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ITEMS FROM INDIA

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Current activities: Improvement of wheat quality and rust resistance in Indian wheat.

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

Improvement of wheat for quality in an Indian wheat background is being carried out by using HMW-glutenin subunits as a selection criterion. The rust resistance genes *Sr31/Lr26/Yr9* and *Sr26*, *Sr24/Lr24* are being combined with high yielding ability and specific HMW subunits. Selected lines from several intervarietal crosses in different generations (F_2, F_3, and F_4) are being evaluated.

Radiation-induced mutations in wheat.

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

Earlier, the cultivar C306, known for its good chapati-making quality was treated with gamma rays, and mutants with early flowering were isolated in the M_2 generation. The parent showed anthesis in about 75 days, whereas the mutants showed anthesis in 50 to 63 days. Seven mutant lines were analysed for quality traits. Grain-protein content ranged from 11.9 to 14.9% compared to 13.1% in the parent. SDS-PAGE of total grain protein showed that the mutants had an unaltered HMW-glutenin subunit pattern. Rheological properties estimated using a Brabender Farinograph showed that the mutant lines had comparable water absorption, dough-development time, dough stability, degree of softening, and quality number. The early mutants are being carried forward.

MP3054 and Hindi 62 were treated earlier with gamma rays. M_2-generation plants were grown in 2008-09. Plants that flowered early and had reduced culm length were identified as mutants and harvested individually.

A bread wheat genetic stock with morphological markers for dark glumes, hairy glumes, hairy leaf, purple culm, and red grain was mutagenized with gamma rays. In the M_2 generation, plants with altered morphology were identified and individually harvested. The M_3 was grown as plant-to-row progeny. Although variations for the extent of glume pigmentation or hairiness, spike morphology, and culm length were observed, lines were found to segregate for the mutant traits.

Validation and marker-assisted selection for rust resistance and quality-related genes in Indian wheat.

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

Validation of SCAR marker $SCS1302_{609}$ for gene *Sr24*. Molecular markers developed for traits such as disease resistance using a specific genotype may not necessarily work in others. Hence, validating markers in diverse genotypes is important. In this study, marker $SCS1302_{609}$ (Gupta et al. 2006) reported for *Lr24/Sr24* was validated by analyzing

wheat genotypes/cultivars with wide genetic background and also in segregating populations. PCR conditions were optimized by gradient PCR at different temperatures (60.3°C, 61.1°C, 61.9°C, 62.3°C, and 63°C). The optimum annealing temperature was found to be at 61°C. Forty-one wheat genotypes were screened using the primers for SCAR marker $SCS1302_{609}$. The genotypes with *Sr24* yielded a 607-bp band. Wheat genotypes that were reported to carry other *Sr* genes, i.e., *Sr31*, *Sr26,* and also noncarriers of *Sr24^,* did not amplify this marker, indicating that SCAR marker $SCS1309_{609}$ was specific only to gene *Sr24* in the Indian wheat genotypes/cultivars.

SCAR marker analysis in segregating populations. The SCAR marker $SCS1302_{609}$ also was validated by analyzing two segregating populations (Kalyansona/Vaishali and Kalyansona/Vidisha). The genotypes (RR, Rr, and rr) of individual plants in the F_2 generation were identified by scoring the rust reaction of respective F_3 progenies. Analysis of DNA from these plants using marker $SCS1302_{609}$ showed that, out of the 52 resistant plants, 51 amplified the SCAR marker and one failed to amplify. Of the 21 susceptible plants, 19 did not amplify the marker and two showed amplification. This result deviated from the expected 9:3:3:1 (Res/+:Res/–:Sus/+:Sus/–) ratio for independent assortment between the stem rust-resistance locus *Sr24* and the SCAR marker. Three recombinants were observed in the F_2 population. Using MAPMAKER (version 3.0), the distance between $SCS1302_{609}$ and the *Sr24* locus was estimated to be 4.3 cM.

Similarly, an F_2 population from the cross 'Kalyansona/Vidisha' was screened for rust reaction and the presence of marker $SCS1302_{609}$. A total of 18 plants were screened in the F_2 generation for their phenotype. Of the 14 F_2 plants with a resistant phenotype, five were confirmed to be homozygous and nine were confirmed to be heterozygous based on the phenotypes of their progenies in the F_3 generation, and four F_2 plants were found to be homozygous for a susceptible reaction. All the resistant plants showed amplification of the SCAR marker. All five susceptible plants did not amplify this marker. The marker, therefore, was found to be suitable for screening *Sr24* in early generation material.

Marker-assisted breeding to combe rust resistance genes *Sr24* and *Sr31* and *Glu-D1d* (coding for HMW-glutenin subunits 5+10) is underway in a cross between FLW-2 and Kite. In the F_2 generation, ~220 plants are being analyzed using SCAR markers. Plants with both rust-resistance genes and *Glu-D1d* will be selected and advanced.

Marker-assisted backcrossing. To transfer *Sr24* and *Glu-D1d* into HD2189, marker-assisted backcross breeding (MAB) is being carried out. Thirty BC_3F_1 plants were grown, and DNA from leaves of 4-week-old individual plants was extracted and screened using SCAR markers for the two genes. In the winter of 2008–09, seven plants with both markers were identified. Backcrosses were made using the HD2189 recurrent parent and carriers of both the markers.

Genotyping of an RIL population for variation at the Xgwm261 locus.

S. Bakshi and S.G. Bhagwat.

A 192-bp allele at the *Xgwm261* microsatellite locus is known for its association with reduced height gene *Rht8* in hexaploid wheat. Indian wheat cultivars showed a predominance of 165-bp, 174-bp, and 192-bp alleles at this locus. In our earlier analysis of Indian wheat cultivars, the 192-bp allele at the *Xgwm261* locus did not show association with height reduction at the Trombay location, which is a warm environment. An RIL population of 139 lines derived from the two cultivars Sonalika (165 bp) and Kalyansona (192 bp) was assayed for polymorphism at the *Xgwm261* locus. The RIL segregation fit a 1:1 ratio for the presence of 165-bp and 192-bp alleles. These RILs were grown in the field at Trombay during the winter of 2008–09, and data for phenotypic traits of culm length (cm), spike length, spikelet number, and flag-leaf blade area (cm) were recorded. Plant growth was affected by heat stress during the season. Further analysis is in progress.

Genetic relationships among bread wheat genotypes with different seedling thermotolerance using parentage analysis, SSRs, and agronomic data.

Heat stress affects the productivity of wheat in many wheat-growing regions of India. The tolerance of wheat plants to higher than optimum temperature varies at different plant-growth stages. Seedling thermotolerance was assessed among 56 genotypes using membrane thermostability (MTS) and triphenyl tetrachloride tests (TTC). Twenty genotypes with varying thermotolerance were selected and grown in heat stressed and non-heat stressed environments to evaluate their phenotypic performance. Parentage data were used to find the degree of relationship among these genotypes. The

genotypes also were subjected to an SSR analysis to find molecular similarities among the genotypes. Further analysis is underway to deduce the genetic relationships and commonalities based on quantitative, parentage, and SSR data.

Wheat tissue culture.

C. Chang, P. Suprasanna, and S.G. Bhagwat.

Calli were induced from scutellum-supported embryos of immature seeds in three lines of *T. turgidum* subsp. *dicoccum*, two cultivars of *T. aestivum* subsp. *aestivum*, and two experimental stocks with the sphaerococcum trait. Differences in growth rates of the calli from different cultivars were observed. Calli from experimental stocks carrying the sphaerococcum trait were smaller than the rest. Calli obtained from the scutellum-supported embryos of mature seeds in four cultivars of *T. aestivum* subsp. *aestivum* and the two experimental stocks showed that the growth rate of the calli from experimental stocks carrying sphaerococcum trait were significantly lower.

Calli obtained from scutellum-supported embryos of immature seeds were irradiated with gamma rays. Three days after irradiation, the calli were assayed using TTC (2,3,5-triphenyl tertazolium chloride). At 50 Gy, the reduction in TTC values for Unnath C306 (*T. aestivum* subsp. *aestivum*) was 9% and for DDK1029 (*T. turgidum* subsp. *dicoccum*) was 1%. A 65% and 68% decrease in the TTC value of Unnath C306 and DDK1029, respectively, were observed after a 500-Gy treatment.

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Development and use of molecular markers for wheat genomics and breeding

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 originally were prepared for the following three traits: (i) grain protein content (GPC); (ii) preharvest-sprouting tolerance (PHST), and (iii) grain weight (GW).

Framework linkage maps of GPC, PHST, and GW populations. Previously, we prepared a framework linkage map for the GPC population using 171 SSR markers. The map spanned a genetic distance of 3,272.4 cM and had large gaps in certain regions, which adversely affected the precision of QTL mapping studies. In view of this, a total of 47 markers were added to the existing framework map of the GPC population making the total number of markers in the map 217. The map now spans a total genetic distance of 3,868 cM.

For the PHST population, the genetic map that was prepared consisted of 214 loci (198 SSR, 5 AFLP, and 11 SAMPL loci) that were distributed on all 21 wheat chromosomes with an average of 10.19 loci/chromosome. The map spanned a genetic distance of 3,972 cM. Of the total mapped loci, a maximum of 77 loci were mapped to the A genome (11 loci/chromosome), followed by 73 loci to the B genome (10.42 loci per chromosome), and 64 loci to the D genome (9.14 loci/chromosome).

For the GW population, a total of 294 loci, including 194 SSR, 86 AFLP, and 14 SAMPL loci, were mapped on all the 21 chromosomes of wheat genome (average 14 loci/chromosome) covering a map length of 5,211 cM. SSRs were more abundant in the A genome (110 SSR loci with an average of 15.7 loci per chromosome) than either the B (103 SSR loci with an average of 14.7 SSR per chromosome) or D genomes (81 SSRs with an average of 11.57 SSR per chromosome).

QTL analysis for grain weight and related kernel traits in bread wheat. Kernel size and shape are important traits in bread wheat because of their relationship with yield and milling quality. For the genome-wide genetic dissection of some kernel traits in bread wheat (kernel size including 1,000-kernel weight (GW) and kernel shape), an intervarietal RIL mapping population derived from the cross 'Rye Selection 111/Chinese Spring' was used. Kernels from Rye Selection 111 are larger than kernels from Chinese Spring in all dimensions. The two parental genotypes and RILs were evaluated in six environments for GW; for other traits (kernel length, width, volume, projection area, vertical perimeter, and horizontal axis proportion), the data was recorded over three environments. Digital image analysis was used for recording the data. Using genotypic and phenotypic data, genome-wide, single-locus QTL analysis (involving inclusive composite interval mapping (ICIM)) and two-locus QTL analysis (involving QTLNetwork) were used to identify the main effect QTL (M-QTL), epistatic QTL (E-QTL), and 'QTL × environment' interactions (QE and QQE). Single-locus QTL analysis for GW revealed a total of 11 QTL (including four major and stable QTL). Threshold LOD scores (3.95 to 32.0) were used to score QTL that contributed significantly to the phenotypic variation (PV = 4.37% to 82.0% per QTL). Similarly, for other related traits, a total of 45 QTL were identified (ranging from four for the vertical perimeter to 13 for kernel length) above threshold LOD values (2.52 to 9.27), which contributed significantly to phenotypic variation (PV = 6.97 for kernel length to 29.87 for projection area). Among the above QTL for GW and related traits, 11 were found to control more than one trait (including four for GW) and were, therefore, considered as pleiotropic/coincident QTL. A two-locus QTL analysis for GW resolved a total of 24 QTL, which included three M-QTL (also detected by single-locus analysis) and 21 E-QTL involved in 12 digenic QQ interactions. Similarly for other traits, a total of 35 QTL including seven M-QTL (five of the seven also were detected through ICIM) and 28 E-QTL involved in 15 digenic QQ and two QQE interactions were detected. The molecular markers linked with the major/coincident QTL for GW and other traits may prove useful in marker-assisted selection for the development of improved bread wheat cultivars.

QTL analyses for grain color and preharvest sprouting. Using the GPC population, single- and two-locus QTL analyses resolved a total of 11 QTL for PHS and 12 QTL for GC. These QTL included both the main-effect QTL (M-QTL; seven for PHS and six for GC) and epistatic QTL (E-QTL; four for PHS and six for GC). The MQTL explained a greater proportion of phenotypic variation (PV) than the E-QTL for both the traits. Four QTL for each of the two traits were co-localized, whereas the remaining M-QTL and E-QTL were unique for each of the two traits. Of all the QTL, one major QTL each for PHS and GC are of interest for breeding PHS-tolerant, white-grained, bread wheat genotypes. The major QTL for PHS, which is independent of grain color, was located on chromosome arm 6AL and explained up to 29.47% PV, whereas the major QTL for GC, co-localized with a minor QTL for PHS, was located on chromosome arm 3BL and explained up to 36.18% PV. Physical mapping placed the QTL for PHS within the 53% proximal region of 6AL, whereas the QTL for GC was placed within 19% of the distal region of 3BL. Comparative genomic analysis also identified 5.47 Mb and 1.63 Mb rice genomic regions, which are orthologous to the wheat genomic regions containing the major QTL for PHS and GC, respectively. SSR markers flanking the major QTL for PHS and GC may be used in wheat-breeding programs aimed at developing PHS-tolerant, white-grained wheat genotypes through MAS. Further-

more, the information gained from physical and comparative mapping may be used in the future for fine mapping and map-based cloning of the above two major QTL.

Genetic diversity and population structure analysis among Indian bread wheat cultivars. As a first step towards association mapping in wheat, we carried out genetic diversity and structure analyses in a collection of 263 Indian wheat cultivars (45 developed during before the Green Revolution and 218 developed during thew 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 SSR markers, one from each arm of the 21 individual chromosomes. The above 42 SSRs had a total of 294 alleles (mean 7.0; range 2–14/SSRs), which included 101 (34.35 %) rare alleles occurring at a frequency of <5%. The average number of alleles/locus (5.91 vs. 5.74) and the estimates of genetic diversity (0.65 vs. 0.61) in the cultivars belonging to pre-and post-Green Revolution periods did not differ significantly indicating that the Green Revolution did not lead to any loss of genetic diversity. The model-based *Structure* analysis identified a total of 14 subpopulations including two subpopulations predominantly comprising cultivars from the pre-Green Revolution period and 12 subpopulations mostly comprising cultivars from post-Green Revolution period.

Introgression of QTL for GPC using MAS. Ten F_1 hybrids were derived from the crosses of each of the 10 elite, Indian, bread wheat genotypes with a high GPC donor genotypes and Yecora Rojo, carrying a major QTL for GPC (*GPC-B1*). The F_1 hybrids were backcrossed with the respective elite recipient parental genotype and the BC_1F_1 plants were raised either in off-season nursery at National Phytotron Facility, IARI, New Delhi during 2004–05 or in the rabi season 2005–06 at the Research Farm of CCS University, Meerut. From the BC_1F_1 onwards, MAS (foreground and background selection) was exercised for three successive backcross generations for the rapid introgression of high GPC QTL and reconstruction of the recipient genotypes. The foreground selection for *GPC-B1* QTL was carried out using STS marker *Xuhw89*, which is tightly linked (0.1 cM) to the *GPC-B1* QTL. Background selection for the recovery of the recurrent parent genotype was carried out using 35 SSRs (representing 52 polymorphic loci) and 12 AFLP primer combinations (889 polymorphic AFLP loci). In each of the 10 BC_3F_1 populations, 2–5 positive plants carrying *GPC-B1* QTL showing higher GPC (up to 1.72% higher than the recipient genotypes) and high genomic similarity (up to 100%) with the recipient parental genotype were selected. In the BC_3F_2 generation, progenies of the six crosses could be advanced in National Phytotron Facility at IARI during the off-season 2006–07, and the BC_3F_3 seed from 29 plants homozygous for the GPC-B1 QTL (identified following foreground selection) was obtained. Using BC_3F_3 seed, 29 BC_3F_3 progenies (belonging to six crosses) were evaluated in five replications at the Research Farm of CCS University, Meerut, during the rabi season 2007–08. Out of these progenies, 17 progenies showed significantly higher GPC (1.08 to 2.51%) over their respective recipient parent genotypes. These progenies with significantly higher GPC did not show any adverse effect of increased GPC on tiller number, spike traits, and 1,000-kernel weight, although some of these progenies did show reduction in plant height. The 17 progenies (BC_3F_4) with significantly higher GPC were evaluated in 2-m single-row plots in five replications at each of the three different locations (Meerut, Pantnagar, and Ludhiana) during the rabi season 2008–09 and the data on six agronomic traits (plant height, spike length, number of spikelets/spike, number of seeds/spike, seed weight/spike, and 1,000-kernel weight) were recorded. Out the above 17 BC_3F_4 progenies, 10 BC_3F_4 progenies were evaluated in separate yield trail in 2-m^2 plots in three replications at Meerut during 2008–09. The data were recorded on grain yield and six agronomic traits. Efforts are underway to record the data on GPC of all the progenies in both the trials. Superior BC_3F_4 progenies will be identified after complete data on all the traits is obtained. In addition to the above, BC_3F_2 progenies of the nine crosses (including four crosses involving the recipient genotypes that were not involved in the above BC_3F_4 progenies) were evaluated at the Research Farm of CCS University, Meerut, during the rabi-season 2007–08. Following foreground selection, 99 plants homozygous for the *GPC-B1* QTL were selected and their progenies (BC_3F_3) were evaluated in 2-m, single row plots in five replications during the rabi season 2008–09 at the Research Farm of CCS University, Meerut. Data were recorded on six agronomic traits (plant height, spike length, number of spikelets/spike, number of seeds/spike, seed weight/spike, and 1,000-kernel weight) on these progenies. Data on GPC will be recorded soon. The BC_3F_3 progenies showing significantly higher GPC and high genomic similarity with the recipient parent genotypes will be evaluated in the future in replicated/multilocation trials for GPC and yield-related traits.

Marker-assisted selection for preharvest sprouting tolerance and leaf rust resistance in bread wheat. In wheat, preharvest sprouting and susceptibility to leaf rust are two major problems that lead to the degradation of grain quality associated with significant losses in yield. We earlier identified a major QTL (*QPhs.ccsu-3A.1*) on chromosome 3A that explained >70% phenotypic variation for PHST across a number of environments. The desirable allele of this QTL was introgressed through MAS into the elite, but PHS susceptible, amber-grained wheat cultivar HD2329 carrying alien leaf rust-resistance genes (*Lr24* + *Lr28*). In each of the backcross generation, foreground selection was exercised using

flanking markers (gwm155 and wmc153), and background selection was performed using 52 polymorphic SSR loci (distributed on all the 21 bread wheat chromosomes) and 146 AFLP loci. In the BC_3F_1, the desirable alleles of the two leaf rust-resistance genes *Lr24* and *Lr28* also were tracked using linked SCAR markers. The reconstituted plants, exhibiting upto 93.4 3% genetic similarity with the recipient parent, were selfed to obtain homozygous plants in the BC_3F_2, which were further evaluated in the BC_3F_3. Seven lines with pyramided PHST QTL and Lr genes exhibited high level of PHS tolerance (PHS score 2–4) and resistance against leaf rust under artificial conditions. The present work demonstrates successful application of marker-assisted selection for targeted pyramiding of QTL/genes for more than one trait into an improved wheat cultivar.

Introgression of QTL for GW using MAS. Crosses involving 10 elite Indian bread wheat genotypes as recipient parents and the genotype Rye Selection 111 (RS111) as a donor parent were attempted during the off-season 2005–06 in the Phytotron Facility at IARI, New Delhi ,and the F_1 seed was collected. These F_1s were raised during the rabi season 2006–07 and were 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 above 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 GW 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 both the markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for GW on chromosome 1A) involving recipient genotype PBW343 (*Lr9*), 142 positive plants for the marker *Xwmc24* 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 will be used to raise BC_3F_1 progenies during 2009–10 rabi season.

Orthology between genomes of *Brachypodium*, wheat, and rice. Comparative sequence analysis of 3,818 *Brachypodium* EST (bEST) contigs and 3,792 physically mapped wheat EST (wEST) contigs revealed that as many as 449 bEST contigs were orthologous to 1,154 wEST loci that were bin-mapped on all the 21 wheat chromosomes. Similarly, 743 bEST contigs were orthologous to specific rice-genome sequences distributed on all the 12 rice chromosomes. As many as 183 bEST contigs were orthologous to both wheat and rice genome sequences, which harbored as many as 17 SSRs conserved across the three species. Primers developed for 12 of these 17 conserved SSRs were used for a wet-lab experiment, which resolved relatively high level of conservation among the genomes of *Brachypodium*, wheat, and rice. The study thus confirmed that *Brachypodium* is a better model than rice for analysis of the genomes of temperate cereals like wheat and barley. The whole-genome sequence of *Brachypodium*, which should become available in the near future, will further facilitate greatly the studies involving comparative genomics of cereals.

Analysis of host–pathogen interaction in leaf rust-infected bread wheat. One major objective in wheat-breeding programs is the development of leaf rust-resistant cultivars. However, for the long-term, effective management of resistance against this disease, the molecular basis of disease resistance and the host-pathogen interaction should be known. For the above purposes, we have attempted both *in silico* and wet-lab approaches to study transcriptome analysis.

In silico study. Transcript based UniGene sets provide great potential to identifying the differentially expressed genes upon infection with leaf rust in bread wheat. Three, wheat cDNA libraries containing ~51,000 ESTs were utilized in the present study. The first cDNA library of the uninfected, disease-resistant Thatcher wheat stock (background gene *Lr10*) contained 22,803 ESTs. The second cDNA library of an infected, disease-resistant Thatcher wheat (background gene *Lr10*) contained 22,740 ESTs, and the third cDNA library of an infected, disease-resistant Thatcher wheat stock (background gene *Lr1*) contained 6,698 ESTs. Using the ESTs belonging to the three libraries, digital gene-expression analysis was conducted with the help of Digital Differential Display (DDD) program available at NCBI. Using this approach, a total of 68 differentially expressed UniGenes were identified, which formed three major clusters, each cluster representing a different class of genes including biotic and abiotic stress responsive genes as well as regulatory genes.

Wet-lab study. For transcriptome analysis 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 the 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 γP^{32} labeled primer combinations. Following cDNA-AFLP analysis, over-expressed TDFs in the resistant host following pathogen inoculation are being cloned and sequenced for their functional analysis.

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Preservation of wheat and barley germ plasm under natural storage conditions.

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We preserved seeds of wheat and barley germ plasm for long periods under the natural conditions of Dalang Maidan in the Lahaul Valley to reduce the exorbitant costs of installation and maintenance of artificial and conditioned storage rooms for germ plasm preservation. We also aimed to develop a standby repository for valuable Indian wheat and barley germ plasm presently being maintained in artificial storage rooms at the NBPGR, New Delhi, and DWR, Karnal. Accidental lapses leading to complete seed lethalities in these storerooms always loom large owing to unexpected human error, natural calamities, or electrical failure.

For every 1% decrease in seed moisture and 10°F in storage temperature, the life of seed is doubled (Harrington and Douglas 1970). Therefore, an attempt was made to store wheat and barley germ plasm under natural conditions characterized with low humidity and low temperature year round, at the Regional Station, Directorate of Wheat Research (ICAR), Dalang Maidan, in district Lahaul Spiti (Himachakl Pradesh). This station is located at approximately 32°.21' north latitude and 77°.14' longitude and is about 6-km upstream from the point of origin of the Chenab River, on the banks of the Chandra River at an altitude of approximately 3,300 M (10,000 ft) above mean sea level. This place is located at a very high altitude and enjoys a temperate-dry climate with an average annual rainfall of 250 mm. The area is covered with snow for about 5 months; from December to April.

Temperatures above 20°C during the summer months are a rare phenomenon, even at lower elevations. Records of the natural temperature and relative humidity (monthly means) pertaining to the room used to store the experimental seeds were maintained. The mean monthly temperature inside the storage room varied within a range of –20–20°C, and humidity levels were not above 60% during the 10-year span of the experiment (Table 1, p. 72).

Routinely during the last decade, new germ plasm accessions developed under national wheat program (All India Coordinated Wheat & Barley Improvement Programs) and those collected from international sources are packed in alkathane pouches, arranged together in plastic trays, and stacked in steel boxes at room temperature. This experiment

was initiated in 1997. The oldest seed lot available now is 10-years old and was tested for viability by germination tests. Because the number of lines stored during 1997 at this station was large, the viability test were restricted to 60 bread, 20 durum, 10 dicoccum, and 10 barley lines. In each case, seeds were kept on a wet filter paper sheet in a Petri plate with the lid covered with another piece of wet filter paper. Petri plates with seeds were incubated at room temperature. Percent germination, total normal seedlings, and time to achieve 25% germination were compared to that for 1-year-old seeds to evaluate viability of stored seed. Straight-growing, greenish white seedlings with well-formed roots were treated as normal, while those with a curved appearance, thin texture, and brownish color were treated as abnormal. In each case, 300 grains were examined. Data were pooled for all accessions within the same crop. A mean value and standard deviation of the accessions within the same crop were calcualted.

Table 1. Temperature (°C) and relative humidity (% RH) records of the seed storage site at Dalang Maidan, India.

Month		1997	1998	1999	2000	2001	2002	2003	2004	2005	2006
January	°C	-19	-16	-18	-22	-21	-17	-20	-19	-23	-16
	RH	45	42	43	45	47	42	43	45	43	45
February	°C	-5	-8	-4	-2	-7	-5	-8	-4	-8	-5
	RH	48	49	48	47	43	46	45	46	43	46
March	°C	2	4	4	2	3	6	5	3	2	5
	RH	51	52	54	53	52	52	53	54	54	54
April	°C	9	8	9	9	8	9	6	9	8	7
	RH	56	55	54	58	57	52	56	54	55	53
May	°C	11	13	11	11	12	14	12	11	12	13
	RH	51	52	51	52	54	53	52	51	52	50
June	°C	17	16	18	20	21	21	18	19	18	20
	RH	49	51	52	51	52	55	49	50	51	51
July	°C	22	21	20	23	23	24	23	23	22	21
	RH	58	56	59	54	58	56	56	54	55	56
August	°C	24	23	23	21	19	23	24	23	24	23
	RH	59	53	58	58	54	48	58	56	58	57
September	°C	18	17	18	17	16	18	18	17	18	19
	RH	49	46	49	45	48	42	46	47	47	48
October	°C	11	13	12	13	14	15	12	13	14	12
	RH	44	45	43	42	45	42	43	44	43	42
November	°C	6	5	8	9	11	10	11	12	8	9
	RH	41	42	41	42	40	42	41	40	42	43
December	°C	2	3	3	4	5	3	2	2	3	4
	RH	42	43	42	41	43	42	42	41	41	40

Barley and dicoccum wheat retained germination ability to a greater extent than the durum and bread wheats after storage under natural conditions at Dalang for 10 years (Fig. 1). Also noteworthy is that these crops represented two different groups. The first group, consisting of barley and dicoccum wheat, exhibited germination above 60%, whereas the group of durum and bread wheat were below 60%. Such a grouping also was supported in the counts made for normal vs. abnormal seedlings produced by the germinated seeds (Fig. 2). The another criterion used to assess the viability of 10-year-old seed was the time needed for 25% germination compared to

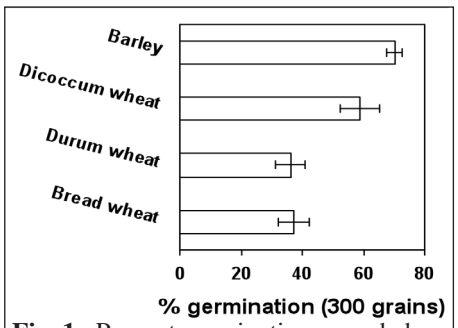

Fig. 1. Percent germination recorded in wheat and barley seeds after storage under the natural conditions for 10 years at Dalang Maidan, India.

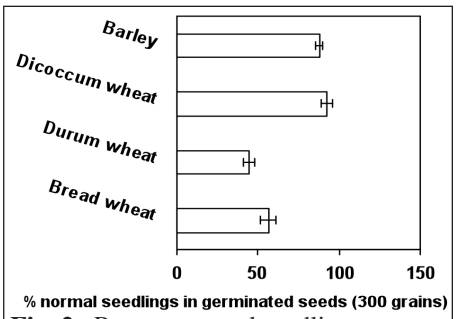

Fig. 2. Percent normal seedlings obtained in germinated seeds of wheat and barley after storage under the natural conditions for 10 years at Dalang Maidan, India.

that for 1-year-old seed of the same crop. All crops except dicoccum wheat experienced an adverse effect from 10 years of storage on the time needed to achieve 25% germination (Fig. 3). The duration was the greatest for bread wheat (72 hours) followed by durum wheat (48 hours) and barley (24 hours).

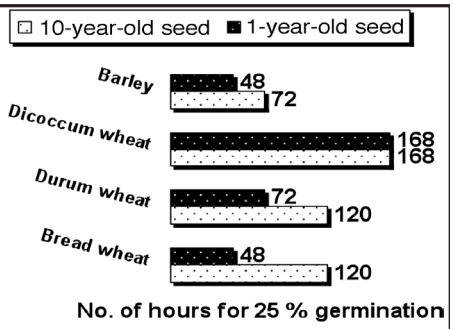

Fig. 3. Time needed for 25% germination of wheat and barley seed after storage under natural conditions for 10 years at Dalang Maidan, India.

From these observations, we conclude that wheat and barley germ plasm can be stored safely at least for 10 years under the natural conditions that prevail at Dalang Maidan, India (monthly mean temperature -20–20°C and mean RH below 60 %). Justice and Bass (1978) reported for wheat a relative storability index of 2 (50% of the seed are expected to germinate after 3–5 years of storage). Our investigations showed that seed germinated normally after 10 years of storage (more than 25% in each case) and in terms of germ plasm maintenance, without spending exorbitant prices to construct and run artificial storage systems. Furthermore, we also concluded that barley and dicoccum seed can withstand long-term storage effects better than bread and durum wheat. However, that dicoccum and barley seed exhibits greater viability compared to bread and durum wheats after 10-years of storage needs further investigations. Seeds of other Gramineae species are known to survive under storage for more than 10 years (Pristley 1986), and we expect that it might prove true for wheat and barley stored under the natural conditions of Dalang Maidan.

Summary. New germ plasm accessions in wheat and barley result from the programs engaged with prebreeding, natural exploration, introductions, and breeding. Due to the scarcity of land at research farms, growing enormous numbers of new accessions every year for maintenance may not be possible. Alternatively, these germ plasm collections may be maintained as seed under storage systems. Conventionally, germ plasm is preserved for long periods in artificially erected storerooms that need huge monetary investments for development and maintenance. Moreover, such structures are prone to accidental handling and unreliable electric supply, which may lead to lethality of valuable stocks. The natural preservation facility available at Dalang Maidan, Regional Station, Directorate of Wheat Research (ICAR) in the Lahaul Valley is envisaged as a potential alternative to unreliable and expensive artificial storage systems. The 10-year-old seed of wheat and barley stored at this station were tested for their viability using a seed-germination test. All seeds were found to have maintained their viability. The dicoccum and barley lines maintained their viability more efficiently than the bread and durum wheats.

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Effect of subculturing on infection potential of Tilletia indica, the incitant of Karnal bunt of wheat.

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Abstract. Karnal bunt resistance in wheat breeding lines was tested by artificial inoculation of emerging spikes with secondary sporidia raised on growth media. The sporidial cultures were maintained through subculturing with weekly transfers. A significant reduction in the production of primary and secondary sporidia was observed in the 2nd, 3rd, 4th, and 5th descendant cultures (DC2, DC3, DC4, and DC5) compared to the parental culture (PC). The budding potential of the primary sporidia to secondary sporidia and self-budding in the secondary sporidia tended to decrease with weekly transfers during subculturing. Secondary sporidia harvested from the cultures were inoculated onto the susceptible wheat cultivar HD 2009 at growth stage Z 49 (emerging spike) for evaluating the infection potential of the parental and descendent cultures (PC and DC). We found that disease severity was reduced significantly in spikes inoculated with descendant cultures compared to the parental culture.

Karnal bunt (KB) of wheat was first reported from northern India by Mitra (1931). The disease is distributed over all of northwest India in an endemic form and occurs in traces over a larger part of south Asia (Warham 1986). Besides India and Pakistan, KB is reported from other countries such as Nepal (Singh et al. 1989), Iraq (CMI 1989), Mexico (Duran 1972), the U.S. (Ykema et al. 1996), and South Africa (Crous et al. 2001). Karnal bunt impairs the quality of wheat-based products and reduces seed germination (Mehdi et al. 1973; Bedi and Meeta 1981; Bansal et al. 1984). The disease also poses serious implications for international trade and exchange of wheat germ plasm in view of the pathogen's migration into new areas (Royer and Ritter 1988). This disease is known to hamper the export of wheat from India because of stringent quarantine restrictions posed by several importing countries as a preventive measure to avoid entry of KB into their territory (Nagarajan et al. 1997).

Cultivation of resistant cultivars offers the best promise for an economical and environmentally safe management of this disease. Resistance to KB in cultivars during their breeding is evaluated by artificial infection tests (Gill et al. 1993). These tests involve inoculation of secondary sporidial suspension of *T. indica* with the help of a hypodermic syringe into the emerging spike at growth stage Z 49 of wheat crop (Aujla et al. 1987). An inoculum density of 10,000 secondary sporidia/mL of water is required for successful creation of artificial epiphytotics of KB (Gill et al. 1993). Sporidial inoculum is prepared by making a water suspension of the sporidia harvested from culture slants maintained for longer periods (Munjal 1974; Dhiman and Bedi 1983). Sporulating mycelium is abundant at 18°C for up to 7 days (the surface of the medium fully occupied by shiny white mycelium; Fig. 4, top left), then gradually deteriorating leading to desiccation (Fig. 4, top right). Therefore, the mycelium needs to be transferred to new agar slants to remain viable and sporulating. Fresh mycelial cultures are initiated from teliospores in December in order to have an adequate amount of inoculum for the large number of breeding populations in February of the next year, when test entries are at growth-stage Z 49. The cultures are transferred at least five times, to fresh potato dextrose yeast extract medium (PDYEA), to maintain their viability before their use as inoculum during the middle of February (average temperature 18–22°C). The effect of repeated transfers of sporidial cultures to fresh growth media on their viability and ability to produce secondary sporidia (responsible for infection) is reported here.

Fig. 4. Mycelium of *Tilletia indica*: fresh and viable (upper left), old and desiccated (upper right); allantoid or secondary (curved) and filiform or primary (thread like) sporidia budding into secondary sporidia (lower).

Materials and methods. Teliospores were germinated at 12°C over a thin layer of 2% agar in a Petri plate after extracting from punctured sorus of an infected kernel. Mycelial cultures were initiated 6, 5, 4, 3, 2, and 1 weeks prior to the onset of growth stage Z 49 in the KB-susceptible wheat cultivar Arjun (HD 2009) by incubating germinated teliospores on the slants of PDYEA at 18°C. On successive transfers to new slants at 7-day intervals, the cultures initiated 6, 5, 4, 3, and 2 weeks attained the 5th, 4th, 3rd, 2nd, and 1st descendant generation, respectively at the onset of growth stage Z 49 in HD 2009. At the time of inoculation, cultures transferred for 5, 4, 3, 2, and 1 times were available. A sporulating culture also was initiated one week before onset of growth stage Z 49 in HD 2009 and was designated as the parent culture (PC) and inoculated without any transfer to serve as a control. The descendent cultures (DC) obtained after the 1st, 2nd, 3rd, 4th, and 5th transfers were designated DC1, DC2, DC3, DC4, and DC5, respectively. The parental and descendant cultures were examined for production of primary and secondary sporidia in actual and budding states (Fig. 4, bottom). One mL of distilled water was poured onto the slant followed by vigorous shaking. Simultaneously, 1 mL of sporidial suspension was mounted on a slide. Six slants were observed in each case and five slides/slant were prepared. Enumeration of sporidia was made in one microscopic field (400X) randomly focused on each slide. The data were subjected to an analysis of standard deviation about the mean. Microsporidia harvested from the PC and DCs were inoculated on the spikes of susceptible wheat cultivar HD 2009 at stage Z 49 (Zadoks et al. 1974) following the methods of Aujla et al. (1987). Each culture was inoculated on nine spikes. The percent coefficient of infection (CI) was calculated individually for each spike after harvest (Aujla et al. 1989). The KB severity of nine spikes was recorded as percent CI, and the data were subjected to an analysis of standard deviation about the mean.

Results and discussion. The PC and their respective DCs up to the fifth generation were examined for their potential to produce primary and secondary sporidia in the actual and budding states. Production of primary and secondary sporidia remained equal between the PC and the DC1. However, a significant reduction in the sporidia count was noted in the 2nd, 3rd, 4th, and 5th DCs compared to the parental cultures. A gradual decrease occurred in sporidia production after from the DC2 to the DC5 generation (Figs. 5A and B, p. 75). Primary and secondary sporidia showing budding to pro-

duce more secondary sporidia (Figs. 5C and D) were at the maximum in the PC, DC1, and DC2 cultures for primary and the PC and DC1 for the secondary without any significant difference. However, budding was reduced significantly in the DC3, DC4, and DC5 for primary sporidia and the DC2, DC3, DC4, and DC5 for secondary sporidia compared to that in the PC (Figs. 5C and D).

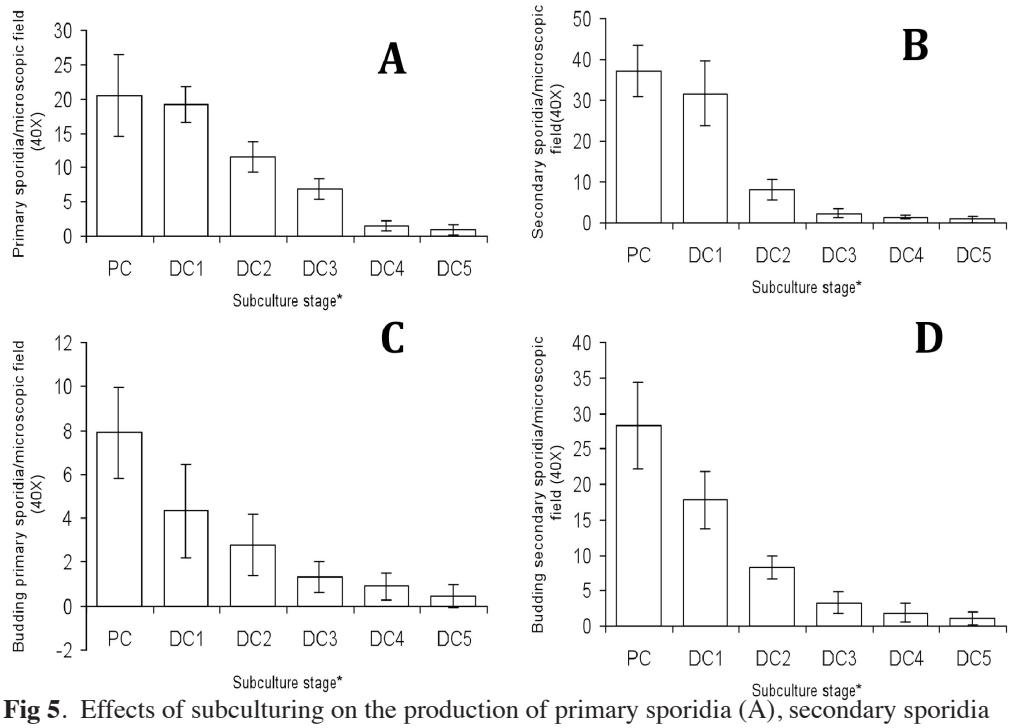

Fig 5. Effects of subculturing on the production of primary sporidia (A), secondary sporidia (B), budding primary sporidia (C), and budding secondary sporidia (D). PC, parent culture obtained from germinated teliospores; DC1, descendant culture generation 1, obtained after subculturing the PC; DC2, descendant culture generation 1 obtained after subculturing the DC1; DC3, descendant culture generation 1 obtained after subculturing the DC2; DC4, descendant culture generation 1 obtained after subculturing the DC3; and DC5, descendant culture generation 1 obtained after subculturing the DC4.

The infection potential of the PC, DC1, DC2, DC3, DC4, and DC5 also was evaluated by inoculating a spore suspension onto spikes of the KB-susceptible HD 2009 at growth stage Z 49. The PC and DC1 inflicted the maximum disease severity without any significant differences (Fig. 6), but disease severity was reduced significantly in spikes inoculated with DC2, DC3, DC4, and DC5.

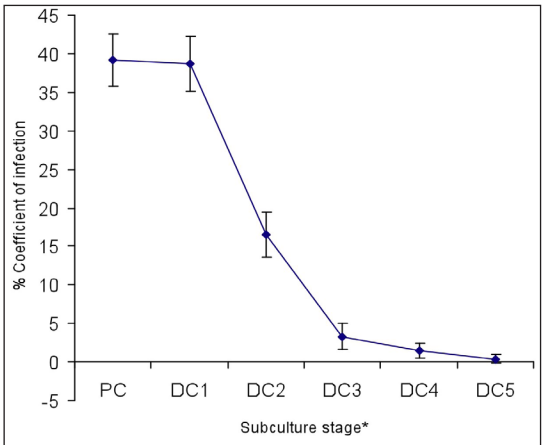

Fig. 6. The effect of subculturing on the infection potential of *T. indica* on the susceptible wheat cultivar HD 2009. See Fig. 2 for description of abbreviations.

Like other major diseases of wheat, evaluating resistance to KB during breeding of a cultivar is an essential practice in Indian wheat programs (Gill and Aujla 1986). Before their release to farmers, wheat cultivars are evaluated in the Karnal Bunt Screening Nursery (KBSN) under artificial and natural conditions (Nagarajan et al. 1997) for resistance in multilocation nurseries at KB hot spots. All popular cultivars now grown in KB-effected areas of northwest India were either rated free of disease or resistant/tolerant based on a percent coefficient of infection below 5 during the artificially inoculated KBSN tests. However, none of the cultivars maintained resistance when cultivated in farmer fields in northwest India. The field susceptibility of the cultivars may be attributed to inadvertent recording of disease escapes, less disease pressure, or a higher level of resistance under artificial testing. Use of inadequate inoculum may be one of the several reasons contributing to a disease escape or less disease pressuer. To ensure ample availability of inoculum at the onset of the critical susceptibility stage Z 49 (Zadoks et al. 1974), a common practice uses cultures initiated in December for inoculations in February and frequent transfer (at least weekly) to fresh growth medium to avoid desiccation. Therefore, fifth generation cultures are inoculated for creation of artificial epidemics.

This study compared the infection potential of cultures originating from teliospores and those obtained as successive descendants after transfer into fresh growth media. The criteria for assessing the infection potential of the cultures was estimated using the secondary sporidia either as such or through the production of primary sporidia that contribute to inoculum potential by producing secondary sporidia through the process of budding (Gill et al. 1993). The budding state was used in the case of secondary sporidia, because it is a natural phenomenon for the mass multiplication of secondary sporidia (Holton 1949; Krishna and Singh 1982, 1983; Aujla et al. 1988).

Secondary sporidia are best produced by PCs that are freshly isolated from the teliospore (Fig. 5B, p. 75). Their transfer to fresh growth medium, if required for the purpose of avoiding desiccation, has no significant impact on their potential to produce secondary sporidia. The same case is true for primary sporidia. The budding potential of sporidia also was the best in the PC and DC1 for secondary sporidia and the PC through the DC2 for primary (Fig. 5C and D, p. 75). The effectiveness of inoculum potential of the PC and DC1 was supported further by the significantly higher severity of disease they caused in spikes of the susceptible HD 2009 compared to other descendant cultures (Fig. 6, p. 75). KB symptoms did not appear in spikes inoculated with cultures obtained after fourth subculturing. The percent CI was reduced significantly from 37.60 to 15.80 in spikes inoculated with cultures resulting from the second transfer (Fig. 6, p. 75).

Based on these findings, we suggest that for satisfactory creation of artificial epidemics of Karnal bunt, inoculating test materials with cultures obtained directly from teliospores or from their first descendant cultures is important.

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Genetic analysis of Karnal bunt (Tilletia indica) resistance in bread wheat.

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Abstract. Karnal bunt of wheat caused by *Neovossia indica* (Mitra) Mundkur (Syn. *Tilletia indica*) has serious implications for the international trade of commercial grain and exchange of wheat germ plasm. In this study, generation mean analysis was carried out on six generations in six crosses of bread wheat to study the genetics of Karnal bunt resistance. A scaling test indicated the presence of nonallelic epistatic interactions. A six-parameter model revealed that dominance (h) was more effective than the additive (d) gene action due to higher magnitude of resistance. Among the epistatic effects, 'additive × additive' (i) action was more important as compared with the 'additive × dominance' (j) component. Complementary epistasis was present in three crosses (WL 6975/PBW 343, WL 6975/HD 2687, and WL 6975/HD 2009), whereas duplicate epistasis also was observed in three other crosses (W 485/PBW 343, W 485/HD 2687, and W 485/HD 2009). The implications of various gene actions in breeding for resistance against Karnal bunt in wheat is discussed.

The production of wheat is adversely affected by a number of factors including various biotic stresses. Karnal bunt of wheat (KB) has gained greater note in recent years because of its widespread prevalence in the main wheat-growing region of northern India causing significant qualitative and quantitative losses. Because the disease is soil, air, and seed borne, only limited success in control can be achieved through fungicides. Breeding of resistant cultivars is an effective method to combat this disease. We undertook a systematic study to explore the genetic basis of resistance to KB, which is a prerequisite for breeding KB-resistant cultivars of wheat.

Genetic resources with resistance or a low level of resistance to KB have been identified. Resistance can be transferred from these genotypes to high-yielding wheat cultivars through a breeding program. Much information on the nature and relative magnitude of the genetic components of variation (additive and dominance) has been generated by diallel analysis, which does not provide knowledge on nonallelic gene actions operating in the inheritance. A nonallelic interaction could inflate the measure of additive and dominance components. Therefore, identifying and estimating the components of epistasis, along with the additive and dominance components, is important so that fixed components can be exploited using suitable breeding techniques. The present study was carried out to assess the nature and magnitude of gene action on disease resistance.

Materials and methods. Two KB-resistant stocks (W485 and WL 6975) and three well-adapted and promising but KB-susceptible cultivars (PBW 343, HD 2687, and HD 2009) were sown in an RBD design with two replications at the Experimental Farm of DWR, Karnal. Crosses were made among promising wheat cultivars and the resistant genetic stocks in a diallel fashion. After harvest, a portion of the F_1 seed and the parental lines were sown for backcrossing BC_1 ($F_1 \times P_1$) and BC_2 ($F_1 \times P_2$) progenies at the Wheat Summer Nursery (WSN), Dalang Maidan, Lahaul Spiti (H.P.) during 2006. Twenty-nine populations consisting of six F_2, six F_1, six BC_1, six BC_2, and the parents were sown in a randomized block design with two replications during the 2006–07 crop season. Each plot consisted of five 2-m rows spaced 30 cm apart and maintaining a 5-cm plant-to-plant distance for the parents, F_1s, BC_1, and BC_2, and 10 2-m rows of spaced 30 cm apart maintaining a 5-cm plant-to-plant distance for the F_2s. In each replication, 10 plants of each parent, BC_1, and BC_2; five plants from each F_1; and 25 plants from each F_2 were randomly selected and tagged. All selected plants were artificially inoculated with an aqueous suspension of allantoid sporidia of *T. indica* (50,000 spores/mL) into the boot (growth stage 49) using a hypodermic syringe, followed by misting by a perfo-spray system (Warham 1984). At maturity, separate spikes of each plant in different generations were harvested. Threshed seeds were examined for disease incidence by manual sorting and counting percent infection.

Seeds were rated for resistance based on the type of sorus produced. Sorus size was grouped broadly into four grades and a numerical rating of 0.25, 0.5, 0.75, and 1.0 was assigned to each grade (Aujla et al., 1989). The percentage of grain showing KB infection with the numerical rating and the partial coefficient of infection (CI) value was obtained. The data were subjected to a scaling test (Mather 1949) and generation mean analysis (Hayman 1958).

Results and discussion. The cultivars W 485 and WL 6975 showed resistant to Karnal bunt, whereas PBW 343, HD 2687, and HD 2009 were susceptible. The F_1 mean infection was significantly lower than the midparent value, indicating the predominance of resistance over susceptibility in all the six crosses (Table 2). In the F_2, mean infection was significantly less than that of the respective P_2 in all crosses. Infection scores in the BC_1 were less than those of the P_2 and F_2, which indicated the transfer of dominant resistance genes from the P_1 (resistant parent), whereas in the BC_2, it was higher than in F_1 and BC_1, indicating a corresponding dilution of the resistance genes by crossing with a susceptible parent (P_2).

Table 2. Mean performance of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) for percent coefficient of infection for resistance to Karnal bunt.

Cross	Mean					
	P_1	P_2	F_1	F_2	BC_1	BC_2
W 485 / PBW 343	0.16 ± 0.11	28.19 ± 2.08	4.16 ± 0.89	13.27 ± 1.63	0.15 ± 0.07	9.28 ± 1.67
W 485 / HD 2687	0.16 ± 0.11	37.06 ± 3.82	0.70 ± 0.38	26.69 ± 2.54	1.78 ± 0.31	8.07 ± 1.29
W 485 / HD 2009	0.16 ± 0.11	42.26 ± 2.19	1.23 ± 0.82	19.04 ± 2.90	0.35 ± 0.15	15.43 ± 1.56
WL 6975 / PBW 343	0.74 ± 0.29	28.19 ± 2.08	14.96 ± 1.68	17.53 ± 2.34	17.74 ± 2.45	36.87 ± 4.09
WL 6975 / HD 2687	0.74 ± 0.29	37.06 ± 3.82	2.06 ± 0.84	14.10 ± 1.67	0.22 ± 0.12	16.57 ± 1.79
WL 6975 / HD 2009	0.74 ± 0.29	42.26 ± 2.19	5.91 ± 1.14	14.23 ± 1.86	2.30 ± 0.27	16.92 ± 1.39

A generation mean analysis was made separately for each cross to determine additive, dominance, and epistatic gene effects. Of the four scaling tests (A, B, C, and D) at least one, two, three, and four scales were found significant in all crosses, indicating the presence of nonallelic, epistatic interactions (Table 3). The A, B, C, and D individual scaling tests indicated the presence of an epistatic interaction for resistance to KB in all the crosses; at least one scaling test was significant. Therefore, the six-parameter model was applied. Estimates of standard notations of the six parameter model for resistance to KB are presented in Table 4 (p. 79). All types of epistatic interactions, additive (d), dominance (h), additive × additive (i), additive × dominance (j), and dominance × dominance (l), were significant in four crosses (WL 6975/HD 2009, W 485/PBW 343, W 485/HD 2687, and W 485/HD 2009), whereas additive (d), dominance (h), additive × additive (i), and dominance × dominance (l) types of epistasis were found significant in two crosses (WL 6975/PBW 343 and WL 6975/HD 2687).

Table 3. A, B, C, and D scaling tests in the different cross combinations of wheat for Karnal bunt resistance. * and ** indicate significance at the 5 and 1 percent levels, respectively.

Crosses	Scaling test			
	A	B	C	D
W 485/PBW 343	-4.03** ± 0.91	-13.80** ± 4.03	16.43* ± 7.07	17.13** ± 3.66
W 485/HD 2687	2.70** ± 0.74	-21.62** ± 4.62	68.17** ± 10.89	43.54** ± 5.25
W 485/HD 2009	-0.69 ± 0.88	-12.63** ± 3.89	31.29** ± 11.91	22.30** ± 6.00
WL 6975/PBW 343	19.78** ± 5.19	30.59** ± 8.61	11.27 ± 10.18	-19.55** ± 6.69
WL 6975/HD 2687	-2.37* ± 0.92	-5.98 ± 5.30	14.48* ± 7.89	11.41** ± 3.80
WL 6975/HD 2009	-2.06 ± 1.29	-14.33** ± 3.72	2.10 ± 8.09	9.24* ± 3.98

Chand et al. (1989) reported both additive and dominance gene effects of a diallel set involving the parents WL 711 and HD 2009 (KB susceptible) and WL 2217, UP 1008, WL 1562, Sonalika, VL 421, HB 208, TZPP, and WG 2038

Table 4. Components of generation means using a six-parameter model for Karnal bunt resistance in six cross combinations. m, mean; d, additive effect; h, dominance effect; i, additive × additive; j, additive × dominance, and l, dominance × dominance type of gene interactions. * and ** indicate significance at the 5 and 1 percent levels, respectively.

Crosses	Parameters					
	m	d	h	i	j	l
WL 6975/PBW 343	17.53** ± 2.34	-19.14** ± 4.77	39.60** ± 13.52	39.10** ± 13.38	-5.41 ± 4.88	89.46** ± 21.62
WL 6975/HD 2687	14.10** ± 1.67	-16.36** ± 1.80	39.66** ± 07.88	-22.82** ± 07.60	1.81 ± 2.63	31.16** ± 10.67
WL 6975/HD 2009	14.23** ± 1.86	-14.63** ± 1.42	34.07** ± 08.12	-18.48* ± 07.97	6.14** ± 1.80	34.87** ± 09.88
W 485/PBW 343	13.27** ± 1.63	-9.13** ± 1.67	-44.27** ± 07.45	-34.26** ± 07.32	4.89* ± 1.97	52.08** ± 09.73
W 485/HD 2687	26.69 ± 2.54	-6.3** ± 1.33	-104.99** ± 10.69	-87.09** ± 10.59	12.16** ± 5.33	106.01** ± 12.11
W 485/HD 2009	19.04** ± 2.90	-15.08** ± 1.56	-64.59** ± 12.08	-44.61** ± 12.00	5.97** ± 1.91	57.92** ± 13.45

(KB resistant). The predominant role of additive gene effects was shown in the inheritance of KB resistance by Nanda et al. (1995) and Sharma et al. (2005). Singh et al. (1995) reported three, independently segregating loci with partial dominance. Other genetic studies on KB resistance in wheat have indicated that one to nine major genes control the resistance to KB in various wheat germ plasm. The genes have been identified as influencing reaction to the pathogen (Morgunov et al. 1994; Fuentes-Davila et al. 1995; Singh et al. 1995a, b, 1999. Villareal et al. (1995) and Singh et al. (1994) also reported the analysis of six basic generations of intervarietal crosses between three resistant (HD 29, W 485, and HP 1531) and two susceptible (WL 711 and HD 2329) parents amplifying the involvement of one to two major genes together with some minor genes/modifiers imparting resistance. In the widely studied cross 'HD 29/WL 711', resistance has been shown to be controlled by a single recessive gene (Bag et al. 1999). In another study, additive gene action was observed to be more important in the genetic control of KB % infection, whereas dominant gene action was pronounced for coefficient of infection (Sharma et al. 2001).

A comparison between dominance (h) and 'dominance × dominance' (l) for negative and positive signs of gene effects revealed the preponderance of duplicate type of epistasis for resistance to KB in three cross combinations, W 485/PBW 343, W 485/HD 2687, and W 485/HD 2009. Duplicate-type epistasis will be a hindrance for the improvement of the population where dominance-type gene effects also exist and, thus, heterosis can not be exploited. Gill and Aujla (1987) reported that resistance was dominant over susceptibility and subject to duplicate epistasis.

The preponderance of complimentary type of epistasis for resistance to KB was observed in three cross combinations, WL 6975/PBW 343, WL 6975/HD 2687, and WL 6975/HD 2009, evidence for the occurrence of dominance (h) and 'dominance × dominance' (l) for negative or positive genes effects in contrast to complimentary gene effects where both positive and negative signs appear. Complementary-type epistasis, which is more favorable genotype improvement, was found in this study. The complementary type of epistasis also has been reported by Villareal et al. (1995).

The high frequency of epistasis observed in the present study proves the importance of nonallelic interactions for genetic control of resistance to KB in wheat. Our results show that dominance (h) effects and 'dominance × dominance' (l) epistatic effects were comparatively more important for the inheritance of KB resistance in all cross combinations, supporting the active role of nonallelic gene interactions for genetic improvement of KB resistance in wheat. Therefore, breeding methods such as reciprocal and recurrent selection by intermating desirable F_2 segregates followed by selection will help in breeding KB-resistant cultivars.

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Evaluation of wheat genotypes under different soil, tillage and production conditions through participatory varietal selection approach in India.

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Summary. Field experiments assessed the genetic potential of improved and promising wheat genotypes under different soil types, tillage options (zero and surface seeding), and production conditions (timely and late sowing) for their suitability to eastern and far-eastern parts of India. A benchmark survey identified the issues and problems of the region and four to five major problems were identified. Based on the survey results, a set of 12–15 promising, bread wheat genotypes, including released cultivars, was selected. Experiments were conducted under different production conditions (late and timely sowings), tillage options (zero and surface seeding), and problematic soils (saline and alkaline soils). We concluded that in undulating areas where soil moisture is very high, cultivars HUW 468, HW 2045, and NW 1014 performed better and gave higher yields when sown through surface seeding. Similarly, under late-sown conditions, DBW 14, NW 1014, HW 2045, HD 2643, and DL788-2 performed better than others. Zero-tillage technology was found more useful than other tillage options, because it helped to advance wheat sowing by 10–15 days in otherwise late-sown areas, and cultivars such as PBW 343, DBW 14, and HW 2045 were found suitable, because they outyielded others. At each site, one or more of the experimental genotypes showed high or good grain yield, acceptable maturity, plant height, and disease resistance compared to the check cultivars. These improved cultivars already are released in the region and many have been used in breeding programs as parents. Identification of wheat genotypes with high grain yield in individual sites underlines their value for increasing grain yield and agronomic performance. An impact assessment identified the preferred traits/cultivars of the farmers and revealed that yield is still the first choice of farmers, followed by maturity duration, plant height, plant stand, early vigor, and grain appearance. The results of this study will help breeders to produce cultivars that would be quickly accepted among farmers.

Bread wheat is a major staple food in the Indo-Gangetic Plains (IGP) of south Asia. India is one of the largest wheat producers in the world with about 27 x 10^6 ha under cultivation and production hovering around 70 x 10^6 tons (Anonymous 2001, 2005a). The demand for wheat is expected to be approximately 109 x 10^6 tons to feed a 1.3 billion population by the year 2020 to provide 180 g of wheat per person per day in India. The IGP comprise the northwestern and eastern parts of the major wheat-growing area of the country. The North Eastern Plains Zone (NEPZ) is an eastern region of India that includes the eastern UP, Bihar, Jharkhand, West Bengal, Assam, and Orissa provinces and accounts for almost 9 x 10^6 ha out of the total 27.0 x 10^6 ha area under wheat. Although the yield potential of wheat in NEPZ is about 4.5 t/ha, farmers realize a yield of just 2.2 t/ha. The constraints to potential and actual yield (technology gap, socio-economic factors, and climate) and the effects of a rice–wheat cropping system on wheat production have been discussed (Singh 1998; Jag Shoran 2003). Wheat generally is grown during the winter (mid-November to mid-April), but late receeding

of rains coupled with a delayed harvest of the preceding wet-season crops, such as basmati rice, groundnut, toria, pigeon pea, cotton, potato, and sugarcane, force wheat to be sown late, even into mid-January (Aslam et al. 1989). Wheat planting is often delayed due to the dominant rice–wheat cropping (Hobbs and Giri 1997).

Another important factor to consider is the temperature regime wherein a sizeable area in this region of India gets hot winds that coincide with grain filling (spike initiation to anthesis) and ripening (anthesis to maturity) in late-sown wheat, thus adversely affecting the grain growth and quality during the months of March and April (Anonymous 2001; Nagarajan 2002). Low productivity is observed under high temperatures, due to a reduction in the number of effective tillers/plant or per unit land area, number of grains/spike, and 1,000-kernel weight. Identifying high-yielding wheat genotypes for the IGP is a challenging task, because wheat cultivation practices and microclimates in the region are diverse (Sharma and Duveiller 2004). Keeping all the above in view, we initiated a multipronged strategy to deal with the problems directly or indirectly affecting wheat yields and to give an impetus to a lagging wheat-improvement program in this region through a project planned and executed by the Directorate of Wheat Research, Karnal.

Materials and methods. The wheat area in the eastern and far eastern parts of the country is ridden with number of diverse production factors related to soil types, temperature fluctuations, and moisture regimes that limit production potential of available wheat cultivars. The farmers grow only a few of the improved wheat cultivars available for cultivation in this region. Considering these problems, the northeastern region was chosen for participatory cultivar selection involving the farmer's participation. The experimental sites selected were near Pusa, Ranchi, Bilaspur, and Varanasi. To facilitate trial management and data recording at different sites, a field book, containing details of layout, blank data recording sheets, and other necessary instructions for trial management and data recording was provided to each collaborator. Different sets of improved but promising cultivars (12–15) along with checks were selected for specific production conditions such as saline-alkaline soils, timely and late-sown conditions, high-moisture areas along with different tillage options such as zero and surface (Table 5).

Table 5. List of the improved wheat cultivars and checks tested at four sites using farmers' preferred attributes.

Center	Cultivars and checks used	Preferred attributes
IARI–Pusa	Test cultivars: HD 2733, PBW 343, HP 1731, HP 1761, HP 1744, HD 2643, HW 2045, PBW 443, PBW 373, HUW 468, K 9107, NW 1012, NW 1014, HI 1418, HI 1454, HI 149 Checks: UP 262, HUW 234, C 306, Sonalika	Grain yield, maturity duration, plant height
IGKV–Bilaspur	Test cultivars: GW 190, DL 788-2, GW 273, HW 2004, GW 173, LOK 1, MP 5013, GW 322, DL 803-3, HI 1500, HI 1490, HD 2781, HI 1498, RAJ 1555, GW 1172 Checks: Sujata, C 306, WH 147, Sonalika	Plant stand, early vigor
BAU–Ranchi	Test cultivars: HP 1731, HP 1633, HD 2733, HD 2643, HUW 468, LOK 1, NW 1012, NW 1014, K 9107, DL 788-2, DL 803-2, PBW 343, PBW 373, HW 2045, PBW 443, HP 1761, UP 2338 Checks: UP 262, RR 21, Kanchan, Kundan, C 306, HUW 234, Sonalika	Grain appearance, spike size
BHU–Varanasi	Test cultivars: HUW 468, PBW 343, HD 2643, RAJ 3765, HUW 533, KRL 1-4, KRL 19 Checks: HUW 234, UP 262, Sonalika	Disease resistance, foliage color

The field trials were planted in completely randomized block design with two replicates. Individual plots were seeded using the standard seed rate of 120 kg/ha. Each genotype was grown in an individual plot having 50 30-m rows spaced 0.25 m apart. In most cases, the trials were planted within the recommended sowing period under each production condition. Recommended doses of fertilizers, irrigation schedule, and other management practices were applied at each site.

Data were recorded for the predecided attributes under each production condition. At maturity, plant height was measured for each plot from ground level to the tip of the spikes. Days-to-maturity was recorded when peduncles changed color. After maturity, plots were individually harvested and threshed. Grain yield was recorded on an indi-

vidual plot basis at each site. Thousand-kernel weight was recorded from grains randomly taken from each plot. Each 'year × site' combination was considered a unique and random environment, whereas genotypic effect was analyzed as fixed. The highest yielding genotype was compared with the checks to assess their genetic superiority. Along with grain yield, other agronomic characters were considered to determine superiority and adoption potential of the highest yielding experimental lines. Each experiment was conducted at a minimum of five locations for 3 years. The farmers and scientists were invited for a joint evaluation of the experiments. Only the farmers determined the traits of preference for each production condition. The location data were analyzed, and the results are presented below.

Results and discussion. The production condition experiments conducted for 3 years were analyzed for the cultivars that suited each production condition and tillage option along with the preferred traits. A significant effect was observed for location on grain yield, 1,000-kernel weight, days-to-heading and maturity, and plant height each year (ANOVA not shown). The genotypes differed significantly ($P < 0.05$) for most of the traits each year. The 'genotype × site' interaction was significant ($P < 0.05$) for all traits, suggesting that the relative genotypic values for these traits changed significantly over sites. A wide range of values among genotypes for individual traits indicated wide variation. Variation among sites for each production condition in all years suggested significantly distinct environments (data not shown). The least significant difference was estimated and used for comparing the performance of genotypes under saline soils. Performance, with respect to grain yield, greatly varied across sites and production conditions, suggesting diversity among the sites. The most suitable genotypes for each production condition and for the different sites were identified based on performance primarily judged by grain yield, mean 1,000-kernel weight, maturity, plant height, and resistance.

Table 6. Performance of promising wheat genotypes under saline soil conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India.

Genotype		HUWL 2081	NWL(S) 13	KRL 19	LSD
Salinity	pH	8.3	8.5	8.3	—
	Ece	0.32	0.28	0.33	—
Maturity duration		123	124	125	2.11
1,000-kernel weight (g)		41.4	38.1	40.4	2.93
Yield (Q/ha)		39.5	38.8	37.3	1.40

Evaluation of genotypes for salinity tolerance. Of the 15 genotypes, including advanced lines that were evaluated at five locations, and based on the mean yield performance and attributing traits for salinity/alkalinity resistance, only two genotypes, HUWL 2081 and NWL(S) 13, recorded significantly higher grain yields than the best check cultivar KRL 19. The rest of the genotypes, including the checks KRL 1-4 and KH 65, were found comparable to the best check cultivar KRL 19 (Table 6).

Evaluation of genotypes under zero tillage. We observed that wheat sown after November has a decrease in grain yield by 30 kg/ha/day; the decrease after December is 50 kg/ha/day. To advance wheat sowing and minimize losses, using zero-tillage technology was emphasized (Singh 1994; Singh et al. 2004). Zero-tillage technology involves wheat seeding in untilled rice fields with the help of a specially designed fertilizer and a seed drill with an inverted T-type furrow opener. In addition to savings on tillage costs for timely and late-sown conditions, this technology has the potential for higher productivity where wheat sowing is delayed due to the late maturity of forecrops such as sugarcane, potato, toria, rice, cotton, or pigeon pea**.** Based on the results from three crop seasons, comparative performance of promising wheat genotypes under zero-tillage technology are presented (Table 7). From 3 years of experiments, the yield levels of late-sown cultivars under zero tillage were comparable to a timely sown wheat crop. However, cultivar differences for yield under zero tillage were conspicuous (Table 7).

Table 7. Performance of promising wheat genotypes under zero-tillage conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India (IR-TS, irrigated timely sown; IR-LS, irrigated late sown; ± the standard error.

Genotype	PBW 343	HUW 468	HW 2045	HP 1744	DBW 14	NW 1014
Production condition	IR-TS	IR-TS	IR-TS	IR-LS	IR-LS	IR-LS
Duration (days)	130 ± 3.5	120 ± 2.9	115 ± 4.1	113 ± 4.6	106 ± 4.0	115 ± 3.8
Plant height (cm)	95 ± 2.3	90 ± 1.9	100 ± 2.4	100 ± 2.8	79 ± 1.4	100 ± 3.7
1,000-kernel weight (g)	40 ± 1.5	43 ± 0.8	39 ± 1.0	39 ± 1.1	40 ± 2.1	37 ± 1.7
Yield (Q/ha)	50 ± 2.4	40 ± 2.7	45 ± 1.9	43 ± 1.7	46 ± 4.1	45 ± 3.9
Protein (%)	11.5 ± 0.4	10.5 ± 0.7	12.5 ± 1.2	12.5 ± 1.0	12 ± 0.6	11.5 ± 1.0

Surface seeding needs no tillage. Surface seeding is the broadcasting of dry or soaked wheat seeds a few days before or after harvest of paddy crop under wet/saturated soil conditions (Singh 2004). This technology was used in lowland rice fields for taking wheat crop after the harvest of paddy crop. Three genotypes, HUW 468, HW 2045, and NW 1014, gave significantly higher grain yield in comparison to other genotypes. We concluded that in the undulating areas of eastern India where soil moisture restricts the wheat sowing, the above three cultivars could be grown under surface seeding to harness the maximum profit by increasing the cropping intensity (Table 8).

Table 8. Performance of promising wheat genotypes under surface seeding at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India (IR-TS, irrigated timely sown; IR-LS, irrigated late sown; ± the standard error.

Genotype	HUW 468	HW 2045	NW 1014
Production condition	IR-TS	IR-TS	IR-LS
Duration (days)	120 ± 1.4	115 ± 1.2	115 ± 1.3
Plant height (cm)	90 ± 2.0	100 ± 1.9	100 ± 1.7
1,000-kernel weight (g)	43 ± 0.8	39 ± 0.9	37 ± 0.7
Yield (Q/ha)	40 ± 3.2	45 ± 3.4	45 ± 2.9

Table 9. Performance of wheat cultivars under late sown conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India.

Genotype	Yield (Q/ha)	Plant height (cm)	Disease score		Grain size
			Leaf blight	Brown rust	
DBW 14	45.75	85.0	24	0	Bold
NW 1014	43.97	105.0	35	0	Medium
HW 2045	37.82	98.0	35	0	Medium
RAJ 3765	37.32	89.0	46	0	Medium
HD 2643	36.97	95.0	34	0	Medium
DL 788-2	35.00	85.0	46	0	Bold
HUW 234	23.97	87.0	35	60S	Small
CD (P= 0.05)	4.16	5.3	—	—	—

Suitability of cultivars to late-sown conditions. A set of 15 promising wheat genotypes was taken for evaluation under late-sown conditions in eastern India where the recently released genotype DBW-14 outyielded others. This unique genotype, in addition to high yield, shorter duration, and better disease tolerance, also possessed a good degree of terminal heat tolerance and produced bold grains. Some of the other better-performing genotypes included NW 1014, HW 2045, HD 2643, DL 788-2, and RAJ 3765 (Table 9).

A number of promising genotypes were identified from the different trials conducted in three production conditions (timely, late, and rainfed) and used for on-farm seed production to increase the horizontal spread of modern, high-yielding wheat genotypes (Table 10). Cultivation of any of the farmer-preferred wheat genotypes based on need

Table 10. Performance of promising wheat genotypes under different production conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India.

Genotype	Duration (days)	Plant height (cm)	1,000-kernel weight (g)	Yield (Q/ha)	Protein (%)
Irrigated, timely sown					
PBW 343	130	95	40	50	11.5
HD2733	125	85	42	50	11.0
K 9107	125	105	45	45	12.0
NW 1012	115	90	38	45	10.5
HUW 468	120	90	43	40	10.5
CD (P= 0.05)	3.7	5.2	2.1	4.3	1.2
Irrigated, late sown					
HW 2045	115	100	39	45	12.5
RAJ 3765	110	90	40	40	10.5
HD 2643	110	85	41	40	13.0
HP 1744	113	100	39	43	12.5
DBW 14	106	79	40	46	12.0
NW 1014	115	100	37	45	11.5
CD (P= 0.05)	2.8	7.4	1.9	3.0	1.4
Rainfed					
K 8027	115	98	43	30	10.0
K 8962	100	115	50	30	11.5
HDR 77	105	75	36	25	11.5
CD (P= 0.05)	4.5	7.4	3.3	2.9	1.0

and production conditions will improve yield and reduce the cost of cultivation if matching production technology is followed.

Wheat cultivars meeting the ranking of traits preferred by the farmers' choice. Wheat cultivars possessing high grain yield along with high 1,000-kernel weight, early maturity, medium to tall plant height, and acceptable resistance levels are of paramount importance to the farmers in the regions. This study is the first comprehensive effort to employ collaborative efforts to identify improved wheat genotypes for different production conditions. Using information generated through an impact-assessment survey, we observed that the farmers still rank grain yield as the first choice followed by maturity duration and plant height when deciding which cultivars to grow for different production conditions. The participatory, cultivar-selection approach might help in increasing the extent of genetic diversity by using number of genotypes fulfilling the farmers' choice of traits (Witcombe et al. 2001). The rank of the farmers' preferred traits and choice of cultivars available are summarized in Table 11.

Table 11. Ranking of farmers' preferred traits and their available choices.

Trait	Rank	Available choices
Grain yield	I	HD 2733, DBW 14, NW 1014,HW 2045, HUW 468, HD 2643
Maturity duration	II	NW 1014, DBW 14, DL 788-2
Plant height	III	DBW 14,HUW 468, HD 2733
Plant stand	IV	DBW 14,HUW 468, NW 1014
Early vigor	V	DBW 14,HD 2643, NW 1012
Grain appearance	VI	DBW 14, K 9107, HW 2045
Ear head size	VII	K 9107, HW 2045, DBW 14
Disease resistance	VIII	HUW 468, HW 2045, DBW 14
Foliage color	IX	DBW 14,NW 1014, HUW 468

We found that grain yield continued to be the number one choice of the farmers when selecting a cultivar, followed by maturity duration, plant height, plant stand, early vigor, grain appearance, and spike size. In the northeast plains of India, however, maturity duration obviously is an important trait to fit into the shorter wheat-growing season and avoid grain shrivelling from the adverse effects of late heat. The resource-poor farmers in theses remote areas, who still grow old genotypes (Ortiz-Ferrara et al. 2006), would benefit the most by adopting these high-yielding cultivars. The tolerance mechanism of a genotype to biotic and abiotic stresses will help in improve the yield ability even under stressed environments (Ortiz et al. 2008), which may be the reason that early vigor and grain appearance are traits considered by farmers when selecting a cultivar. These efforts are being linked with participatory approach of germ plasm dissemination in the IGP especially benefiting small and marginal farmers (Ortiz-Ferrara 2001; Witcombe et al. 2001; Ortiz-Ferrara et al. 2007). The superior performance of identified genotypes over the checks indicates that farmers across the regions could benefit by adopting the high-yielding wheat genotypes for specific production conditions. In particular, resource-poor farmers in the remote areas who still grow Sonalika (Ortiz-Ferrara et al. 2006) would benefit the most by adopting these high-yielding, experimental lines.

We concluded that suitable wheat cultivars are available to fulfil the farmers' preferred traits. These results demonstrate the important role that PVS experiments play in identifying the production conditions of specific wheat genotypes to increase wheat yields in regions where the livelihood of farmers are integrally associated with wheat production. The adoption of different tillage technologies for growing wheat under diversified soils and production conditions also can enhance wheat yields significantly in eastern India. A future wheat-improvement program should combine as many traits of farmers' preference as possible in a cultivar to be developed for commercial cultivation.

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Characterization of wheat accessions for various metric and morphological traits.

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Summary. Advanced material of 430 wheat genotypes developed through the All India Coordinated Wheat Improvement Project (AICWIP) were characterized for 10 metric and 25 morphological traits as per DUS norms. These genotypes were grouped into different classes with respect to various traits and promising genotypes for each metric trait that was identified. Character association between these metric traits showed a high association between days-to-heading and maturity, spikelets/spike, and seeds/spike; protein content; and heading and maturity period. Desirable correlations also were observed between the traits, which can be harnessed in germ plasm improvement activities.

India is the second largest wheat-producing country at the global level. Wheat yield in the past few decades has increased, mainly due to improved germ plasm. The All India Coordinated Wheat Improvement Programme has the primary mandate to develop cultivars for different agroclimatic zones and production conditions for which wheat genotypes are put in a 3-tier, multilocational testing system consisting of the National Initial Varietal Trial (NIVT), the Advanced Varietal Trial-I (AVT-I), and the Advanced Varietal Trial-II (AVT-II). These genotypes are supposed to be high yielding, resistant to biotic stresses, and tolerant to abiotic stresses. Presently, wheat cultivars are available that suit different climatic conditions and can be fitted into different cropping sequences. Although all cultivars tested in final trial year are not identified for release, these materials are promising for many aspects and can be further utilized in breeding programs as donor lines. A trial was conducted to characterize such elite genotypes and some released cultivars for various metric and morphological traits following DUS norms.

Materials and methods. The experimental material consisted 430 wheat genotypes pooled from AVT-II trials including some released cultivars. The experimental material represented *T. aestivum* subsp. *aestivum,* and *T. turgidum* subsps. *durum* and *dicoccum*, and triticale strains. These genotypes were planted at the DWR farm for two consecutive seasons under timely sown conditions in an augmented block design along with three checks Sonalika, Kalyansona, and PDW 215 (Surum). The plot size was a double row 2.5-m long. The recommended practices were followed in order to raise a healthy crop. Data were recorded on metric and morphological DUS characters using 10 randomly selected plants/spikes

for as per the standard norms (Kundu and Nagarajan 1998) (Table 12). The data were analyzed to work out range and mean for metric traits and frequency of genotypes in different classes of all the traits was also calculated.

Results and discussion. The 430 genotypes included in the study consisted of 364 *T. aestivum* subsp. *aestivum,* 60 *T. turgidum* subsp. *durum,* two *T. turgidum* subsp. *dicoccum,* and four Triticale cultivars. The analysis showed a wide range and more variability for all the metric traits (Table 13). The frequency of genotypes in different classes was calculated for all traits under study (Fig. 7; Table 14, p. 87). The identification of promising genotypes for each of the metric characters suggested that there is hope for further improvement of wheat cultivars. Promising genotypes for various metric traits are shown in Table 15 (p. 88). Early maturing genotypes are considered desirable to fit in various crop sequences. Spike length, number of spikelets, and seeds/spike are the trait that directly or indirectly contribute to the yield. Similarly, high

Table 12. Metric and morphological DUS characters recorded on 450 wheat genotypes pooled from the Advanced Varietal Trial-II, Karnal, India.

Metric traits
Days-to-50% heading, days-to-maturity, plant height (cm), spike length (cm), number of spikelets/spike, number of seeds/spike, flag leaf length (cm), flag leaf breadth (cm), 1,000-kernel weight (g), and protein content (%)
Morphological traits
Plant growth habit, coleoptile color, auricle color, auricle pubescence, flag leaf angle, waxiness, foliage color, angle of spike, spike color, spike shape, spike density, awn length, awn color, outer glume shoulder shape, outer glume pubescence, glume beak length, glume beak curvature, grain color, grain shape, grain texture, grain size, brush hair length, brush hair profile, germ width, and grain crease

Table 13. Range, mean, coefficient of variability, and standard error for metric traits recorded on 450 wheat genotypes pooled from the Advanced Varietal Trial-II, Karnal, India.

Character	Minimum	Maximum	Range	Mean	Coefficient of variability	Standard Error
Days-to-heading	71.0	125.0	54.0	93.0	6.85	0.31
Days-to-maturity	121.0	175.0	54.0	133.0	6.04	0.39
Plant height (cm)	61.0	151.0	90.0	95.0	10.61	0.49
Spike length (cm)	6.0	16.8	10.8	10.4	16.09	0.08
Number of spikelets / spike	14.0	28.0	14.0	19.0	10.43	0.10
Number of seeds / spike	30.0	96.0	66.0	55.0	17.28	0.46
Flag leaf length (cm)	16.7	42.0	25.3	28.1	14.20	0.19
Flag leaf breadth (cm)	1.1	2.8	1.7	1.9	15.05	0.02

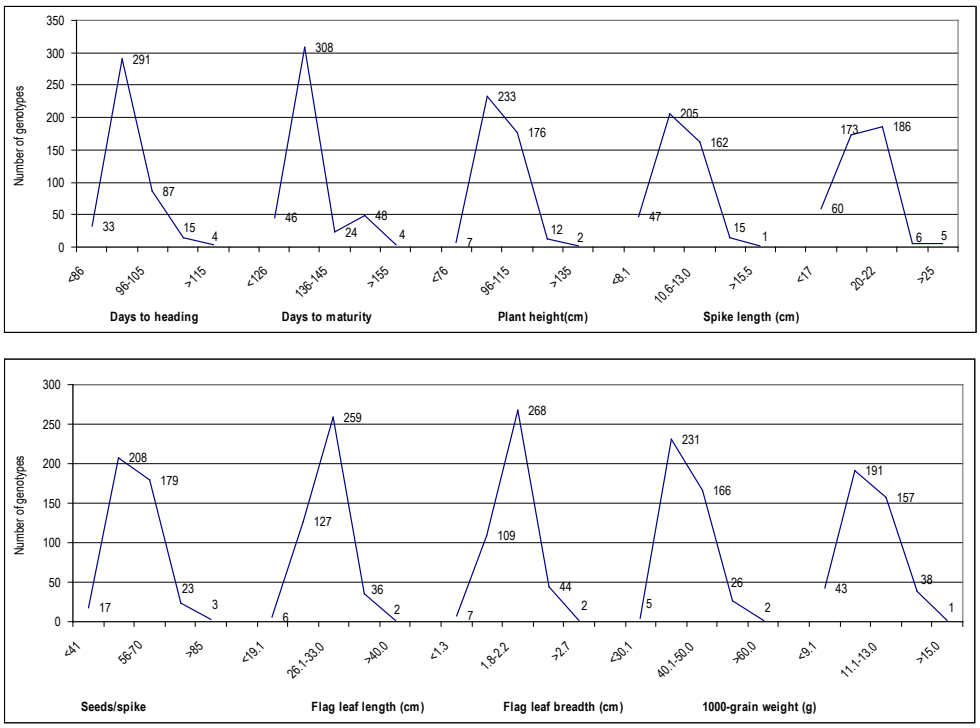

Fig. 7. Frequency distribution for the ten metric traits of days-to-heading, days-to-maturity, plant height (cm), spike length (cm), seeds/spike, flag leaf length (cm), flag leaf width (cm), and 1,000-kernel weight (g) for the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India.

Table 14. Frequency distribution for various morphological characters of the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India.

Character	Frequency of genotypes in different classes
Plant growth habit	Erect – 233, Semi-erect – 191, Semi-spreading – 6
Coleoptile color	Green – 402, Pink – 6
Auricle color	Dark purple – 81, Purple – 83, Colorless – 266
Auricle pubescence	Dense –58, Moderate – 202, Sparse – 98, Absent – 70
Flag leaf angle	Erect – 220, Semi-erect – 199, Semi-curved – 9, Recurved – 2
Waxiness	Waxy – 126, Partially waxy – 304, Nonwaxy – 1
Foliage color	Dark green – 53, Green – 335, Light green – 42
Angle of spike	Erect – 181, Semi-erect – 198, Semi-drooping – 41, Drooping – 10
Spike color	White – 361, Brown – 69
Spike shape	Tapering – 331, Parallel – 99
Spike density	Lax – 85, Intermediate – 221, Dense – 79, Very dense – 45
Awn Length	Long (> 10cm) – 76, Medium (6.6–10 cm) – 277, Short (< 6.5 cm) – 77
Awn color	White – 319, Brown – 68, Black – 43
Outer glume shoulder shape	Sloping – 79, Round – 133, Square – 150, Elevated – 68
Outer glume pubescence	Densely pubescent – 19, Pubescent – 32, Nonpubescent – 379
Glume beak length	Long (> 5 mm) – 178, Medium (2–5 mm) – 196, Short (< 2 mm) – 56
Glume beak curvature	Strong – 8, Medium – 209, Weak – 212
Grain color	White – 25, Amber – 396, Red – 8
Grain Shape	Ovate – 145, Oblong – 238, Elliptical – 45
Grain texture	Hard – 153, Semi-hard – 24, Soft – 36
Grain size	Bold – 97, Medium – 290, Small – 43
Brush hair length	Long – 102, Medium – 212, Short – 116
Brush hair profile	Pointed – 133, Medium – 148, Blunt – 149
Germ width	Wide–62, Medium–311, Narrow–57
Grain crease	Shallow–72, Medium–180, Deep–178

thousand-grain weight shows grain boldness that is one of the major yield components. Among the bold seeded genotypes, most are durum but few aestivum genotypes, such as RW 482, HW 3029, K 9266, HS 396, K 9706, K 9263, HD 2733, and K 9545, also have been identified to possess bold grains. Flag leaf is considered as most efficient leaf for photosynthesis and for this reason, large flag leaf is desirable for selecting the genotypes that can have efficient carbon assimilation system. Protein content is an important quality parameter and the genotypes having more protein content coupled with bold grains may be promising for improving nutritional quality.

Correlations between the metric traits were computed and the results revealed a high and positive correlation between days-to-heading and maturity, spikelets/spike, seeds/spike, protein content, heading, and maturity period (Table 16, p. 88). Genotypes with delayed heading and maturity had comparatively more protein content. Protein content also was positively associated with spike length and seeds/spike. Plant height showed positive association with maturity period and spike length. Number of spikelets/spike and seeds/spike had good association with heading and maturity period as well as spike length. Flag leaf length and breadth were found positively associated with each other. We concluded that there is a wide range of variation for almost all the metric traits in the experimental material, and promising genotypes for various metric traits can be further utilized in germ plasm improvement programs. The correlations between various traits can be utilized for selection of better genotypes for various purposes.

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Table 15. Promising wheat genotypes for various metric traits of the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India (D, *T. turgidum* subsp. *durum*; Di, *T. turgidum* subsp. *dicoccum*; and T, triticale.

Character	Criteria	Genotypes
Days-to-heading	< 85	BW 267, AKW 381, BW 1055, UP 2447, HD 2680, PBW 276, HD 1925, HD 2122, HUW 227, HW 135, K 9262, K 9323, K 9324, K 9334, K 9533, PBN 332, PBW 332, RAJ 3385, WH 423, BW 1050, DL 975-1, DL 3776, K 9545, VL 687
Days-to-maturity	< 123	AKW 1071, BW 1055, HP 1659, HPW 54, HUW 326, HUW 327, HUW 435, HW 135, HW 517, K 9305, K 9334, K 9351, PBW 332, VW 189
Plant height (cm)	< 76.0	HD 1941, HD 2160, HD 2412, HW 1085, K 9451, Lal Bahadur, UP 2418
Spike length (cm)	> 13.0	K 8708, HD 2747, HPT 6 (T), HW 2045, GW 147, HI 1277, HS 361, HS 369, K 9545, VL 802, VL 804, HD 2122, HD 2705, UP 2425, HS 396, K 9743
Number of spikelets/spike	> 22	HPT 6 (T), TL 2780 (T), TL 2877 (T), HS 355, HS 361, K 9706, VL 801, WH 534, PDW 276 (D), TL 2908 (T), DDK 1013 (Di)
Number of seeds/spike	> 80	K 9451, VL 801, DWR 241, GW 147, K 9743, VL 802, HS 396, HUW 516, HW 2062-1
Flag leaf length (cm)	> 37.0	J 411, HP 1529, HD 2504, J 407, UP 2447, VL 707, HD 2747, K 8965, K 8946
Flag leaf breadth (cm)	> 2.4	HUW 55, RW 482, BW 267, GW 147, HB 501, HPW 89, HPW 143, HS 322, HS 361, HUW 311, HUW 510, HW 1085, K 9212, UP 2375
1,000-kernel weight (g)	>52.0	PDW 274 (D), MACS 2846 (D), TL 2908 (T), RW 482, AKW 38-5(D), DW 1001 (D), PDW 251 (D), HW 3029, HI 8498 (D), DWR 1013 (D), K 9266, HS 396, PDW 247 (D), K 9706, K 9263, HD 2733, NIDW 9 (D), NIDW 15 (D), PDW 248 (D), K 9545, MACS 3125 (D)
Protein content (%)	>13.0 & TGW>40g	K 8504 (D), WH 882 (D), K 8904, K 8705, DWR 1013 (D), P 10950, HD 2643, PBW 276, NI 8841, J 478, MACS 2846 (D), NIAW 129, K9743, JU 126 (D), K 8706, PBW 271, NG 14-4-1-10, JU 69 (D)

Table 16. Correlation coefficients between the various metric traits of the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India.

Character	Days to maturity	Plant height	Spike length	Number of spikelets/spike	Number of seeds/ spike	Flag leaf length	Flag leaf breadth	1,000-kernel weight	Protein content
Days-to-heading	0.779	0.118	0.065	0.263	0.219	-0.066	-0.208	0.013	0.351
Days-to-maturity		0.236	0.160	0.261	0.265	0.108	-0.281	0.173	0.504
Plant height			0.303	0.228	0.057	0.195	0.013	-0.032	0.107
Spike length				0.313	0.224	0.268	0.055	-0.152	0.279
Spikelets/spike					0.549	-0.043	0.065	-0.039	0.145
Seeds/spike						0.027	0.093	-0.067	0.225
Flag leaf length							0.218	0.091	0.116
Flag leaf breadth								0.158	-0.254
1,000-kernel weight									0.060

Genotypic effects of spring wheat on yield and nitrogen uptake, utilization efficiency, and harvest index.

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Summary. Ten spring wheat genotypes (four Indian and six Mexican) were evaluated after 180 and 300 Kg N/ha applications at CIMMYT (Centro Internacional de Mejoramiento de Maiz y Trigo), near Ciudad Obregon, Sonora, Mexico, during 1997–98 and 1998–99 for their yield potential, N concentration in grain and straw, and their relationships. From a pooled analysis, the effect of N rates on biomass, yield, and yield-attributing characters was not significant, whereas

genotypic effects on the abovementioned characters as well as on grain N concentration, uptake, nitrogen harvest index (HI), and utilization efficiency were significant. From the combined analysis across years, grain yield ranged from 7.81 t/ha (Pavon 76) to 9.13 t/ha (Baviacora 92) and HI from 39.5 % (Pastor) to 45.1 % (Baviacora 92). The range of grain N concentration was from 1.99 % (Baviacora 92) to 2.23 % (Rayon 89), uptake from 147.6 kg/ha (Pastor) to 169.5 kg/ha (UP 2338), and nitrogen utilization efficiency from 29.8 kg grain/kg N uptake (Pavon 76) to 35.6 kg grain/kg N uptake (Baviacora 92). Grain yield correlated (r) positively with HI (0.66), NHI (0.62), and grain N uptake (0.77), and negatively with N concentration in grain (-0.68) and straw (-0.64). The correlation between HI and NHI was highly positive (0.89), suggesting that enhancing these two indices could lead to higher grain yield and protein content. Therefore, these two indices should be given more emphasis for enhancing yield potential of spring wheat genotypes.

Introduction. The advent of semidwarf wheat increased yield potential during the mid-1960s. The high yielding, semidwarf, photo insensitive, wheat cultivars released after the 'Green Revolution' were selected to respond to high N input (Earl and Ausubel 1983). Genetic selection was for high harvest index (HI) under medium to high N rates, whereas, HI and NHI (nitrogen harvest index) in wheat might respond differently to N fertilizer depending on the amount and timing of the application. Efficiency in dry matter partitioning or HI is defined as the ratio of grain yield to total biomass at maturity (Donald 1962). Efficiency in N partitioning or N harvest index is defined as the ratio of N uptake by grain to total N uptake at maturity (Austin and Jones 1975).

Generally, an inverse relationship between grain yield and grain N concentration has been reported in bread wheat (Cox et al. 1985; Stoddard and Marshall 1990). However, the degree of this relationship varies with soil fertility, water availability, and other environmental factors. Maximizing grain yield and N concentration in grain with optimum N use also is essential. Nitrogen dose depends upon the yield level of the crop and the apparent nitrogen recovery. Hobbs et al. (1997) envisage that a wheat crop yielding 7.0 t/ha might require 330, 254, and 206 kg N/ha provided it shows 50, 65, and 80 % apparent N recovery, respectively. They assumed that a wheat crop without N can yield only up to 2 t/ha. Nitrogen use efficiency can be defined as the product of uptake efficiency (total N uptake/applied N through fertilizer) and utilization efficiency (yield/total N uptake). At low N rates, uptake efficiency is dominant compared to utilization efficiency, whereas utilization efficiency is relatively more dominant than uptake efficiency at high N rates (Ortiz Monasterio et al. 1997). In the past, more emphasis was given to higher grain yield irrespective of the N concentration in the grain. Therefore, our objective was to evaluate important Indian and Mexican spring wheat genotypes released during the last quarter of the 20th century for yield potential, N concentration in grain and straw, and their relationships.

Materials and methods. The experiment was at CIMMYT near Ciudad Obregon, Sonora, Mexico (27.33'N, 109.09'W, and 38-m above sea level). The soil type was a coarse sandy clay, mixed montmorillonitic typic calciorthid, low in NO_3^- N (29.5 ppm) and NH_4^+ N (6.1 ppm), medium in available P (7.7 ppm) and organic matter (0.89 %), high in K (557 ppm), and alkaline (pH = 8.0) in nature. The minimum temperature in November, December, January, and March was about 1°C lower in 1998–99 than in 1997–98.

The study consists of two N levels (180 and 300 kg/ha) in main plots and 10 historical spring wheat genotypes (six from Mexico; Baviacora 92, Seri 82, Pastor, Pavon 76, Rayon 89, and Bacanora 88 and four from India; PBW 343, UP 2338, WH 542, and HD 2329) in subplots, which were grown in a split-plot design with three replications. The crop was sown during the last week of November by plot drill into dry soil followed by irrigation to give about 300 viable seeds/m^2 in rows, 20 cm apart. At sowing time, 100 kg N/ha was applied as urea and 46 kg/ha phosphorous as Single Super Phosphate. Potash was not applied due to inherent high content of potassium (557 ppm) in the soil (0–15 cm depth). A top dressing of 200 kg N/ha through urea was made at stage DC 31 (Zadoks et al. 1974) followed by irrigation. Herbicides, such as Topik (Clodinafop-propargyl) at 250 ml/ha and Brominal (Bromixinil at 1.5 l/ha) + Harmony (Thiofensulfuron @ 25 g /ha) were used with a Knap Sack sprayer at the two-leaf weed stage for control of grassy and nongrassy weeds, respectively.

A net plot of 3.6 m^2, excluding border rows and ends, was harvested manually 7–10 days of after physiological maturity. All yield and yield-attributing characters were obtained using methods as described by Bell and Fischer (1994). At physiological maturity, a subsample of 50 tillers/plot was taken and dried for 48 hours at 70°C. Thereafter, these were threshed and 'straw + chaff' samples were collected. Grains collected from these tillers were weighed and added in yield of the plot. Afterwards, these grain and 'straw + chaff' samples were dried and ground separately. Nitrogen estimation of grain and straw was performed by the Kjeldahl method (Humphries 1956). The data of the experiment were analyzed on pooled basis by using MSTATC. The mean of the two years data were used for correlation study of important parameters.

Results and discussion. From an across years analysis, the effect of N rates of on biomass, yield, and other component characters was equal (data not given), whereas cultivar differences were significant (Table 17). Baviacora 92 was significantly taller (103 cm) and HD 2329 significantly shorter (84.4 cm) than other cultivars. Generally, the genotypes studied took 132 to 136 days between emergence to maturity, except HD 2329, which was about one week earlier. The Mexican cultivar Baviacora 92 produced the maximum biomass (17.82 t/ha), grain yield (9.13 t/ha), and 1,000-kernel weight (48.2 g) despite being lowest in spikes/m^2 (370). Seri 82 recorded the highest HI (45.9 %) and grain/spike (46.7), whereas Pastor had the lowest HI (39.5 %) and HD 2329 the lowest grain/spike (31). Cultivar differences in grain yield were in agreement with those of others (Stapper and Fischer 1990 b). At the same place, in a set of historical cultivars, Sayre et al. (1997) reported that average yield increased linearly from 66.8 q/ha (Pitic 62) to 84.8 q/ha (Bacanora 88). Generally, cultivars possessing higher spikes/m^2 showed lower 1,000-kernel weight and vice versa.

Table 17. Genotypic differences in plant height, biomass, yield and its attributing characters in pooled analysis across years.

Parameter	Plant height (cm)	Biomass (kg/ha)	Yield (kg/ha)	HI (%)	1,000-kernel weight (g)	Spikes/m^2	Grain/ spike
PBW 343	94.4	16,117	8,281	45.2	47.0	408	38.2
UP 2338	90.0	17,554	8,837	44.3	45.1	407	42.4
Baviacora 92	103.3	17,815	9,134	45.1	48.2	370	45.4
Seri 82	91.9	16,683	8,708	45.9	42.0	392	46.7
Pastor	100.9	17,687	7,924	39.5	44.8	460	34.3
WH 542	86.7	17,093	8,572	44.1	35.4	481	44.4
HD 2329	84.4	15,549	7,971	45.1	44.7	510	31.0
Pavon 76	99.2	17,191	7,808	40.0	38.7	541	33.2
Rayon 89	96.9	17,746	8,082	40.2	36.2	522	37.9
Bacanora 88	86.8	17,766	8,815	43.8	36.4	490	43.8
LSD (P=0.05)	1.7	727	302	1.5	1.2	31	2.7

The effect of N rates on nitrogen concentration and uptake in the grain and NHI was not significant, whereas straw N concentration, uptake, and NUTE were significantly higher at 300 kg N/ha compared to the 180 kg N/ha application rate (data not given). From the means of two years data (Table 18), the range of grain N concentration, uptake, and total uptake was from 1.99 % (Baviacora 92) to 2.23 % (Rayon 89), from 147.6 kg/ha (Pastor) to 169.5 kg/ha (UP 2338), and from 223 kg/ha (Pastor) to 241 kg/ha (Pavon 76), respectively. The range of straw N concentration was from 0.58 % (Bacanora 88) to 0.79 % (Pavon 76) and uptake from 53.6 kg/ha (PBW 343) to 80.4 kg/ha (Pavon 76). The maximum NUTE value was 35.6 kg grain/kg N uptake in Baviacora 92 and a minimum 29.8 kg grain/kg N uptake in Pavon 76. The highest

Table 18. Cultivar differences in N concentration in grain and straw, uptake, NUTE and NHI in pooled analysis across years.

Parameters	N Concentration (%)		N Uptake (kg/ha)			NUTE (kg grain/ kg N uptake)	NHI (%)
	Grain	Straw	Grain	Straw	Total		
PBW 343	2.19	0.60	159.6	53.6	213	34.3	74.9
UP 2338	2.18	0.66	169.5	64.3	233	33.3	72.5
Baviacora 92	1.99	0.66	160.3	65.1	225	35.6	71.1
Seri 82	2.14	0.64	163.9	57.3	221	34.7	74.2
Pastor	2.12	0.71	147.6	76.8	224	31.2	65.9
WH 542	2.07	0.63	157.8	59.5	217	35.2	72.6
HD 2329	2.20	0.71	154.3	60.4	215	32.7	71.9
Pavon 76	2.19	0.79	152.5	80.4	233	29.8	65.5
Rayon 89	2.23	0.66	158.3	70.6	229	31.0	69.3
Bacanora 88	2.08	0.58	161.9	57.9	220	35.3	73.5
LSD (P=0.05)	0.04	0.05	6.94	6.93	9.8	1.24	2.6

NHI was in PBW 343 (74.9 %) and lowest in Pavon 76 (65.5 %). Similar findings also have been reported by various workers (Halloran and Lee 1979; Dhugga and Waines 1989).

Grain yield correlated positively with HI (0.66), NHI (0.62), grain N uptake (0.77), and negatively with N concentration in grain (-0.68), straw (-0.64), and straw N uptake (-0.54). The correlation between HI and NHI was highly positive (0.89), whereas between HI and straw N uptake, it was highly negative (-0.89). Sinclair (1998) showed that NHI is directly dependent on HI and, therefore, a positive association between HI and NHI is generally expected. A positive correlation between HI and NHI has been reported in durum wheat (Desai and Bhatia 1978) and in bread wheat (Loffler and Busch 1982). Nitrogen harvest index also showed a positive association with N uptake by grain (0.72) and negative trend with straw N concentration (-0.83) and straw N uptake (-0.98), as is generally expected. To gain more information on the relationship between HI and NHI, mean NHI over two N rates and years was regressed on mean HI. The slope (b = 0.67) of the regression line, 1% increase in HI was accompanied by 0.67 % increase in NHI, suggests that improvement in NHI has lagged behind HI in wheat-breeding programs. Recently, Ehdaie and Waines (2001) also observed that a 1% increase in HI was accompanied by 0.84% increase in NHI, corroborating our findings. Biomass at maturity did not correlate well with any of the important parameters. Therefore, grain yield and protein could be maximized with selection of cultivars with high HI and NHI.

Conclusion. This study of important Indian and Mexican spring wheat cultivars at high N levels (180 and 300 kg/ha) resulted in significant differences in yield, N concentration, uptake, NUTE, and NHI. The positive correlation of grain yield with HI (0.66), NHI (0.62), and grain N uptake (0.77), and negative correlations with grain (-0.68) and straw (-0.64) N concentration exhibited the possibility of further increases in yield under high-input conditions. HI and NHI correlated positively (0.89), which suggests that enhancing these two indices could lead to higher grain yield.

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Effect of delayed nitrogen application on yield and quality of wheat.

S.C. Tripathi.

Abstract. A field experiment was conducted at Karnal to enhance grain yield, nitrogen use efficiency, and protein content by initially stressing the crop for nitrogen and rescheduling at later stages when the demand is generally high. Omitting basal nitrogen and applying it whe the plants are two-thirds at the first node plus one-third in flag leaf/flowering or three-fourths at first node plus one-fourth at anthesis gives an additional grain yield (about 2 q/ha) due to higher 1,000-kernel weight and grains/spike, compared to recommended applications when the plants at one-half basal plus one-half at crown-root initiation (CRI) or one-third basal plus two-thirds at first node. The number of spikes/m^2 was higher with the recommended N application than when it is delayed application. Furthermore, skipping basal N and applying it at later stages resulted in significantly higher N content and uptake in the grain. These treatments also recorded higher NUE (6–10 %), protein content, total N uptake (7–15 kg/ha), and nitrogen harvest index (NHI) than under recommended N application practices. However, full N applied at the first-node stage had the lowest NUE (58.0 %). This study emphasizes that initial N stress followed by a split application of N at crucial stages enhances the protein content by utilizing more N uptake, higher NUE (68-72 %), and NHI.

Nitrogen use efficiency in wheat decreases with an increase in nitrogen rate and ranges from 30–77 % (Kumar et al. 1995; Sarkar et al. 1994). Generally, nitrogenous fertilization of a wheat crop is recommended in two, equal applications, at the basal, crown-root initiation stage and when the plant leaves are one-third basal and two-thirds at the first node, i.e., stage DC 31 (Zadoks et al. 1974). However, timing the exogenous N application should be based on the demand of the crop and N capacity of the soil. The wheat crop germinates approximately 6–8 days after sowing under timely sown conditions and the crown roots, responsible for nutrient extraction, start developing at 21 days after sowing. The nutrients stored in the endosperm of the seed and the inherent N present in the soil are sufficient for crop emergence and to meet N demand up to the development of the crown-root system. Therefore, a majority of the applied basal N remains unutilized by the crop during early stages and might be lost leading to lower nitrogen recovery. Under initial condition of N stress, roots will penetrate deeper for nutrients resulting in plants tolerant to lodging.

During formation of the first node (stage DC 31), the crop requires maximum N because of the simultaneous processes of stem elongation/development and forming the number of spikelets/spike. Therefore, this time is when the crop should be given maximum N, so that full potential can be achieved. Generally, an inverse relationship exists between grain yield and grain N concentration in bread wheat (Cox et al. 1985; Stoddard and Marshall 1990). Thus, maximizing yield and grain N concentration to harness maximum N recovery and protein content is needed. We evaluated initial N stress and different timings of subsequent nitrogen applications, including the existing recommendations as a control, with the objective of enhancing yield, NUE, NHI, and protein content in wheat.

Materials and methods. A field experiment was conducted at the Directorate of Wheat Research, Karnal (Latitude 29°43' N, longitude 76°58' E; altitude 245 m) during the winter seasons of 1999–2000 and 2000–01. The average annual precipitation at Karnal is >600 mm and is erratic. The trial included eight N application timings (T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis) replicated three times in a randomized block design. The soil of experimental plot was a sandy loam with low organic carbon (0.359 %) and available nitrogen (139.0 kg/ha) and medium in available phosphorous (17.6 kg/ha) and potassium (151.0 kg/ha). Phosphorous and potash were applied at 60 and 40 kg/ha, respectively, through single super phosphate and muriate of potash, and 150 kg N/ha was applied through urea. During both years, sorghum was raised as a forecrop to exhaust soil fertility and the wheat PBW 343 was sown during the second week of November. Irrigation was applied at all critical stages of the crop. Weeds were controlled by an application of Clodinafop (60 g ai/ha) in 400 L of water at 2–3 leaf stage of the weed. Biomass, harvest index (HI), and yield and its attributing characters were recorded/calculated as per standard procedures. Estimation of nitrogen in the grain and straw was by the Kjeldahl method (Humphries 1956). Nitrogen harvest index, calculated as the ratio of N uptake by grain to total N uptake at maturity (Austin and Jones 1975), was used to estimate the efficiency of N partitioning. Yearly and pooled data for all the parameters were analyzed using MSTATC.

Results and discussion. From the pooled analysis, maximum grain yield (66.09 q/ha) was recorded when N was applied whe plants were at two at stage T_6, which was about 1–2 q/ha more than all other treatments. In general, providing an initial N stress resulted in higher grain yield (T_5–T_8 treatments) compared to other treatments, mainly due to higher

Table 19. Effect of timing of N application on yield attributes and yield of wheat in experiments at Karnal, India. Treatments were T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis.

Treatment	Grain yield (q/ha)			Straw yield (q/ha)			Spikes/m²			Grain/spike			1,000-kernel weight (g)		
	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled
T_1	25.91	19.80	22.86	54.9	31.1	43.0	228	243	236	25.4	18.4	21.9	45.95	42.45	44.19
T_2	64.74	61.74	63.24	121.9	86.5	104.2	462	411	436	29.1	33.0	31.1	48.22	46.25	47.23
T_3	65.46	62.99	64.23	114.0	82.5	98.3	454	430	442	30.9	32.5	31.7	46.83	45.41	46.12
T_4	64.96	60.48	62.72	108.3	69.9	89.1	448	378	413	31.3	36.4	33.9	46.47	44.49	45.48
T_5	67.02	63.90	65.46	112.4	83.4	97.9	443	373	408	32.5	36.7	34.6	46.76	47.59	47.17
T_6	66.96	65.21	66.09	114.3	72.3	93.3	451	363	407	31.4	37.0	34.2	47.44	48.73	48.08
T_7	66.49	61.92	64.21	117.3	78.3	97.8	461	339	400	29.3	37.4	33.4	48.35	49.11	48.73
T_8	67.34	64.15	65.74	119.3	68.9	94.1	482	314	398	29.4	40.4	34.9	47.78	50.75	49.26

Table 20. The effect of N scheduling on N content and uptake in grain and straw in field experiments at Karnal, India. Treatments were T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis.

Treatment	N Concentration (%)						N uptake (kg/ha)						Total N uptake (kg/ha)		
	Grain			Straw			Grain			Straw					
	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled
T_1	1.256	1.253	1.254	0.307	0.290	0.298	32.6	26.0	29.3	16.8	9.1	12.9	49.4	35.2	42.3
T_2	1.628	1.586	1.607	0.345	0.347	0.346	105.3	97.9	101.6	42.0	30.0	36.0	147.4	127.9	137.6
T_3	1.641	1.503	1.572	0.348	0.350	0.349	107.4	94.7	101.1	39.7	28.9	34.3	147.1	123.7	135.4
T_4	1.593	1.519	1.556	0.357	0.372	0.364	103.5	91.7	97.6	38.6	26.0	32.3	142.0	117.7	129.9
T_5	1.730	1.641	1.685	0.343	0.348	0.346	115.9	104.9	110.4	38.6	29.2	33.9	154.5	134.0	144.3
T_6	1.794	1.711	1.753	0.342	0.348	0.345	120.1	111.6	115.9	39.0	25.3	32.2	159.2	136.9	148.0
T_7	1.761	1.729	1.745	0.347	0.355	0.351	117.0	107.1	112.1	40.6	27.9	34.3	157.6	134.9	146.3
T_8	1.823	1.775	1.799	0.340	0.345	0.342	122.8	113.9	118.4	40.6	23.8	32.2	163.4	137.6	150.5
CD (P = 0.05)	0.095	0.126	0.077	0.01	0.01	0.007	8.5	11.7	7.0	3.3	6.4	3.5	8.2	13.3	7.6

1,000-kernel weight and number of grain/spike (Table 19, p. 93). Even a 75% N application at the first node (DC 31) and 25% at flag leaf or flowering stage significantly increased 1,000-kernel weight compared to N applications at the recommended time. These observations were similar to Sharma and Tiwari (2004), who reported higher wheat yields at different N levels (60, 120, and 180 kg/ha) by skipping a basal, N dressing and splitting the application in contrast to traditional practices. Similar N stress treatments followed by split applications yielded lower spike/m^2 compared to treatments T_2 or T_3. Grain and straw yield, number of spike/m^2, and 1,000-kernel weight in 1999–2000 were higher than 2000–01 because of more favorable climatic conditions. The number of grains/spike were higher in 2000–01 compared to 1999–2000.

Exposing the crop to initial N stress and followed by augmentaion with two split doses resulted in significantly higher grain N concentration and uptake compared to other treatments (Table 20, p. 93). On the other hand, straw N concentration and uptake were equal among treatments with initial N stress and recommended practices. Significantly higher straw N concentration (0.364%) were found when whole N was applied at first node stage in the pooled analysis. Total N uptake in treatments with delayed N (T_6 or T_7) was higher than in the recommended N application. Initial N stress followed by a split application of N enhanced the ability of plants to absorb more N. The pooled analysis (Table 21) showed a significantly higher NUE (68–72%) with delayed N treatments (T_5 to T_8) compared to the recommended N practice (58–63 %). The lowest NUE was recorded when full N was applied at the first-node stage. A higher NHI is more significant than higher NUE in reflecting higher yields. In this study, delayed N application (T_5 to T_8) recorded high NHI (76.6 to 78.9 %) compared to T_2 and T_3 (73.9–74.8%). In a study of ten, high-yielding spring wheat genotypes (Indian and Mexican) at CIMMYT, Mexico, Tripathi et al. (2004) reported that high yield could be achieved with higher HI (r = 0.66) and NHI (r = 0.62). Furthermore, omitting basal N application and splitting the N doses (T_5 to T_8 treatments) gave significantly higher protein content (10.5–11.3%) compared to the recommended practice (9.8–10.0%). Therefore, delayed N application enhances wheat yield, total N uptake, NUE, NHI, and protein content.

Table 21. Effects of N scheduling on protein content, NUE, and nitrogen harvest index (NHI) in field experiments at Karnal, India. Treatments were T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis.

Treatment	Protein content (%)			NUE (%)			NHI		
	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled
T_1	7.85	7.83	7.84	—	—	—	0.655	0.724	0.690
T_2	10.17	9.91	10.04	65.33	61.80	63.53	0.714	0.765	0.739
T_3	10.26	9.39	9.83	65.13	59.00	62.06	0.730	0.766	0.748
T_4	9.96	9.49	9.72	61.73	55.00	58.04	0.728	0.777	0.752
T_5	10.81	10.26	10.53	70.06	65.86	68.04	0.750	0.782	0.766
T_6	11.21	10.69	10.95	73.20	67.80	70.46	0.754	0.816	0.785
T_7	11.01	10.81	10.91	72.13	66.46	69.73	0.742	0.795	0.768
T_8	11.39	11.09	11.25	76.00	68.26	72.13	0.751	0.828	0.789
CD (P=0.05)	0.59	0.79	0.48	4.7	5.4	3.5	0.029	0.045	0.026

In this two-year study, we observed that providing an initial N stress followed by split applications of N at later stages (T_2 and T_3 recorded higher yield compared to T_5 to T_8). Protein content, NUE, and NHI also improved significantly compared to conventional practices. In wheat, delayed N application enhances nitrogen use efficiency and NHI with a simultaneous increase in grain quality.

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Induced, high-yielding mutants in wheat.

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Mutation techniques are a novel approach for enhancing the level of genetically conditioned variability of a species within a short time. Selection can isolate superior genotypes (mutants) for various traits. Because wheat is a self-pollinated crop, mutagenesis is an alternative approach for generating variability. Investigations on the effects of chemical mutagens in inducing variability have received much attention because of their utmost importance in plant breeding. Among chemical mutagens, ethyl methane sulphonate (EMS) and sodium azide (SA) were used for inducing mutations in cereals (Panse and Sukhatme 1967; Awan et al. 1980). An experiment was aimed at isolating and characterizing the mutants for yield traits using EMS and SA in wheat.

For the mutagen treatment, 1,000 healthy seeds of four high yielding wheat genotypes, HP1633, HP1731, K9006, and K9107, were presoaked in distilled water for 1 hour and, thereafter, treated in separate sets containing freshly prepared 0.01, 0.02, 0.03, and 0.04M EMS and 0.5, 1.0, 1.5, and 2.0 mM SA in phosphate buffer. The pH was 7.0 for EMS and 3.0 for SA. The seeds were completely submerged in the solutions (500 mL) for 4 hours and then washed thoroughly in running water for two hours before sowing to remove the residual chemicals. One thousand untreated dry seeds of all the four genotypes were soaked separately in distilled water for 4 hours and served as a control for comparison with mutagen-treated seeds.

A total of 36 treatment combinations, including four controls, were sown immediately after treatment with EMS and SA at the Agriculture Research Farm, Banaras Hindu University, Varanasi. The plot size was 20 5-m rows of with an inter- and intrarow spacing of 25 cm (EMS) and 10 cm (SA). From each treatment, all the plants that represented the M_1 generation were harvested separately for raising the M_2 generation. Seeds from individual M_1 plants were space planted in single, 5-m row. Untreated seeds (control) also were sown after each tenth row for comparison. Individual plants were observed for various yield traits, and nine plants showing wide differences were selected and harvested separately for raising the M_3 generation. These mutants showing variability for yield traits were observed at various doses of EMS and SA. The mutants were confirmed as true breeding, because all the mutant seeds gave rise to morphologically similar plants in the M_3 that were quite distinct from the control.

All the nine mutants were harvested and planted in randomized block design with 3 replications in double row plots of 5-m length. Ten plants from each mutant progeny row were taken at random and characterized for plant height (cm), number of tillers/plant, openness of flower glumes (degree), ear length (cm), number of grains/spike, 100-seed weight (g), yield/plant (g), grain shining, ear position, and lodging. The data were subjected to ANOVA according to Georgiev (1982).

The ANOVA for yield traits, using mutant and control populations, indicated that all the treatments differed significantly for plant height, number of tillers/plant, openness of floret, spike length, number of grains/spike, 100-seed weight, and yield/plant (Table 22, p. 96). Both EMS and SA were effective in inducing variability in wheat genotypes at both low and high concentrations that depended on the sensitivity of the genotype to the chemical and their concentra-

Table 22. Analysis of variance for various traits in wheat mutants (** Significant at the 1% level).

Source	df	Plant height (cm)	Number of tillers/plant	Openness of flower (degree)	Spike length (cm)	Number of grains/ spike	100-kernel weight (g)	Yield/ plant (g)
Replication	2	0.56	0.02	0.002	0.001	0.01	0.001	0.03
Treatment	12	453.62**	11.79**	1.27**	9.63**	22.12**	0.95**	16.85**
Error	24	0.64	0.03	0.004	0.006	0.03	0.001	0.06
Total	28							

Table 23. Performance of mutants and their control for various traits in wheat (characters in *italics* are the alterations/mutations compared to control; ** significant at the 1% level).

Mutant	Treatment	Yield/ plant (g)	Plant height (cm)	Number of tillers/ plant	Open-ness of flower (degree)	Spike length (cm)	Number of grains/ spike	100-kernel weight (g)	Grain	Spike position	Lodging
HP1633											
Control	—	15.43	96.89	9.56	3.17	11.38	45.68	3.56	Normal	Semi drooping	Susceptible
1	0.5 mM SA	18.45**	97.23	9.39	5.47**	11.56**	51.68**	4.63**	Normal	Semi drooping	Susceptible
HP1731											
Control	—	18.46	90.01	10.22	2.83	12.10	53.19	3.57	Normal	Semi erect	Susceptible
2	0.01 M EMS	20.42**	91.56	9.87	3.13**	12.32**	54.35**	3.74**	*Shining*	Semi erect	Susceptible
3	2.0 mM SA	16.62	75.27 **	10.25	3.03**	12.10	53.47	3.01	Normal	Semi erect	Susceptible
K9006											
Control	—	19.24	108.26	9.28	3.37	13.78	55.32	4.03	Normal	Semi erect	Susceptible
4	0.01 M EMS	22.18**	104.26**	9.81**	3.17	15.27**	55.40	4.63**	*Shining*	Semi erect	Susceptible
5	0.02 M EMS	20.99**	105.07**	15.40**	3.53**	15.11**	55.65*	3.95	*Shining*	Semi erect	*Resistant*
6	1.5 mM SA	19.77*	105.45**	9.54	3.63**	16.37**	55.47	3.75	Normal	*Erect*	Susceptible
K9107											
Control	—	21.71	108.74	9.37	3.10	12.86	52.42	4.69	Normal	Erect	Resistant
7	0.03 M EMS	23.81**	107.64	9.54	3.27**	12.43	53.62**	4.93**	*Shining*	Erect	Resistant
8	1.0 mM SA	18.33	76.60**	9.63	3.47**	11.13	52.91**	3.62	Normal	Erect	Resistant
9	1.5 mM SA	22.01	79.78**	14.33**	3.37**	10.46	55.98**	2.83	Normal	Erect	Resistant
S.E. ±		0.20	0.65	0.14	0.05	0.06	0.14	0.03			

tion. Mutant 1 was derived from the parent HP1633, whereas mutants 2 and 3 were isolated from HP1731. Three mutants were isolated from each of the remaining parents, K9006 (mutants 4, 5, and 6) and K9107 (mutants 7, 8, and 9). Out of these nine mutants, six showed a significant yield advantage over the respective parent cultivar on a per plant basis (Table 23) and also were promising for yield-component characteristics. In addition to these six high-yielding mutants, three dwarf mutants were isolated from HP 1731 and K 9107. Among these, mutant 9 was dwarf mutant with high tillering and more grain/spike. All mutants except mutant 4 had a high degree of openness of florets compared to the parents, which is expected to promote out-crossing and could be utilized effectively in a hybrid development program.

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Augmenting the Indian wheat improvement program through national nurseries.

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Summary. The Directorate of Wheat Research (DWR) coördinates five national nurseries each year in which genotypes are evaluated in multilocation testing and promising genotypes showing superiority over respective checks for three or more years are identified/confirmed as donors for specific traits. These genetic stocks are important in Indian wheat-improvement programs.

Introduction. India has a very rich biodiversity in wheat. The Green Revolution in India is the result of the introduction of exotic wheat genotypes from the USDA and CIMMYT. CIMMYT, as an international center for wheat improvement, has played an important role in enriching our wheat biodiversity through various international nurseries and trials, which were utilized extensively by various wheat-improvement programs in India. Similarly, the DWR is recognized as a major wheat program in India and has played a significant role in developing and distributing wheat germ plasm in the form of national nurseries to various coördinating centers. At the national level, the DWR coördinates five nurseries every year through which genotypes are evaluated in multilocation testing. These nurseries are the Yield Component Screening Nursery (YCSN), the Salinity/Alkalinity Tolerance Screening Nursery (SAN), the Short Duration cum Late Heat Tolerance Screening Nursery (SDN), the Drought and Heat Tolerance Screening Nursery (DHTSN), and the Quality Component Screening Nursery (QCSN). These national nurseries are for multilocation evaluation and identification of donors along with their utilization at various centers. In this study, the effectiveness of the different national nurseries and their role in wheat-improvement programs is explored.

Methods. The nurseries constituted by the DWR each year consist of genotypes developed from various wheat programs at the Directorate as well as at the various centers. During their evaluation, genotypes contribute in different nurseries as their objectives are evaluated primarily at the Directorate and promising/suitable genotypes are promoted to the multilocation evaluation. The genotypes that perform better for three or more years are confirmed as genetic stocks for a particular character. Information regarding confirmation of the genotypes as genetic stocks has been collected since 1985, and their utilization is based on three criteria, tested/identified/released in coördinated trials as a cultivar, registered as a genetic stock, and used as a parent of an entry.

Results and discussion. A large number of genotypes (269) have been confirmed as genetic stocks during last 20 years.

Yield Component Screening Nursery – AKW 810, AKW 2862-2, DBPY 2000-3, DBPY 2000-4, DBPY 2000-5, DL 218-6, DL 153-2, K 9212, K 9941, Lok Bold, M 81-195-5, PBN 1479, Raj 3461, RD 45, RD 108, RD 185, RD 211, RD 213, RD 214, RD 524, RD 557, Sel.III-50, UP 2425, UP 2467, UP 2468, UP 2490, WR 180, WR 196, WR 765, WR 775, WR 887, WW 2084, YCN 28, and YCN 33 for 1,000-kernel weight; CMH-74, AKW 1948, AKW 2248, AKW 2344, AKW 2591, AKW 2660, AKW 2956, AKAW 2264, AKAW 2665, CMH 76A-962, GW 9906, JNGW 4, JNGW 11, KYZ 9712, LBP 98-301, LBP 98-304, MP 3054, MP 3075, NI 8729, PBN 1786, Raj 3486, UP 2327, VW 9113, VW 9641, WR 107, WR 201, WR 484, WR 782, WR 783, WR 798, WR 885, WR 999, YC-BW-13, YCN 39, and YCN 41 for grain/spike; HI 601, ISD 8, K 9006, LBP 98-307, NI 9768, PBN 4456, RWS 3331, RWS 3332, UNC 39-13, UNC 47-2, WW 2180, WW 2218 and YCN 35 for tillers/meter; AKAW 2344, JNGW 9, SW 2005, VW 9676, WR 829, and WR 849 for grain and tiller number; K 9922 and Lok 2 for 1,000-kernel weight and tiller number, and AKW 1071 for 1,000-kernel weight and grain and tiller number.

Quality Component Screening Nursery – CPAN 1946, CPAN 2016, CPAN 2019, GW 9912, HD 2674, HD 2793, HP 1765, ISD 215, K 9006, K 9107, K 9507, K 9906, KC 974, KYZ 9652, KYZ 9718, KYZK2K 13, MBL 2, MBL 5, NP 761, PR 2, PR 3, PR 5, PR 8, PR 9, PR 12, PR 19, PR 21, PR 22, PR 23, PR 42, PR 48, QBS 102, QBS 103, RD 363, RD 524, Sel. III 50, UP 301, VL 490, WR 5, and WR 758.

Short Duration cum Late Heat Tolerance Screening Nursery – GW 9715, GW 9904, WR 544, NCS 209 AKW 770, 85D-245, GW 2000-6, AKW 50, AKW 204, DL 7-6, J 83-39, M 80-239, P 2045, RD 191, and WH 423-6 for early heading and maturity; DBW 11, GW 2000-4, HD 2327, HD 4594, UP 2425 and WR 251 for 1000-Grain weight; CBW 12, PBN 4588, RWP 9912, RS 386, UP 2496, and WJ 89 for grain/spike; 85D-47, 85D-50, AKW 2862-1, DL 218-6, HD 2469, HD 2472, KC 975, P 10987, P 10988, WR 225, WR 703, and WR 704 for short duration and 1,000-kernel weight; AKW 619, GW 9711, GW 9712, HD 2402, HW 2045, HD 2316, HD 2367, HD 2449, HD 2516, NCS 157, UP 2260, UP 2281, UP 2282, and VH 36 for short duration and grain yield; and 85D-204, AKW 90-1, AKW 381, and Lok 1 for short duration, 1,000-kernel weight and grain yield.

Salinity/Alkalinity Tolerance Screening Nursery – AKW 65-1, BAU 2267, BW 1022, BW 1052, DL 770-2, HD 2385, HP 1529, Job 603, Job 666, Job 673, K 9006, K 9351, K 9353, K 9507, Kharchia 65, KNS 7, KNS 11, KNS 57, KNS 59, KNS 75, KRL 1-4, KRL 2-22, KRL 3-4, KRL 4-1, KRL 4-4, KRL 4-6, KRL 4-8, KRL 4-10, KRL 13, KRL 28, KRL 32, KRL 35, KRL 36, KS 133, Lok 1, M 3096, M 3097, M 3098, MPJ 12, NI 5439, NW 1001, NW 1032, NW 1053, NW 1065, NW 1067, NW 1082, NW (S) 93-3, NW (S) 93-9, NW (S) 93-11, NW (S) 93-21, Raj 3077, Raj 3730, Raj 3732, RK 59, RK 67, RK 76, SNH 9, Sonalika, WH 157, and WR 814.

Drought and Heat Tolerance Screening Nursery – 21 (S) Ad, A-9-30-1, AKW 65-1, AKW 470-7, CM 59, GWL 331, HD 2815, Hindi 62, Hyb 65, Job 828, K 8027, Kharchia 65, MP 3054, Narmada 4, NI 5439, NI 8223, Pissi local, RS 352, RS 488, RS 491, RS 519, RS 626, RS 629, RS 634, Sujata, WR 502, WR 741, and WT 245

Among the nurseries, most germ plasm lines confirmed as sources for different traits were from the YCSN, followed by those from the SAN and SDN. The YCSN and SDN evaluate genotypes for yield-component traits and a number of genotypes were confirmed as a source either singly or in combination. Out of 91 genotypes confirmed through the YCSN, 34 were confirmed for 1,000-kernel weight, 35 for grain/spike, and 14 for high tiller number. AKW 1071 was confirmed as a source for all three characters under the YCSN, whereas K 9922 and Lok 2 were confirmed for high grain weight and tiller number. Similarly, promising genotypes having short duration and yield components were confirmed as donors after 3–4 years of evaluation. Of the 57 genotypes confirmed from the SDN, four genotypes, 85D-204, AKW 90-1, AKW 381, and Lok 1, were high-yielding genotypes with short duration and bold seeds.

Three groups, based on utilization, included genotypes tested/identified/released in a coördinated system as a cultivar, used as a parent in breeding programs, or registered as genetic stocks with the National Board of Plant Genetic Resources (NBPGR). In the study, utilizing germ plasm lines as parents was considered only for those entries that were included in the All India Coordinated Trials. Out of 269 genotypes confirmed through the various national nurseries, only 59 (approximately 21.93%) genotypes passed these three criteria (Table 24). A maximum 35.09% of the genotypes

Table 24. Utilization pattern of genetic stocks confirmed from the various national nurseries. Genotypes used as parents are in *italics*, and genotypes tested/identified/released as cultivars are underlined. An asterisk (*) indicates that the line was registered with National Board of Plant Genetic Resources as a genetic stock. Nurseries include the Yield Component Screening Nursery (YCSN), the Salinity/Alkalinity Tolerance Screening Nursery (SAN), the Short Duration cum Late Heat Tolerance Screening Nursery (SDN), the Drought and Heat Tolerance Screening Nursery (DHTSN), and the Quality Component Screening Nursery (QCSN).

Nursery	Genotypes identified	Utilization (%)	Genetic stocks
YCSN	91	16.48	*DL 218-6*, *DL 153-2, JNGW 4, JNGW 11*, *K 9006*, *K 9212*, K 9941, *NI 8729*, *SW 2005*, UP 2425, *WR 107*, *WR 484*, *WW 2218, YC-BW-13, YCN 39*
SDN	57	35.09	*AKW 381,* AKW 619, *AKW* 770, AKW 2862-1*, CBW 12, DBW 11, *DL 218-6*, *HD 2327, HD 2367*, *HD 2402*, *HD 2449*, *HD 2469*, *HD 4594*, *HW 2045*, *Lok 1, UP 2282, UP 2425, WR 225,* WR 251, *WR 544*
SAN	60	25.00	*DL 770-2*, *HD 2385*, *K 9006*, *K 9351*, *K 9507*, *Kharchia 65*, *KRL 1-4*, *KRL 3-4**, *Lok 1*, *NI 5439*, *Raj 3077*, *Sonalika*, *WH 157*
DHTSN	28	32.14	*A-9-30-1*, HD 2815, *Hindi 62**, *Hyb 65*, *K 8027*, Kharchia 65, Narmada 4, NI 5439, Sujata
QCSN	40	20.00	ISD 215*, *K 9006*, *K 9107*, *K 9507*, K 9906, MBL 2*, MBL 5*, *UP 301*
Total	269	21.93	

utilized were from the SDN followed by the DHTSN (32.14%) and SAN (25%) (Fig. 5, p. 99). The utilization trend of germ plasm lines revealed that out of 269 genotypes confirmed as genetic stocks, 15% were used as parents and about 12% were evaluated as an entry in a coördinated trial. When the performance of genotypes from an individual nursery was studied, we found that highest percent of entries evaluated as cultivars was from the DHTSN (28.57%) and SDN (19.30%). More genotypes from the SAN (21.67%) and SDN (15.79%) were used as donor parents in breeding programs (Fig. 5, p. 99). Three genotypes, ISD 215, MBL 2, and MBL 5, were confirmed from the QCSN and registered as genetic stocks with the NBPGR. In addition, three genotypes registered as genetic stocks with the NBPGR, AKW 2862-1, KRL 3-4, and Hindi 62, from the SDN, SAN, and DHTSN, respectively, were confirmed as donors for different traits.

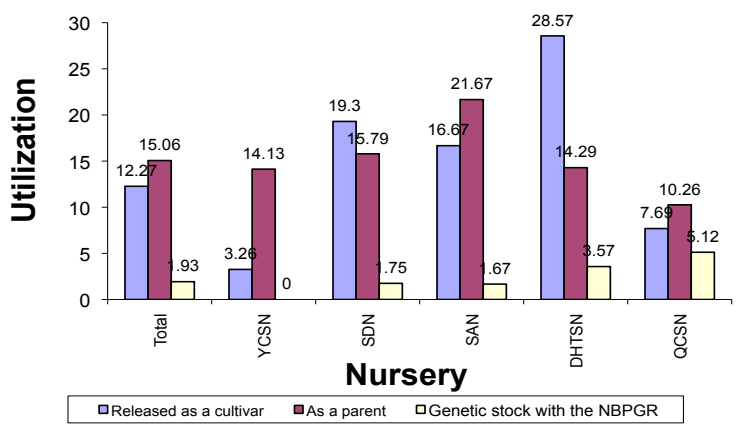

Fig. 5. Utilization of genotypes from the various multilocation nurseries in India, including the Yield Component Screening Nursery (YCSN), the Salinity/Alkalinity Tolerance Screening Nursery (SAN), the Short Duration cum Late Heat Tolerance Screening Nursery (SDN), the Drought and Heat Tolerance Screening Nursery (DHTSN), and the Quality Component Screening Nursery (QCSN).

The study also revealed that a few genotypes were confirmed as donors through different nurseries. Among these, K 9006 was identified as good source for tillers from the YCSN, for high protein and bold grain through the QCSN, and for tolerance to salinity/alkalinity through the SAN. Other genotypes that were identified as donors from different nurseries were DL 218-6 from the YCSN (1,000-kernel weight) and SDN; Sel.III-50 from the YCSN (1,000-kernel weight) and QCSN; MP 3054 from the YCSN (grain/spike) and DHTSN; Lok 1 from the SDN and SAN; and K 9507 from the SAN and QCSN.

Inferences can be drawn from this information regarding role of these national nurseries in Indian wheat-improvement programs. From the time of the Green Revolution, Indian wheat-improvement programs have benefited very much from exotic materials and, as a result, most of the cultivars released have had their origin either as a direct selection from this exotic material or from 'indigenous × exotic' combinations (Fig. 6). At the same time, the indigenous wheat-improvement programs also existed through direct selection; 'indigenous × indigenous', and 'indigenous × exotic crosses' (Singh et al. 2006). These indigenous materials include landraces of economic importance, especially as donors for quality and heat stress and indigenously developed breeding lines. Although the overall utilization of the identified genotypes from these national nurseries was less (21.85%), their role in germ plasm improvement and enhancement is encouraging. The genotypes identified from the DHTSN and SDN were utilized as genotype tested/identified/released under the AICWIP, whereas a maximum percent of genotypes used as donors were from the SAN and SDN. Genotypes identified from various nurseries or registered with the NBPGR are made available to various centers for their efficient utilization through the NGSN. The future prospects for these nurseries is very hopeful. Although the pace of utilizing these materials is slow, their effective and efficient use is encouraging and will enhance further genetic variability in wheat-improvement programs.

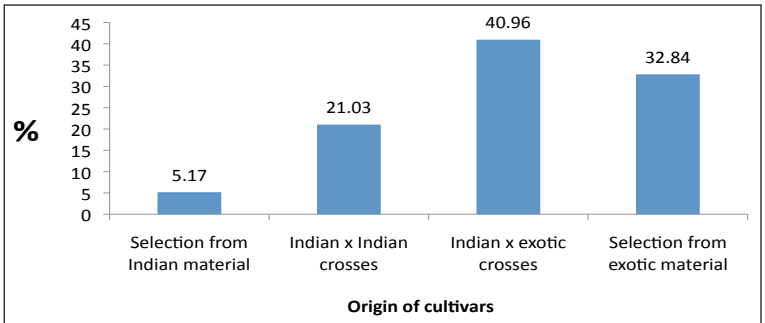

Fig. 6. Origin of released cultivars under the under All India Coordinated Trials.

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