ITEMS FROM INDIA

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Current activities: Genetic improvement for rust resistance and quality traits in Indian wheat.

B.K. Das and S.G. Bhagwat.

Rust resistance genes, such as *Sr31*/*Lr26*/*Yr9*, *Sr26*, *Sr24*/*Lr24*, and *Lr34*, and specific HMW-glutenin subunits are being recombined with good agronomic traits. Selected lines from several intervarietal crosses are in different generations (F_2–F_5) and are being evaluated. Marker-assisted selection is being used to screen for specific rust resistance genes.

Using induced mutations, some early flowering mutants in the cultivars C-306 and MP-3054 were isolated and are being further evaluated. The early mutants were crossed with HW-2004 (C-306 + *Sr24*/*Lr24*) to recombine earliness and rust resistance. With the aim of isolating mutants resistant to rust diseases, the cultivars PBW343 and NI917 were mutagenized with gamma rays and populations from the M_1 generation were grown.

Marker-assisted backcrossing is being used to improve the rust resistance and dough strength of HD2189 wheat by incorporating the *Lr24*/*Lr24* and *Glu-D1d* genes. Eighteen BC_4F_1 plants were grown, and DNA from leaves of four-week old individual plants was extracted and screened using SCAR markers for these two genes. In the winter of 2009–10, five plants carrying both markers were identified. Backcrosses were made using the recurrent parent HD2189 and carriers of both the markers.

Marker-assisted selection to combine rust resistance genes (*Sr24* and *Sr26*) and *Glu-D1d* (coding for HMW-glutenin subunits 5+10) is being carried out in a cross between FLW-2 and Kite. In the F_2 generation, ~220 plants were analyzed using SCAR markers. Plants carrying markers for rust resistance genes *Sr24* and *Sr26* and *Glu-D1d* were selected and will be evaluated for their field performance.

Validation of a SCAR marker (Sr26#43) for stem rust resistance gene Sr26 in Indian wheat genotypes and segregating populations.

B.K. Das, Ruchi Rai, and S.G. Bhagwat.

Stem rust is a potential threat to the wheat crop and causes significant losses worldwide. Ug99, a race of black stem rust detected in Uganda, shows virulence to a great majority of wheat cultivars. The stem rust resistance gene *Sr26* is translocated to wheat from *Thinopyrum elongatum* and no virulence towards the *Sr26* gene has been reported. A SCAR marker, Sr26#43, was reported for this gene by Mago et al. (2005). To validate this marker in Indian wheat genotypes, 49 wheat genotypes were screened using SCAR marker Sr26#43. Analysis of these genotypes showed that the SCAR marker was present in all the genotypes carrying *Sr26*, except HW2090, which was reported to carry *Sr26* gene. The marker was absent in the genotype that lacked *Sr26* or carried any other stem rust resistance genes.

Two F_2 populations from crosses involving susceptible (Kalyansona (-*Sr26*) and resistant (Kite (+*Sr26*) and Takari (+*Sr26*) genotypes were used for validation. The phenotypic rust reaction data and marker data matched one-to-one, indicating that this marker can be used in early generations to selecte for the *Sr26* gene. Incorporating this gene is recommended to prevent stem rust epidemics caused by Ug99. The validated marker Sr26#43 will facilitate incorporating this gene in new breeding lines. The durability of *Sr26* can be enhanced by pyramiding it with other rust resistance genes. Multiplex PCR for the simultaneous screening of *Sr26* and *Sr24* is in progress.

The help of the DWR Regional Station, Flowerdale, Shimla, for phenotypic screening of some F_3 lines is acknowledged. The genotypes carrying *Sr26* were provided by DWRRS, Shimla, and IARIRS, Wellington. During this period, Shri. K. Arun participated in some of the experiments as project trainee.

Analysis of semidwarfing genes and polymorphisms at the Xgwm261 locus in a recombinant inbred population of bread wheat.

Suman Bakshi and S.G. Bhagwat.

Recombinant inbred lines (RILs) derived from a cross between cultivars Sonalika and Kalyansona in the F_9 generation were grown in the winter season of 2009–10. Leaves of one individual from each line were harvested and used for DNA extraction. The parental cultivars and the RILs were analyzed for the presence of *RhtB1b* and *RhtD1b* using perfect markers (Ellis et al. 2002). Variation at the microsatellite locus *Xgwm261* was studied. The parent cultivar Kalyansona had a 192-bp allele; the other parent Sonalika had a 165-bp allele. The RILs showed a 1:1 ratio for the presence of these alleles. Culm height was recorded on the RILs by measuring the culm of the main tiller of five plants when the plants were near maturity. The results showed that the RILs carrying *Rhtb1a* and *RhtD1a* were the tallest, followed by those with *RhtB1b* and *RhtD1b*. Plants with both semidwarfing genes were shortest. The RILs with a given a *Rht* gene composition were further classified according to the presence of *Xgwm261*. The results indicate that there was no reduction in culm height associated with the presence of the 192-bp allele. Further analysis is in progress.

Canopy temperature depression studies in bread wheat.

Heat stress is one of the most important stresses in subtropical, wheat-growing areas of the world and results in grain yield losses. The stage at which the wheat crop faces heat stress varies with the location and cropping season. In some areas, the stress is experienced at either at the seedling stage or at the grain-filling stage, in other cases the stress is felt through out the life of the plant. Heat stress affects the crop by altering many traits. Wheat cultivars differ in their canopy architecture, and this may result in differences in canopy temperature. Canopy temperature depression, the difference between air temperature and canopy temperature, can be measured. An experiment was carried out at the experimental field in Trombay in the winter of 2009–10. Seventeen wheat cultivars, which included both heat stress tolerant and susceptible cultivars, were grown in a replicated experiment. Canopy temperature was measured with an infrared thermometer. Measurements were made around 12:00 PM from tillering to flag leaf senescence at weekly intervals. At harvest, data on agronomic parameters were recorded using five plants from each replicate of each cultivar. Canopy temperature values appeared to vary across cultivars and growth stages. Data are being analyzed.

Threshability in recombinant inbred lines of bread wheat.

S.G. Bhagwat.

In wheat, threshability is an important trait. Very soft glumes and loose attachment to the rachis results in deciduous glumes that fall off if the spikes are not harvested in a timely fashion resulting in some grain loss. Thick glumes, with a strong attachment to rachis, make threshing hard. Tough glumes are associated with a brittle rachis, which is know as the nonfreethreshing habit.

Studies on the genetics of tough glumes and brittle rachis have been reported. Using interspecific crosses, QTL for threshability have been identified. Crosses between semi-wild and common wheat indicated that the fragile rachis and nonfreethreshing character of semi-wild wheat are dominant to the tough rachis and freethreshing character of common wheat. Rachis fragility and glume tenacity of semi-wild wheat were each controlled by a single gene (Cao et al. 1997). In hexaploid wheat, the glume tenacity gene *Tg* and *Q* locus control threshability. The *Tg* gene was mapped on 2DS of *T. aestivum* in the distal region (Sood et al. 2009). RILs evaluated for kernel shattering, glume strength, glume-pair angle, open-floret percentage, spike density, and plant height in different environments showed that glume strength consistently correlated with kernel shattering in all test environments, but their correlation was moderate. One QTL for glume strength was identified in the genomic regions containing the kernel-shattering QTL, suggesting that glume

strength is not the only genetic factor that determines kernel shattering. These results indicate that glume pair angle and open floret percentage might be the direct causes of kernel shattering (Zhang et al. 2009).

We are developing RILs from a cross between the cultivars Sonalika and Kalyansona, and RILs in the F_9 generation were grown in field. Single spikes were harvested at maturity, threshed by hand, and classified according to their ease or difficulty in threshing. Kalyansona was easier to thresh than Sonalika. The RILs varied for the trait. Lines easier to thresh than Kalyansona and harder to thresh Sonalika were observed. Each line was given a major category rating as follows: 1, deciduous glumes or very soft threshing; 2, similar to cultivar Kalyansona; 3, similar to cultivar Sonalika; 4, tougher glumes and hard to thresh; and 5, tough glumes very hard to thresh. Data were taken on 138 RILs in 2009–10. Based on the hand feel, the RILs were given scores in between the major categories mentioned above (Table 1).

Table 1. Scoring of glume and threshing traits in field-grown, F_9 RILs between the cultivars Sonalike (tough threshing) and Kalyansona (freethreshing).

Description	Rating	Frequency
Very soft and deciduous	1.0	00
Intermediate	1.5	09
Kalyansona type	2.0	31
Intermediate	2.5	12
Sonalika type	3.0	40
Intermediate	3.5	22
Tougher glumes, hard threshing	4.0	14
Intermediate	4.5	05
Tough glumes, very hard threshing	5.0	05

The data showed transgressive segregation for the trait. Observations also were taken in the F_7 and F_8 generations in 2007–08 and 2008–09, respectively, however the RILs were not rated as in 2009–10. Of the 18 RILs that were rated 4.0 or above in 2009–10, 14 were rated as hard or medium hard to thresh in 2007–08 and 12 were rated as hard or medium hard to thresh in 2008–09. Five lines were rated as soft in 2007–08 and four in 2008–09. Of the 40 lines that were rated from 1.0 to 2.0 in 2009–10, data on 26 were available from 2008–09; 24 were rated soft and two were rated as hard or medium hard. In 2007–08, 37 were rated as soft threshing, and three were rated hard or medium hard. These results indicate that some consistency between years. The disagreement could be due to error in judgment, environmental variation, or segregation.

Rachis breaking on 138 RILs was recorded in 2009–10. Fragile rachis was observed in 19 lines, the rachis remained intact in 98 cases, and was intermediate in 21. Of the 19 lines rated as fragile, 13 rate 4.0–5.0, indicating that the fragile rachis was largely accompanied by tougher glumes and hard threshing. Two lines with fragile rachis were rated 1.0, 3.0, and 3.5.

The RILs and parents were classified according to number of spikelets/cm of spike length. This value indicated whether the spike was compact or lax. Kalyansona showed a more compact spike with 2.47spikelets/cm; Sonalika had 1.72 spikelets/cm. RILs with lax spikes were more frequent than those with denser spikes. Fifty-six percent of the RILs were in the category of less than or equal to the Sonalika parent. More compact spikes (with 2.0 or more spikelets/cm) were observed in 30% of the RILs.

The RILs with denser spikes were classified according to their threshability rating. Of the 43 RILs, 18 were easy to thresh (rating 2.0 or lower), 21 were in the medium range (rating 2.5 to 3.5), and four were in the hard threshing range (rating 4.0 or more). The rachis remained intact in 31 of the 43 RILs, was intermediate in seven, and fragile in five. These results showed that there was an incomplete association between high spike density and easy threshability or nonfragile rachis. These RILs originated from intervarietal crosses and could be useful in identifying loci governing threshability trait in bread wheat.

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Deployment of molecular markers for the improvement of some important quality traits in bread wheat.

Construction of framework linkage map(s) using trait-specific, intervarietal RIL populations. Three framework linkage maps using three mapping populations have been prepared in our laboratory for QTL interval mapping of various agronomically important traits. These three mapping populations were originally developed for the following three traits by Dr. H.S. Dhaliwal and his coworkers at Punjab Agricultural University (PAU), Ludhiana, India: (i) grain protein content (GPC); (ii) preharvest sprouting tolerance (PHST), and (iii) grain weight (GW).

QTL analyses for 11 yield and yield-related traits. The GPC and ITMI populations were used to identify QTL for nine yield traits including plot yield and its components, plant height, and peduncle length. For this purpose, single-locus (using QTL Cartographer) and two-locus (using QTLNetwork) QTL analyses were conducted. For all 11 traits, a total of 80 putative M-QTL on 19 chromosomes in the GPC population and 140 putative M-QTL on 20 chromosomes in ITMI population were detected. QTLNetwork identified a total of 113 and 190 QTL that included QTL with significant main effect and/or significant interaction effect (epistatic QTL or QTL involved in interaction with the environment). An important genomic region harboring important major co-localized QTL for each of the six yield traits was identified on chromosome arm 2DS in both the GPC and ITMI populations. In the ITMI population, this QTL influenced plot yield, spike weight, spike length, spikelets/spike, seed weight, and 1,000-kernel weight (explaining from 13.00% to 37.85% PV for individual trait), whereas in the GPC population, the QTL influenced plot yield, tiller number, spike length, spike compactness, number of seeds, and 1,000-kernel weight (explaining from 8.93% to 19.81% PV for individual trait). The genomic region with the above QTL was physically located in the distal bin (2DS5-0.47-1.00) covering 53% region of 2DS. Comparative mapping revealed that the genomic region harboring the QTL in wheat spans a distance of 11.51 Mb on rice chromosome 7 (R7). This information may prove useful for high-resolution mapping leading to map-based cloning of the above major QTL.

Marker-assisted selection for GPC and leaf rust resistance. In bread wheat, high grain protein content (HGPC) determines nutritional value, processing properties, and quality of the end-product. In view of this, marker-assisted selection (MAS) was used to introgress a major gene for high GPC (*Gpc-B1*) into six wheat genotypes. These six wheat genotypes included (i) three elite Indian bread wheat cultivars and (ii) three advanced lines derived from the cultivar PBW343 (each containing the leaf rust resistant gene *Lr*24). During backcrossing, foreground selection was exercised using tightly linked markers. Background selection was performed using SSR markers evenly distributed throughout the genome. As a result, 14 BC_3F_4 lines carrying *Gpc-B1* were developed and evaluated for GPC and grain yield. Ten of

these lines, homozygous for *Gpc-B1*, had significantly higher GPC, the increment ranging from 0.42% to 2.50% of the GPC (increment on the original concentration was ~4% to 25%). One of the derived lines with enhanced GPC also had significantly higher grain yield (others were equal with their recipient genotypes). No negative correlation was observed between grain yield and GPC (%), suggesting no yield penalty with improved GPC. The results presented in this study suggest that introgression of *Gpc-B1* gene through MAS, in combination with phenotypic selection, is a useful strategy for development of wheat genotypes combining high GPC with higher grain yield.

Marker-assisted selection for preharvest sprouting tolerance and leaf rust resistance. Preharvest sprouting and susceptibility to leaf rust are two major problems in wheat that lead to the degradation of grain quality and significant losses in yield. Development of PHST and leaf rust resistant wheat genotypes was undertaken in our laboratory using MAS. A major QTL (*QPhs.ccsu-3A.1*) for PHST, which we had earlier identified, was introgressed into HD2329, an elite but PHS-susceptible cultivar that has two *Lr* genes (*Lr24* + *Lr28*) earlier introgressed at IARI by Dr. K.V. Prabhu and coworkers using MAS. In each backcross generation, foreground selection for the PHS QTL was exercised using flanking markers (*Xgwm155* and *Xwmc153*), and background selection was performed using 61 simple sequence repeat markers mapped at loci spread over the whole genome. During backcrossing, desirable alleles of *Lr24* and *Lr28*, also were tracked using linked SCAR markers. Seven BC_3F_3 progenies having both the desirable PHST QTL and *Lr* genes and showing up to 93.44% genetic similarity with the recipient parent were selected. These lines exhibited a high level of PHST (PHS score 2–4) and resistance against leaf rust under artificial conditions. The study demonstrated successful application of MAS for targeted pyramiding of QTL/genes for more than one trait into an improved wheat cultivar (Kumar et al. 2009).

Introgression of QTL for grain weight using MAS. Crosses involving 10 elite Indian bread wheat genotypes as recipient parents and the genotype Rye Selection111 as a donor parent were attempted during the off-season of 2005–06 in a Phytotron Facility at IARI, New Delhi, and the F_1 seed collected. These F_1s were raised during the rabi season 2006–07 and backcrossed with their respective recurrent parents to obtain the BC_1F_1 seed. A total of 470 BC_1F_1 seeds belonging to five crosses (RS111/HD2329, PBW343 (*Lr9*)/RS111, HI977/RS111, K9107/RS111, and RAJ3765/RS111) were obtained. Using this seed material, ~259 BC_1F_1 plants were raised during rabi 2007–08. Following foreground selection, 27 positive plants for markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for grain weight on chromosome 1A), 127 positive plants for the marker *Xwmc24* and 57 positive plants for the marker *Xwmc59* were selected. The selected BC_1F_1 plants were backcrossed with their respective recurrent parents and BC_2F_1 seeds was obtained, which were used to raise BC_2F_1 progenies in the field during the rabi season 2008–09. Following foreground selection, three positive plants for markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for grain weight on chromosome 1A) involving the recipient genotype PBW343 (*Lr9*); 142 positive plants for the marker *Xwmc24* only involving recipient genotypes PBW343 (*Lr9*), K9107, and Raj3765; and 18 positive plants for the marker *Xwmc59* involving recipient genotype PBW343 (*Lr9*) were selected. The selected plants were backcrossed with their respective recurrent parents to obtain BC_3F_1 seed, which was used to raise the BC_3F_1 progenies during the rabi season 2009–10. The selfed seed (BC_3F_2 seed) of the corresponding progenies was harvested and phenotypic data on 1,000-kernel weight is being recorded. The BC_3F_2 seed will be used to raise the BC_3F_2 progenies during the rabi season 2010–11, and both foreground and background selections (for progenies possessing the desired QTL) will be undertaken to identify desirable plants for raising the BC_3F_3 progenies.

Genetic dissection of grain weight in bread wheat through QTL analysis. For the genome-wide genetic dissection of GW in bread wheat, both QTL interval mapping and regional association mapping were undertaken. QTL interval mapping involved preparation of framework linkage map with 294 loci (194 SSRs, 86 AFLP, and 14 SAMPL) using a biparental RIL mapping population derived from the cross 'Rye Selection111/Chinese Spring'. Using the genotypic data and data on GW of RILs collected over six environments (3 locations × 2 years), genome-wide single-locus QTL analysis (using inclusive composite interval mapping, ICIM) and two-locus QTL analysis (using QTLNetwork) were conducted to identify main effect QTL (M-QTL) and epistatic QTL (E-QTL). Single-locus QTL analysis identified 10 QTL (including four major and three stable QTL), contributing >20% phenotypic variation for GW. Two-locus QTL analysis resolved a total of 24 QTL, which included three M-QTL (also detected by single-locus analysis) and 21 E-QTL, the later involved in 12 digenic Q × Q interactions; no Q × E and Q × Q × E interactions were detected. The total PV due to all the M-QTL was 28.11%, whereas the PV due to all the E-QTL was 43.36%, which suggested that nearly three quarters (71.47%) of PV for GW was fixable. This study was further supplemented with association mapping, which allowed validation of seven QTL (including above two QTL) and helped to identify two new markers in the genomic regions that were not reported to contain QTL for GW in earlier studies. The validated markers linked with QTL for high grain weight may prove useful in marker-assisted selection for the development of cultivars with high GW in bread wheat.

Genetic diversity and population structure analysis among Indian bread wheat cultivars. As a first step towards association mapping in wheat, we analyzed genetic diversity and structure in a collection of 263 Indian bread wheat cultivars (45 developed during pre-Green Revolution period and 218 developed during post-Green Revolution period) that were released over a period of ~100 years (1910 to 2006). For this purpose, we used a set of 42 unlinked neutral SSRs and 48 SSRs (60 loci) from the genomic regions reported to have QTL for GW. The 42 SSRs detected a total of 295 alleles (mean 7.02; range 2-14/SSR), which is more than a total of 273 alleles (mean 4.55; range 2–9 alleles/SSR) detected by 60 SSR loci subjected to selection. The average number of alleles/locus (5.91 vs. 5.74) and the estimates of genetic diversity (0.65 vs. 0.61) in the pre- and post-Green Revolution period cultivars did not differ significantly indicating that the Green Revolution did not lead to any loss of genetic diversity. However, to better understand the scenario, decadal diversity also was studied, which indicated gradual loss in diversity during three decades (1970s-2000s). This loss in diversity is alarming and, therefore, needs attention of breeders. The model-based *Structure* analysis identified a total of 14 subpopulations including two subpopulations largely comprising cultivars from pre-Green Revolution period and the 12 subpopulations mostly comprising cultivars from post-Green Revolution period. These results suggest that modern wheat-breeding practices in India are slowly decreasing genetic diversity and, therefore, this issue need to be addressed by involving diverse/synthetic wheat germ plasm in Indian wheat-breeding programs.

Association analysis for grain weight, grain protein content, and preharvest sprouting tolerance. We attempted association analyses for the grain-quality traits GW, PHST, and GPC. For this purpose, only 230/263 of the above cultivars were used, because for the remaining 33 cultivars, either phenotypic data was not available, they had similar pedigrees, or they flowered/matured too early or very late making them unsuitable for study. The model-based *Structure* analysis identified a total of 13 subpopulations. These included two subpopulations largely containing pre-Green Revolution cultivars and the remaining 11 subpopulations containing post-Green Revolution cultivars.

The *Structure* analysis was used to make marker-trait associations for GW and GPC using a set of 48 SSR markers mapped in the genomic regions harboring QTL for GW. The association mapping allowed identification of nine and four markers ($P < 0.05$) having significant association for GW and GPC, respectively. The study validated two markers on chromosome 1A that earlier were reported to be associated with QTL for GW (through QTL analysis), and also helped in identification of two new markers for GW in the genomic regions that were not reported to contain QTL for GW in earlier studies. Five new markers also were identified in the genomic regions previously reported to have QTL for GW, so that relatively more closely linked markers with the QTL were identified in these cases.

Marker-assisted pyramiding of quality traits and leaf rust resistance in the background of PBW343. Pyramiding the QTL/genes for quality traits and leaf rust resistance in the background of PBW343 also was undertaken using the genetic stocks developed through MAS by us at our research farm and Punjab Agricultural University (PAU), Ludhiana, India. We decided to develop the following two single cross hybrids (i) PBW343 (*Lr24+GPC-B1*) / PBW343 (PHST) developed by us and (ii) PBW343 (*Lr24+Lr28*+GW) / PBW343 (*GluAx-Ay*) developed by PAU. F_1 seeds of these two hybrids were distributed between each institute (CCSU and PAU) for producing double cross hybrids for carrying out MAS for pyramiding the genes/QTL for leaf rust resistance, PHST, GW, and *GluAx-Ay*.

The above two hybrids were raised at CCSU and PAU in an off-season (2009) nursery at Keylong (a research station for raising off-season nurseries) for preparing the double cross hybrid seed. The two hybrids were intercrossed, and double cross hybrid seed (F_1 seed) was obtained. The double cross population comprising a set of ~192 plants were grown at CCSU during 2009–10 and foreground selection was undertaken using a set of six SSR/SCAR markers linked to corresponding gene/QTL for GPC, PHST, GW, and leaf rust resistance. Following foreground selection, four plants containing all the above genes/QTL in homozygous condition were selected and bagged to allow them self pollinate. An additional two plants containing all the above genes but showing heterozygosity for markers associated with GW or GPC loci also were selected and allowed to self pollinate. To increase the frequency of plants possessing all the important genes, we selected ~15 plants possessing either four or more than four genes and intercrossed them in different combinations and F_1 seeds were obtained.

Molecular marker-assisted transfer and pyramiding of one or more of the QTL/genes for quality traits.
To mobilize or pyramid one or more QTL/genes for grain quality into high-yielding wheat cultivars to develop genotypes/cultivars combining improved, five institutions from India, including CCSU, will focus on developing wheat cultivars combining grain quality traits (high GW, high PC, PHST, grain hardness, and flour quality) with leaf rust resistance and high grain yield using molecular MAS.

Analysis of host-pathogen interaction in leaf rust-infected bread wheat: wet-lab approach. To understand the host-pathogen interaction in detail, it is essential not only to study temporal and spatial expression of a particular gene, but also those of other genes that may be similarly co-regulated, at both seedling and adult-plant stage. The well known, classical method cDNA–AFLP analysis is most suitable for the above purposes, because it covers the whole transcriptome. For the study of seedling resistance provided by the gene *Lr28*, total RNA was isolated from seven-day-old seedlings of each of the resistant (HD2329 + *Lr28*) and susceptible (HD2329) wheat stocks (a) before inoculation, i.e., at 0 h; (b) at 48 h, 96 h, and 168 h after inoculation with leaf rust pathogen race 77-5; and (c) at 168 h after mock inoculation. Using the above RNA samples, high-quality cDNA samples were obtained. These cDNA samples were utilized to study the transcript derived fragments (TDFs) following cDNA–AFLP analysis using 17 *Eco*RI+3/*Mse*I+3 γP32 labeled primer combinations. Highly reproducible, single banded, and over-expressed, 37 TDFs in the resistant and susceptible hosts following pathogen inoculation were isolated, cloned, and sequenced. Analysis of the sequences showed that 29 TDFs had significant similarity with known nucleotide or protein sequences in the database, including a number of wheat BAC clones and known proteins. To gain more information regarding expression of the above TDFs across different treatments, quantitative RT-PCR analysis is being conducted.

For the study of adult-plant resistance provided by the gene *Lr48*, total RNA was isolated from leaves of a 120-day-old, leaf rust inoculated and mock inoculated APR resistant wheat stock CSP44 + *Lr48* at (a) 0 h, (b) 24 h, (c) 48 h, (d) 72 h, and (e) 168 h. Using the above derived 10 purified RNA samples, 10 high quality cDNA samples were synthesized followed by cDNA-AFLP analysis using 16 *Eco*RI+3/*Mse*I+3 γP32 labeled primer combinations. A total of 483 differentially expressed TDFs were identified, and 52 TDFs (out of 483) were eluted from the gels. A total of 48 TDFs were cloned and sequenced successfully. Some of these TDFs showed similarity with known genes which include genes expressed in leaf rust and stripe rust infected bread wheat plants and other stress responsive genes. A few TDFs did not match with nucleotide or protein sequences in the database and were considered new. One TDF showed similarity with a genomic sequence of *P. triticina* and was considered to be of pathogen origin. Primers for quantitative RT-PCR were designed using software primer express.

Analysis of host–pathogen interaction in leaf rust-infected bread wheat: *in-silico* approach. The availability of wheat UniGenes and ESTs from cDNA libraries of leaf rust infected susceptible and resistant wheat plant stocks in UniGene and the dbEST database of the NCBI are powerful resources to identify differentially expressed wheat genes expressed during resistance reaction . Using these transcriptomic resources, and with the help of the data-mining tool Digital Differential Display (DDD), three pair-wise comparisons were performed on three cDNA libraries, each derived from leaf rust inoculated susceptible wheat stock (i) Thatcher, leaf rust inoculated resistant wheat stock, (ii) Thatcher + *Lr10* and leaf rust inoculated resistant wheat stock, and (iii) Thatcher + *Lr1* . A total of 68 differentially expressed UniGenes were identified. Using the Cluster 3.0 program, the differentially expressed UniGenes were clustered in five major clusters based on correlated expression pattern . In this exercise, resistance specific up- and down-regulated genes were identified for both genes *Lr10* and *Lr1* in the cultivar Thatcher. Some of the differentially expressed UniGenes encode for proteins similar to DNAJ heat shock family protein, thiol-disulfide exchange intermediate (*A. thaliana*), Triticain gamma (CTSH), membrane-binding proteins, and many known and unknown but novel gene sequences. Further tissue-based cluster analysis of the differentially expressed UniGenes was performed and revealed that all the identified UniGenes are highly expressed in leaves, have moderate expression in the sheath, stem, and inflorescence, and have low expression in the seed, root, flower, crown, callus, and cell culture. The present study will be followed by wet-lab experiments to identify differentially expressed genes in leaf rust infected wheat.

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Behavior of spring wheat genotypes under late and very late situations in northwestern India.

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Summary. A field experiment conducted during the winter seasons in 2000–01 to 2001–02 at the Directorate of Wheat Research, Karnal, evaluated new, promising genotypes under late and very late sowing situations. The mean of 2 years data revealed reductions of 16.96% and 17.15% in biomass and yield, respectively, when sowing was delayed from late to very late. This decline was due to 8.38% and 11.77% reductions in 1,000-kernel weight and grains/spike, respectively, and a more than 10 days less grain-filling period between late to very late sowings. Cultivar differences were observed for yield and yield-attributing parameters. For mean basis, cultivar HD 2643 produced the maximum biomass (106.95 q/ha) followed by Raj 3765 (106.77 q/ha); the lowest was by genotype WR 251 (94. 72 q/ha). Similarly, genotype PBW 435 recorded the maximum grain yield (42.86 q/ha) and lowest by UP 2425 (37.37 q/ha). Differential responses suggested different cultivars were suited for late sown conditions.

Wheat is the second most important crop after rice in India, occupying approximately 28 x 10^6 ha with a production of 78.4 x 10^6 metric tons during 2008–09, the highest level of production since the Green Revolution. Considering environmental and technological adaptation, India is broadly divided in to six wheat-growing regions, the Northern Hill Zone (NHZ; Jammu and Kashmir, Himachal Pradesh, and Uttarakhand), the North Western Plain Zone (NWPZ; Punjab, Haryana, Western Uttar Pradesh, and some parts of Rajasthan), the North Eastern Plain Zone (NEPZ; Eastern Uttar Pradesh, Bihar, West Bengal, Orissa, and Eastern states), the Central Zone (CZ; Madhya Pradesh, Gujrat, Southern Rajasthan, and the Bundel Khand region of Uttar Pradesh), the Peninsular Zone (PZ; Maharashtra and Karnataka), and the Southern Hill Zone (SHZ; Tamil Nadu). The growing period of wheat is variable from one agroclimatic zone to another, which affects vegetative growth and grain-filling duration leading to differences in attainable yield. The maximum wheat growing duration is in the Northern Hills Zone and the mininum is in the Peninsular Zone.

Farmers generally grow wheat in a cropping system that maximizes their total production. In this process, wheat is generally preceded by crops such as rice, cotton, sugarcane, maize, sorghum, potato, toria, and pigeon pea. In this plethora of cropping sequences, some crops, such as basmati rice, cotton, sugarcane, potato, toria, and pigeon pea, delay wheat sowing in different parts of the country. Due to late harvests of sugarcane, potato, and toria, wheat generally is sown in the first week of January. Under late and very late sowing conditions, low temperatures occur during seedling establishment and hot, dry spells prevail during grain-filling. Maturity is accelerated/forced because of high temperature and/or water stress, which reduces grain size and weight.

In India, wheat is sown from November to January, whereas the most appropriate time for sowing is the first two weeks of November. A delay in sowing to late mid-November to first two weeks of December resulted in decreases in yield of 15.5, 32.0, 27.6, 32.9, and 26.8 kg/ha/day in the NHZ, NWPZ, NEPZ, CZ, and PZ, respectively, for timely sown cultivars. Corresponding yield losses were 7.6, 18.5, 17.7, 17.0, and 15.5 %. For late-sown cultivars, a delay in sowing from late to very late, first two weeks of December to first two weeks of January, decreased grain yield by 42.7, 44.8, 51.6, and 44.2 kg/ha/day or 22.8, 27.1, 30.9, and 25.6 % in the NWPZ, NEPZ, CZ, and PZ, respectively (Tripathi et al. 2005). This huge reduction in yield due to delayed sowing prompted us to evaluate late and very late sown genotypes for maximum production. An effort was made to grow advance genotypes/cultivars under late (December sowing) and

very late (January sowing) sowning conditions to evaluate their flowering, maturity, grain filling period, biomass, yield and yield attributes.

Materials and Methods. A field experiment was conducted for two years, from 2000–01 to 2001–02, at the Directorate of Wheat Research, Karnal (Latitude 290°43' N, longitude 760°58' E and altitude 245 m). The experimental soil was sandy clay loam in texture (22% clay), low in organic carbon (0.37%) and available N (145 kg/ha), and medium in available P (17.2 kg/ha) and available K (155 kg/ha) content. The experiment was a split-plot design and replicated three times. The main plots included two sowing times, late sown (9 December in 2000 and 10 December in 2001) and very late sown (22 January in 2001 and 9 January in 2002), and nine genotypes, PBW 435, UP 2425, HD 2643, HP 1744, DL 788-2, WR 251, WR 544, Raj 3765, and PBW 373, were grown as subplot treatments. After the rice forecrop was harvested, the field was prepared by cultivator and disk, and 250 viable seeds were seeded in each subplot. Fertilizer (120 N, 60 P_2O_5, 40 K_2O) was applied to the crop. A one-third dose of nitrogen, in the form of urea, full phosphorous, in the form of di-ammonium phosphate, and potash, in the from of muriate of potash, was applied as before sowing and the remaining nitrogen was top dressed in two splits at the first node stage (DC 31) (Zadoks et al. 1974) and at boot stage (DC 41). Irrigation was applied as needed. Weeds were controlled with the application of isoguard plus (a chemical blend of isoproturon and 2, 4-D (at 0.5 + 0.125 Kg/ha) in 500 liters of water 30 days after sowing. Observations were recorded on biomass, anthesis, maturity, grain-filling period, grain production rate, yield, and yield component characters. Standard statistical methods were were followed for the parameters under study (Gomez and Gomez 1984).

Results and Discussion. Two years of data reveals that during 2000–01 biomass, 1,000-kernel weight, spikes/m^2, and grains/spike were not significant under late and very late sowning condition, whereas during 2001–02, only spikes/m^2 was at not significant. All other parameters under study in late and very late sowning conditions were significant. From the mean of two years, we observed that biomass and yield declined 16.96 and 17.15%, with 8.38% and 11.77% reductions in 1,000-kernel weight and grain/spike and more than 10 days less grain-filling period, from late to very late sowning conditions, respectively (Tables 1 and 2, p. 67). The grain production rate under very late sowning conditions was significantly higher than that under late sowning conditions in both years, probably because of the shorter grain-filling period under very late sowing conditions.

Table 1. The effect of sowing time and genotype on biomass, yield, harvest index, 1,000-kernel weight, and spikes/m^2 for spring wheat genotypes sown at the Directorate of Wheat Research, Karnal, India (NS indicates nonsignificance).

	Biomass (q/ha)		Yield (q/ha)			Harvest index		1,000-kernel weight (g)		Spikes/m^2	
Treatment	2000–01	2001–02	2000–01	2001–02	Mean	2000–01	2001–02	2000–01	2001–02	2000–01	2001–02
Sowing time											
Late	103.31	121.58	40.19	46.55	43.37	0.415	0.384	44.77	42.78	406	406
Very late	97.35	89.38	36.65	35.21	35.93	0.371	0.395	42.65	37.08	424	435
CD at 5 %	NS	8.05	3.55	3.77		0.202	0.04	NS	3.35	NS	NS
Genotype											
PBW 435	93.25	107.04	40.27	45.45	42.86	0.432	0.427	42.93	39.80	396	456
UP 2425	84.25	108.95	34.30	40.44	37.37	0.375	0.376	49.10	44.73	378	363
HD 2643	102.77	111.12	37.32	39.61	38.47	0.370	0.356	46.96	43.27	419	363
HP 1744	108.14	104.83	39.96	40.83	40.40	0.382	0.390	43.15	35.80	415	391
DL 788-2	105.75	107.11	43.31	41.00	42.16	0.412	0.386	42.59	35.87	467	517
WR 251	93.65	95.79	36.17	37.73	36.95	0.417	0.394	47.27	50.27	378	356
WR 544	98.21	96.24	39.17	38.64	38.91	0.408	0.403	39.73	38.00	398	403
Raj 3765	102.77	110.76	39.78	44.32	42.05	0.399	0.402	41.54	36.87	439	442
PBW 373	104.17	107.51	35.53	39.91	37.72	0.342	0.375	40.08	34.80	444	491
CD at 5 %	NS	8.96	6.27	3.93		NS	0.037	3.52	2.39	NS	71

Among the cultivars under study, biomass, harvest index and spikes/m^2 were statistically similar in 2000–01, whereas all other parameters were significant (Table 1). Based on means, the maximum biomass was produced by cultivar HD 2643 (106.95 q/ha) followed by Raj 3765 (106.77 q/ha). In contrast, the lowest biomass was exhibited by genotype WR 251 (94. 72 q/ha). Similarly, genotype PBW 435 recorded the maximum grain yield (42.86 q/ha) but was

Table 2. Effect of sowing time and genotypes on grains/spike, anthesis, maturity, grain-filling period, and grain production rate for spring wheat genotypes grown in the field at the Directorate of Wheat Research, Karnal, India (NS indicates nonsignificance).

	Grain/spike		Anthesis (days)		Maturity (days)		Grain-filling period (days)		Grain production rate (kg/ha/day)	
Treatment	**2000–01**	**2001–02**	**2000–01**	**2001–02**	**2000–01**	**2001–02**	**2000–01**	**2001–02**	**2000–01**	**2001–02**
Sowing time										
Late	22.6	27.5	84	82	112	114	28	33	144.6	144.3
Very late	21.1	23.1	71	62	89	82	18	20	203.6	174.3
CD at 5 %	NS	4.3	0.8	0.3	1	0.4	1	1	16.4	14.9
Genotype										
PBW 435	23.9	25.1	79	71	106	100	28	28	149.4	162.6
UP 2425	18.8	25.5	79	72	108	100	29	28	118.2	148.6
HD 2643	19.2	25.1	82	75	106	100	25	25	152.5	163.5
HP 1744	22.7	29.3	78	72	106	100	28	28	143.5	147.6
DL 788-2	22.2	22.9	77	71	105	100	28	28	157.7	148.7
WR 251	20.9	21.2	71	67	102	94	31	27	120.2	150.3
WR 544	25.5	25.7	71	67	102	94	31	27	128.7	157.0
Raj 3765	22.3	28.4	78	75	107	99	29	24	139.4	187.9
PBW 373	20.8	24.2	83	75	107	100	24	24	145.1	167.1
CD at 5 %	5.11	4.9	2.4	0.6	1.7	0.3	2	0.7	27.1	15.3

followed closely by DL 788-2 (42.16 q/ha) and Raj 3765 (42.05 q/ha). The lowest yield was in UP 2425 (37.37 q/ha). Harvest index ranged from 0.342 to 0.432 and 1,000-kernel weight 34.80 to 50.27 g. The highest mean for grain-filling period (29 days) was recorded in genotype WR 251 and WR 544 due to early anthesis (69 days) whereas lowest grain filling period (24 days) was recorded in cultivar PBW 373 because of delayed anthesis (79 days). From the two-year mean, the maximum grain production rate was observed in Raj 3765 (163.65 kg/ha/day) followed by HD 2643 (158 kg/ha/day) the lowest was in UP 2425 (133.40 kg/ha/day). Under late sowning conditions, cultivars are more sensitive to temperature stress during grain filling, and the critical temperatures required at a specific stage for effective screening can not be repeated in the field (Chatrath at al. 2008).

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Evaluating molecular markers associated with preharvest sprouting resistance in wheat.

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Preharvest sprouting (PHS) refers to the precocious germination of grain in the spike prior to harvest as a result of moist weather conditions at harvest time. The wheat crop grown in the northeastern and far-eastern states of India (West Bengal, Assam, and other eastern hill states) is prone to PHS losses due to pre-monsoon rains and high humidity around maturity. Resistance to PHS is based on seed dormancy, i.e., the ability of the physiologically mature seed to withstand sprouting under conditions otherwise favorable for germination. PHS in wheat represents a major constraint for consistent production of high-quality grain because it causes downgrading of grain, severely limits end-use applications for wheat flour, and results in substantial economic losses to farmers and food processors. A large number of QTL have

been reported and screening of diverse genotypes with the molecular markers associated with PHS resistance will help to identify diverse sources of PHS resistance. In view of this, a set of 216 wheat genotypes was phenotyped for PHS resistance and screened with two markers associated with QTL for PHS resistance on chromosomes 4A and 3B.

Phenotyping for PHS resistance. A set of 216 wheat genotypes was phenotyped for PHS resistance based on germination index (GI). A majority of the genotypes were found susceptible to PHS based on GI. Only 7.8% of the genotypes were resistant to PHS (Table 3). As expected, none of the Indian wheat cultivars were resistant, and only five germ plasm entries were resistant to PHS. However, 22% of the genotypes from the High Rainfall Wheat Yield Trial (HRWYT) and the High Rainfall Wheat Screening Nursery (HRWSN) were resistant and, thus, have potential as donor lines for improving PHS tolerance in future wheat genotypes targeted for cultivation in the regions that are otherwise favorable for PHS. The results also indicated that GI information supports assumption of susceptibility of Indian material as no selection pressure was exerted for this trait. Only one genotype in the hybridization block was found to be resistant to PHS.

Table 3. Germination index of wheat genotypes phenotyped for resistance to preharvest sprouting in various trials in India.

Entries	No. of genotypes	Germination index			
		0.00–0.25	0.26-0.50	0.51–0.75	0.75–1.00
High Rainfall Wheat Yield Trial	23	6	3	8	6
High Rainfall Wheat Screening Nursery	27	5	13	5	4
Indian cultivars	17	—	—	—	17
Germ plasm lines	88	5	7	11	65
Hybridization block	61	1	1	3	56
Total	216	17	24	27	148

Genotyping with markers associated with PHS resistance. Using diverse mapping populations in bread wheat, all chromosomes have been reported to carry QTL/genes for PHS or dormancy. These large numbers of QTL suggest a complex trait controlled by numerous genes that are influenced by environmental conditions and genetic background. However, homoeologous chromosome group 3 and chromosome 4A carry major loci for PHS resistance, which weere revealed in several earlier studies. In the present study, the genotypes were screened with two molecular markers associated with QTL for PHS resistance on chromosome 4A and 3B. One marker, *DuPw004* was mapped in the QTL region on chromosome 4A (Singh et al. 2010) and other marker, *Vp-1B3*, was derived from the vivipary gene on chromosome 3B (Yang et al. 2007). Ninety-nine genotypes amplified the PCR band associated with PHS resistance with *DuPw004*, and the remaining 117 genotypes amplified the PCR band associated with PHS susceptibility. The *Vp-1B3* marker was used in 67 genotypes and amplified three different alleles; 58 genotypes amplified the allele associated with PHS susceptibility.

Eleven out of 17 genotypes having a GI range of 0–0.25 amplified the PCR band with marker *DuPw004* associated with PHS resistance (Fig. 1), whereas, seven out of nine genotypes with a GI range of 0–0.50 amplified the PCR

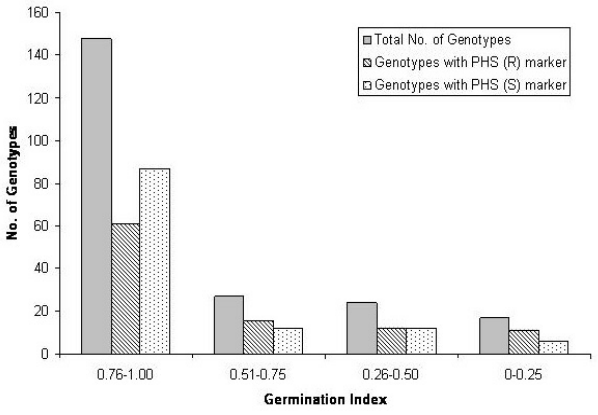

Fig 1. Association between germination index and marker *DuPw004*.

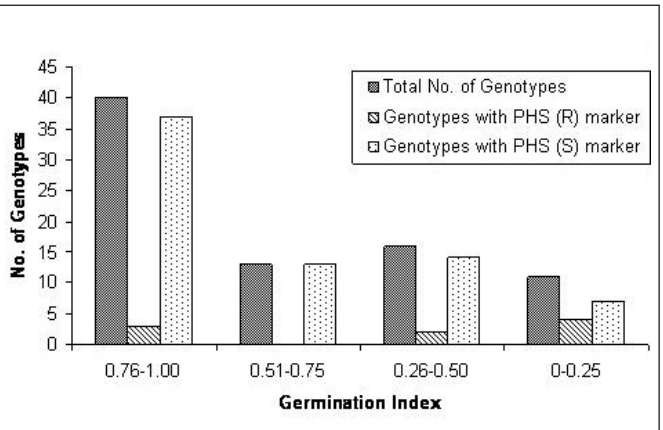

Fig 2. Association between germination index and marker *Vp-1B3*.

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 *DuPw004* and *Vp-1B3* 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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Gene action for quantitative traits in bread wheat.

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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 P_1, P_2, F_1, F_2, BC_1, and 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

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 (l), 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 P_1, P_2, F_1, F_2, BC_1, and BC_2. The material of five crosses was evaluated in a randomized block design with three replications in a plot size with 2.5-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 F_1, F_2, BC_1, and 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 F_1 and 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 $F_1$and 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 F_1 and 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 F_2 generation higher than the 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 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 F_2 population over their 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 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 (A, B, 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';

Table 1. Mean performance of different generations for yield and yield components in five cross combinations of bread wheat (G=generation; D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

Cross	G	D75H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S (g)	S/P	TKW (g)	GY/P (g)	HLB-1	HLB-2	HLB-3
DBW14/HUW 468 (I)	P_1	57.00 ±0.58	117.00 ±0.58	79.33 ±2.73	7.33 ±0.88	9.00 ±0.58	18.00 ±1.15	49.33 ±2.03	1.98 ±0.14	351.00 ±4.10	41.00 ±1.15	13.66 ±0.04	12.33 ±0.33	30.33 ±3.67	45.33 ±0.33
	P_2	80.00 ±20.8	123.00 ±0.58	85.00 ±0.58	7.33 ±0.33	10.00 ±0.58	16.00 ±1.15	44.33 ±1.86	1.71 ±0.05	310.33 ±8.35	39.00 ±2.08	11.60 ±0.50	12.00 ±0.58	27.00 ±4.00	56.33 ±0.33
	F_1	78.67 ±0.88	125.00 ±0.58	83.00 ±1.15	10.00 ±0.58	11.00 ±0.58	19.33 ±1.76	45.00 ±1.15	1.26 ±0.05	447.33 ±4.91	28.00 ±0.58	12.58 ±0.06	12.33 ± 0.33	23.33 ±0.33	38.00 ±3.51
	F_2	81.67 ±1.86	120.67 ±0.88	89.00 ±3.06	11.67 ±0.88	11.33 ±0.67	19.67 ±0.88	47.67 ±0.33	1.24 ±0.03	565.33 ±37.12	31.00 ±0.58	14.19 ±0.53	12.33 ±0.33	45.33 ±0.33	56.33 ±0.33
	BC_1	63.67 ±1.76	116.00 ±1.00	80.67 ±1.33	11.00 ±0.58	11.00 ±0.58	21.00 ±0.58	48.33 ±0.88	1.06 ±0.03	546.00 ±34.43	32.00 ±0.58	13.92 ±0.26	8.67 ±3.33	19.67 ±3.33	38.00 ±3.51
	BC_2	81.33 ±1.76	126.33 ±1.45	82.33 ±0.88	9.67 ±0.33	10.67 ±0.88	20.33 ±0.33	52.67 ±1.76	1.39 ±0.14	519.00 ±29.48	32.33 ±0.88	17.59 ±0.30	5.33 ±3.33	13.00 ±0.00	42.00 ±3.51
DL788-2/PBW 502 (II)	P_1	79.00 ±0.58	124.33 ±1.76	78.33 ±1.45	9.67 ±0.67	9.00 ±0.58	18.00 ±1.15	43.00 ±2.02	1.34 ±0.11	422.67 ±6.17	32.67 ±0.33	13.60 ±0.19	19.33 ±3.67	34.67 ±0.33	59.67 ±3.67
	P_2	84.00 ±0.58	125.00 ±0.58	82.67 ±2.33	9.33 ±0.33	9.00 ±0.58	18.00 ±115	41.00 ±1.53	1.46 ±0.06	386.00 ±6.51	36.00 ±0.58	13.62 ±0.30	5.67 ±3.67	26.33 ±3.84	49.00 ±7.51
	F_1	80.67 ±1.20	128.00 ±1.00	81.00 ±3.21	11.67 ±0.33	11.00 ±0.58	18.00 ±1.15	41.33 ±1.20	1.27 ±0.07	472.33 ±2.40	31.33 ±0.88	14.73 ±0.35	12.33 ±0.33	27.33 ±3.84	52.67 ±3.33
	F_2	76.00 ±0.58	125.00 ±0.58	94.00 ±1.53	14.00 ±0.58	12.00 ±0.58	22.00 ±1.15	35.00 ±1.15	1.00 ±0.01	488.33 ±3.53	28.67 ±0.67	13.70 ±0.12	16.00 ±3.51	56.67 ±6.06	74.00 ±4.00
	BC_1	78.67 ±0.88	131.00 ±0.58	84.00 ±1.53	11.00 ±0.58	10.00 ±0.58	20.00 ±0.58	43.00 ±0.58	1.08 ±0.04	455.33 ±8.84	30.67 ±0.88	11.33 ±0.12	2.00 ±3.51	23.33 ±0.33	53.00 ±7.00
	BC_2	86.33 ± 1.86	126.67 ±0.88	88.00 ±3.61	9.00 ±0.58	11.00 ±0.58	21.33 ±0.67	50.00 ±3.21	1.26 ±0.07	467.20 ±19.61	31.67 ±0.88	11.87 ±0.74	2.00 ±3.52	23.00 ±0.58	45.67 ±6.06
DBW14/HUW 533 (III)	P_1	58.67 ±0.88	117.67 ±0.88	82.00 ±1.73	10.67 ±0.33	9.67 ±0.33	18.33 ±1.45	44.33 ±0.88	1.72 ±0.01	467.33 ±11.62	38.67 ±0.33	18.43 ±0.36	12.00 ±3.51	20.00 ±3.51	34.67 ±6.39
	P_2	84.00 ±1.15	124.67 ±1.20	105.67 ±1.45	10.00 ±0.58	8.00 ±0.58	17.33 ±1.76	40.67 ±0.33	1.24 ±0.09	404.67 ±21.42	29.67 ±0.69	11.34 ±0.88	9.00 ±0.27	27.00 ±3.51	45.67 ±0.33
	F_1	78.33 ±0.88	127.33 ±0.88	99.00 ±1.15	12.00 ±0.58	11.00 ±0.58	20.00 ±1.15	36.67 ±1.20	0.95 ±0.03	428.00 ±6.56	31.67 ±0.33	11.15 ±0.19	5.00 ±3.51	16.33 ±3.33	38.67 ±3.18
	F_2	76.00 ±0.58	128.33 ±0.88	111.33 ±1.20	11.67 ±0.33	10.00 ±0.58	20.00 ±1.15	41.67 ±1.45	1.06 ±0.03	468.33 ±9.35	31.67 ±0.33	11.74 ±0.34	5.33 ±3.33	34.67 ±0.33	56.67 ±0.33
	BC_1	77.33 ±0.88	126.33 ±0.88	95.67 ±1.86	11.00 ±0.58	10.00 ±0.58	20.00 ±0.58	43.67 ±2.40	1.05 ±0.06	464.33 ±8.41	31.00 ±1.00	11.70 ±0.30	1.67 ±0.33	16.00 ±3.00	56.00 ±0.58
	BC_2	87.00 ±0.58	126.00 ±0.58	93.00 ±1.53	12.33 ±1.20	10.00 ±0.33	20.00 ±0.58	38.67 ±4.26	1.07 ±0.12	466.33 ±5.36	32.67 ±1.20	12.36 ±0.10	5.33 ±3.33	16.33 ±3.33	42.67 ±3.84

Table 1 (continued). Mean performance of different generations for yield and yield components in five cross combinations of bread wheat (G=generation; D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

Cross	G	D75H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S (g)	S/P	TKW (g)	GY/P (g)	HLB-1	HLB-2	HLB-3
GW273/HUW 468 (IV)	P_1	80.00 ±2.52	127.33 ±0.88	89.67 ±2.33	9.00 ±0.58	8.33 ±0.88	20.00 ±1.15	38.33 ±0.67	1.05 ±0.06	339.67 ±21.15	27.67 ±1.20	8.91 ±0.21	9.00 ±7.00	30.33 ±7.33	56.33 ±0.67
	P_2	81.33 ±0.88	124.67 ±0.33	86.67 ±0.88	10.33 ±0.33	10.67 ±0.33	17.33 ±0.67	45.00 ±1.53	1.54 ±0.05	464.00 ±4.04	33.67 ±0.33	15.36 ±0.05	5.00 ±3.51	15.67 ±3.67	42.67 ±3.84
	F_1	81.33 ±0.88	124.00 ±0.58	91.00 ±0.58	12.00 ±0.58	12.00 ±0.58	22.00 ±1.15	39.00 ±0.58	1.14 ±0.33	470.33 ±31.42	29.33 ±0.33	13.74 ±0.68	12.33 ±0.33	27.33 ±3.33	56.33 ±0.33
	F_2	76.00 ±0.58	125.33 ±1.20	89.33 ±1.20	11.33 ±0.67	10.67 ±0.33	20.00 ±1.15	38.00 ±1.15	1.08 ±0.03	430.67 ±20.85	29.00 ±0.33	12.17 ±0.40	20.33 ±3.67	49.67 ±3.71	70.33 ±2.85
	BC_1	82.00 ±0.58	126.67 ±0.88	86.67 ±0.88	10.33 ±0.33	11.00 ±0.58	22.00 ±1.15	38.00 ±2.31	0.91 ±0.05	405.00 ±7.51	30.00 ±1.15	9.69 ±0.11	8.33 ±3.67	20.00 ±3.51	56.67 ±6.06
	BC_2	84.33 ±1.20	128.00 ±0.58	85.33 ±1.20	10.00 ±0.58	12.00 ±0.58	22.00 ±1.15	35.33 ±1.76	1.19 ±0.09	338.00 ±3.51	33.67 ±0.88	11.31 ±0.14	2.00 ±0.00	20.00 ±3.51	52.33 ±3.67
PBW443/HUW 533 (V)	P_1	83.00 ±1.53	125.13 ±0.47	79.67 ±1.20	9.67 ±0.33	7.67 ±0.33	17.33 ±1.76	35.33 ±2.60	1.10 ±0.08	349.00 ±16.48	31.00 ±1.00	10.16 ±0.18	12.33 ±6.06	30.67 ±7.17	59.33 ±7.17
	P_2	84.67 ±1.45	125.80 ±1.17	106.00 ±1.53	11.00 ±0.58	8.67 ±0.88	18.00 ±1.15	40.33 ±0.67	1.15 ±0.01	442.33 ±14.50	28.67 ±0.33	12.24 ±0.22	1.33 ±0.33	15.67 ±3.67	45.67 ±6.06
	F_1	84.67 ±0.88	126.20 ±0.81	81.00 ±1.15	10.33 ±0.67	10.67 ±0.88	18.00 ±1.15	36.00 ±2.00	1.05 ±0.07	386.33 ±3.53	29.00 ±0.58	10.89 ±0.11	5.33 ±3.33	34.33 ±0.33	52.67 ±7.17
	F_2	82.33 ±0.88	125.73 ±0.87	94.33 ±2.91	10.00 ±0.58	11.00 ±0.58	20.00 ±1.15	37.00 ±2.08	1.07 ±0.08	361.33 ±12.88	29.33 ±1.33	10.19 ±0.18	16.67 ±3.67	53.33 ±3.67	63.33 ±3.18
	BC_1	83.00 ±1.53	125.20 ±0.53	68.67 ±0.67	10.67 ±0.88	10.00 ±0.58	18.00 ±1.15	31.33 ±1.20	0.97 ±0.04	341.33 ±22.92	30.33 ±0.33	10.18 ±0.64	8.67 ±3.33	37.67 ±7.33	59.67 ±3.67
	BC_2	86.67 ±0.88	125.47 ±0.87	105.33 ±0.88	12.33 ±0.87	10.67 ±0.88	16.00 ±1.15	34.33 ±1.45	0.99 ±0.03	408.00 ±13.11	29.33 ±0.33	11.69 ±0.45	1.67 ±0.33	23.33 ±0.33	49.33 ±3.33

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 (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

Table 2. Estimation of scaling tests for testing the adequacy of additive-dominance model for different traits in five crosses of wheat (P=scaling test parameters (A, B, C, and D); D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

Cross	P	D75%H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S	S/P	TKW	GY/P (g)	HLB-1	HLB-2	HLB-3
DBW14/HUW 468 (I)	A	-8.00* ±3.68	-10.00** ±2.20	-1.00 ±3.98	4.66** ±1.56	2.00 ±1.41	4.66 ±2.40	2.33 ±2.92	-1.12** ±0.16	293.33** ±69.15	-5.00** ±1.73	1.59** ±0.53	-7.33 ±6.68	-14.33 ±7.61	-7.33 ±7.85
	B	4.00 ±4.18	4.67 ±3.01	-3.33 ±2.18	2.00* ±0.94	0.33 ±1.94	5.33* ±2.21	16.00** ±4.14	-0.20 ±0.29	280.33** ±59.75	-2.33 ±2.78	10.99** ±0.78	-13.66* ±6.69	-24.33** ±4.01	-10.33 ±7.85
	C	32.33** ±7.93	-7.33 ±3.80	25.67* ±12.74	12.00** ±3.82	4.33 ±3.01	6.00 ±5.24	7.00 ±3.82	-1.24** ±0.21	704.99** ±149.10	-12.00** ±3.51	6.35** ±2.17	0.33 ±1.63	77.33** ±5.62	47.66** ±7.16
	D	18.33** ±4.47	-1.00 ±2.49	15.00* ±6.31	2.66 ±1.88	1.00 ±1.69	-2.00 ±1.88	-5.66** ±2.08	0.04 ±0.15	65.66 ±86.98	-2.33 ±1.56	-3.12** ±1.13	10.66* ±4.76	58.00** ±3.39	32.66** ±5.01
DL788-2/ PBW 502 (II)	A	-2.33 ±2.21	9.66** ±2.33	8.66 ±4.66	0.66 ±1.37	0.00 ±0.00	4.00* ±1.63	1.66 ±2.62	-0.45** ±0.15	15.66 ±18.87	-2.66 ±2.00	-5.67** ±0.46	-21.00* ±7.61	-15.33** ±3.91	-6.33 ±14.85
	B	8.00* ±3.94	0.33 ±2.10	12.33 ±8.23	-3.00* ±1.24	2.00 ±1.41	6.66** ±2.10	17.66* ±6.71	-0.21 ±0.16	76.06 ±39.82	-4.00* ±1.97	-4.62** ±1.54	-14.00** ±3.68	-7.66 ±5.43	-10.33 ±14.64
	C	-20.33** ±3.43	-5.33 ±3.57	53.00** ±9.28	13.66** ±2.51	8.00** ±2.70	16.00** ±5.41	-26.66** ±5.79	-1.32** ±0.19	200.00** ±17.39	-16.66** ±3.21	-1.90* ±0.92	14.33 ±14.98	111.00** ±25.73	82.00** ±19.24
	D	-13.00** ±2.35	-7.66** ±1.56	16.00** ±4.96	8.00** ±1.41	3.00* ±1.41	2.66 ±2.40	-23.00** ±4.00	-0.32** ±0.08	54.13* ±22.63	-5.00** ±1.82	4.19** ±0.78	24.66** ±7.77	67.00** ±12.13	49.33** ±12.23
DBW14/HUW533 (III)	A	17.66** ±2.16	7.66** ±2.16	10.33* ±4.25	-0.66 ±1.33	0.66 ±1.33	1.66 ±2.18	6.33 ±5.03	6.33 ±5.03	33.33 ±21.47	-8.33** ±2.05	-6.18** ±0.72	-6.67 ±5.01	-4.33 ±7.71	38.67* ±7.13
	B	11.66** ±1.85	0.00 ±0.00	-18.66** ±3.57	2.66 ±2.53	1.00 ±0.81	2.66 ±2.40	0.00 ±0.00	0.00 ±8.60	100.00** ±24.83	4.00 ±2.58	2.23** ±0.39	-3.33 ±8.31	-10.66 ±8.23	1.00 ±8.32
	C	4.66 ±3.24	16.33** ±4.21	59.66** ±5.79	2.00 ±1.88	0.33 ±2.66	4.33 ±5.64	8.33 ±6.35	8.33 ±6.35	145.33** ±46.52	-5.00* ±1.76	-5.11** ±1.46	-2.67 ±15.86	59.00** ±8.41	69.00** ±9.11
	D	-12.33** ±1.56	4.33* ±2.05	34.00** ±3.39	0.00 ±1.49	0.00 ±1.29	0.00 ±2.44	1.00 ±5.68	1.00 ±5.68	6.00 ±21.19	-0.33 ±1.69	-0.58 ±0.74	3.67 ±7.46	37.00** ±4.53	14.66 ±3.90
GW273/HUW468 (IV)	A	2.66 ±2.90	2.00 ±2.05	-7.33* ±2.98	-0.33 ±1.05	1.66 ±1.56	2.00 ±2.82	-1.33 ±4.70	6.33 ±5.03	33.33 ±21.47	-8.33** ±2.05	-6.18** ±0.72	-6.67 ±5.01	-4.33 ±7.71	38.67* ±7.13
	B	6.00* ±2.70	7.33** ±1.33	-7.00* ±2.62	-2.33 ±1.33	1.33 ±1.33	4.66 ±2.66	-13.33** ±3.88	0.00 ±8.60	100.00** ±24.83	4.00 ±2.58	2.23** ±0.39	-3.33 ±8.31	-10.66 ±8.23	1.00 ±8.32
	C	-20.00** ±3.94	1.33 ±5.03	-1.00 ±5.53	2.00 ±2.98	-0.33 ±2.00	-1.33 ±5.33	-9.33 ±5.04	8.33 ±6.35	145.33** ±46.52	-5.00* ±1.76	-5.11** ±1.46	-2.67 ±15.86	59.00** ±8.41	69.00** ±9.11
	D	-14.33** ±1.76	-4.00 ±2.62	6.66* ±2.82	2.33 ±1.49	-1.66 ±1.05	-4.00 ±2.82	2.66 ±3.71	1.00 ±5.68	6.00 ±21.19	-0.33 ±1.69	-0.58 ±0.74	3.67 ±7.46	37.00** ±4.53	14.66 ±3.90
PBW443/HUW533 (V)	A	-1.66 ±3.52	-0.93 ±1.41	-23.33** ±2.13	1.33 ±1.91	1.66 ±1.49	0.66 ±3.12	-8.66* ±4.06	-0.21 ±0.14	-53.00 ±48.84	0.67 ±1.33	-0.70 ±1.29	-0.33 ±9.60	10.33 ±16.32	7.33 ±12.51
	B	4.00 ±2.44	-1.06 ±2.24	23.66** ±2.60	3.33 ±1.97	2.00 ±2.16	-4.00 ±2.82	-7.66* ±3.59	-0.21 ±0.10	-12.67 ±30.17	1.00 ±0.94	0.24 ±0.92	-3.33 ±3.41	-3.33 ±3.74	0.33 ±11.51
	C	-7.66 ±4.47	-0.40 ±4.02	29.66* ±12.00	-1.33 ±2.74	6.33* ±3.05	8.66 ±5.57	0.33 ±9.62	-0.07 ±0.37	-119.00* ±56.42	-0.33 ±5.55	-3.43** ±0.80	42.33* ±17.21	98.33** ±16.74	43.00* ±21.34
	D	-5.00* ±2.49	0.80 ±2.00	14.66* ±5.91	-3.00 ±1.69	1.33 ±1.56	6.00* ±2.82	8.33 ±4.57	0.17 ±0.17	-26.67 ±36.88	-1.00 ±2.70	-1.49 ±0.85	23.00* ±8.06	45.67** ±10.37	17.67* ±8.06

Table 3. Estimation of adequacy for simple additive-dominance model in different traits of five crosses of wheat (P=parameter; D75H=days-to-75% maturity; DM=days-to-maturity; PH=plant height; T/P=effective tillers/plant; SL=spike length; S/S=spikelets/spike; G/S=grains/spike; GW/S=grain weight/spike; S/P=seeds/plant; TKW=1,000-kernel weight; GY/P=grain yield/plant; and HLB-2, HLB-2, and HLB-3=Helminthosporium leaf blight infection, at 77–80 d (dough stage), 83–86 d (soft dough stage), and 87–89 d (hard dough stage), respectively).

HLB-3Cross	P	D75%H	DM	PH (cm)	T/P	SL (cm)	S/S	G/S	GW/S (g)	S/P	TKW	GY/P (g)	HLB_1	HLB-2	HLB-3
DBW14/HUW 468 (I)	m	69.19** ±0.64	119.47** ±0.64	82.66** ±0.64	8.07** ±0.64	9.76** ±0.64	17.76* ±0.64	48.11** ±0.64	1.72** ±0.64	385.31** ±0.64	39.21** ±0.64	13.55** ±0.64	10.94** ±0.64	28.66** ±0.64	51.19** ±0.64
	d	-12.73** ±0.63	-4.46 ±0.63	-2.60** ±0.63	0.26 ±0.63	-0.33 ±0.63	0.93 ±0.63	1.13 ±0.63	0.04 ±0.63	21.80** ±0.63	0.73 ±0.63	0.09 ±0.63	0.79 0.63	2.66** ±0.63	-5.20** ±0.63
	h	10.86** ±1.18	4.47** ±1.18	1.33 ±1.18	3.41** ±1.18	1.76 ±1.18	3.09* ±1.18	-0.54 ±1.18	-0.69 ±1.18	170.98** ±1.19	-12.78** ±1.19	0.88 ±1.18	-1.05 ±1.18	-5.33** ±1.19	-12.47** ±1.18
	c^2	76.720**	24.854**	40.877**	8.188*	**1.238**	**7.338**	42.723**	**0.232**	34,374.200**	8.590*	20.198**	39.994**	570.667**	180.243**
DL788-2/PBW 502 (II)	m	81.23** ±0.64	125.09** ±0.64	83.29** ±0.64	9.76** ±0.64	9.35** ±0.64	19.09** ±0.64	42.35** ±0.64	1.32* ±0.64	415.61** ±0.64	33.45** ±0.64	12.95** ± 0.64	10.86** ±0.64	32.41** ±0.64	55.76** ±0.64
	d	-3.53** ±0.63	0.60 ±0.63	-2.53** ±0.63	0.53 ±0.63	-0.20 ±0.63	-0.20 ±0.63	-0.60 ±0.63	0.085 ±0.63	12.29** ±0.63	-1.53* ±0.63	-0.114 ±0.63	6.13** ±0.63	3.40** ±0.63	5.73** ±0.63
	h	-1.09 ±1.18	3.76** ±1.18	3.29** ±1.18	2.43* ±1.18	2.35 ±1.18	1.09 ±1.18	-0.31 ±1.18	-0.21 ±1.19	79.27** ±1.18	-3.88** ±1.19	0.458 ±1.18	-1.80 ±1.19	-1.25 ±1.18	-0.23 ±1.18
	c^2	39.638**	20.616**	132.491**	12.805*	**3.311**	15.560*	115.178**	**0.093**	2,294.853**	13.167*	8.000*	136.687**	795.466**	430.449**
DBW14/HUW533 (III)	m	73.19** ±0.64	122.09** ±0.64	95.09** ±0.64	10.50** ±0.64	8.86** ±0.64	18.21** ±0.64	43.11** ±0.64	1.42** ±0.64	448.11** ±0.64	33.76** ±0.64	14.50** ±0.64	6.33** ±0.64	24.35** ±0.64	44.52** ±0.64
	d	-12.06** ±0.63	-2.73** ±0.63	-8.93** ±0.63	0.019 ±0.63	0.66 ±0.63	0.40 ±0.63	2.46** ±0.63	0.18 ±0.63	24.66** ±0.63	3.26** ±0.63	2.70** ±0.63	-2.33** ±0.63	-2.86** ±0.62	-1.73** ±0.63
	h	8.86** ±1.18	7.09** ±1.18	6.43** ±1.18	1.84 ±1.18	2.19 ±1.18	2.54* ±1.18	-5.21** ±1.18	-0.59 ±1.18	4.117** ±1.19	-2.90** ±1.19	-4.12** ±1.20	-2.67** ±1.18	-6.31** ±1.120	2.86** ±1.19
	c^2	68.276**	18.838**	294.894**	**1.464**	**0.287**	**1.756**	8.501*	**0.061**	2,114.602**	17.060**	8.794*	8.388*	240.422**	393.443**
GW273/HUW468 (IV)	m	80.58** ±0.64	126.58** ±0.64	87.29** ±0.64	9.56** ±0.64	9.66** ±0.64	19.01** ±0.64	40.52** ±0.64	1.23* ±0.64	385.99** ±0.64	30.98** ±0.64	11.46** ±0.64	7.16** ±0.65	24.67** ±0.64	51.92** ±0.64
	d	-1.00* ±0.63	0.80 ±0.63	1.46* ±0.63	-0.46 ±0.63	-1.13* ±0.63	1.06* ±0.63	-2.13** ±0.63	-0.23 ±0.63	-36.33** ±0.63	-3.13** ±0.63	-2.90** ±0.63	2.86** ±0.62	5.86** ±0.63	6.33** ±0.63
	h	0.58 ±1.20	-1.41 ±1.19	1.96* ±1.19	2.23 ±1.20	2.66** ±1.18	3.68** ±1.19	-3.80** ±1.19	-0.19 ±1.19	52.67** ±1.19	-1.02 ±1.20	0.94 ±1.18	5.52** ±1.20	6.00** ±1.19	9.25** ±1.20
	c^2	35.421**	9.432*	16.047**	**1.416**	**0.788**	**4.789**	30.243**	**0.034**	11,848.610**	6.645*	7.909*	161.298**	639.733**	236.088**
PBW443/HUW533 (V)	m	83.74** ±0.64	125.34** ±0.64	93.72** ±0.64	10.56** ±0.64	8.56** ±0.64	17.72** ±0.64	36.88** ±0.64	1.09* ±0.64	388.47** ±0.64	29.92** ±0.65	11.07** ±0.64	7.86** ±0.65	26.47** ±0.65	54.21** ±0.65
	d	-1.39* ±0.63	-0.32 ±0.63	-17.86** ±0.63	-0.86 ±0.63	-0.53 ±0.63	0.13 ±0.63	-2.60** ±0.63	-0.025 ±0.63	-50.53** ±0.63	1.13* ±0.63	-1.13* ±0.62	5.80** ±0.63	8.86** ±0.63	7.53** ±0.63
	h	0.74 ±1.18	0.60 ±1.19	-10.94** ±1.18	0.23 ±1.18	2.90** ±1.21	0.39 ±1.19	-2.78** ±1.19	-0.099 ±1.18	-16.86** ±1.18	-0.74 ±1.18	-0.43 ±1.19	-0.47 ±1.18	14.47** ±1.19	1.82* ±1.18
	c^2	7.466	0.298	265.772**	2.527	2.138	8.216*	21.923**	**0.0138**	895.576**	**0.266**	**0.644**	101.076**	489.965**	90.279**

'GW273/HUW468'; and for HLB-2 and HLB-3 in crosses 'DBW14/HUW468' and 'PBW443/HUW533'. Additive (d) components were significant for days-to-75% heading in 'DL788-2/PBW502', 'GW273/HUW468', and 'PBW443/HUW533'; for 1,000-kernel weight in crosses 'GW273/HUW468' and 'PBW443/HUW533'; for grain yield/plant in crosses 'GW273/HUW468' and 'PBW443/HUW533'; for HLB-1, HLB-2, and HLB-3 in cross 'DL788-2/PBW502'; and HLB-1 in cross 'PBW443/HUW533'. Dominance (h) components were important for days-to-maturity and effective tillers/plant in crosses 'DBW14/HUW468' and 'DL788-2/PBW502' and for 1,000-kernel weight in cross 'DBW14/HUW 468'. Both main ef-

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) for16 traits in five crosses of bread wheat (m = mean effect, d = additive effect, h = dominance effect, i = 'additive x additive' interaction, j = 'additive x dominant' interaction, l = 'dominant x dominant' interaction; * and ** equal significance at 5% and 1%, respectively; D = duplicate and C = complimentary).

Cross/ character	Gene effect						Type of epistasis
	m	d	h	i	j	l	
DBW14/HUW 468 (I)							
Days-to-75% heading	81.66**±1.85	-17.66 **± 2.49	-26.49**±9.05	-36.66**±8.94	-6.16*±2.71	40.99**±12.74	D
Days-to-maturity	120.66**±0.88	-10.33**±1.76	7.00±5.03	2.00±4.98	-7.33**±1.81	3.33±8.01	C
Plant height (cm)	89.00**±3.05	-1.67±1.59	-29.16±12.76	-30.00*±12.63	1.16±2.12	34.33*±14.25	D
Effective tillers/plant	11.67**±0.88	1.33*±0.67	-2.67±3.84	-5.33±3.77	1.33±0.81	-1.33±4.67	C
Grains/spike	47.67**±0.33	-4.33*±1.97	9.49*±4.53	11.33**±4.16	-6.83**±2.40	-29.67**±8.76	D
Seeds/plant	56.53**±37.12	27.00±45.32	-14.83±174.10	-131.33±173.97	6.50±45.56	-442.33**±234.74	C
1,000-kernel weight (gm)	31.00**±0.58	-0.33±1.05	-7.33*±3.39	4.67±3.12	-1.33±1.58	2.67±5.48	D
Grain yield/plant (gm)	14.19**±0.53	-3.67**±0.40	6.19**±2.27	6.24**±2.26	-4.69**±0.47	-18.83**±2.70	D
HLB -1	12.33**±0.33	3.33±4.71	-21.16*±9.53	-21.33*±9.52	3.16±4.72	42.33*±18.92	D
HLB -2	45.33**±0.33	6.67*±3.33	-121.33**±7.32	-116.00**±6.79	4.99±4.29	154.67**±14.47	D
HLB -3	56.33**±0.33	-4.00±4.96	-78.17**±10.62	-65.33**±10.02	1.50±4.97	82.99**±21.12	D
DL788-2/PBW502 (II)							
Days-to-75% heading	76.00**±0.57	-7.67**±2.05	25.17**±4.88	26.00**±4.71	-5.17*±2.09	-31.67**±8.90	D
Days-to-maturity	125.00**±0.58	4.33**±1.05	18.67**±3.41	15.33**±3.12	4.67**±1.40	-25.33**±5.53	D
Plant height (cm)	94.00**±1.52	-4.00±3.91	-31.50**±10.53	-32.00**±9.93	-1.83±4.14	11.00±18.20	D
Effective tillers/plant	14.00**±0.58	2.00*±0.82	-13.83**±2.87	-16.00**±2.82	1.83*±0.89	18.33**±4.12	D
Grains/spike	22.00**±1.15	-1.33±0.67	-5.33±5.01	-5.33±4.81	-1.33±1.05	-5.33±6.03	C
Spikelets/spike	35.00**±1.15	-7.00*±3.26	45.33**±8.18	46.00**±8.00	-8.00**±3.50	-65.33**±14.29	D
Seeds/plant	488.33**±3.52	-11.87±21.51	-40.27±45.56	-108.27*±45.27	-30.19±21.97	16.53±87.78	D
1,000-kernel weight (gm)	28.66**±0.67	-1.00±1.24	7.00±3.76	10.00**±3.65	0.67±1.25	-3.33±5.93	D
Grain yield/plant (gm)	13.69**±0.12	-0.53±0.74	-7.27**±1.61	-8.38**±1.56	-0.52±0.76	18.68**±3.12	D
HLB -1	16.00**±3.51	3.33±3.33	-49.50**±15.76	-49.33**±15.54	-3.50±4.22	84.33**±20.06	D
HLB -2	56.67**±6.06	0.33±0.33	-137.17**±24.64	-134.00**±24.26	-3.83*±1.95	157.00**±25.77	D
HLB -3	74.00**±4.00	7.33±9.26	-100.33**±25.05	-98.67**±24.47	1.99±10.15	115.33**±41.74	D
DBW14/HUW 533 (III)							
Days-to-75% heading	76.00**±0.57	-9.67**±1.05	31.67**±3.32	24.67**±3.12	3.00*±1.28	-54.00**±5.32	D
Days-to-maturity	128.33**±0.88	0.33 ±1.05	-2.50±4.26	-8.67*±4.10	3.83**±1.29	0.99±5.96	D
Plant height (cm)	111.33**±1.20	2.67±2.40	-62.83**±6.98	-68.00**±6.79	14.50**±2.65	76.33**±11.22	D
Grains/spike	41.66**±1.45	5.00±4.88	-7.83±11.44	-2.00±11.37	3.17±4.91	-4.33±20.55	C
Seeds/plant	468.33**±9.35	-2.00±9.97	-20.00**±44.59	-12.00±42.39	-33.33*±15.74	-121.33*±61.30	C
1,000-kernel weight (gm)	31.66**±0.33	-1.67±1.56	-1.83±3.44	0.67±3.39	-6.17**±1.63	3.67±6.49	D
Grain yield/plant (gm)	11.74**±0.34	-0.67*±0.31	-2.59±1.51	1.15±1.48	-4.21**±0.38	2.80±1.93	D
HLB -1	5.33**±3.33	-3.67±3.34	-9.33±15.52	-7.33±14.92	-1.67±4.16	17.33±20.76	D
HLB -2	34.67**±0.33	-0.33±4.48	-81.17**±9.97	-74.00**±9.06	3.16±5.12	89.00**±19.81	D
HLB -3	56.67**±0.33	13.33**±3.84	-30.83**±9.01	-29.33**±7.80	18.83**±5.00	-10.33±17.87	C

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 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 DL788-2/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 'DL788-2/PBW502', 'additive x dominant' and 'dominant x dominant' effects were significant in cross 'GW273/HUW468', 'additive x additive' and 'dominant 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/

Table 4 (continued). Estimation of the components of generation mean analysis using six-parameter model of Hayman (1958) for16 traits in five crosses of bread wheat (m = mean effect, d = additive effect, h = dominance effect, i = 'additive x additive' interaction, j = 'additive x dominant' interaction, l = 'dominant x dominant' interaction; * and ** equal significance at 5% and 1%, respectively; D = duplicate and C = complimentary).

Cross/ character	Gene effect						Type of epistasis
	m	d	h	i	j	l	
GW273/HUW 468 (IV)							
Days-to-75% heading	76.0**±0.58	-2.33*±1.33	29.33**±3.87	28.67**±3.52	-1.67±1.88	-37.33**±6.63	D
Days-to-maturity	125.33**±1.20	-1.33±1.05	5.99±5.30	7.99±5.24	-2.67±1.15	-17.33**±6.56	D
Plant height (cm)	89.33**±1.20	1.33±1.49	-10.50*±5.28	-13.33*±5.65	-0.16±1.94	27.67**±8.13	D
Grains/spike	38.00**±1.15	2.67±2.90	-8.00±7.49	-5.33±7.42	6.00*±3.02	20.00*±12.67	D
Seeds/plant	430.67**±20.85	67.00**±8.28	-168.17**±91.29	-236.67**±85.03		495.00**±111.67	D
1,000-kernel weight (gm)	29.00**±0.33	-3.67**±1.45	10.00**±2.99	11.33**±2.90	-0.67±1.58	-18.67**±5.98	D
Grain yield/plant (gm)	12.16**± 0.40	-1.62**±0.17	-5.06**±1.77	-6.67**±1.64	1.61**±0.20	16.43**±2.21	D
HLB -1	20.33**±3.67	6.33±3.67	-55.33**±16.86	-60.67**±16.39	4.33±5.36	78.67**±22.18	D
HLB -2	49.67**±3.71	0.00±4.96	-114.33**±18.62	-118.67±17.86	-7.33±6.43	139.33**±26.95	D
HLB -3	70.33**±2.84	4.33±7.08	-56.50**±18.29	-63.33**±18.18	-2.50±7.35	57.00*±30.80	D
PBW443/HUW 533 (V)							
Plant height (cm)	94.33**±2.90	-36.67**±1.10	-41.17**±11.92	-29.33**±11.83	-23.50**±1.47	29.00**±12.79	D
Spikelets/spike	20.00**±1.15	2.00±1.63	-11.67*±5.86	-12.00**±5.65	2.33±1.94	15.33*±8.58	D
Grains/spike	37.00**±2.08	-2.99±1.88	-18.50*±9.45	-16.67*±9.14	-0.50±2.31	33.00**±12.22	D
Seeds/plant	361.33**±12.87	-67.66**±26.41	43.83±74.67	53.33±73.77	-20.17±28.59	12.33±119.76	C
HLB -1	16.67**±3.67	7.00*±3.34	-47.50**±16.74	-46.00**±16.12	1.50±4.52	49.67**±21.81	D
HLB -2	53.33**±3.67	14.33*±7.34	-80.17**±21.14	-91.33**±20.75	6.83±8.37	84.33**±33.80	D
HLB -3	63.33**±3.17	10.33*±4.95	-35.16*±18.26	-35.33*±16.12	3.50±6.82	27.68±29.13	D

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 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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Detection of heat shock protein in bread wheat through ELISA.

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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°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-kDa HSPs are the second most predominantly

expressed HSPs after the 70-kDa family. These proteins appear to impart thermotolerance, because mutant cells with an impaired capacity to make HSP 90 are incapable of growing at higher temperatures (Borkovich et al. 1989).

Materials and Methods. Twelve wheat genotypes/cultivars were used for the present investigation (Table 1). The experiment was conducted on two sowing dates, 18 November and 18 December, 2006. Protein extracted from the leaves of plants from both sowing dates were used separately for experimentation. ELISA tests were developed with minor modifications as described initially by Engvall and Pedlman (1971) and later by Clark and Adams (1977). Here, microtitre plates were coated with different concentrations of proteins in coating buffers keeping the volume constant, i.e., 100 μl/well of soluble antigen. The plates were incubated for 1 hr at room temperature and kept overnight at 4°C. Following a standard washing procedure, the plates were washed with antibody dilution buffer. A 100 μl dilution of primary antibody (anti-HSP 90 sera) was added and the plates were incubated for 2 hrs at room temperature. The plates were washed again with antibody dilution buffer three times and a substrate of 1:1,000 times diluted alkaline phosphate conjugated secondary antibody were added to the plates (rabbit anti-goat I_gG-ALP conjugate) and incubated for 2 hrs at room temperature. After washing the plates three times with dilution buffer, 100-μl substrate solutions were added in each well and incubated for 30 min. The reaction was terminated by adding 100 μl of 1.5 M NaOH solution. The absorbance of the plates was taken 405 nm in an ELISA reader.

Table 1. Twelve wheat genotypes and their pedigrees used in the detection of heat-shock proteins.

Genotype	Pedigree
Acc 8528	not available
DBW 14	Raj 3765 / PBW 343
Halna (K 7903)	HD 1982 / K 816
HD 2808	WH 542 / DL 377-8
HI 385 (Mukta)	HYB 633 / Baza // PR / PKD 25
NP 846	NP 760 . RN
PBN 51	BUL 'S' / FLS 'S'
Raj 3765	HD 2402 / VL 639
Raj 4014	DL 802-5 / K 9011
UP 2425	HD 2320 / UP 2263
WH 147	E 4870 / C 303 // 5339 / PV 18
WH 1003	WEAVER / JACANA

Results and Discussion. In timely-sown conditions, we observed that the OD value at 405 nm ranged between 0.05 (Raj 3765 and HD 2808) to 0.42 (NP 846). In late-sown conditions, the OD value at 405 nm ranged between 0.05 (Halna) to 0.61 (NP 846). The OD values of both days of sowing of different genotypes are presented in Fig. 1.

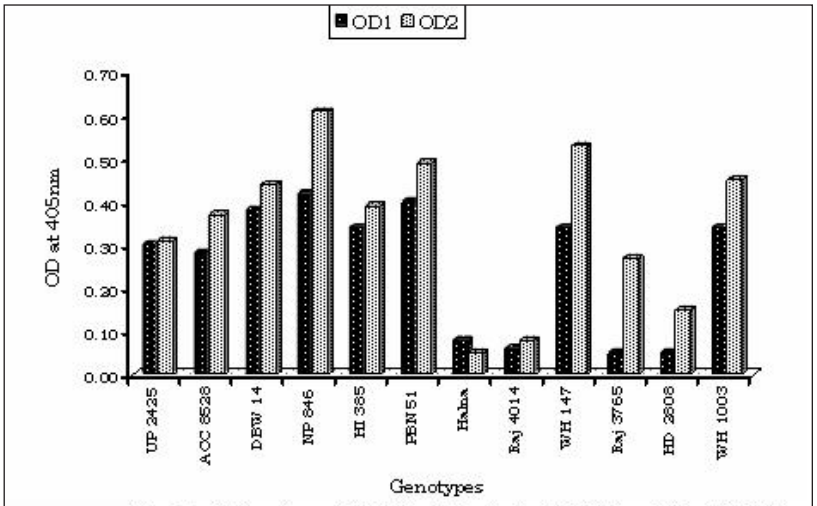

Fig. 1: OD value of ELISA in both D_1 (OD 1) and D_2 (OD 2)

In the ELISA study (which indicates the presence of heat-shock protein), we observed that a majority of the genotypes had high OD values under late-sown conditions compared with the timely sown, and a similar finding was reported by Sharma (2006). Cupina et al. (1979) studied 12 wheat cultivars of varying duration and found that late-maturing types contained more chlorophyll than early cultivars, particularly at heading. This finding indicates that there may be heat-shock protein expressed (HSP 90) in response to heat stress. We found higher ODs for those heat-tolerant genotypes, ACC 8528, DBW 14, NP 846, HI 385, and PBN 51, whereas Raj 4014 had a low OD value and was observed to be heat susceptible. Halna had a very low OD value although it showed heat tolerance on the basis of the heat susceptibility index (result not shown). Because Halna is a heat-tolerant cultivar but matures in a very short period (115 days) in both timely and late-sown conditions, it was not exposed to heat stress, which could be the most plausible explanation of its very low expression of HSP-90 resulting in a very low OD value.

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Performance of brown and black rust resistance genes in some wheat cultivars of central, peninsular, and south India.

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Some of the popular wheat cultivars grown in central, peninsular, and southern India were evaluated for seedling and adult-plant resistance to black and brown rusts. Because the source of rust inoculum for Central and Peninsular India lies mainly in Nilgiri Hills in southern India, the cultivars were tested only with Nilgiri pathotypes. Cultivars were raised as single lines in plastic trays (12 x 5 cm) each accommodating 10 lines (8 seedlings/line). Uredosporic dust of individual pathotypes prevailing in the Nilgiri Hills and maintained artificially at the IARI Regional Station, Wellington, was inoculated on the wet surface of the primary leaves of 7-day-old seedlings of the test cultivars by a uniform rub application from base to tip. Inoculated pots were kept in a fine mist created with a manually operated water sprayer making a free film of water on the leaf surface. The plants were kept in a high humidity atmosphere maintained in glass humidity chambers. After 24 hours, the pots were transferred to benches in the glasshouse. Optimum temperature (20°C for brown and 25°C for black rust) and a light regime of 16:8 hours light:dark cycle maintained in the glass houses permitted full expression of brown and black rust pustules after 12 days. Host–pathogen interactions were recorded by following standard international procedures of Johnston and Mains (1932) in brown rust and Stackman and Levine (1922) in black rust. Cultivars also were sown in an open field environment exposing them to natural rust pathotypes prevailing in Wellington to evaluate adult-plant resistance response. Rust intensities were recorded on these cultivars at growth stage 71 (Zadoks et al. 1974) following the Peterson scale (Peterson et al. 1948) for estimating adult-plant resistance.

Seedling and adult-plant response of cultivars are given in Table 1 (p. 81). In the Central Zone, seven of eight tested cultivars exhibited seedling resistance to all the pathotypes of brown and black rust prevalent in the Nilgiri Hills. These seven cultivars were HI 8498, HI 8381, HI 1544, HI 1531, HI 8627, DL 788-2, and HD 4672 were free of infection from brown and black rusts at the adult stage; their field resistance is robust only if the inoculum in central India originates from the Nilgiri Hills. Only cultivar HI 1500 of central India showed susceptibility but that was only to one race 77-5 (121R63-1) of brown rust. Fortunately, this genotype has strong adult-plant resistance to brown rust (0 rating). Partial susceptibility (10S) of HI 1500 to black rust is a very positive feature because such incomplete resistance restricts the epiphytotic development of disease so that economic losses do not exceed the threshold (field durability; Parlevliet 1977). The majority of the cultivars of the Central Zone possess gene *Sr2*, which is quite desirable for the purpose of preventing black rust epidemics in this zone. Because of the presence of *Sr2*, the rust resistance seems to be stabile in the Central Zone even after 4–5 decades of utilization of the cultivars possessing this gene. This gene is derived from the cultivar Hope, which is responsible for reducing yield losses to only negligible amounts since the late 1960s in

Table 1. Response of popular wheat cultivars of the Central, Peninsular, and South Hill Zones to individual pathotypes at the seedling stage and to a mixture of pathotypes at the adult-plant stage of brown, black, and yellow rusts.

Cultivar	Seedling reaction						Adult-plant reaction		Seedling resistance genes present		
	Brown rust pathotypes				Black rust pathotypes		Brown rust	Black rust	Black rust	Brown rust	Yellow rust
	77A	77-5	77-7	77-8	40A	40-1					
Central Zone											
HI 8498	;	;1	;1	;1	;	0	0	0	*Sr2*	*Lr23*	—
HI 8381	;2	;1	;2	;1	;2+	2+	0	0	*Sr2+Sr9e*	—	—
HI 1544	;2	0;	;1	;1	;1	;1	0	0	*Sr2*	—	—
HI 1531	;2	;2	;2	;2	;	;	0	0	*Sr2+Sr24*	*Lr24*	—
HI 8627	;1	;1	;1	;1	;	0	0	0	*Sr9e*	—	—
DL 788-2	;1	;1	1	0;1	;	0	0	0	*Sr2+Sr5+ Sr24*	*Lr24*	—
HD 4672	;2	;2	;1	;1	;1	1	0	0	—	*Lr23*	—
HI 1500	;1	3+	;2	;2+	;12+	;	0	10S	—	—	—
Peninsular Zone											
Raj 4037	2	3+	2+	;2	2+	2+	80S	20S	*Sr2*	—	—
DWR 162	2+	3+	2+	2+	2	2	60S	10MR	*Sr2+Sr31*	*Lr23+Lr26*	*Yr9*
MACS 2496	2+	3+	2+	22+	2	1	40S	10MR MS	*Sr2+Lr31*	*Lr1+Lr23+ Lr26*	*Yr9*
DDK 1001	;2	0;	;	;1	0;	;1	0	0	—	—	—
DDK1009	;1	;2	;2	;2	;	2	0	0	—	—	—
NIAW 917	0;	0;	0	0;	;1	0	0	0	*Sr2+Sr31*	*Lr26*	*Yr9*
DDK 1025	;2	;1	;1	0;	;	;	0	0	—	—	—
UAS 415	;2	;12	;1	;2	1	;	0	0	—	*Lr23*	—
DWR 195	2+	3+	2+	2+	0;1	2	20S	20MS	*Sr2+Sr31*	*Lr1+Lr23+ Lr26*	*Yr9*
NIAW 34	;2	;2	;2+	;2	;1	2+	60S	0	*Sr11*	*Lr13+Lr34*	*Yr18*
Raj 4083	2+	2+	2+	12+	;1	2	10S	0	—	*Lr23*	—
HD 2781	;1	;1	;1	;1	0	3+	0	0	*Sr2*	—	—
K9644	2+	2+	2+	2	0;	0	20S	0	*Sr2*	*Lr13*	—
MACS 1967	1	;2	2	2	2	2+	0	0	*Sr11*	—	—
AKDW 2997-16	;1	;2	;12	0;	1	;	0	0	—	—	—
Bijaga yellow	1	;1	;2	;2	;1	;	0	0	*Sr2+Sr11*	*Lr23*	—
South Hill Zone											
HW 1085	;1	;1	;1	0;1	0	0	0	0	*Sr24+Sr31*	*Lr24*	—
HW 2044	;1	;1	;2	;2	;1	;	0	0	*Sr2+Sr25*	*Lr19*	—
HW 2045	1	;1	;1	;1	0	0	0	0	*Sr2+Sr25*	*Lr19*	—
HW 3094	;2	;1	;	0;	0	;1	0	0	*Sr24+Sr31*	*Lr24+Lr26*	*Yr9*
HD 2833	22+	;1	;	;1	;1	;1	0	5MRMS	*Sr24*	*Lr24*	—
HW 3083	;	0;	;	0	0;	;2	0	0	—	—	—
HW 2000	;2	;1	;1	;1	;1	;	0	0	—	—	—
HW 5013	;2	;1	;1	0;	;1	;2	0	0	*Sr24+Sr31*	*Lr24+Lr26*	*Yr9*

South America. This resistance is based on the *Sr2* gene complex, which actually consists of *Sr2* plus 4–5 minor genes pyramided into 3–4 gene combinations (Rajaram et al. 1988). *Sr2* alone behaves as a slow-rusting gene. Because there have been no major stem rust epidemic in areas where CIMMYT germ plasm is grown worldwide, the resistance shows promise to be durable also in India. In addition to having *Sr2* protection against black rust, the two cultivars HI 1531 and DL 788-2 also possess *Lr24*, a gene currently resistant to all Indian pathotypes of brown rust and capable of providing simultaneous protection. Fortunately, the *Lr24* gene is present in combination with *Lr26* in cultivars HW 3094 and HW 5013 of the South Hill Zone (Table 1), which is an area of inoculum source. Such a combination may act as an

impediment to risng of new races. The presence of *Sr2* in a majority of cultivars of the Peninsular Zone (Table 1, p. 81) guarantees averting yield losses in this zone in the future bacause of the proven durability of this gene.

In the Peninsular Zone, 16 popular wheat cultivars were evaluated for seedling and adult-stage resistance and 11, DDK 1001, DDK 1009 , NIAW 917, DDK 1025, UAS 415, NIAW 34, Raj 4083, HD 2781, K 9644, MACS 1967, and AKDW 2997-16, showed excellent resistance to Nilgiri flora of black and brown rust pathogens at both the stages (Table 1, p. 81). Three cultivars, Raj 4037, DWR 162, and MACS 2496, were either completely or partially susceptible at seedling stage to brown rust and also susceptible to Nilgiri pathotypes of brown rust pathogen at the adult stage. Thus, the resistance of these three cultivars should be improved or they should be discouraged from cultivation if occupying large acreages in the states of Maharashtra and Karnataka. Nevertheless, these three cultivars need to be retained in the germ plasm pool because of their utility as partially resistant lines for black rust at the adult-plant stage. Such a trait makes these genotypes excellent genetic stocks for deriving durable resistance either for direct cultivation or for incorporation into other high-yielding but susceptible cultivars. Still another genotype, DWR 195, is susceptible to the most predominate pathotype 77-5 (121R63-1) but only at seedling stage. This cultivar holds promise, because it is resistant to black rust at the seedling stage and possesses excellent partial resistance to both black and brown rusts giving it potential to become a durably resistant cultivar in Peninsular India.

Seedling and adult-plant reaction of eight wheat cultivars released for cultivation in the Southern Hill Zone are given in Table 1 (p. 81). All exhibited high levels of resistance (≤ 2 as seedlings and 0–5MR as adult plants) to the Nilgiri flora of both brown and black rusts. In the Southern Hill Zone, wheat is cultivated only in a few thousand ha in the hilly areas of southern Karnataka and parts of Tamil Nadu (Jag Shoran et al. 2009). Because these are the areas where host–pathogen contact is maintained continuously and selection pressure can favor pathogen survival, new, virulent mutants can emerge if host cultivars have single, major genes. Regarding black rust resistance of cultivars released for the Southern Hill Zone, the situation is comfortable because the majority possess more than one gene making them suitable for cultivation in this zone without imminent danger of new pathogenic variants emerging. Brown rust resistance, however, is worrysome with some of the cultivars, e.g., HW 1085, HW 2044, HW 2045, and HD 2833, because they possess only single genes, either *Lr19* or *Lr24*. No virulence for gene *Lr24* is known in India (Mishra et al. 2001), but its singular presence HW 1085 and HD 2833, which are recommended for cultivation in the Southern Indian hills may contribute to new pathogenic mutants by virtue of year round culture. These new variants may not be so threatening for wheat cultivation in South Indian Hills because less area is under wheat cultivation, but they may become a potential constraint in production of *Lr24*-containing wheats such as HI 1531 and DL 788-2 in the Central Zone. Thus, pyramiding more genes in cultivars with *Lr24* grown in the Southern Hill Zone is needed so that they can be cultivated more safely in the rust source areas of hilly Tamil Nadu and southern Karnataka. Such multigenic complexes of rust resistance genes may curtail the arisal of new pathogenic mutants.

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Two new wheat cultivars, Pusa-Navagiri and CoW(SW)2, released for cultivation in the Southern Hill Zone and the nontraditional areas of South India.

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The two disease-resistant, heat-tolerant, high-yielding wheat cultivars developed at IARI, Regional Station, Wellington, were released for cultivation under conditions in the Southern Hill Zone of India. The bread wheat HW 5207 (Pusa Navagiri) was released through All India Co-ordinated Wheat Improvement Progrmme and a *T. turgidum* subsp. *dicoccum* (Samba) wheat cultivar named HW 1095 and also known as CoW(SW)2 was released by Tamil Nadu Agricultural University, Coimbatore, as a state variety for cultivation in the Southern Hill Zone.

The Southern Hills are known as the main foci for leaf and stem rust inoculum to the plains of India. Hence, the development of high-yielding, rust-resistant wheat cultivars and their saturation in these areas is of national importance in order to arrest the dissemination of uredospores to the plains of India.

In the Southern Hill Zone, wheat is not grown commonly except in the areas adjoining Western and Eastern Ghats, which covers some districts of the west and north Tamil Nadu and southern Karnataka states, because of very short winters and unfavorable conditions for cultivation. These areas also have comparatively high temperatures, and the crop is damaged from high infections of Sclerotium foot rot.

The agro-ecological conditions in the Southern Hill Zone, high altitudes prone to frost damage, midaltitudes with erratic monsoon, and low hills with frequent water shortages during the short winters, prompted us to develop the early maturing, thermo-tolerant, rust- and foot-rot resistant bread wheat genotype HW5207. This bread wheat fits well in the local crop rotation with wider adaptability. HW 5207 has a yield potential up to 5.96 t/ha under need-based/restricted irrigation (up to five irrigations) and exhibiting remarkable resistance to all three rusts. Because HW 5207 matures in 100–102 days, it could become a choice and alternative crop for the resource-poor farmers in the areas where erratic and unpredictable northeastern monsoons occur. HW 5207 consistently yields under varied levels of irrigation and has a 32.5% yield advantage over control cultivars under two irrigation levels. HW5207 will ensure both grain and fodder for sustaining the livelihood of resource-poor farmers.

Salient features of the proposed cutlivar HW 5207.

- The genotype HW 5207 (Pusa navagiri) recorded the highest mean grain yield (52.1 q/ha) over the best check COW(W)1(48.75 q/ha) over the testing period. The superiority yield ranged from 7–18%.
- HW 5207 ranked in the first nonsignificant group eight out of 12 times (66.6%) over four years of testing at different locations indicating its wider adaptability and stability in its performance.
- HW 5207 exhibited a high degree of resistance to stem, leaf, and stripe rusts under both artificial and natural epidemic conditions against all the pathotypes occurring in the Nilgiris. The resistance to rusts and powdery mildew is attributed to the likely presence of a combination of genes, *Sr2* (based on the presence of pseudo-black chaff, tightly linked to *Sr2*), *Sr31*, and *Sr24* for stem rust; *Lr24* and *Lr26* for leaf rust; *Yr9* and *Yr15* for yellow rust; and *Pm8* for powdery mildew. These genes likely were derived from the parents involved in the cross.
- HW 5207 yielded consistently higher over the best check HW 2044 when tested at more locations in areas adjoining the Nilgiri and Palani Nills and nontraditional areas, indicating its elasticity.
- HW 5207 recorded highest mean grain yield of 58.7 q/ha under two irrigation levels in trials as compared to the best check HW 2044 . The over-all gain with two irrigations is 32.5%, which is the most favorable feature of the cultivar. The 12.1% advantage in mean yield obtained over HW 2044 under different irrigation levels indicats an ability for increased yield under varied soil moisture levels.
- HW 5027 has the ideal plant height (90 cm) with strong and resilient stems that provide resistance to lodging. The very nutritious grain registers 40.5 g mean test weight with > 11% protein and a high levels of iron (53.1 ppm), zinc (46.3 ppm), copper (5.33 ppm), and manganese (47.5 ppm) when compared to the checks indicating the nutritional quality of the grain it produces. In addition, HW 5027 has high scores for bread-making quality (7 out of 10), chapatti quality (7.42 out of 10), a *Glu-1* score of 8 out 10, mean sedimentation value of 45.5, and a high hectolitre weight of 78.3 (kg/hl).

Cultivation of HW 5207 will provide an alternative to HW 2044 and Cow(w)1 and create additional genetic diversity to contain rust from the foci of rust inoculum and will have an added yield advantage as HW5207 shown better adaptability; suit cultivation in high altitudes, at middle elevations, and in lower hills as well as areas adjoining the hills; offer protection against the prevailing rusts and minor foliar diseases such as leaf blight, powdery mildew, and Sclerotium foot rot under field conditions; produce more grain (50 q/ha) along with fodder ensuring farm sustainability; and confer a high degree of resistance at field level in the zone, which could be attributed to the likely presence of *Lr24+Sr24*, *Sr31+Lr26+Yr9+Pm8*, and *Yr15* possibly derived from the parents involved in the cross, evidenced from the Seedling Response Test. In addition, the presence of prominent pseudo-black chaff, which is tightly linked to *Sr2* (a race nonspecific APR gene), in combination with other stem rust genes is expected to offer durable resistance against the most frequent pathotypes of rust in the Southern Hill Zone, a hot spot for foliar diseases of wheat in India.

Release of HW 1095, a semidwarf dicoccum as CoW(SW)2.

HW 1095, a semidwarf, disease-resistant, nutritionally rich, economically viable and high yielding dicoccum (Samba wheat) wheat developed at IARI, Regional Station, Wellington, using mutation techniques, is released for parts of Tamil Nadu and the Southern Hill Zone, including nontraditional areas, in collaboration with Tamil Nadu Agricultural University, Coimbatore, as state release. Wheat is one of the most important cereal crops in the world, ensureing food security to humankind. Although as many as 18 species of wheat were described and recognized by Percival (1921). only a few are of importance in agriculture. India is one of the very few countries in the world that cultivates all three important commercially cultivated species of wheat, *T. aestivum* subps. *aestivum* (common bread or chappati wheat), *T. turgidum* subsp. *durum* (macaroni or durum wheat), and *T. turgidum* subsp. *dicoccum* (emmer, dicoccum, or Samba wheat). Bread wheat is the most important species accounting for a little over 87% of the total wheat production in India followed by durum (about 12%) and dicoccum (about 1%). Unlike aestivum and durum wheat, dicoccum wheat is grown on only limited acreage in Tamil Nadu, Karnataka, and parts of Maharastra. Even today, a considerable area under dicoccum can be found in the northwestern Tamil Nadu, Karnataka, Maharastra, and parts of Andhra Pradesh states. The farmers have preserved this wheat species becaues of its nutritional, nonshattering, and drought-tolerant traits. Currently, the tall land races that were released as NP 200, NP201, and NP 202, from IARI, Wellington, during 1960s are under cultivation in the southern Indian states for the traditional food preparation are made from dicoccum.

Incorporating dietary fiber-rich, dicoccum, whole-wheat flour in the regular diet of a diabetic significantly reduced total lipids ($p \leq 0.01$), triglycerides ($p \leq 0.01$), and LDL cholesterol ($p \leq 0.05$) (Yenagi N et al. 2001). Dicoccum wheat has therapeutic properties that can effectively reduce the cardiovascular risk factors. Managing diabetes, a life-long ailment, with medicine is very expensive and a dicoccum diet plays a crucial role in reducing the levels of plasma cholesterol and lowering glycemic response. The hulled grain of dicoccum wheat is used mainly in the alternative or health food markets. Most of the suggested beneficial effects of this cereal is from the specific characteristics of the fiber. Pyrolysis fragments derived from the polysaccharide fraction were significantly more abundant in dicoccum than in the other genotypes, whereas the highest percentage of lignin-derived pyrolysis fragments was detected in durum wheat. Results suggest that dicoccum genetic material may represent a source of high-value dietary fiber; dicoccum is much higher in fiber than common wheat. Future wheat-breeding programs should aim to preserve such characters.

In India, first three dicoccum cultivars, NP 200, NP 201, and NP 202, which were selected from Rishi Valley collections in Andhra Pradesh, were released for commercial cultivation during 1960s from the IARI Regional Station, Wellington. These cultivars are tall, tend to lodge, and are susceptible to yellow rust. Attempts were made to develop semidwarf dicoccum cultivars using dwarfing gene(s) derived from closely related tetraploid durum species, and a number of semidwarf cultivars were released from the University of Agricultural Sciences, Dharwad (DDK 1001, DDK 1009, DDK 1026, and DDK 1029) and from the Agharkar Research Institute, Pune. Although the dwarfing gene(s) derived from durum helped in developing semidwarf dicoccum wheats, most of them are now susceptible to yellow, particularly against pathotype 'I' (38S102) prevalent in the Southern Hills, and also produced undesirable end-product, grain traits, such as slightly sticky, reduced-quality fiber Rawa 'Uppuma', and were less preferred by the millers.

Therefore, a meticulously planned, dicoccum-improvement program was undertaken at IARI, Wellington, during 2002 for developing semidwarf dicoccum wheats without altering the quality of NP200, NP 201, and NP 202 by mutation breeding. Gamma irradiation of 10 (100 Gy (Gray is the unit of absorbed dose and is 1 Joul/kg)), 20 (200 Gy), 30 (300 Gy), and 40 (400 Gy) Kr γ-rays was given at optimal seed moisture levels. The irradiated seed were sown as M_1

and desirable plants were selected in the M^2 at 200 Gy dose. A stable population was fixed at M_4 that was entered into the All India Co-ordinated Trials as HW 1095 in 2005.

The salient features of HW 1095 (released as CoW(SW)2).

– dicoccum wheat HW 1095 developed at IARI, Regional Station, Wellington, is a NP200-mutant through gamma irradiation (200 Gray) maturing in 110 days, belonging to the early duration group.
– Culture HW 1095 recorded a mean grain yield of 4,040 kg/ha, which is an increase of 26% over NP 200 in a total of 98 trials over the past five years. NP 200 was used as a check. The yield of NP 200 was 3,190 kg/ha.
– Culture HW 1095 has 10–12 productive tillers with long and slightly tapering ears. A special attribute of this culture is the broad and waxy green foliage, drooping leaves, lodging resistance, and nonshattering grains. Rich in protein (13.2%) with a high sedimentation value (25), the reddish colored grain provides a good grain appearance and score of 8.
– The culture is resistant to black (stem), yellow (stripe), and brown (leaf) rusts. No major incidence of pests occurred in this Samba wheat culture. In view of a high and stable yield performance over locations and resistance to leaf and stem rust diseases, the culture HW 1095 is proposed for release as wheat COW (SW) 2 in collaboration with Department of Millets, Tamil Nadu Agricultural University, Coimbatore, as state release.
– The released cultivar HW 1095-CoW(SW)2 was significantly superior in yield over NP 200 and DDK 1029 during the testing period.
– HW 1095 occurred 11/18 times in first nonsignificant group indicating wider adaptability and stability in performance across zones.

The release of this Samba wheat CoW(SW)2 is likely to boost the re-introduction of dicoccum wheat in the traditional dicoccum belt. In addition, resource-poor farmers will earn a better livelihood, because dicoccum grain garners a higher price in the market than other types of wheat. Our efforts at IARI, Wellington, now are to improve NP201 and NP202, and of these, one promising entry HW 1098 already has been entered in AICWIP Co-ordinated Trials.

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A protein marker as a tool to detect the Secale cereale-derived linked genes Sr31, Lr26, Yr9, and Pm8 genes in wheat.

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Introduction. Much of the widely adapted wheat germ plasm generated and distributed by CIMMYT throughout the spring wheat production areas in low latitude countries carry a T1BL·1RS translocation. The wheat-breeding community has relied particularly on the use of the *Sr31* gene derived from wheat–rye hybrid derivatives produced in Germany in the 1930s (Mettin et al. 1973; Zeller 1973) that gave continued protection against stem rust worldwide. The T1BL·1RS segment carries genes for resistance to three rusts, *Sr31*, *Lr26*, and *Yr9*, and *Pm8* for resistance to powdery mildew (Zeller 1973). However, in many genetic backgrounds, especially wheat lines of CIMMYT origin, the expression of *Pm8* is suppressed by a gene(s) located in chromosome 1A (Ren et al. 1997) or 7D (Zeller et al. 1993). In addition, the translocation may contribute positively to agronomic traits such as yield and drought tolerance (Rajaram et al. 1983). On the negative side, wheat lines with the translocation generally produce lower quality flour than their non-T1BL·1 RS counterparts (Dhaliwal et al. 1987), indicating that the rye genes present are responsible for low gluten quality.

Singh et al. (1990) used SDS–PAGE to examine the genetic linkage between the genes controlling secalins (*Sec-1*) and those for resistance to the three rust diseases. The rust resistance genes are located 5.4±1.7 cM from the *Sec-1* locus, suggesting a close linkage (Afshari 2006). Because of the lack of pairing between the wheat and rye chromatin (IB and TIBL·IRS) in a wheat background, *Sec-1* acts as a marker for *Sr31*, *Lr26*, *Yr9*, and *Pm8*.

The ineffectiveness of *Sr31* against the new stem rust race Ug99 (Singh et al. 2004, 2006), which threatens wheat grain production worldwide, offers much hope to diversify the genetic base of the cultivar by pyramiding effective genes with or without *Sr31*.

The six Indian popular wheat cultivars, HD 2329, HD 2285, HP 1205, WH 147, J 24, and Lok-1, already with *Sr24+Lr24* that were introgressed with the *Sr31* gene complex through conventional backcross methods, were obtained for the confirmation of the presence of *Sr31*.

For the molecular analysis, protein was extracted using a protein-extraction buffer and separated in a vertical dual-gel unit (Sigma-Aldrich). Electrophoresis was at a constant 30 mA or until the bromophenol blue dye migrated to 1.5–2 cm above the gel base. SDS–PAGE used Laemmli (1970) buffer. The gel was then rinsed with distilled water and destained in 10% (v/v) acetic acid and 30% (v/v) methanol for 20 minutes, followed by washing in distilled water for 50 minutes with gentle shaking. The protein bands were documented on a digital gel documentation unit. The data on phenotyping of the constituted lines was done at IARI, Regional Station, Wellington.

Results and discussion. The SDS–PAGE procedure revealed patterns of water-soluble proteins that detected the T1BL·1RS translocation in wheat cultivars. The SDS–PAGE results showed that all the wheat stocks introgressed with the *S. cereale*-derived, linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8*, HW 4042 (HD 2329 with *Lr28*), HW 4044 (Lok-1 with *Lr28*), HW 4047 (WH 147 with *Lr28*), HW 4049 (HD 2285 with *Lr28*), and HW 4062 (J 24 with *Lr28*), carried the *Sec-1* band and the presence of the linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8* thus confirming the T1BL·1RS translocation. The recurrent parent HP 1205 also with the *Sr31* gene complex shows the *Sec-1* band. The protein bands corresponded to the secalins of the rye parent, which were present in the wheat cultivars carrying T1B·1R translocation. The *Sec-1* band was not found in the recurrent parents HD 2329, HD 2285, WH 147, J 24, and Lok-1, which do not have *Sr31* and suggesting the absence of the T1B·1R translocation. The lines pyramided with *T. ponticum*-derived linked genes *Lr24+Sr24*, and the *S. cereale*-derived gene comples are expected to yield better than the recurrent parent under field conditions.

Table 2. Adult-plant response to black (Sr), brown (Lr), and yellow (Yr) rust and powdery mildew (Pm, 0–4 scale) diseases in wheat genotypes that carry specific rust-resistance genes and their recurrent parents.

Stock	Back-ground of recurrent parent	Genes	Adult-plant response			
			Sr	Lr	Yr	Pm
HW 2037	HD 2329	*Lr28*	90S	F	90S	2
HW 4042	HD 2329	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	10R–MR	F	F	3
HW 2038	HD 2285	*Lr28*	50MS–S	F	30S	2
HW 4049	HD 2285	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	10R–MR	F	F	3
HW 2036	J 24	*Lr28*	90S	F	100S	2
HW 4062	J 24	*Sr25*, *Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	20R–MR	F	F	4
HW 2032	Lok-1	*Lr28*	90S	F	80S	3
HW 4044	Lok-1	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	15R–MR	F	F	3
HW 2033	WH 147	*Lr28*	100S	F	90S	2
HW 4047	WH 147	*Sr31*, *Lr26*, *Yr9*, *Pm8*, and *Lr28*	15R–MR	F	F	3
HW 4444	HP 1205	*Sr25+Lr19*	30MS–S	F	90S	4
	HP 1205	*Sr25+Lr19*, *Sr31*, *Lr26*, *Yr9*, and *Pm8*	F	F	F	3

The phenotyping data (Table 2) showed that the recurrent parents HW 2037, HW 2036, HW 2032, and HW 2033 (all carrying the *Ae. speltoides*-derived leaf rust resistance gene *Lr28*) were highly susceptibility to all stem and stripe rusts, except HW 2038, which was attributed to the presence of the *Sr8+Sr9b+Sr11* gene complex. However, HW 4444 in the background of HP 1205 showed resistance to leaf and stem rust because of the presence of *Lr19+Sr25*. The stocks HW 4042, HW 4049, HW 4062, HW 4044, HW 4047, and HW 4444 with *Sr31*, *Lr26*, *Yr9*, and *Pm8* from *S. cereale* clearly showed remarkable resistance against all three rusts. The *Sec-1* band clearly demonstrates and confirms that these lines carry *S. cereale*-derived, *Sr31*+gene complex.

Because *Sec-1* is tightly linked with the three rust resistance genes, SDS–PAGE is a useful method to identify and confirm the presence of rye chromatin and the three genes. The protein marker band associated with *Sec-1* is 5.4±1.7 cM from the linked genes *Sr31*, *Lr26*, *Yr9*, and *Pm8* and can be exploited for detecting the T1RS·1BL translocation and developing lines with or without the *Sr31* gene complex (Fig 1.). Because *Sr31* is not effective against the emerging threat posed by the Ug99 stem rust pathotype and associated with poor gluten quality, this technique can be used to select lines without *Sr31*. *Sec-1* can be introgressed with other effective stem rust resistance genes such as *Sr24* (virulent pathotype 40-1 already reported from India), *Sr25*, *Sr26*, or *Sr27* for developing cultivars that produce better quality flour. Otherwise, *Sec-1* can be pyramided with other effective stem rust gene(s) to exploit the positive yield traits associated with the *Sr31* gene complex. The *Sec-1* marker will be a quick and economical method for screening large numbers of wheat germ plasm lines for the presence of *Sr31* in the laboratory without any greenhouse facility in a short period of time.

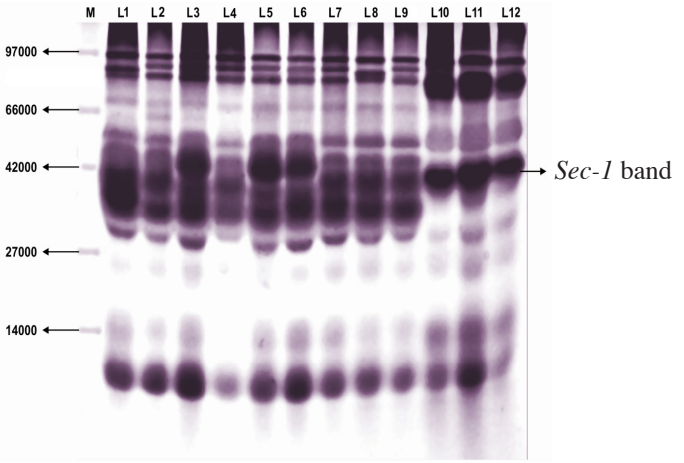

Fig. 1. Banding patterns of seed protein extracts from wheat stocks and various controls subjected to SDS-PAGE eletcrophoresis (lanes L to R: M, marker (14–97 Kda); L1, HW 4444 (+); L2, WH 542 (donor) (+); L3, HW 4049 (+); L4, HW4042 (+); L5, HW 2038 (rye parent) (–); L6, HW 2037 (Recurrent parent) (–); L7, HW 4062 (+); L8, HW 4044 (+); L9, HW 4047 (+); L10, R–1 (+); L11, R–2 (+); and L12, R–4 (+). The presence or absence of the Sec-1 band the presence or absence of T1BL·1RS is indicated by (+) and (–), respectively.

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Developing elite, durable disease resistant wheat cultivars combining high grain yield and end-use quality by introgressing effective genes employing conventional and modern breeding approaches.

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Introduction. A meticulously planned, wheat-improvement program employing back-cross methodology to introgress effective rust and powdery mildew resistance genes was initiated during late eighties and early nineties. Popular Indian bread wheat and dicoccum wheat cultivars were used. The reference stocks (RILs) obtained were initially evaluated for resistance, and only effective genes conferring resistance to existing pathotypes were taken for the program. The effec-

tive resistance genes were introgressed initially through a conventional back-cross hybridization method taking advantage of Wellington where in all three rusts and other foliar diseases occur on a susceptible line throughout the year and is considered as natural 'hot spot'. Later, when markers were made available, both conventional and MAS approaches are used. Initially, the number of backcrosses effected were 8–9, but now we stop with BC_3. For molecular confirmation, the mapping populations were used at the BC_1F_2 stage.

Alien rust-resistance genes in the back-cross program at IARI, Wellington (Table 3, p. 89).

Stem rust resistance genes:	*Sr2* (linked to pseudo-black chaff (*Pbc*)), *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr27* (linked to apical claw on spike), *Sr29*, *Sr30*, *Sr31*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr38*, *Sr39*, *Sr42*, and *Sr43*.
Leaf rust resistance genes:	*Lr9* (not effective in India), *Lr19* (new virulence reported), *Lr24*, *Lr26* (not effective in India), *Lr28*, *Lr32*, *Lr34* (adult-plant resistance (APR) is race nonspecific and linked to leaf tip necrosis), *Lr35* (APR), *Lr37*, *Lr39*, *Lr40*, *Lr41*, *Lr42*, *Lr45* (linked to pink awn/glume at milk stage under low temperature), *Lr46* (APR, race nonspecific), *Lr47*, *Lr48*, *Lr49*, *Lr53*, and *Lr57*.
Stripe rust resistance genes:	*Yr9*, *Yr10*, *Yr15*, *Yr16*, *Yr17*, *Yr18*, *Yr24*, *Yr25*, *Yr26*, *Yr29*, *Yr30*, *Yr35*, and *Yr40*.
Powdery mildew resistance genes:	*Pm6*, *Pm8*, *Pm38*, and *Pm39*

Pleiotropic or closely linked to genes (race nonspecific) exploited that are effective to other diseases include *Lr34*/*Yr18*/*Pm38*/*Bdv1*/*Sr* resistance/*Ltn*, *Lr46*/*Yr29*/*Pm39*/*Ltn*, and *Sr2*/*Yr30*/(*Lr27*)/*Pbc*.

Linked genes that are exploited include *Lr19*+*Sr25*, *Lr24*+*Sr24*, *Yr30*+*Sr2*+*Lr27*, *Lr26**+*Yr9*+*Sr31*+*Pm8*, *Lr37**+*Yr17*+*Sr38*, and *Sr39*+*Lr35*.

Pyramiding of effective stem rust-resistance genes currently under progress to over come threat from Ug99 and its variants of stem rust race virulent on *Sr31*, *Sr24*, and *Sr36* virulence spectrum of Ug99 (TTKSK). Genes that currently are effective against Ug99 are *Sr25* (*Lophopyrum ponticum*); *Sr28* [1], *Sr29* [2], and *SrTmp* [1] (*T. aestivum* subsp. *aestivum*); *Sr2*, *Sr13* [1,2], and *Sr14* [1] (*T. turgidum* subsp. *turgidum*); *Sr22* and *Sr35* (*T. monococcum* subsp. *monococcum*); *Sr36* [1] and *Sr37* (*T. timopheevii* subsp. *timopheevii*); *Sr32* and *Sr39* (*Ae. speltoides*); *Sr33* [2] and *Sr45* (*Ae. tauschii*); *Sr40* (*T. timopheevii* subsp. *armeniacum*); *Sr26* and *Sr43* (*Th. elongatum*); *Sr44* (*Th. intermedium*); and *Sr27* [1] and *Sr1A·1R* [1] (*S. cereale*). For genes marked with a [1], virulence for the gene is known to occur in other races; for those with a [2], the level of resistance conferred in the field usually insufficient (Singh et al 2008).

Markers available in public domain used at the Indian Agricultural Research Institute, Regional Station, Wellington. Stem rust: *Sr1A*, *Sr2*, *Sr9a*, *Sr11*, *Sr13*, *Sr14*, *Sr15*, *Sr17*, *Sr19*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr28*, *Sr29*, *Sr31*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr37*, *Sr38*, *Sr39*, *Sr40*, *Sr43*, *Sr44*, *Sr45*, *Sr46*, *SrR*, *SrTmp*, *SrTt3*, and *SrD5*; leaf rust: *Lr19*, *Lr24*, *Lr28*, *Lr32*, *Lr35*, *Lr37*, *Lr39*, *Lr26*, *Lr47*, *Lr50*, and *Lr51*; and yellow rust: *Yr9*, *Yr10*, *Yr15*, *Yr17*, *Yr18*, *Yr26*, and *Yr28* (Bariana et al. 2007).

Accomplishments.

- Combinations of *Sr24*+*Sr25, Sr25*+*Sr26, Sr25*+*Sr27*, *Sr25*+*Sr36*, *Sr25*+*Sr38*, *Sr24*+*Sr26*, *Sr24*+*Sr27*, and *Sr24*+*Sr36* are pyramided with *Yr10* in at least 20 adapted Indian bread wheat cultivars and the material is ready for sharing. Even stocks with *Lr19*+*Sr25*+*Sr36*+*Pm6* and *Yr15*, which are free from leaf, stem, and stripe rusts and powdery mildew have been developed and published (Table 4, pp. 90-91).
- Popular Indian bread wheat cultivars with *Lr24*+*Sr24* and *Lr19*+*Sr25* along with *Sr36*+*Pm6*, *Lr28*, and *Lr37* developed in 20 cultivar backgrounds have been completed and published.
- Corrective crosses for *Lr19*+*Sr25* where Sunstar was used are using 'wheatear'.
- Corrective crosses for *Lr32* (Thatcher *Lr32*) also is in progress at the BC_3F_2 stage.
- Incorporated of new leaf rust genes *Lr35*+*Sr39* (during Kharif 2010), *Lr39* (BC_3), *Lr42*, *Lr44*, *Lr45* (at BC_3F_3 stage) in 28 popular Indian bread wheat cultivars.
- Current efforts to incorporate/pyramid *Lr46*, *Lr47*, *Lr48*, and *Lr57* in combination with *Yr10* and *Yr15*.
- Pyramiding of *Sr24* with *Sr31*, *Lr19*+*Sr25* with *Sr31*, and *Lr19*+*Sr25* with *Lr24*+*Sr24* completed in 20 popular cultivars and published.
- *Lr28*, *Lr32*, and *Lr37* with *Sr36*+*Pm6* in 20 popular cultivars complete.

Table 3. Effective rust-resistance genes used in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington (* reference stock attributes are listed in Table 4, pp. 90-91).

Gene	Source	Reference stock used*	Chromosome location
Lr9 (ineffective at Wellington since 1995)	*Ae. umbellulata*	Abe	6BL
Lr19+Sr25, *Sr36+Pm6* (77-8 race reported in Peninsular Zone, India, during 2008)	*Th. ponticum*	Sunstar and Cook and now wheatear	7DL
Lr24+Sr24 (40-1 race reported in Wellington on *Sr24*)	*Th. ponticum*	Tr380-14*7/3Ag#14 Janz, Sunleg, RL6064, Agent	3DL
Lr26+Sr31+Yr9+Pm8 (77-1 race reported from Wellington for *Lr26*)	*S. cereale* (Petkus rye)	WH 542 (Bucanora)	T1BL1RS
Lr28	*Ae. speltoides*	CS 2A/2M 4/2	4AL
Lr32	*Ae. tauschii*	C86-8/KalyansonaF$_4$/ Thatcher *Lr32*	3DS
Lr34+Yr18+BDV1 Pm38+Sr resistance/*Ltn* (APR race nonspecific)	*T. aestivum* subsp. *aestivum* cultivar Terenizo	RL6058	7DS
Lr35+Sr39	*Ae. speltoides*	Thatcher+*Lr35*	2B
Lr37+Sr38+Yr17	*Ae. ventricosa*	Thatcher*8/VPM1, RL6081	2AS
Lr39	*Ae. tauschii*	KS92WGRC15, EZ 350692	2DS
Lr40	*Ae. tauschii*	LC+*Lr40*, KS89WGRC07	1D
Lr41	*Ae. tauschii*	EC381200, KS90WGRC10	2DS
Lr42	*Ae. tauschii*	EC381201, KS91WGRC11	1D
Lr44	*T. aestivum* subsp. *spelta*	EC381202, RL6147	1BL
Lr45	*S cereale* (Imperial rye)	EC 381203, RL6144	TAS·2R
Lr46	*T. aestivum* subsp. *aestivum*	Pavon 76, Dimond Bird	1BL
Lr47	*Ae. speltoides*	Pavon 7 S3 Lr47, KS90H450	7AS
Sr2+Lr27+Yr30+Pbc (pseudo-black chaff)	*T. aestivum* subsp. *aestivum*	Maden, Lok-1, HW 5207	3BS
Sr22 (APR)	*T. monococcum* subsp. *monococcum*		7AL
Sr24	*Th. ponticum*	Tr380-14*7/3Ag#14	3DL
Sr25+Lr19+Sr36+Pm6	*Th. ponticum*		7DL
Sr26	*Th. ponticum*	DARF*6/3Ag3/Kite	6AL
Sr27	*S cereale* (Imperial rye)	Kalyanasona*4/*Sr27*	3A
Sr29	*T. aestivum* subsp. *aestivum*	Pusa 4/Etoile de choisy	6DL
Sr30	*T. aestivum* subsp. *aestivum*	BtSr30Wst	5DL
Sr32	*Ae. speltoides*	CnsSr32 AS	2A, 2B, 2AS
Sr33	*Ae. tauschii*	RL5405	1DL, 1DS
Sr35	*T. monococcum* subsp. *monococcum*	Mq(2)/5*G2919	3AL
Sr36+pm6	*T. timopheevii* subsp. *timopheevii*	Cook*6/C 80-1	2BS
Sr38	*Ae. ventricosa*	Thatcher*8/VPM1, RL6081	2AS
Sr39	*Ae. speltoides* (APR)	Thatcher+*Lr35*	2B
Sr42	*T. aestivum* subsp. *aestivum*	EC381206	6DS
Sr43	*Th. ponticum*	EC381210	7DL
Sr44	*Th. ponticum*		7AS?, 7DS
Yr10	*T. aestivum* subsp. *spelta*	Moro, *Yr10*+WH 542	1BS
Yr15	*T. turgidum* subsp. *dicoccoides*	*T. dicocoides* G-25	1BL
Yr16	Capelle-Desprez	Capelle-Desprez	2DS
Yr17	*Ae. ventricosa*	Thatcher*8/VPM1, RL6081	2AS
Pm6	*T. timopheevii* subsp. *timopheevii*	Cook*6/C 80-1, Abe	2BS

Table 4. *Triticum aestivum* subsp. *aestivum* donor parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s)	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew
Abe	*Lr9 Sr36* (Not effective in India)	15R MR	F	40S	1
Sunstar*6/C80-1 (molecularly confirmed not carrying *Lr19*, 'wheatear' used now)	*Lr19 Sr25*	10R MR–30R MR	F	F	4
	Lr19+Sr25	F	F	10MR–MS	3
Cook*6/C 80-1	*Lr19 Sr25 Sr36 Pm6*	F	F	F	1
Tr380-14*7/3Ag#14	*Lr24 Sr24* (*Sr24* not effective in India)	15R MR	F	5MR	2+
DARF*6/3Ag3/Kite	*Lr24 Sr24 Sr26*	10R MR–20R MR	F	10MS	3
WH 542	*Lr26* (not effective in India) *Sr31 Yr9 Pm8*	10R MR	80S	F	3
CS 2A/2M 4/2	Lr28 Sr34 Yr8	90S	F	F	0–1
C86-8/Kalyansona F_4 (not carrying *Lr32*; Thatcher Lr32 used now	*Lr32*	70S	F	90S	3
	Lr32	60S	F	20S	2
RL6058	*Lr 34 Yr18 BDV1 Pm38*	F	30MR–MS	F	0–1
Thatcher+*Lr 35*	*Lr35* (Race specific APR) *Sr39*	F	F	F	2
Thatcher*8/VPM1, RL6081	*Lr37 Sr38 Yr17*	20R MR MS	F	15MS	4
KS92WGRC15, EZ350692	*Lr39*	40S	F	F	2
LC+*Lr40*	*Lr40*	S	S	F	2
EC381200	*Lr41*	5S	F	30S	3
EC381201	*Lr42*	F	F	40S	3
KS92WGRC16	*Lr43*	F	F	40S	2
EC381202	*Lr44*	20S	20S	F	2
EC381203	*Lr45*	S	F	S	3
Pavon 76	*Lr46*		20MS		
Pavon	*Lr47*	F	F	10S	2
Tr380-14*7/3Ag#14	*Sr24 Lr24*	15R MR	F	5MR	2+
DARF*6/3Ag3/Kite	*Sr24 Sr26 Lr24*	10R MR–20R MR	F	10MS	3
Sunstar*6/C80-1 (molecularly confirmed not carrying *Lr19*, 'wheatear' used now)	*Sr25 Lr19*	10R MR-30R MR	F	F	4
Cook*6/C 80-1	*Sr25 Sr36 Lr19 Pm6*	F	F	F	1
Kalyanasona*4/Sr27	*Sr27*	F–Tr	80S	90S	3
Pusa 4/Etoile de Choisy	*Sr 29*	F			
BtSr30Wst	*Sr 30*	F			
WH 542	*Sr31 Lr26 Yr9 Pm8*	10R MR	80S	F	3
CnsSr 32 AS	*Sr 32*	F			
RL5405	*Sr33*	F			
CS 2A/2M 4/2	*Sr34*	90S	F	F	0–1
Mq(2)/5*G2919	*Sr35*	F			
Abe	*Sr36*	15R MR	F	40S	1
	Sr37	F	80S	30S	2
Thatcher*8/VPM 1,RL 6081	*Sr38*	20R MR MS	F	15MS	4

Table 4 (continued). *Triticum aestivum* subsp. *aestivum* donor parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s)	Reaction to (adult-plant response)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew
EC381198	*Sr38*	F	F	F	4
Thatcher+*Lr35*	*Sr39*	F	F	F	2
EC381204	*Sr39*	F	F	F	2
RL6087	*Sr40*	F	60S	F	2
EC381206	*Sr42*	F	40S	5S	2
EC381210	*Sr43*	F	80S	F	1
CS 2A/2M 4/2	*Yr8 Lr28 Sr34*	90S	F	F	0–1
WH 542	*Yr9 Lr26 Sr31 Pm8*	10R MR	80S	F	3
Moro, WH 542	*Yr10*	F	F	F	0–1
T. dicocoides G-25	*Yr15*	F	F	F	0–1
Capelle-Desprez	*Yr16*	F	F	F	0–1
Thatcher*8/VPM1, RL6081	*Yr17 Lr37 Sr38*	20R MR MS	F	15MS	4
EC463655	*Yr17*	F	90S	F	NA
EC463057	*Yr24*	F	40S	20S	NA
EC463658	*Yr26*	F	20S	30S	NA

Table 5. Number wheat cultivars released for commercial use developed through the alien gene backcross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Cultivar	Pedigree	Year of release	Release target zone
HW 2004 (Amar)	C 306//Tr 380-14*7//3 Ag # 14	1997	Central zone, rainfed
HW 1085 (Bhavani)	HW 2002A//CPAN 3057	1998	Southern Hill Zone, medium fertility, timely sown
HW 2044 (Kurinji)	PBW 226*5//Sunstar*6/C 80 -1	2000	Southern Hill Zone, medium fertility, timely sown
HW 2045 (Kaushambi)	HD2402*5//Sunstar*6/C80-1	2003	North Eastern Plain Zone, late sown
HS 375 (HIMGIRI) (In collaboration)	BB/G11/CJ 71/3/TAEST//KAL/BB	2003	Northern Hill Zone, very high altitude, timely sown
HS 420 (Shivalik) (In collaboration)	RAJ3302//cmh 73a-49*7/3*CNO 79	2003	Northern Hill Zone, late sown
HD 2833 (In collaboration)	PBW 226/HW 1042 (Tr 380-14*7/3 Ag#14)// HD 2285	2005–06	Peninsular Zone
MACS 6145 (HW 2034) (In collaboration)	C 306*9/CS 2A/2M*4/2	2004	North Eastern Plain Zone, rainfed
COW(W) 1 (HW 3094) (In collaboration)	HD 2646//HW 2002A/CPAN 3057	2004	Areas adjoining Southern Hills and hills in Tamil Nadu/Karnataka (wheat for warmer areas)
HW 5207 (Pusa Navagiri)	HW 3029//*Yr15*	2009–10	Southern Hill Zone, medium fertility, timely sown
Hw 1095 as CoW(SW)2 (Dicoccum)	NP200 - Mutant through Gamma Irradiation (y)(200 Gray)	2010	Areas adjoining Southern Hills and hills in Tamil Nadu/Karnataka (wheat for warmer areas)

Targeted breeding program to tackle the Ug99 threat accomplishments.

– Introgression of pyramided genes involving *Sr2* and *Sr22* with *Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr29*, *Sr30*, *Sr33*, *Sr35*, *Sr36*, and *Sr44* in at least 20 important, currently popular cultivars across the zones is under progress, many

Table 6. *Triticum aestivum* subsp. *aestivum* recurrent parents in the back-cross program at the Indian Agricultural Research Institute, Regional Station, Wellington.

Stock	Gene(s) already carrying	Reaction to (adult-plant respone)			
		Stem rust	Leaf rust	Stripe rust	Powdery mildew (0–4 scale)
C 306	*Lr34+Yr18+BDV1+Pm38+Sr* resistance/*Ltn* (unknown resistance gene for yellow rust)	90S	90S	F	3
HD 2009		40S	60S	100S	3
HD 2285	*Lr23+Sr9b+Sr11+Yr2*	30MS	100S	30S	3
HD 2329	*Lr13+Lr10+Lr34*, *Sr8+Sr9b+Sr11+Yr2+Yr18*	80S	90S	90S	3
HD 2402	*Lr34*+ unknown resistance gene for yellow rust	30S	100S	F	3
HD 2687	*Sr31 Lr26 Yr9 Pm8*	15R MR	80S	F	3
HI 1077	*Lr14a*	30MS S	50S	40S	3
HS 240	Sr31 Lr26 Yr9 Pm8	5R MR	70S	F	3
HUW 234	*Lr14a+Sr9b+Sr11+Yr2*+(Ks) and *Sr31 Lr26 Yr9 Pm8*	20MS S	100S	F	3
J 24		90S	100S	100S	3
Kalyansona	*Yr2*	80S	90S	90S	3
Lok-1	*Lr13+Sr2+Sr9b+Sr11+Yr18*	70S	80S	80S	3
NI 5439	*Lr34+Yr18+BDV1+Pm38+Sr* resistance/*Ltn* and *Sr11+Yr2*	90S	90S	100S	3
PBW 226		20S	90S	F	3
Sonalika	*Lr11* and *Lr13* (Gupta et al. 1984; Rao et al. 2001)	60S	80S	60S	3
UP 262		50S	50S	50S	3
UP 2338	*Lr26+Lr34+Sr31+Yr9+Yr18*	10MR	60S	F	3
VL 421		60S	90S	80S	3
WH 147	*Lr34*	90S	90S	90S	3
WH 542	*Lr34*, *Sr31 Lr26 Yr9 Pm8*	10R MR	80S	F	3
WL 711	*Lr11* and *Lr13* (Gupta et al. 1984; Rao et al. 2001)	100S	100S	90S	3
HI 977		F	60S	40S	2
HP 1205		60SS	80SS	90S	3
PBN 51		20MR	40S	S	2
PBW 343	*Lr34*	20MR	60S	5S	3
Raj 3077		5MR	60SS	60SS	1
HD 2877	*Sr31*	5MR	40SS	F	3
HW 3070	*Lr24+Sr24*, *Sr31*	F	F	10MR-10S	2
HD 2733	*Sr31*	20MR	60S	F	3

at BC_2 stage in Rabi 2009–10.
– Simultaneous molecular confirmations are under taken
– More than 400 near isogeneic lines carrying various specific rust resistance genes developed.

Some salient observations made on the introgression lines with above-mentioned rust resistance genes.

– *Lr24+Sr24* are tightly linked, but snew pathotype virulent on *Sr24* (40-1/62G29) was reported from this station.
– *Sr31*, *Lr26*, *Yr9*, and *Pm8* are tightly linked and linked to slow senescence of leaf and high susceptility to powdery mildew. A new pathotype virulent on *Lr26* (77-5) was reported from Wellington, *Pm8* is ineffective in a spring wheat back ground, the virulent races available at Wellington were showing 5MR–MS reaction to yellow rust, *Sr31* gave a 20MR–MS reaction.
– *Lr28* and *Lr32* were observed to be associated with fast rusting to stem rust susceptibility and a reduced level of infection to powdery mildew, *Lr28* and *Lr32* have association with fast rusting to stem rust.
– *Lr24+Sr24* and *Sr27* are associated with phenotypical markers of apical claw on the spike.
– *Lr19+sr25* seems to be associated with slow leaf senescence and increased yield, however, the susceptibility level for powdery mildew increases.
– *Lr37+Sr28+Yr17* introgression not giving yellow rust resistance in all backgrounds indicating the existance of certain suppressor genes at that particular loci.
– *Sr31* is associated with red grain, in derivatives there is always a chance to get amber grains.

Table 7. Maintenance and utilization of wild species of wheat at the Indian Agricultural Research Institute, Regional Station, Wellington, under this program 2009–09.

Species	Gene pool	Genome	Ploidy level (2n)	Total accessions
Ae. biuncialis	Tertiary	UM	28	122
Ae. columanaris	Tertiary	$U^{co}M^{co}$	28	17
Ae. comosa	Tertiary	M	14	3
Ae. comosa var. *comosa*	Tertiary	M	14	1
Ae. comosa var. *subventricosa*	Tertiary	M	14	1
Ae. crassa	Secondary	DJ, DJX	28, 42	9
Ae. cylindrica	Secondary	CD	28	75
Ae. geniculata	Tertiary	$U^{g}M^{g}$	28	110
Ae. juvenalis	Secondary	DMU	42	1
Ae. kotschyii	Tertiary	USS	28	9
Ae. longissima	Secondary	SB	14	36
Ae. markgrafii	Tertiary	CC	14	39
Ae. neglecta	Tertiary	UM	28	102
Ae. peregrina	Tertiary	US	28	55
Ae. peregrina var. *brachythera*	Tertiary	US	28	3
Ae. peregrina var. *peregrina*	Tertiary	US	28	1
Ae. searsii	Secondary	SS	14	50
Ae. sharonensis	Secondary	S^{sh}	14	77
Ae. speltoides	Secondary	S	14	29
Ae. speltoides var. *ligustica*	Secondary	S	14	9
Ae. speltoides var. *speltoides*	Secondary	S	14	6
Ae. tauchii	Primary	D	14	81
Ae. triuncialis	Tertiary	UC	28	239
Ae.triuncialis var. *persica*	Tertiary	$U^{t}C^{t}$	28	2
Ae.umbellulata	Tertiary	U	14	52
Ae.uniaristata	Tertiary	Mt	14	2
Ae.ventricosa	Secondary	$D^{v}N^{v}$	28	1
T. monococcum subsp. *aegilopoides*	Primary	A^{m}	14	742
T. timopheevii subsp. *armeniacum*	Secondary	AG	28	252
T. timopheevi subsp. *timopheevii*	Secondary	AG	28	22
T. turgidum subsp. *dicoccoides*	Primary	AB	28	595
T. urartu	Primary	A		171
Secale cereale	Tertiary	R	14, 16, 20	136
Total accessions				2,938
Total from tertiary gene pool				155

– *Yr9* is ineffective in a spring wheat background.
– *Lr45* seems to linked to pink awn and glumes at milk stage under low temperature.
– *Lr32* and *Lr28* in combination with *Sr31* are observed to give enhanced yield, to be investigated and exploited.
– Lr35 and Lr45 seems to not enhancing the yield and need further investigation.
– *Lr45* can easily be selected for based on pink awn color.
– Combinations of major and minor genes pyramided in certain elite cultivars is the long-term solution.
– *Lr19* and *Sr31* seem to be associated with high susceptibility to powdery mildew.
– *Lr45* seems to be associated with lax spikes although fertility in the lowest spikelet is restored.

Other externally funded projects in operation now at IARI, Regional Station, Wellington include 1. a DBT-funded Net work project 'Molecular Marker Assisted development of biotic stress resistant wheat varieties' and 2. an Indo-Australian breeding program on 'Molecular markers for broadening the genetic base of stem rust resistance genes effective against strain Ug99'.

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Ug99 virulence of wheat stem rust pathogen yet not detected in India.

J. Kumar and M. Sivasamy.

The virulence of race Ug99 of *Puccinia graminis* Pers..f.sp. *tritici* Eriks. & E.Henn. causing stem rust of wheat was recognized first in Uganda during 1999. Ug99 has the potential of migrating into India as documented by other rust races migrating from eastern Africa to southern Asia. A huge area in India is under cultivation of the mega-cultivar PBW 343 and other Veery cultivars with the gene *Sr31*, which has been rated to be highly susceptible when tested in Kenya (Singh et al. 2006). Owing to the inherent capability of stem rust spores for wind dipersal for long distances, the Nilgiri Hills in Tamil Nadu the state of South India are one of the prospective Indian targets of Ug99 virulence. A continuous vigil thus becomes imperative for tracking the supposed introduction of Ug99 and variants at this location, especially because wheat and stem rust survives here throughout the year.

The Wellington Station of theIndian Agricultural Research Institute situated in the Nilgiri Hills of Tamil Nadu in India is an ideal place to undertake Ug99 surveillance because stem rust survives here in vivo on wheat grown year round as winter and summer (off-season) crops. This IARI research station is well prepared to track the field incidence (if it happens) of new pathogenic strains such as Ug99 with a battery of well-maintained greenhouses for accomplishing virulence analysis in wheat rust pathogens. A quick, differential set comprising wheat lines capable of capturing Ug99

and its variants is regularly planted in a staggered way with repeating sowing at three-month intervals to maintain adult-stage plants continuously in the field. The quick set is comprised of the wheat lines Morocco (no *Sr* gene), LMPG (no *Sr* gene), Seri–MACS 2496, Bacanora–WH 542, Attila–PBW 343, *Sr31*/LMPG, *Sr24* (Tr 380–14), *Sr36* (Cook-2), *Sr36* (Cook), and *Sr36* (LMPG).

In the month of November 2009, the quick set also was planted at all regional stations of IARI; Shimla (North Hill zone), the Wheat Division of IARI headquarters in Delhi (North Western Plain Zone), Indore (Central Zone), and Wellington (South Hill Zone). These station cover all the agro-ecological situations in India suitable for wheat cultivation. Uredosporic dust was collected from 146 leaf samples of stem rust from the premises of the IARI Regional Station, Wellington, between April 2009 and April 2010 from the regular winter (March–April 2009 and October 2009–April 2010) and the summer crops (July–November, 2009). Seedlings of the quick set were inoculated and seedling reactions recorded following Bahadur et al. (1985). These samples yielded only the existing Indian pathotypes and none resembled Ug99 or its reported variants. The adult-stage reactions recorded in the first week of April, 2010, following the scale of Roelfs et al. (1992) indicated that all lines of the quick set were free of stem rust except Morrocco, which was susceptible at Indore and Wellington. We have concluded that Ug99 has not yet reached in Nilgiri Hills or other parts of India so far.

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ITEMS FROM ITALY

CONSIGLIO PER LA RICERCA E LA SPERIMENTAZIONE IN AGRICOLTURA, Unità di ricerca per la valorizzazione qualitativa dei cereali (CRA–QCE), Via Cassia, 176, 00191 Rome, Italy.

Pyramiding of leaf rust-resistance genes in common wheat using marker-assisted selection.

F. Nocente, L. Gazza, L. Sereni, and M. Pasquini.

Foliar diseases, such as leaf rust caused by *Puccinia triticina* Eriks. (*Pt*), have been important factors limiting wheat production worldwide. This pathogen is regarded as potentially the most damaging causal agent of rust disease on wheat in Italy, where it is widespread and needs constant monitoring.

One strategy for increasing the durability of resistance in commercial cultivars is to pyramid multiple resistance genes into a single wheat genotype. Pyramiding two or more genes, irrespective of whether they are major or minor, with different modes of action can greatly delay or even prevent the breakdown of resistance. The introgression of two or more genes into the same genetic background is difficult to monitor by traditional phenotypic analysis alone because of the epistatic or dominance effects of some genes or the lack of pathotypes with virulences matching the corresponding resistance gene(s). The availability of specific molecular markers tightly linked to respective resistance genes makes the detection of multiple genes in one genotype possible; such markers are the basis for efficient marker-assisted selection (MAS) in breeding work to speed up the identification of lines carrying two or more resistance genes.

Several known genes for resistance to leaf rust, often derived from related species and genera, have confirmed their efficacy in Italy over a long period. Epidemiological field controls in different locations in Italy and greenhouse