type of epistasis, which is more favorable for genotype improvement, was present in cross I for days-to-maturity, effective tillers/plant, and seed/plant; in cross II for spikelets/spike; in cross III for grains/spike, seed/plant, and HLB-3; and in cross V only for seed/plant. Cross IV had duplicate-type gene interactions for all the characters ( Yadav et al. 1997). The results suggest that the nature and magnitude of gene effects vary within the different crosses for different characters, necessitating specific breeding strategys need to be adopted for particular crosses to obtain improvement (Kaur et al. 2004). Characters that were predominantly additive gene effects can use simple selection procedures efficiently, however, dominant and epistasic effects for most of the character in some crosses would slow progress. In such a situation, exploiting additive, dominant, and nonadditive gene effects simultaneously would be benificial.

For characteristics that are controlled by fixable genes, simple selection or any other breeding methodology that can exploit additive effects might be adopted. For characteristicss that are controlled by both additive and dominant gene effects, a breeding plan that exploits both gene effects, such as intermating in early segregating generations followed by selection or reciprocal recurrent selection, might be useful for improvment. For characteristics with complementary-type epistasis in crosses, heterosis breeding may be useful. We observed that a generation mean analysis for most of the characteristics conform with those of previous workers (Luthara et al. 1991, 1996; Singh et al. 1998; Ghannadha et al. 1999; Mehla et al. 2000; Satyavart et al. 2000; Shekhawat et al. 2000; Hamada 2003; Sharma et al. 2001, 2002, 2003, 2004).

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## G.B. PANT UNIVERSITY OF AGRICULTURE AND TECHNOLOGY Pantnagar, Uttarakhand, 263 145, India.

## Detection of heat shock protein in bread wheat through ELISA.

P.K. Bhowmick, J.P. Jaiswal, and D.S. Gupta (Genetics \& Plant Breeding, GBPUAT, Pantnagar), and Anil Grover (University of Delhi, South Campus, New Delhi).

Introduction. High temperature stress is an important abiotic factor that reduces drastically wheat yields in the arid and semi-arid tropics. Howard (1924) reported that for every one degree rise of mean temperature over the range of 12.2$27.53^{\circ} \mathrm{C}$, the crop yield is reduced by $4 \%$. To overcome the limits created by higher-temperature stress, a major impetus is on the use of suitable screening techniques to identify heat-tolerant genotypes. Under natural conditions, abiotic stress is usually encountered gradually. Plants, therefore, are exposed to a sublethal stress before being subjected to severe stress. Several studies have shown that plants develop the ability to withstand lethal temperatures upon exposure to sublethal temperatures (known as induction stress). This phenomenon has been termed 'acquired thermo-tolerance' (Hahn and Li 1990). During the induction stress, many stress-inducible genes are triggered ,which alters several physiological and biochemical processes relevant for stress tolerance. Heat shock proteins (HSP) have been known to play a role in cell protection, survival, and recovery in several species (Vierling 1991; Nguyen et al. 1992). Mild heat treatment induces a so-called heat shock response leading to the immediate induction of a set of new proteins or the over-expression of already existing HSPs that persist over time at high temperature. The $90-\mathrm{kDa}$ HSPs are the second most predominantly

