III. CONTRIBUTIONS

PRIVATE COMPANIES

WESTBRED, LLC
Northern Great Plains – 1725 1st Ave. N., #G, Fargo, ND, 58103, USA.

Greg Fox and John Davies.

Dr. John Davies has joined our program as a wheat breeder and will head up the Hard White Spring Wheat program at this location and assist in all breeding projects. John has a Ph.D. and an M.S. in Plant Breeding and Genetics from North Dakota State University and a B.Sc. in Agriculture from the University of Western Australia.

We have released two new HRSW cultivars that possess improved scab tolerance combined with excellent standability, early maturity, and high protein. **Rush** has better adaptation to North Dakota and **Chamberlin** is better adapted to South Dakota. Certified seed will be available through the WestBred Associates in this region.

Southern Great Plains – 14604 S. Haven Rd., Haven, KS 67543, USA.

Sid Perry, Roy Dare, and Robynn Sims.

New cultivars.

Keota, a HRWW that was tested as HV9W98-143R. Keota is best adapted to the western high plains. Keota was derived from the cross 'Jagger/Custer'. The cultivar has strong straw, good shattering resistance, moderate resistance to WSMV, and good resistance to stripe rust.

Tarkio, a HRWW developed from the cross 'OK90604/KSSB-369-7//SnowWhite' was tested as HV9W99-191R. This cultivar has a strong foliar protection bundle and will be used primarily in blends for north central and northeast Kansas.

Shavano, a HWWW developed from a bulk population was tested as HV9W98-926W. Shavano has exceptional milling and baking properties suitable for whole-wheat applications.

Pacific Northwest – 81 Timberline Drive, Bozeman, MT 59718, USA.

Dale Clark, Dan Biggerstaff, Craig Cook, and Gail Sharp.

New cultivars.

Ledger, a HRWW that was tested as BZ9W96-788-d, is an early maturing, semidwarf cultivar adapted to the Golden Triangle area of Montana. Ledger was developed from the cross 'BZ9W92-709/MTSF1142'. BZ9W92-709 is a solid-stemmed lines selected by WestBred from the cross 'Hatton/SS-14'. SS-14 is a WestBred selection from a composite cross winter wheat population that resulted from the cross of WestBred's hard red winter Male Sterile Facilitated

Recurrent Populations (MSFRSP) with the wheat stem sawfly-tolerant spring wheat cultivars Fortuna, Lew, and Rambo. MTSF 1142 is a solid-stemmed line selected by Montana State University from the cross 'Lew/Tiber//Redwin'.

Waikea, a HWSW, was tested as BZ998-447W. Waikea is tolerant to the current biotypes of Hessian fly and the current races of stripe rust found in the PNW. This cultivar is a high-yielding, mid-tall, low PPO, semidwarf that was developed from the cross 'Spillman/WestBred 906R'.

Corbin is a HRSW that was tested as BZ996-434. This cultivar was derived from the cross 'Border/Conan'. Corbin has shown high yields with moderate tolerance to the wheat stem sawfly, although it is not solid stemmed. The quality is similar to other HRSWs in its market area.

WestBred, LLC continues to breed for high quality hard white wheat, along with the other market classes found in the PNW. The WestBred hard white spring cultivars Snow Crest and Pristine are currently being produced under IP programs for the U.S. milling and baking industry.

One-gene, Imazamox-tolerant SWWW will be released in 2008, and two-gene tolerant hard red and hard white spring wheat cultivars will be released in 2007.

Stripe rust continues to be a challenge to the breeding program in the PNW. This program coöperates with the Southwest program run by Kim Shantz in Arizona and California. Through joint efforts the programs will be releasing hard spring wheat cultivars with at least two genes for stripe rust resistance in 2007.

In addition, two stripe rust-tolerant SWWW lines are being increased for possible release in 2007.

ITEMS FROM ARGENTINA

CÓRDOBA NATIONAL UNIVERSITY
College of Agriculture, P.O. Box 509, 5000 Córdoba, Argentina.

Eight cycles of recurrent selection in bread wheat.

J.G. Astolfi, I. Robbiano, M.N. Casanova, G. Manera, and R.H. Maich.

Conducting a plant breeding program under rainfed conditions it is not a natural enterprise. Slow genetic progress is the result of the presence of 'G x E' interactions, grain-yield component compensation, and the enigmatic origin of drought tolerance. However, increasing breeder efficiency is necessary in order to satisfy the world's food requirements. With the objective to measure changes in agronomic characteristics after eight cycles of a recurrent selection program, 90 S_1-derived families (10/cycle) and 10 commercial cultivars were grown under the rainfed conditions of the central semiarid region of Argentina. Taking into account the more progressed cycles of recurrent selection (C_7 and C_8), a significant increment of 17.9 % was observed for spike biomass (C_7). Similarly, increases of 20.9 % (C_7) and 18.6 % (C_8) were measured for spike straw. Several workers have found positive associations between the number of grains and dry weight of spikes/m^2 in response to the phenotypic variation in the absence of water or nutritional limitations. However, establishing a direct relationship between the tendency to increase spike dry weight and genetic progress for grain yield should be cautiously considered.

Recent progress in divergent selection in bread wheat and hexaploid triticale.

R. Argenti, V. Davidenco, A. Masgrau, and R.H. Maich.

Our objective was to evaluate the actual agronomic performance in bread wheat and hexaploid triticale (X *Triticosecale*) using a selection index constituted by eleven traits measured at the plot level. Two samples of 118 S_0 hexaploid triticale

and 111 S_0 bread wheat progenies were sown under rainfed conditions. A disruptive selection intensity of 17 % (triticale) and 18 % (bread wheat) was applied in both directions on the frequency distributions for the selection index. The 40 S_1 triticale families (20/group) and 40 S_1 bread wheat families (20/group) were evaluated during 2005. Grain and biological yield (gr/m^2), spikes (#/m^2), and harvest index (%) were measured. Differentials and responses to selection were estimated from the S_0 progenies and S_1-derived families, respectively. Significant differences ($P < 0.05$) between the higher and lower index group mean values were observed in both species for all the variables except harvest index. In addition, mean values corresponding to the higher group were greater than those observed in the lower one. Taking into account previous results (Cereal Res Commun: in press) where realized heritability estimates were approximately 6–7 % obtained under good environmental conditions, the estimates were higher despite the more severe conditions of cultivation.

Plant breeding effects on morphological characteristics of bread wheat.

S.P. Gil, M.E. Reyna, C.S. Perrone, M.M. Cerana, and R.H. Maich.

We currently are analyzing eight cycles of recurrent selection in bread wheat. The plants were grown in the semiarid conditions of the central region of Argentina at the Experimental Farm of the College of Agriculture in Córdoba (31^o 29'S and 64^o 00'W) during 2005. We compared the C_0 (initial); C_1, C_2, C_3, C_4, C_5, C_6, and C_7 (intermediates); and C_8 (more advanced) cycles. The variables measured were spike length; spike internode length; and length, width, and area of flag leaves. Data were evaluated with ANOVA and Duncan's Multiple Range Test ($P < 0.05$).

The results indicated that the C_8 spike length was higher than other cycles with the longest spike internodes. With respect to leaves, the more evolved cycle had shorter flag leaves but wider and higher areas, regardless of the degree of significance. The shortening of the flag leaves in the more advanced cycle was observed after studying the morphological changes after three and six cycles of recurrent selection. Perhaps this behavior could be related to the plant adapting to stress conditions.

ITEMS FROM AUSTRALIA

SOUTH AUSTRALIA

UNIVERSITY OF ADELAIDE
Grain Biochemistry Group, Waite Campus, School of Agriculture, Food and Wine, Glen Osmond, SA 5064, Australia.

Daryl Mares, Kolumbina Mrva, Robert Asenstorfer, Imelda Soriano, Judith Rathjen, and Michael Quinn.

Research interests.

1. Biochemistry and genetic control of factors that cause deterioration of wheat quality prior to harvest (preharvest sprouting and tolerance to preharvest sprouting, grain dormancy, late maturity α-amylase, and black point).
2. Biochemical and genetic control of color and color stability in Asian noodles (grain and flour constituents involved in color of wheat flour and color and color stability in Asian noodles; xanthophylls, flavonoids, polyphenol oxidase, peroxidase, lipoxygenase, and nutritive aspects of cereal xanthophylls; and lutein and lutein esters).
3. Durum germ plasm with tolerance to hostile soils and root diseases and better adaptation to southern Australia.

Preharvest sprouting tolerance in white-grained wheats.

A highly significant QTL on chromosome 4A was associated with dormancy in three wheat genotypes, AUS1408, SW95-50213, and a dormant single gene red genotype, AUS1490, of diverse origin. Additional SSR markers, gwm269, and barc170, located near the center of the QTL have recently been identified and should provide near-diagnostic tools for MAS. The phenotype of lines containing the 4A alleles from the dormant parent varied from dormant to intermediate dormant with both the range and absolute values dependent on temperature during grain ripening. As temperature during ripening increased, dormancy decreased, and the range for lines containing the 4A dormancy alleles increased. A doubled-haploid population, dormant x intermediate dormant, that is fixed for the 4A dormancy allele but varies with respect to putative additional dormancy genes, has now been phenotyped and currently is being genotyped using markers specific for a number of chromosome regions previously reported to be associated with grain dormancy.

Late maturity α-amylase (LMA) in wheat.

LMA is a genetic defect that can give rise to high grain α-amylase activity, low falling number (typically 200–300 sec but in some instances < 200 sec.), in the absence of sprouting and depending on the environmental conditions during the middle stages of grain filling. The defect is present at low levels in Australian wheat breeding programs and has been identified in genotypes from the U.K., Japan, China, South Africa, Mexico (CIMMYT) and the U.S. (California) and in primary and derived synthetic wheats. Once introduced, the defect is very difficult to eliminate from breeding programs.

Our current work focuses on populations involving different sources of LMA, the underlying biochemical mechanisms involved, the duration and temperature differential required for maximal expression, and a comparison of LMA expression in genotypes with semidwarfing genes such as *Rht8* that do not depend on insensitivity to GA. Earlier work indicated that the expression of LMA was reduced in the presence of *Rht1* or *Rht2* and almost completely inhibited in the presence of *Rht1* + *Rht2* or *Rht3*, suggesting that GA was involved in this genetic defect. A recent study comparing patterns of cell death in the aleurone of LMA affected and germinating grains with GA-treated aleurone provided further evidence. Cell death was absent in control genotypes but pockets of dead or dying cells were observed distributed at random through the aleurone of LMA-affected grains but were concentrated near the scutellum in germinating grains.

Biochemical and genetic control of color and color stability in Asian noodles.

Polyphenol oxidase (PPO). Australian cultivars vary from high (unacceptable for alkaline noodles due to excessive darkening) to low in benchmark cultivars such as Sunco. Recently, a bread wheat genotype with PPO levels significantly less than Sunco and number of primary synthetic wheats with zero PPO have been identified. These appear to provide incremental improvements in color stability (i.e., reduced rate of darkening). In the absence of PPO, there is still significant darkening contributed by non-PPO enzymic activity. Synthetic derived zero PPO has been backcrossed into locally adapted, semidwarf backgrounds and separated from undesirable agronomic traits such as adhering glumes.

Flavonoids. Water and 0.1 M hydroxylamine extract compounds from whole meal or flour that are colorless at neutral pH but that turn yellow at higher pH (e.g., as in yellow alkaline noodles, YAN). The germ tissues contain both the free form and phenolic esters of apigenin-C-diglycosides that contribute to the total yellow color of YAN, whereas the seed coat or bran contains other phenolic compounds that have a minor role. Unfortunately, the endogenous hydroquinone precursor of these latter compounds reacts with hydroxylamine to give a product that has a high color yield at alkaline pH. As a result, the total color of hydroxylamine extracts cannot be used to give an accurate measure of genetic variation or to predict YAN color.

Lipoxygenase (LOX). This enzyme is implicated in the degradation of yellow xanthophyll pigments in wheat-based end-products. Variation in both 'Sunco/Tasman' and 'Opata/Synthetic' was associated with a QTL on chromosome 4B located close to the centromere and in the case of 'Sunco/Tasman', *Rht1*. A number of other populations involving low and high LOX genotypes have now been phenotyped and will be used to validate the 4B QTL. Many durum wheats have very low LOX and although low LOX is not common in bread wheats, very low or near-zero LOX synthetic wheats have now been identified.

Publications.

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ITEMS FROM BRAZIL

NATIONAL WHEAT RESEARCH CENTRE — EMBRAPA TRIGO
Centro Nacional de Pesquisa de Trigo, Rodovia BR 285, Km 174, Caixa Postal 451, 99001-970, Passo Fundo, Rio Grande do Sul, Brazil.

Brazilian wheat production and grain yield – 2004 crop and perspectives

Leo J.A. Del Duca and Eliana M. Guarienti

Brazilian wheat consumption is nearly 10 x 10^6 t/year. The 2003 national wheat crop represented an increase of 90 %, relative to the previous crop. Influenced by policy changes favoring exports and hindering imports, the production started to have prices with positive effects on Brazilian agrobusiness (P. M. Rabelo, http://conab.gov.br). Production was a result of a 20 % increase in the cultivated area and of a productivity gain of 49.5 % relative to the previous year. Farmers were stimulated by good prices in 2002 and by industrial partnerships. This progress was due to the reliability of research recommendations and a favorable climate. In the crop estimate for December 2004, CONAB (Companhia Nacional de Abastecimento; National Company of Provisioning), projected wheat production for the 2004–05 crop at 6,021.6 x 10^3 tons (Table 1). The states with the

Table 1. Production and grain yield for the 2003–04 and 2004–05 Brazilian wheat crops. Source: CONAB (December 2003 and December 2004) http://conab.gov.br.

	Production (1,000 t)		Grain yield (kg/ha)	
State	2003–04	2004–05	2003–04	2004–05
Paraná	2,954.0	3,038.9	2,500	2,250
Santa Catarina	159.5	185.2	2,150	2,300
Rio Grande do Sul	2,346.3	2,306.0	2,250	2,100
Total for southern Brazil	**5,459.8**	**5,530.1**	**2,375**	**2,187**
Minas Gerais	30.8	61.0	4,400	4,450
São Paulo	104.7	130.0	2,200	2,429
Total for southeast Brazil	135.5	191.0	2,482	2,842
Mato Grosso	—	1.7	—	3,300
Mato Grosso do Sul	184.1	204.0	1,980	1,500
Goiás	66.4	86.8	3,950	4,000
Distrito Federal	5.5	5.5	4,600	4,600
Total for west-central Brazil	**256.0**	**298.0**	**2,306**	**1,870**
Bahia	—	2.5	—	5,000
Total for northeast Brazil	**—**	**2.5**	**—**	**5,000**
Total for all Brazil	**5,851.3**	**6,021.6**	**2,375**	**2,185**

highest grain yield production were Paraná and Rio Grande do Sul, although effected by adverse climatic conditions, still had good crops. Because of the 2004–05 crop, the national wheat sector for the second consecutive time will supply 60 % of the domestic needs. Although this production benefits the trade balance by reducing imports, it increases commercialization and depresses prices for farmers. The state of Rio Grande do Sul produces a surplus of 1.5 x 10^6 tons of soft wheat that would be consumed in northeast Brazil. The high cost of freight and/or the lack of competitive prices for shipping (coastal traffic) represent the biggest problems that hurt Brazilian wheat commercialization. In addition, Argentina, which consumes only 5 x 10^6 of the 15 x 10^6 ton annual production, depresses the Brazilian wheat market with the availability for export of a volume of wheat nearly equal to the total Brazilian consumption. Imports are facilitated with extensive benefits that keep the Brazilian producer from competing equally. The Federal Government, seeking to support to national production, made available to the market some means of support for commercial producers (AGF, Contract of Option, and PEP) that can lead to the recovery of some profit. However, some measures seeking to correct structural problems, must be implemented soon or a permanent government intervention will be needed. The Brazilian wheat production needs special attention from outside the farm, where problems in infrastructure and transport are responsible for establishing limits for the sustained growth of the wheat chain sector (http://www.conab.govbr/download/safra/safra20042005Lev02.pdf).

BRS Guatambu – an alternative cultivar for crop–cattle integration in southern Brazil.

L.J.A. Del Duca, C.N A. Sousa, P.L. Scheeren, A. Nascimento Júnior, E. Caierão, M. Sóe Silva, R.S. Fontaneli, H.P. Santos, J.B. Lhamby, O. Carvalho, J.B. Marques, A.G. Linhares, L. Eichelberger, O. Rodrigues, G.R. Cunha, E.M. Guarienti, M.Z. Miranda, L.M. Costamilan, M.I.P.M. Lima, M.S. Chaves, W.C. da Luz, and A. Prestes.

The wheat cultivar **BRS Guatambu** was released in 2004 for southern Brazil, seeking to supply an alternative for early green cover of soil in no-tillage systems and favor the crop-cattle integration. BRS Guatambu was tested for double purpose (forage production and grain) and showed adaptation to that practice in trials sown in Rio Grande do Sul and Paraná in 2001–03. Developed at Embrapa Trigo from the backcross 'Amigo/2*BR 23', the cultivar is semi-late and medium to high in stature. BRS Guatambu is resistant to natural dehiscence of the spike, moderately susceptible to lodging, resistant in the field to mildew, and moderately resistant to resistant to soil aluminum conditions. BRS Guatambu is susceptible to scab, tan spot, and glume blotch when artificially inoculated. Seedling reaction in both the greenhouse and field indicate APR to leaf rust. BRS Guatambu is classified preliminarily as a soft wheat for use in crackers, cookies, sweet shop products, pizzas, fresh pasta, and in mixes with wheat for bread and/or domestic use.

BRS Tarumã – a new, double-purpose wheat cultivar for southern Brazil.

L.J.A. Del Duca, C.N.A. Sousa, P.L. Scheeren, A. Nascimento Júnior, E. Caierão, M. Sóe Silva, R.S. Fontaneli, H.P. Santos, J.B. Lhamby, A.G. Linhares, O. Carvalho, J.B. Marques, L. Eichelberger, O. Rodrigues, G.R. Cunha, E.M. Guarienti, M.Z. Miranda, L.M. Costamilan, M.I.P.M. Lima, M.S. Chaves, W.C. da Luz, and A. Prestes.

The wheat cultivar **BRS Tarumã** was released in Rio Grande do Sul in 2004 to promote technology integrating crop–cattle production. Income also is anticipated from dry matter transformed into meat, milk, or wool providing flexibility and sustainability to the croping system. Developed by Embrapa Trigo, BRS Tarumã was derived from the single cross 'Century/B 35' made in Passo Fundo in 1990. The cultivar is semi-late after early sowing (it was selected by looking for a late-early cycle with a heading period longer than the conventional early cultivars) and low stature. BRS Tarumã is resistant in the field to powdery mildew under natural infection, moderately resistant to scab under inoculation and soil borne mosaic virus in the field, moderately susceptible to tan spot and glume blotch, preliminarily classified as resistant to frost in the vegetative phase, and moderately resistant to sprouting and BYDV. In spite of its seedling susceptibility to the group of leaf rust races, BRS Tarumã consistently has been resistant under field conditions under high inoculum pressure over the years. Seedling reaction under both greenhouse and field conditions indicate resistance is expressed in the adult plant. BRS Tarumã is resistant to spike shattering and moderately resistant to soil aluminum toxicity and to lodging under normal soil fertility. Tested in early sowing for double purpose (forage production and grain) in Rio Grande do Sul and south-central Paraná in 2001 and 2003, BRS Tarumã produced 1,381 kg/ha (one clipping) and 2,075 kg/ha (two clippings) of dry matter, 19 % and 23 % better, respectively, than that of the common black oat (dry matter check). In those treatments, in the average from different sites varied by year. Tested in these same places and period, grain-yield averages were 2,996 kg/ha (without clipping), 2,568 kg/ha (1 clipping), and 2,432 kg/ha (2 clippings).

outyielding by 11 %, and 31 %, treatments with one and two clippings, respectively, the average of the two better wheat checks (from among BR 23, BR 35, CEP 24, CEP 27, and OCEPAR 21). BRS Tarumã is classified as a bread wheat for baking and pasta.

ITEMS FROM CROATIA

BC INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS
Marulicev trg 5/1, 10000 Zagreb, Croatia.

Slobodan Tomasovic, Rade Mlinar, Branko Palaverasic, Ivica Ikic, and Kristijan Puakaric.

Winter wheat breeding at the Bc Institute–Zagreb with special reference to resistance to the main fungus diseases with the goal of protecting environment.

Breeding and genetics work at the Bc Institute for Breeding and production of Field Crops is a constituent part of the program for winter wheat cultivars for Croatia. A very successful activity by the Bc Institute in the area winter wheat breeding, the results of which are known both in Croatia and abroad. Wheat breeders at the Bc Institute–Zagreb have created 81 winter wheat cultivars since 1964, when the first cultivar Vuka was introduced. By its genetic potential the fruitfulness of this varieties presents top achievements in the selection. Of 31 cultivars, some were strong standards (Baranjka and Korona, Hungary), and Marija, introduced in 1988, is still a strong standard in the Republic of Slovenia. The Croatian Committee also has strong standards (Zlatna Dolina and Super Zlatna), among which is the highly successful and stable cultivar Sana, introduced in 1983. In our breeding program, considerable attention has been given to resistance to fungal diseases. The Croatian breeders have been successful in developing resistant cultivars that have been used in commercial production and represent a source of resistance for breeding purposes. We are increasingly concerned about not polluting the environment and about producing food without using chemicals. Wheat breeders and geneticists are expected to develop cultivars that can grow with less chemical inputs.

Sources of resistance in wheat and crosses of the F_1 and F_1 x F_1 generations in resistance to Fusarium graminearum.

Over 1,500 sources of resistance to *Fusarium* were tested under artificial infection and seven genotypes were chosen and intercrossed using partial diallel crosses. The level of resistance differed markedly, ranging from 0.65 to 3.69 (on a 0–5 scale). Improved level of resistance was obtained in the F_1 generation and in 'F_1 x F_1' crosses in several combinations. Additive gene effects (i.e., minor gene effects) and dominance were noticed. The highest level of resistance was found in the F_1 and crosses involving the cultivars Bizel and Poncheau.

Testing for high quality in Bc winter wheat cultivars in large-scale trials.

The Bc winter wheat cultivars Zdenka, Mihelca, and Aura were evaluated for their rheological properties in large-scale trials at Vinkovci, Belje, and Kutjevo in 2001–02, 2002–03, and 2003–04. Laboratory testing included wet-gluten quantity and farinographic and extensographic measurements. The rheological properties of Zdenka, Mihelca, and Aura proved that they had a high genetic potential for stabile technological quality in the kernel and flour. Flour from these cultivars contributes to higher nutritive value in baking products.

Yield of Bc winter wheat cultivars from large-scale trials in 2005.

Bc winter wheat cultivars also were tested in large-scale trials in Croatia in 2004–05. The trials included both cultivars developed by domestic breeding companies and introductions, covering the majority of winter wheats grown in Croatia. The trials were at Belje, Vinkovci, and Kutjevo in 2005. Performance data of the Bc winter wheats again proved that these cultivars possess the genetic potential for high grain yield. Bc Institute wheats can assure high and stable yields for wheat producers.

Publications.

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ITEMS FROM GERMANY

INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK
Correnstraße 3, 06466 Gatersleben, Germany.

A. Börner, O. Dobrovolskaya, E.K. Khlestkina, U. Lohwasser, S. Navakode, M.S. Roeder, V. Schubert, A. Weidner, and K. Zaynali Nezhad.

Leaf rust resistance.

The majority of *Aegilops* species is characterized by the valuable potential of resistance against economically important diseases such as powdery mildew, yellow rust, and leaf rust. The *Ae. caudata* accession S740-69 possesses, among others, resistance to leaf rust inherited at the seedling stage by one dominant gene and some minor factors. The C genome of *Ae. triuncialis* and *Ae. caudata* is known to cause gametocidal effects. The expression of these effects was slightly reduced in the *Ae. caudata* accession S740-69. Therefore, six of the seven possible monosomic addition lines could be selected from the cross of *T. aestivum* subsp. *aestivum* cv. Alcedo with *Ae. caudata* accession S740-69. Selfing of these lines permitted the selection of lines with 42 chromosomes and introgressions of *Ae. caudata* caused by the gametocidal effects of the C genome on the wheat background. By using microsatellite markers, segments of *Ae. caudata* chromatin in the wheat background were detected on chromosomes 2AS, 2BS, 3BL, 4AL, and 6DL. Different F_3 populations from backcrosses of leaf rust-resistant introgression lines with a wheat like growth habit and Alcedo will be used to investigate the leaf rust resistance at the seedling stage and the location of responsible genes.

Drought stress.

In order to find QTL related to postanthesis drought tolerance in wheat two accessions, one tolerant line from Pakistan and one sensitive line from Sweden were selected as parental lines, and 143 lines of the F_2 and $F_{2:3}$ families derived from their cross were used for population genotyping using SSR markers and for phenotypic investigations. Based on a chemical desiccation method, drought stress was induced and the stress-tolerance index was calculated with a range from 23 to 55 %. For population genotyping, 550 primers were tested and a total of 356 polymorphic primers (65 %) were found. With these selected primers, all wheat genetic linkage groups will be covered. Finally, these linkage groups and data from field experiments will be used for QTL analysis.

Aluminum tolerance.

A set of 85 *T. aestivum* subsp. *aestivum* cv. Chinese Spring–*Ae. tauschii* introgression lines developed at IPK Gatersleben were grown in nutrient solutions and characterized at the seedling stage for tolerance to aluminum and to map the genetic loci involved. The experimental principle is based on a comparative evaluation between aluminum-stress conditions and a control with nutrient solution only. The root tolerance index (RTI = length of roots grown with Al / length of roots grown without Al*100) was calculated. Using microsatellite markers, a major QTL was mapped on the long arm of chromosome 4D near the centromere indicating the influence of the D genome on aluminum tolerance in wheat.

Preharvest sprouting / dormancy.

Two wheat mapping populations, the International Triticeae Mapping Initiative (ITMI) population and D-genome introgression lines, were evaluated for the domestication traits of preharvest sprouting and dormancy. Cultivation in the field and the greenhouse was used to discover the influence of environmental conditions on detecting QTL for these traits. No significant correlation between the evaluated traits and the environmental conditions was found. Under field

conditions, major QTL could be localized for preharvest sprouting on chromosome 4AL and for dormancy on chromosome 3AL in the ITMI population. Under greenhouse conditions, a major QTL on chromosome 4AL was found for both traits. The major QTL on chromosome 3AL could not be detected again. The D-genome introgression lines were researched under greenhouse conditions at first. A major QTL for dormancy was localized on chromosome 6DL, but no QTL was found for preharvest sprouting. Under field conditions, the major QTL on chromosome 6DL could not be identified again. For preharvest sprouting, it was not possible to find an important genome region. The influence of environmental conditions could not be researched.

Duplicate identification in germ plasm collections.

Genebank accessions of the Gatersleben collection were selected based on the screening of the passport data for identical cultivar names or accession numbers of the donor genebanks. Twelve potential duplicate groups consisting of three to nine accessions with identical names/numbers were selected and analyzed with DNA markers (microsatellites). A bootstrap approach based on resampling of both microsatellite markers and alleles within marker loci was used to test for homogeneity. Although several homogenous groups were identified, it became clear that only cultivar name did not allow the determination of duplicates. A combination of SSR-analysis followed by the bootstrap method and database survey considering the botanical classification and other data (origin, growth habit, donor) available is necessary in order to determine duplicates.

Leaf pubescence genes.

A study was initiated to map genes determining hairy leaves in cultivated wheat and a wheat/*Ae. speltoides* introgression line. A QTL-mapping approach also was performed to investigate the ITMI mapping population and consider the hairiness of leaves and auricles. Two major genes controlling leaf pubescence were mapped on chromosomes 4BL (*Hl1*) and 7BS ($Hl2^{Aesp}$) in the hexaploid wheat Saratovskaya 29 and a wheat/*Aegilops* introgression line ($102/00^{i}$), respectively, together with QTL determining hairiness of leaf margin (*QHl.ipk-4B*, *QHl.ipk-4D*) and auricle (*QPa.ipk-4B*, *QPa.ipk-4D*) on the long arms of chromosomes 4B and 4D. The QTL on chromosome 4D were contributed by the synthetic wheat and, therefore, originated from *Ae. tauschii*. The homoeologous, group-4 wheat/*Ae. tauschii* genes/QTL detected in the present study line up with the barley pubescence genes *Hln*/*Hsh* and Hs_b and the hairy peduncle rye gene *Hp1*. The locus seems to be pleiotropically responsible for the pubescence of different plant organs in different species of the Triticeae. Another homoeologous series may be present on the short arms of the homoeologous group-7 chromosomes, concluded from an allelic test cross between the Chinese local cultivar Hong-mang-mai carrying *Hl2* and the wheat/*Ae. speltoides* introgression line 102/00'.

Glume color and pubescence.

Microsatellite markers were used for the precise mapping and comparative studies of the genes determining the traits red glume color (*Rg3* on chromosome 1A and *Rg1* on chromosome 1B), black glume color (*Bg* on chromosome 1A), smoky-gray glume color (on chromosome 1D), and hairy glume (*Hg* on chromosome 1A). The loci were mapped to the distal regions of the chromosomes 1AS, 1BS, and 1DS, respectively, between markers *Xgwm1223* (in proximal or closely linked position) and *Xgwm0033* (distal). From the results and from the known close linkage of these genes with homoeologous gliadin loci, we concluded that we had mapped a homoeologous series and proposed the designation *Rg-A1*, *Rg-B1*, and *Rg-D1*. Genes *Rg3* and *Bg* were considered to be different alleles of the locus *Rg-A1*. Both *Rg3* and *Bg* were found to be closely linked to the major glume pubescence gene *Hg*, also mapped in the present study. The smoky-gray glume gene and *Rg2* (1D), the latter mapped previously in a synthetic wheat, were proposed to be different alleles of the locus *Rg-D1*.

Purple grain color.

Three genes for purple grain color, *Pp1*, *Pp2*, and *Pp3* (now designated *Pp1*, *Pp3b*, and *Pp3a*, respectively), were mapped using crosses between the purple-grained hexaploid wheats Purple (*Pp1Pp1Pp3Pp3* (*Pp1Pp1Pp3aPp3a*)) and Purple Feed (*Pp1Pp1Pp2Pp2* (*Pp1Pp1Pp3bPp3b*)) with the nonpurple-grained cultivars Novosibirskaya 67 and

Saratovskaya 29. The genes *Pp2* (*Pp3b)* and *Pp3 (Pp3a)* were inherited as monofactorial dominant when purple grained wheats were crossed to Novosibirskaya 67. Both were mapped in the centromeric region of the chromosome 2A. Therefore, they were suggested being different alleles at the same locus and designated *Pp3a* and *Pp3b*. In the crosses between purple-grained wheats and Saratovskaya 29, a segregation ratio of 9 (purple) to 7 (nonpurple) was obtained suggesting a complementary interaction of two dominant genes, *Pp1* and *Pp3*. To map *Pp1* as a single gene, the influence of the other *Pp* gene was taken into consideration by determining the *Pp3* genotype of the F_2 plants. The gene was mapped on chromosome 7BL, about 24 cM distal to the centromere. The *Pp1* gene was shown to be nonallelic to the *Rc-1* (red coleoptile) and *Pc* (purple culm) genes, contrary to what was previously suggested. The coloration caused by the *Pp* genes was found to have no effect on preharvest sprouting.

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ITEMS FROM HUNGARY

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Wheat season. The last wheat growing season was characterized by extreme weather and above-average rainfall. A mild January was followed by a cold February, although no freezing out was observed. The abundant rainfall in spring caused frequent early lodging. After flowering, the weather was unusually hot, after which cold weather delayed ripening. A long period of wet weather began just before the harvest, leading to a considerable deterioration in the wheat quality. Approximately 5 x 10^6 t of wheat was produced in Hungary, with a moderate yield average (4.49 t/ha).

Breeding.

Z. Bedö, L. Láng, O. Veisz, G. Vida, I. Karsai, K. Mészáros, M. Rakszegi, D. Pribék, S. Bencze, K. Puskás, and A. Uhrin.

Breeding. One new winter wheat cultivar was registered in 2005.

Mv Gorsium (Mv 04-02) is an early maturing, high-yielding cultivar with good abiotic stress resistance, selected from the cross 'GT6687-12R/F6038W12-1'. This cultivar has very good frost resistance, a firm stem, and tolerates high temperature during the grain-filling period. Mv Gorsium is moderately resistant to powdery mildew and leaf rust, and resistant to stem rust. This cultivar is a medium quality hard red bread wheat.

MAS selection. The resistance gene *Lr37*, originating from *Ae. ventricosa*, has been identified using the SC-Y15 F/R PCR marker in a set of wheat genotypes. From 219 cultivars and lines tested, gene *Lr37* was identified in 35 genotypes originating from various countries where its presence was not previously reported. One of them is Vekni, a very promising breeding line from Martonvásár, which confirms year by year the continued effectiveness of resistance against leaf rust under field conditions.

Durum wheat breeding. The most recent success in the winter durum wheat breeding project is the state registration of **Mv Gyémánt**, a high-yielding winter durum wheat variety with excellent cold tolerance and good technological quality. Two further cultivars are being tested in state variety trials that gave satisfactory results for yield and technological quality in the first year. They have been sown in the second year of the state trials.

Molecular markers linked to the yellow pigment content of durum wheat have been identified using the bulk segregant analysis model. After combining the DNA of the ten lines with the highest and the ten with the lowest yellow index, these two samples were used to look for polymorphism mainly using RAPD primers. The experiment is expected to end in February 2006.

Investigations were made on a combination developed using breeding lines with widely different values of yellow pigment content (the Austrian line PWD1216, which had high pigment content, and MvTD10-98, which had an extremely low pigment content). Based on data for the last two years, ANOVA demonstrated a significant difference between the yellow index values of the families, but the year and 'genotype x year' interaction also were significant. The difference between the yellow index values of the two parents was well in excess of the $LSD_{5\%}$ value (1.94). The yellow index was also significantly influenced by the year. The mean value for the families and parents was 25.61 in 2004 and 21.95 in 2005. The order of progeny with values close to those of the parents did not change to any great extent in the two generations, so effective selection for yellow pigment content can be carried out in both the positive and negative direction even in early progeny generations.

Disease resistance studies. Within the framework of an international (Bioexploit-EU FP6) project, molecular marker selection is being used to incorporate known resistance genes (*Lr9, Lr19, Lr24, Lr25, Lr29, Lr35, Lr37, and Lr47*) into varieties adapted to Hungarian conditions as part of a backcross program. Progeny similar to the recurrent cultivar but resistant to leaf rust have been selected from populations sown in field experiments for phenotypic testing.

The degree of infection of genotypes carrying known genes for leaf and stem rust resistance was tested in an artificially inoculated nursery. The resistance genes *Lr9, Lr19, Lr24, Lr25, Lr29, Lr35,* and *Lr37* continued to provide effective protection against leaf rust in Martonvásár, as did gene *Lr47*, which had not been previously tested. Cultivars with the gene *Sr36* were still not infected by stem rust. The resistant reaction type and less than 20 % infection was observed for genotypes carrying genes *Sr11, Sr27, Sr30* or *SrDr*, or the gene combination *Sr5+6+8+17*.

Powdery mildew isolates collected in the neighborhood of Martonvásár were used to determine the race composition of the pathogen population, the degree of virulence, and the effectiveness of known resistance genes. The following wheat powdery mildew races were dominant in 2005 (frequency in brackets): 51 (24.4 %), 72 (17.2 %), 76 (14.4 %), and 77 (12.2 %). The number of virulence genes in the pathogen population averaged 5.67. Almost complete protection against the wheat powdery mildew isolates tested was provided by the *Pm4a* + resistance gene, whereas cultivars with genes *Pm1+2+9, Pm3b or Pm3d* exhibited less than 20 % infection.

Winter wheat genotypes with adult resistance to powdery mildew were identified in field and greenhouse experiments. For the majority of the genotypes tested, the area under the disease progress curve was similar to that of Massey, the resistant control, but cultivars and lines with significantly better resistance also were found. Among the genotypes in the Martonvásár breeding stock, Mv Táltos, Mv Panna, and line Mv07-03 were found to have excellent adult powdery mildew resistance.

The field FHB resistance of lines developed from populations of old Hungarian cultivars was investigated in an artificially inoculated nursery, together with that of foreign resistance sources. The level of spike infection for 19 of the lines developed from populations of old Hungarian cultivars was less than 10 %. The average spike infection of resistant spring wheat genotypes obtained from the Nanjing partner institute as part of a Chinese-Hungarian project was 16.5 %, the most resistant line being *Ning894013*. Analysis of the genetic background of FHB resistance using microsatellite markers revealed gene effects on several chromosomes in line *Ning8331*.

Among the Martonvásár genotypes, a low level of FHB infection was recorded for *Mv Emese*, while *Mv Palotás* and line *Mv08-03* also performed well in the experiment. The Martonvásár varieties *Mv Táltos*, *Mv Csárdás* and *Mv Marsall* proved to have above-average resistance to the spread of FHB within the spike.

A survey was made of the virus composition of winter wheat, winter barley, durum wheat, winter oat, and triticale crops. The wheat dwarf virus (WDV) was identified on almost 100 % of plants exhibiting symptoms. Work was begun under field conditions on the elaboration of an artificial inoculation method using *Psammotettix alienus* Dahl., the vector of WDV.

Abiotic stress resistance studies. The effect of heat, drought, and combined heat and drought stress was studied in an artificially created environmental system on wheat cultivars with diverse genetic backgrounds. Changes in the photosynthetic processes, chlorophyll content, and chlorophyll fluorescence induction of 12 wheat cultivars grown in phytotron chambers were recorded on the basis of biophysical measurements during 15-day stress treatments starting on the 12th day of heading. Among the 12 cultivars, Fatima 2 and Mv Mambó proved to have good heat tolerance based on changes in the chlorophyll content, whereas Plainsman V gave the most sensitive response. Drought stress also was tolerated best by Mv Mambó. The most sensitive response to heat stress was observed in the photosynthetic processes of Mv Makaróni and Bánkúti 1201.

The wheat cultivars tested could be divided into two groups on the basis of the response of their chlorophyll fluorescence values to drought stress. Mv Mambó, Plainsman V and Bánkúti 1201 proved to be drought-tolerant, while Bezostaya 1, Mv Magma and Mv 15 were classified in the drought-sensitive group.

High temperature and drought had a negative effect on physiological processes both separately and in combination. Similar reductions, which gradually became more severe, were observed as a response to extreme heat stress, drought stress and combined stress.

Among the abiotic stress factors the varieties exhibited better tolerance to high temperature in all cases, because the optimum water supplies helped them to avoid becoming stressed. Drought had a greater effect on the biomass production and yield of the varieties, while a combination of the two stress factors resulted in the most drastic reduction.

The leaf nitrogen content of winter wheat cultivars Mv 15 and Alba was found to decrease in response to a rise in the atmospheric CO_2 level, but this decline was smallest when the soil N content was around optimum. The effect of doubling the CO_2 level was greatest in the suboptimum and supraoptimum ranges. At low nitrogen supplies, this difference could be attributed to the C surplus, and at high N levels to the excess of nitrogen. At low soil nitrogen levels, the nutrient uptake of the plants was unable to keep up with the increase in nitrogen requirements even when the root mass increased. At high nitrogen levels, however, the plants were unable to prevent the uptake of excess nitrogen, so the dilution of the toxic level could be attributed to greater C incorporation. The results proved that high CO_2 level only caused substantial dilution of the nitrogen content in plant tissues in the suboptimum and supraoptimum N ranges.

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Effect of aluminium stress on the androgenic development of wheat microspores. Wheat anther culture is a feasible system for the *in vitro* selection of aluminium-tolerant plants. However, no detailed investigation has yet been reported on the effect of aluminium on the sporophytic development of microspores. In this study, the cell division pattern and viability of microspores, embryoid formation, and green plant regeneration were monitored in the control and in cultures given a single or repeated aluminium treatment.

Although the free Al concentration was higher than 20 mM during the first week of the incubation period, no cytological effect of Al could be detected during the first week irrespective of the Al treatments. By the 14th day, when the anther walls were extensively necrotized, microspore embryogenesis were affected in both cases. In cultures treated with aluminium only at the beginning of the incubation period, the number of nuclei was lower and their distribution in the multinucleate structures was more heterogeneous than in the control cultures. The microspore embryogenesis and plant regeneration were possible, but were delayed and occurred with lower frequency. In the cultures treated repeatedly with Al (weekly), the aluminium toxicity was much more severe, resulting in very few viable microspores. The cells were highly vacuolated, frequently contained micronuclei, and had unusually thick walls. These cells were unable to develop further. These results indicate that the anther walls may delay the manifestation of the effects of Al on microspore development. Microspores can survive a single Al treatment, but perish when they are exposed to Al toxicity for a long time.

Molecular cytogenetic characterization of *Ae. biuncialis* and its use for the identification of 5 derived wheat/*Ae. biuncialis* addition lines. The aim of the experiments was to produce and identify different *T. aestivum–Ae. biuncialis* disomic addition lines. To facilitate the exact identification of the *Ae. biuncialis* chromosomes in these *T. aestivum–Ae. biuncialis* disomic additions, we analyzed the FISH pattern of *Ae. biuncialis* (2n=4x=28, $U^bU^bM^bM^b$), comparing it to the diploid progenitors (*Ae. umbellulata* 2n=2x=14, UU, and *Ae. comosa* 2n=2x=14, MM). In order to identify the *Ae. biuncialis* chromosomes, FISH was done using two DNA clones (pSc119.2, pAs1) on *Ae. biuncialis* and its two diploid progenitor species. Differences in the hybridization patterns of all chromosomes were observed between the four *Ae. umbellulata* accessions, the four *Ae. comosa* accessions, and the three *Ae. biuncialis* accessions analyzed. The hybridization pattern of the M genome was more variable than that of the U genome. Five different wheat-*Ae. biuncialis* addition lines were produced from the wheat–*Ae. biuncialis* amphiploids produced earlier in Martonvásár. The 2M, 3M, 7M, 3U, and 5U chromosome pairs were identified with FISH using three (pSc119.2, pAs1, and pTa71) repetitive DNA clones in the disomic chromosome additions produced. Genomic *in situ* hybridization was used to differentiate the *Ae. biuncialis* chromosomes from wheat, but no chromosome rearrangements between wheat and *Ae. biuncialis* were detected in the addition lines.

Ability of chromosome 4H to compensate for 4D in response to drought stress in a newly developed and identified wheat–barley DS4H(4D) line. A spontaneously produced wheat–barley DS4H(4D) line was identified cytogenetically

using GISH, multicolor FISH, and microsatellite markers. The ability of the barley 4H chromosome to compensate for wheat 4D in response to mild drought stress also was investigated.

In the barley cultivar Betzes and the DS4H(4D) line mild osmotic stress induced intensive stomatal closure, resulting in reduced water loss through transpiration and unchanged RWC in the leaves. Because the CO_2 assimilation rate remained relatively high, the water use efficiency, which is an important factor associated with drought tolerance, increased intensively under mild osmotic stress in these lines. In the case of the parental wheat genotypes, however, mild drought stress induced less intense stomatal closure and a greater decrease in the CO_2 assimilation rate than in barley or in the substitution line, resulting in unaugmented or reduced water use efficiency. The results demonstrate that genes localized on the 4H chromosome of barley were able to increase the water use efficiency of the wheat substitution line, which is suitable for improving wheat drought tolerance through intergeneric crossing.

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Genetic and physiological studies.

G. Galiba, G. Kocsy, A. Vágújfalvi, V. Szilágyi, A. Soltész, and T. Kellcs.

Gene expression studies in cold-treated wheat. An international effort (Hungarian – Italian – American) has shown that the expression of three cold-inducible *cbf* genes have a positive correlation with the freezing tolerance of wheat. These genes were mapped to a QTL region (*Fr-A2*) on chromosome 5A of wheat that determines freezing tolerance. In a German–Hungarian joint research project, (Plant Resource) the comparison of cold-induced changes in the transcript profile of wheat chromosome substitution lines having different freezing tolerances showed which genes exhibited a change in expression as the result of the 5A chromosome.

Publications.

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Research activities in the Cereal Genebank.

G. Kovács.

Evaluation of selected genetic resources and breeding lines of *T. monococcum* subsp. *monococcum* and *T. turgidum* subsp. *dicoccum* under organic farming conditions. The growing interest in hulled wheat cultivation has been stimulated, no doubt, by the increasing demand for traditional foods with a natural image, especially in the organic market. The new economic situation could stimulate the breeding and production of emmer and einkorn as the source of an especially valuable foodstuff. Based on intensively growing market needs, the establishment of organic breeding procedures was initiated for einkorn and emmer. Several hundred genebank accessions of these two species have been characterized in recent years. The results suggest that their direct use in breeding is greatly hindered, however, by the fact that the genebank accessions are very heterogeneous populations. In recent years, several pure lines have been produced using the single-seed descent, and the lines obtained have been agronomically described. Genetically extreme genotypes were crossed to produce mapping populations for further molecular studies. The best lines were used in organic breeding. In the case of einkorn, the lines obtained were tested under low-input conditions, and their yielding capacity has found to be already higher than 3 t/ha. During the einkorn improvement procedure, a new semidwarf genotype was identified and genetically analyzed. According to the results of a recent experiment, this genotype carries a recessive monogenic dwarf gene, which should be highly useful in producing semidwarf einkorn cultivars.

Organic wheat and einkorn breeding. Organic farming differs from conventional agricultural practices in that it aims to maximize dependence on naturally occurring biological systems. Such systems are less important in conventional agriculture, which is highly dependent on synthetic, external inputs. Our comparative experiments underlined that there is a significant difference between the agronomic performance and adaptability of conventionally bred cultivars under organic and conventional growth conditions and only a few of them are really useful in organic farming. Therefore, developing cultivars and populations that are bred and selected under organic conditions is essential to ensure good performance and quality for organic production.

During the last 3 years, new einkorn breeding lines have been produced using organic-breeding techniques, which resulted in very good adaptability, weed competitive ability, stable quality parameters, and acceptable yield. Meanwhile, einkorn lines selected under conventional conditions, which had very good agronomic performance and productivity (but unstable quality parameters) under conventional conditions, were not at all competitive with the organically bred lines under organic conditions.

In the case of bread wheat, a new project was initiated on the basis of evolutionary breeding theory. In these experiments, different composite cross populations were produced using 4, 6, and 7 parents. The F_2 generations were grown at a range of organic and nonorganic sites and compared with conventionally bred varieties. The results suggest that genetically diverse populations have better adaptability, especially in the case of low-input, organic conditions, whereas under high-input, conventional growth conditions, they cannot compete with conventionally bred varieties.

ITEMS FROM INDIA

BHABHA ATOMIC RESEARCH CENTRE
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Identification, validation, and use of molecular markers for combining quality with durable rust resistance in Indian wheat.

B.K. Das [1], A. Saini [2], S.G. Bhagwat [1], and N. Jawali [2].
[1] Nuclear Agriculture & Biotechnology Division, [2] Molecular Biology Division.

Genetic improvement of wheat for quality and rust resistance is continuing. The HMW-glutenin subunits are being used as a criterion for selection. Rust resistance genes such as *Sr31* and *Sr24/Lr24* are being combined with high yielding ability. Selections made on the basis of good agronomic characters are being advanced.

Marker-assisted selection for pyramiding stem rust resistance genes *Sr31* and *Sr24* in Indian wheat is being carried out. SCAR markers that identify the *Sr31* gene in homozygous or heterozygous condition were developed. DNA markers reported in literature for the *Sr24/Lr24* gene ($SCS73_{719}$) was validated in Indian wheat cultivars and segregating populations. Phenotypic scoring for stem rust reaction and a cosegregation study with the marker was made in an F_2 population from the cross 'Kalyansona (-*Sr24/Lr24*)/Vaishali (+*Sr24/Lr24*)'. The SCAR marker for the *Sr24* gene, along with the SCAR markers for *Sr31*, are being used for pyramiding these two genes.

Selections for *Glu-D1d* (coding for HMW-glutenin subunits 5+10), *Sr24*, and *Sr31* are being made from intercultivar crosses by use of molecular markers.

Identification of DNA markers for stem rust resistance gene Sr26.

Ruchi Rai, B.K. Das, and S.G. Bhagwat (Nuclear Agriculture and Biotechnology Division).

The stem rust-resistance gene *Sr26* has the potential to provide durable resistance to stem rust if it is pyramided with other *Sr* gene(s). Two markers, one based on a RAPD marker and the other based on an AP-PCR marker associated with stem rust resistance conferred by *Sr26*, were identified. Linkage analysis was done by studying cosegregation of the markers with resistant phenotype in a F_2 population from a cross between Kalyansona and the Australian cultivar Kite (*Sr26*).

Thermotolerance in wheat.

Suman Sud and S.G. Bhagwat (Nuclear Agriculture and Biotechnology Division).

High temperature stress is a major environmental constraint that lowers wheat productivity in warmer areas. In India, wheat cultivars are developed for different agroclimatic zones and, thus, show wide variability. We explored the cultivated germ plasm to mine genes for thermotolerance for further utilization. Fifty-six Indian bread wheat genotypes were assayed for acquired thermotolerance at the seedling stage. Ten-day-old seedlings were hardened and then subjected to membrane thermostability (MTS) and cell viability (TTC reduction) assays. Six thermotolerant genotypes identified from the assays and one relatively nontolerant genotype were grown in the field till maturity. Flag leaf area was estimated 10 days after emergence, and flag leaf senescence was recorded 17, 24, and 31 days after flag leaf emergence. Daily maximum and minimum air temperatures were recorded throughout the crop season. Variability was detected among the 56 genotypes for acquired thermotolerance. Significant correlation was observed between MTS and TTC values. The TTC assay, which measured cell viability after heat shock treatment, showed significant positive association

with grain yield/plant and yield/meter. Variation among the thermotolerant genotypes for yield and yield components was observed. Because the TTC assay showed positive correlation with yield under high temperature stress, it can be used as a selection criterion in breeding for warmer areas. To improve the productivity in warmer areas selection for heat stress tolerance accompanied by superior yield components will be needed. The tolerant genotypes identified in this study can serve as parents in improvement of thermotolerance of wheat.

Agronomic characterization, Rht genotyping, and high-molecular-weight glutenin subunit profiling of oligo-derived lines.

Suman Sud and S.G. Bhagwat (Nuclear Agriculture & Biotechnology Division).

Wheat is cultivated world wide in cooler environments. There is increasing interest in cultivation of wheat in nontraditional areas, including warmer environments. Also, a growing problem concerns the rise and fluctuation in temperature at the time when wheat is cultivated. Higher temperature during early phase of growth affects tillering, number of spikelets/spike, and biomass production. Oligoculm wheat is known to have high vigor and Gigas features. The vigor of oligoculm wheat expressed as long culms, thick stem, large leaves, long spikes with a high number of spikelets, and large grains. A set of 14 oligoculm derivatives obtained from the cross 'oligoculm wheat/Kundan//selection 212' was evaluated for their field performance under high temperature stress conditions. Grain yield/spike were higher in 10 derivatives, whereas on area basis the derivatives were poorer. Biomass/plant and biomass/meter were significantly higher in many of the oligoculm derivatives indicating their superior ability to accumulate biomass. The spikelet number/spike and flag leaf area were significantly higher than the checks, hence the derivatives can be used as a source of these yield components for improvement in warm environment. Harvest index in the derivatives was generally lower. The oligoculm derivatives lacked major dwarfing gene as observed by their responsiveness to gibberellin and by use of perfect markers, as a result these were taller than the semidwarf check cultivars. The oligo derivatives were found to vary in their HMW-glutenin subunit composition. Two derivatives, 8-44-1 and 8-44-2, had the subunit composition N, 7+9, and 2+12 (*Glu-1* score 5). Ten derivatives showed subunit composition N, 13+16, 2+12 (*Glu-1* score 6). One line each showed subunit composition 1, 7+8, 2+12, and 1, 7+9, 2+12 (*Glu-1* scores 8 and 7, respectively). The variability in *Glu-1* scores offers scope to select for strong or weak dough. The oligo derivatives lacked tolerance to heat stress as indicated by their rapid leaf senescence. The performance of the derivatives may be improved by introduction of semidwarfing gene(s) and by improving tolerance to high temperature.

Identification of Rht genes and pin a and pin b status of Indian wheat cultivars.

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The semi dwarfing genes *Rht1* and *Rht2* are common among Indian wheat cultivars. Forty-five cultivars were analyzed using PCR-based, allele-specific perfect markers. Thirteen had *Rht-B1b* and 24 had *Rht-D1a*. Grain hardness is an important quality related trait. Sixty bread wheat cultivars were analyzed for their status of *pin a* and *pin b* genes. The null form of *pin a* was found to be most frequent among the hard Indian bread wheats. Mapping of wheat genome using a intervarietal cross between cultivars Kalyansona and Sonalika is in progress.

Artificial neural network for identification of wheat grains.

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Observing the shape, size and color of grains is normally employed for identification of a wheat cultivar. Use of computer based image analysis may be a good alternative to visual identification. Grain shape and size are considerably influenced by changes in environment. The Artificial Neural Network (ANN), when combined with digital imaging, may have the potential for cultivar identification. Three bread wheat varieties were grown in different environments to create variation in the grain shape and size. Morphometric features of these grains were quantified

using Comprehensive Image Processing Software. Data on 45 parameters were used to train ANN with different combinations of nodes and iterations. Similar samples were used for testing. A commercial and an in-house developed ANN software packages were used in this study. Best results were obtained with the resilient back propagation architecture for both. The success of correct identification was about 88 % for all the grains together and ranged from 84–94 % for individual varieties. The results showed that ANN, combined with image analysis has excellent potential for wheat cultivar identification.

Publications.

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Breeding for rust resistance in some Indian hexaploid wheat cultivars.

K. Gajalakshimi and V.R.K. Reddy.

Specific genes for rust (stem, leaf, and stripe) resistance were transferred from hexaploid wheat stocks into the Indian hexaploid wheat cultivars HW 2084, PDSN-32, and K 9107. Among the three recipient wheat parents, HW 2084 and K 9107 were free from leaf rust and stem rust, respectively, however, both were susceptible to the other two wheat rusts. The third cultivar, PDSN-32, was susceptible to all the three rusts. Thus, we improved these Indian wheat cultivars by incorporating the respective rust-resistance genes for which they are susceptible. The donor parents included 10 hexaploid wheat stocks carrying a total of five leaf rust-resistance genes (*Lr19, Lr24, Lr26, Lr28,* and *Lr37*), six stem rust-resistance genes (*Sr24, Sr25, Sr27, Sr31, Sr36,* and *Sr38*), and seven stripe rust-resistance genes (*Yr8, Yr9, Yr11, Yr13, Yr15, Yr16,* and *Yr17*), present either singly or in combinations (linked condition). Transfers were made using a simple backcross-breeding method followed by selection.

Selection was made in the BC_2/BC_3 and/or BC_5 generations, and one NIL each in the BC_2F_5/BC_3F_5 and BC_5F_5 was selected from all 29 cross combinations. All the lines were screened against individual rust races at the seedling stage in the glasshouse with a mixture of rust races and at the adult-plant stage in natural and artificial conditions in the field. An immune to moderately resistant reaction at the seedling stage and a highly resistant reaction at the adult-plant stage provided by the incorporated genes strongly advocate the use of specific rust-resistance genes for durable resistance.

All the rust resistance genes used provided a moderate to high degree of resistance under field conditions (Table 1, p. 36). Specific rust resistance from single genes included *Lr19, Lr24, Lr28, Lr37, Sr27, Sr38, Yr9, Yr11, Yr13, Yr15,* and *Yr16*. Other rust-resistance genes, *Lr26, Sr24, Sr25, Sr31, Yr8*, and *Yr17,* were useful in combination with other resistance genes already present in the genetic background of recurrent parents.

Table 1. Adult plant reactions of Indian wheat cultivars and constituted near-isogenic lines against wheat rusts.

Indian wheat cultivars / NILs (BC_2F_5 / BC_3F_5 and BC_5F_5)	Rust reaction		
	Stem	Leaf	Stripe
HW 2084 (*Lr19 + Sr25*)	40MS	F	100S
HW 2084 / Veery'S' (*Sr31 + Lr26 + Yr9*)	F	F	F
HW 2084 / Joss Chambier (*Yr11*)	40MS	F	F
HW 2084 / Longbow (*Yr13*)	40MS	F	F
HW 2084 / G 25 (*Yr15*)	F	F	F
HW 2084 / Cap - 5BL - 7BL (*Yr16*)	5R	F	F
HW 2084 / RL 6081 (*Sr38 + Lr37 + Yr17*)	TR	F	15MS
HW 2084 / WRT 238-5 (*Sr27*)	F	F	40MS
HW 2084 /Cook*6/C 80-1 (*Lr19 + Sr25 + Sr36*)	F	F	F
HW 2084 / Darf*6 / 3 Ag / Kite (*Lr24 + Sr24*)	F	F	10S
HW 2084 / CS 2A/2M # 4/2 (*Lr28 + Sr34 + Yr8*)	40MS	F	10RMR
PDSN-32 / (*Sr7b, Sr9 , Lr14*)	60S	70S	90S
PDSN-32 / Veery'S' (*Sr31 + Lr26 + Yr9*)	10R	10MS	F
PDSN-32 / Joss Chambier (*Yr11*)	70S	50S	F
PDSN-32 / Longbow (*Yr13*)	70S	60S	F
PDSN-32 / G 25 (*Yr15*)	F	20R	F
PDSN-32 / Cap-5BL-7BL (*Yr16*)	20S	F	F
PDSN-32 / RL 6081 (*Sr38 + Lr37 + Yr17*)	5RMR	TR	15MS
PDSN-32 / Cook*6/C 80-1 (*Lr19 + Sr25 + Sr36)*	F	F	F
PDSN-32 / Darf*6/3 Ag/Kite (*Lr24 + Sr24*)	10RMR	F	10S
PDSN-32 / WRT 238-5 (*Sr27*)	TR	20RMR	40MS
PDSN-32 / CS 2A/2M#4/2 (*Lr28 + Sr34 + Yr8*)	60S	F	5RMR
K 9107 (*Sr2, Sr5, Sr8b, Sr11, Lr13, Yr2*)	F	40S	80S
K 9107 / Veery'S' (*Sr31 + Lr26 + Yr9)*	F	F	F
K 9107 / Joss Chambier (*Yr11*)	F	10MR	F
K 9107 / Longbow (*Yr13*)	F	10MR	F
K 9107 / G 25 (*Yr15*)	F	5R	F
K 9107 / Cap-5BL–7BL (*Yr16*)	F	F	F
K 9107 / RL 6081 (*Sr38 + Lr37 + Yr17*)	F	F	F
K 9107 / Cook*6/C 80-1 (*Lr19 + Sr25 + Sr36*)	F	F	F
K 9107 / Darf*6/3 Ag/Kite (*Lr24 + Sr24*)	F	F	10S
K 9107 / CS 2A / 2M # 4/2 (*Lr28 + Sr34 + Yr8*)	F	F	TMR

Yield performance of the NILs was tested under rust-free conditions. Many of the NILs were significantly higher in grain yield than the chemically treated control plants. In general, the agronomic performance of the plants at the BC_2F_5/ BC_3F_5 was superior to those of BC_5F_5-selected plants for plant height, tiller number/plant, spike length, number of spikelets/spike, 1,000-kernel weight, and grain yield. However, the various agronomic characters recorded in the BC_5F_5 also were comparatively superior to those of the untreated recurrent parents (Table 2, p. 37). The NILs of the BC_2F_5/BC_3F_5 had very good agronomic characteristics, but the seed quality (plumpness, weight, size, and color) was not improved in many lines. Based on seed quality coupled with good agronomic characters and yield, 20 lines were finally selected for commercial purposes, and the remaining nine lines were grouped as genetic stocks for use in breeding programs.

Confirming the transfer of rust-resistance genes to Indian wheat cultivars. Transfer of rust-resistance genes into Indian wheats was confirmed through morphological, genetical, biochemical, and molecular markers. The presence of morphological markers of the donor parents, such as awnless spike (Darf*6/3Ag/Kite, *Sr24+Lr24*; Joss Chambier, *Yr11*; Longbow, *Yr13*; and Cap-5BL-7BL, *Yr16*), lax spike (RL 6081, *Sr38+Lr37+Yr17*), reduced yellow pigment in the seed flour (Cook*6/C 80-1, *Lr19+Sr25+Sr36*), clubby tip (G-25, *Yr15*), waxy color (Veery'S', *Sr31+Lr26+Yr9*), and powdery mildew severity in the F_1 hybrid derivatives of different crosses between Indian wheats and donor parents suggests the successful transfer of these morphological characters along with rust-resistance genes from the donor parents to recipient Indian wheats.

Inheritance studies in the NILs for *Yr9*; *Lr24* (HW 2084); *Yr11*, *Yr13* (PDSN-32); and *Lr19*, *Sr27* (K 9107); which involved crossing each of the NILs with the universally susceptible wheat cultivar Agra Local, showed that rust resistance in the NILs was due to a single, dominant gene. The F_1 hybrids exhibited complete rust resistance, whereas the F_2 plants segregated as 3 resistant : 1 susceptible to the respective rusts. Similarly, the BC_1 hybrids segregated 1 resistant : 1 susceptible to respective rusts. These results confirm the transfer of rust-resistance genes into Indian wheats.

Table 2. Comparative mean grain yield (Q/ha) performance of Indian hexaploid wheat cultivars (untreated and chemically treated controls) and the constituted NILs in the BC_2F_5/ BC_3F_5 and BC_5F_5 generations.

		Constituted lines		
Control / Constituted lines	Generation	HW 2084	PDSN-32	K 9107
Control (untreated)	—	32.68	30.92	31.26
Control (chemically treated)	—	41.96	39.47	38.62
Veery'S' (*Sr31+Lr26+Yr9*)	BC_2F_5	46.82	43.62	45.78
	BC_5F_5	45.79	42.80	44.95
Joss Chambier (*Yr11*)	BC_2F_5	41.88	40.16	39.36
	BC_5F_5	41.81	39.74	39.04
Longbow (*Yr13*)	BC_2F_5	42.16	39.52	40.98
	BC_5F_5	41.99	38.81	40.12
G - 25 (*Yr15*)	BC_3F_5	40.26	35.34	38.87
	BC_5F_5	38.12	34.59	38.72
Cap-5BL-7BL (*Yr16*)	BC_2F_5	43.14	40.75	41.45
	BC_5F_5	42.78	40.46	41.08
RL-6081 (*Sr38+Lr37+Yr17*)	BC_3F_5	44.66	41.45	42.93
	BC_5F_5	43.47	40.87	41.68
Cook*6/C 80-1 (*Lr19+Sr25+Sr36*)	BC_2F_5	46.45	43.12	45.16
	BC_5F_5	45.63	42.56	44.08
Darf *6 / 3Ag / Kite (*Lr24+Sr24*)	BC_2F_5	39.95	37.34	38.95
	BC_5F_5	35.82	36.18	38.68
CS 2A/2M# 4/2 (*Lr28+Sr34+Yr8*)	BC_2F_5	40.38	39.26	40.24
	BC_5F_5	36.45	38.42	39.87
WRT 238-5 (*Sr27*)	BC_2F_5	42.74	39.84	—
	BC_5F_5	41.69	39.49	—
		SEM	CD (0.05%)	
Population		0.342 **	0.243 **	0.276 **
Treatment		0.573**	0.438 **	0.524 **
P x T interaction		0.768 NS	0.597 NS	0.746 NS

The F_2 segregation data of the monosomic and disomic F_1 hybrids of crosses between the complete set of CS monosomics and the NILs for *Sr27* (HW 2084), *Lr24* (PDSN-32), and *Lr19* (K 9107) were studied for their respective rust resistance. A segregation ration of 3:1 (resistant:susceptible) except for lines 3A, 3D, and 7D in HW 2084, PDSN-32, and K 9107, respectively, confirmed the successful incorporation of these genes on to the respective chromosomes of the recipient wheat parents.

We studied changes in enzymatic activities of peroxidase, polyphenol oxidase, catalase, and lipoxygenase in the leaves of 25-day-old plants of rust-susceptible wheat parents and rust-resistant NILs inoculated with respective rust pathogens and found altered activity. The constituted lines had a higher peroxidase activity compared to healthy controls 2–7 days after inoculation. Polyphenol oxidase activity increased in all NILs 3–7 days post inoculation, whereas activity declined in the susceptible parents. Catalase activity was higher in susceptible wheat parents than the resistant NILs. Lipoxygenase activity increased in both the susceptible wheat parents and their NILs 2 days after inoculation but subsequently declined 7 days after inoculation in resistant plants. A consistent increase was noticed in plants of the susceptible parents. Esterase activity increased in all the NILs 3–7 days after inoculation but declined activity was observed in the susceptible parents.

The total lipid content of the leaves increased in both susceptible and rust-resistant NILs 2 days after inoculation but subsequently decreased with an increase in post inoculation time. The percent decrease was greater in the susceptible parents than in the resistant NILs. Soluble protein content increased in resistant NILs 24 hours after inoculation but decreased during later stages of infection. The percent decrease was more in susceptible than resistant lines 7 days after inoculation. Specific activities of ribonuclease-I and combined ribonuclease-II and nuclease-I was high at

day15 compared to day 10 in susceptible and resistant lines. Resistant NILs had relatively higher chlorophyll content than that of the susceptible parents. Total free amino acid content increased up 8 days after inoculation in both susceptible and resistant lines followed by a slight reduction in both the cases. Respiration rate increased to a greater extent in the resistant NILs compared to susceptible parents. On the third day after inoculation, the reduction in respiration rate was drastic in the susceptible parents, whereas in resistant NILs, respiration was more or less constant. A significant increase in total free phenols and tannin content was observed in the NILs over their respective recurrent parents. The NILs had significantly higher nuclear DNA than their respective susceptible parents.

A change in the intensity of isoenzyme bands of polyphenol oxidase, peroxidase, esterase, and superoxide dismutase in susceptible and their resistant NILs were noted with Rf values. Isozyme analysis of polyphenol oxidase shows some specific bands only in NILs with different rust-resistance genes. Esterase activity of some specific esterase activity bands was present only in rust-resistant NILs, whereas these specific bands were absent in the susceptible lines. Specific SOD activity bands were observed only in resistant lines and were missing in susceptible lines. SDS–PAGE analysis of soluble protein did not show any major qualitative difference in the protein profiles in the leaves of susceptible parents and its resistant NIL. However, quantitative changes were observed in the intensity of the banding pattern; some of the major protein bands were found to increase in intensity in NILs with rust-resistance genes *Yr9, Sr27, Yr17* (HW 2084); *Lr19, Sr27, Yr9* (PDSN-32); and *Lr19, Lr28, Yr16* (K 9107) over their susceptible (recurrent) parents. The intensity of specific protein bands with Rf values of 0.13, 0.26, 0.29, 0.36, 0.74, 0.78, 0.82, and 0.85 decreased in the leaves of susceptible plants. SDS–PAGE analysis of seed-storage proteins, under reduced conditions for the presence to *Sec-1,* revealed that all Veery 'S' derivatives, Veery'S', and Kavakaz (aºknown standard for the T1B·1R translocation) showed a *Sec-1* band with an Rf value of 0.56, which is a characteristic feature of T1B·1RS lines. This result confirmed the successful incorporation of rye segment carrying the gene complex *Sr31+Lr26+Yr9*.

Molecular screening of NILs for *Yr15* with the RAPD primers OPA-19 and OPB-13 confirmed the transfer of *Yr15*. The RAPD primers OPA-19 and OPB-13 amplified the diagnostic fragments at 1,420 bp and 1,500 bp and resulted in one additional band in the resistant NIL. This band was absent in susceptible parent.

Distribution of necrosis genes and evaluation of resistance to rusts in some bread wheats.

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Introduction. Hybrid necrosis are frequently met with inter and intraspecific wheat crosses and are serious barriers to the transfer of genes in a planned hybridization program. Hybrid necrosis, causing gradual death or debility of F_1 hybrids is often noticed in wheat crosses and this kind of weakness can be clearly distinguished phenotypically. The genetic trait of hybrid necrosis is governed by two complementary genes, *Ne1* and *Ne2* (Caldwell and Compton 1943; Hermsen 1963), located on chromosomes 2BS and 2BL (Tsunewaki 1960; Nisikawa et al. 1974), respectively. Hybrid necrosis proves to be a hurdle in the process of gene transfers from alien or other diverse sources of resistance to disease. Thus, documenting information on the different genes for resistance to diseases relevant to India as well as the information about the genes in wheat stocks is important. The present study determines the genes for necrosis. Stocks also were evaluated for resistance to rusts in wheats.

Materials and methods. Eighty-two *T. aestivum* cultivars were crossed to two *T. aestivum* subsp. *aestivum* testers, C306 (*Ne1ne2*) and Klein Lucero (*ne1Ne2*). The F_1 hybrids and parents were raised in field as well as in greenhouse under optimal conditions for the expression of *Ne* genes. The genotypes of the parents with respect to *Ne* were determined from the phenotype of the F_1 hybrids. The stocks were also evaluated for resistance to rusts under high incidence of natural infection.

Results and discussion. Study of hybrid necrosis. Eighty-two wheat stocks were tested for the presence or absence of necrosis gene(s). The results are presented in Table 3 (pp. 39-41) and indicate that out of 82 cultivars, eight stocks were Ne_1 carriers, 35 stocks were *Ne2* carriers, and the remaining 39 were noncarriers for the necrosis genes (*ne1*, *ne2*). Tsunewaki (1971) tested two strains of *T. aestivum* subsp. *sphaerococcum* and reported on of them as *Ne1* carrier, whereas Zeven (1971) recorded one strain that had the gene *Ne1*. Cultivars of *T. turgidum* subsp. *dicoccum*, like other tetraploid species of wheat, are either *Ne1* carriers or noncarriers (Nishikawa 1967; Tsunewaki 1969). The *Ne2* gene, found restricted to the western 6X wheats, is presumed to have originated by mutation at the hexaploid level in Europe

(Tsunewaki and Kihara 1962). Zeven (1966) and Tsunewaki and Nakai (1973) reported high frequencies of *Ne1* and *Ne2* carriers in the hexaploid wheats of Asian and Western populations, respectively.

Similarly, eight *Ne1* carriers, 35 *Ne2* carriers, and 39 noncarriers of the necrosis genes were found among the 82 stocks of *T. aestivum* subsp. *aestivum*. Pukhal'skii (1980) found that *Ne2* occurred especially in winter wheat and *Ne1* in spring wheat, but Zeven (1981) suggested that spring and winter wheats were possibly derived from two different groups, one carrying the necrosis gene *Ne1* and the other *Ne2*. Narula et al. (1971) and Kochumadhavan et al. (1980) have reported that the Indian bread wheat cultivars predominantly have *Ne1*, whereas the western European and North American wheats are mainly *Ne2* carriers. Tsunewaki (1971) studied 22 accessions of compactum wheats from the U.S. and reported 5 % *Ne1* carriers, 18 % *Ne2* carriers, and 77 % noncarriers, whereas 34 strains of *T. aestivum* subsp. *compactum* from Asia were either *Ne1* carriers (32 %) or noncarriers (68 %). Similarly, (9.76 %) *Ne1* carriers, (42.68 %) *Ne2* carriers, and (47.56 %) noncarriers were found among the 82 stocks of *T. aestivum* subsp. *aestivum*.

Table 3. Disease reaction and genotype with respect to the genes for necrosis in some bread wheats.

Stock	Gene(s) present	Reaction to rust			Tester		Genotype of tester
		Stem	Leaf	Stripe	C 306 (Ne_1ne_2)	Klein Lucero (ne_1Ne_2)	
Abe	*Sr36 Lr19*	5R	60S	30S	Normal	Normal	ne_1ne_2
Riley 67	*Lr9*	F	50S	40S	Normal	Normal	ne_1ne_2
Oasis	*Lr9*	10R	40S	F	Normal	Normal	ne_1ne_2
Sonali	*Lr9*	60S	60S	60S	Necrotic	Normal	ne_1Ne_2
Transfer	*Lr9*	80S	50S	F	Normal	Necrotic	Ne_1ne_2
Terral	*Lr9*	15MS	50S	F	Necrotic	Normal	ne_1Ne_2
Sunnan	*Sr25 Lr19*	10S	F	5S	Normal	Normal	ne_1ne_2
Oasis 86	*Sr25 Lr19*	5MS	F	40S	Necrotic	Normal	ne_1Ne_2
Sears 7D/Ag translocation	*Sr25 Lr19*	10S	F	F	Normal	Necrotic	Ne_1ne_2
CS2D/2M#3/8	*Lr28*	80s	F	F	Normal	Necrotic	Ne_1ne_2
Agent	*Lr24 Sr24*	5MS	F	10S	Normal	Normal	ne_1ne_2
Cloud	*Sr24 Lr24*	5MS	F	F	Necrotic	Normal	ne_1Ne_2
Collin	*Sr24 Lr24*	10MS	F	F	Normal	Normal	ne_1ne_2
Fox	*Sr24 Lr24*	15MS	F	20MS	Necrotic	Normal	ne_1Ne_2
Gamka	*Sr24 Lr24*	5MS	F	20MS	Necrotic	Normal	ne_1Ne_2
Jasper	*Sr24 Lr24 Sr31 Lr26 Yr9*	10MS	F	TS	Necrotic	Normal	ne_1Ne_2
TC*8/VPM 1.R.L. 6081	*Sr38 Lr37 Yr17*	15MRMS	F	20MS	Normal	Normal	ne_1ne_2
RL 6043	*Lr21 Sr33*	30MR	20R	60S	Normal	Normal	ne_1ne_2
Rio Blanco	*Sr24 Lr24*	15MS	F	TS	Necrotic	Normal	ne_1Ne_2
Sage	*Sr24 Lr24*	5MS	F	15S	Normal	Normal	ne_1ne_2
Sears' translocation 3Ag # 3	*Sr24 Lr24*	10MS, S	F	F	Normal	Necrotic	Ne_1ne_2
Sears' translocation 3Ag # 14	*Sr24 Lr24*	10MS	F	F	Normal	Necrotic	Ne_1ne_2
TR 380-16 *7/3 AG 3	*Sr24 Lr24*	TS	F	20MR	Normal	Normal	ne_1ne_2
TR 548 # 7/ 3 AG 3	*Sr24 Lr24*	5MS	F	15MS	Normal	Normal	ne_1ne_2
TC* 7/ Transec,R.L. 6084	*Lr25*	70S	F	70S	Normal	Normal	ne_1ne_2
Eagle	*Sr26*	10RMR	70S	50S	Normal	Normal	ne_1ne_2
King	*Sr26*	5R	70S	20S	Normal	Normal	ne_1ne_2
Bass	*Sr26 Sr36*	10R	60S	30S	Normal	Normal	ne_1ne_2
Terra	*Sr26*	15MR	70S	TS	Normal	Normal	ne_1ne_2
Gabric	*Sr26*	10MR	40S	60S	Normal	Normal	ne_1ne_2
Takari	*Sr26*	5R	20MS	20S	Necrotic	Normal	ne_1Ne_2
WRT 238-5	*Sr27*	F-TR	20MR	30S	Normal	Necrotic	Ne_1ne_2
Mediterranean	*Sr30*	30MS	80S	50S	Necrotic	Normal	ne_1Ne_2
Romany	*Sr30*	10MS	TR	40S	Necrotic	Normal	ne_1Ne_2
Sunstar	*Sr30*	15MR	70S	40S	Necrotic	Normal	ne_1Ne_2

Table 3 (continued). Disease reaction and genotype with respect to the genes for necrosis in some bread wheats.

Stock	Gene(s) present	Reaction to rust			Tester		Genotype of tester
		Stem	Leaf	Stripe	C 306 (Ne_1ne_2)	Klein Lucero (ne_1Ne_2)	
Webster	*Sr30*	10R	80S	40S	Normal	Normal	ne_1ne_2
Banks	*Sr30*	15MR	70S	F	Normal	Normal	ne_1ne_2
Festiguay	*Sr30*	30MR	70S	F	Normal	Normal	ne_1ne_2
Hartog	*Sr30*	TR	50MS	30S	Necrotic	Normal	ne_1Ne_2
Orlando	*Sr31 Lr26 Yr9*	10MS	70S	F	Normal	Normal	ne_1ne_2
Pakistan 81	*Sr31 Lr26 Yr9*	10MR	70S	F	Necrotic	Normal	ne_1Ne_2
Seri 82	*Sr31 Lr26 Yr9*	15MR	80S	F	Necrotic	Normal	ne_1Ne_2
Zorba	*Sr31 Lr26 Yr9*	15MR	70S	F	Normal	Normal	ne_1ne_2
W3 563	*Sr37*	5R-15MR	90S	70S	Normal	Normal	ne_1ne_2
TAF 2d	*SrAgi*	F-10R	20RMR	5S	Necrotic	Normal	ne_1Ne_2
Kenya Civet	*Sr36*	5R	20S	TS	Normal	Normal	ne_1ne_2
Kenya Leopard	*Sr36*	10R	50S	F	Normal	Normal	ne_1ne_2
Maris Envoy	*Sr36*	F-TR	60S	F	Necrotic	Normal	ne_1Ne_2
Maris Nimrod	*Sr26*	10R	80S	F	Necrotic	Normal	ne_1Ne_2
Cook	*Sr36 Lr3*	5R	70S	F	Normal	Normal	ne_1ne_2
Dipka	*Sr26*	F-10R	60S	F	Necrotic	Normal	ne_1Ne_2
Timvera	*Sr36*	F-TR	80S	40S	Normal	Normal	ne_1ne_2
Mendos	*Sr36*	TR	60S	40S	Normal	Necrotic	Ne_1ne_2
Songlen	*Sr36*	TR	60S	15S	Normal	Normal	ne_1ne_2
Weique		30MS	TMS	80S	Normal	Normal	ne_1ne_2
PBW 226/6//CS 24/2M 4/2	*Lr28*	70S	F	F	Necrotic	Normal	ne_1Ne_2
PBW 226/6//C 86-8/Kalyansona F_4	*Lr32*	30S	F	F	Necrotic	Normal	ne_1Ne_2
RL 5406/6*Thatcher	*Sr33 Lr21*	30MR	20MR-MS	60S	Normal	Normal	ne_1ne_2
Sonalika*6//Sunstar*6/C80 1	*Sr25 Lr19*	10MR	F	80S	Necrotic	Normal	ne_1Ne_2
Sonalika*8//CS 2A/2M/ 4/2	*Lr28*	70S	F	80S	Necrotic	Normal	ne_1Ne_2
Sonalika*6//C86-8/ Kalyansona F_4	*Lr32*	60S	F	60S	Necrotic	Normal	ne_1Ne_2
Sonalika*5/Thatcher*8/VPM-1	*Sr38 Lr37 Yr17*	20S	F	40S	Necrotic	Normal	ne_1Ne_2
Tetracanthatch/*Ae. tauschii* RL5288	*Sr33 Lr21*	20MR	15R	50S	Normal	Normal	ne_1ne_2
Thatcher*8/VPM-1, RL6081	*Sr38 Lr37 Yr17*	15MR	F	10S	Normal	Normal	ne_1ne_2
UP262*2//C 86-8/ Kalyansona F_4	*Lr32*	80S	F	40S	Necrotic	Normal	ne_1Ne_2
UP262*2//CS 2A/2M 4/2	*Lr28*	80S	F	30S	Necrotic	Normal	ne_1Ne_2
UP262*2//Thatcher*8/VPM-1	*Sr38 Lr37 Yr17*	30S	F	70S	Necrotic	Normal	ne_1Ne_2
Transfer	*Lr25*	80S	F	15S	Normal	Normal	ne_1ne_2
UNNAT C306	*Sr27 Lr28*	F	F	F	Normal	Necrotic	Ne_1ne_2
Lok-1*3//Cook*6/C 80-1	*Sr25 Sr36 Lr9*	F	F	70S	Necrotic	Normal	ne_1Ne_2
Lok-1*7//Sunstar*6/C 80-1	*Sr25 Lr19*	10MS	F	60S	Necrotic	Normal	ne_1Ne_2
Lok-1*7//CS 2A/2M 4/2	*Lr28*	100S	F	90S	Necrotic	Normal	ne_1Ne_2
Lok-1*6//C 86-8/ Kalyansona F_4	*Lr32*	70S	F	70S	Necrotic	Normal	ne_1Ne_2
Lok-1*5//Thatcher*8/VPM-1	*Sr38 Lr37 Yr17*	40S	F	60S	Necrotic	Normal	ne_1Ne_2
Lovrin 10	*Sr31 Lr26 Yr9*	5MR	80S	F	Normal	Normal	ne_1ne_2

Table 3 (continued). Disease reaction and genotype with respect to the genes for necrosis in some bread wheats.

Stock	Gene(s) present	Reaction to rust: Stem	Leaf	Stripe	Tester: C 306 (Ne_1ne_2)	Tester: Klein Lucero (ne_1Ne_2)	Genotype of tester
NI 5439*6//Sunstar*6 /C 80-1	*Sr25 Lr19*	15MS	F	80S	Normal	Normal	ne_1ne_2
NI 5439*6// TR 380-14*7/3 Ag #14	*Sr24 Lr24*	10MR	F	80S	Normal	Normal	ne_1ne_2
NI 5439*7//CS 2A/2M 4/2	*Lr28*	80S	F	80S	Normal	Normal	ne_1ne_2
NI 5439*6//C 86-8/ Kalyansona F_4	*Lr32*	80S	F	80S	Normal	Normal	ne_1ne_2
NI 5439*2/Thatcher*8/VPM-1	*Sr38 Lr37 Yr17*	60S	F	80S	Normal	Normal	ne_1ne_2
PBW 226/5//Sunstar*6/C 80-1	*Sr25 Lr19*	TR	F	F	Necrotic	Normal	ne_1Ne_2
PBW 226/6//TR 380-14*7/3 Ag #14	*Sr24 Lr24*	T- MS	F	F	Necrotic	Normal	ne_1Ne_2

Disease resistance. This study reveals that the alien genes *Lr9*, *Lr28*, *Lr32*, and *Lr37* and *Lr19*, *Lr24*, *Sr24*, *Sr25*, *Sr26, Sr27, Lr25*, and *Sr31* condition a high degree of resistance. The gene *Lr37* showed a high degree of resistance at the adult-plant stage, and this resistance gene, linked with *Sr38* and *Yr17*, provides a high degree of resistance. The genes *Lr21* and *Sr33* conferred moderate resistance. *Sr30* and *Sr37* showed moderate resistance to stem rust. *Sr36* and *SrAgi* conferred high degree of resistance to stem rust. The gene *Yr9* is associated with *Lr26* and *Sr31*, *Yr9* has resistance to stripe rust, and *Lr26* was found to be susceptible to leaf rust. Genes *Lr19, Lr24, Lr25*, and *Lr28* confer effective seedling resistance to different pathotypes of leaf rust (Sawhney and Goel 1983) and also APR. Gene *Lr24* is known to be linked with *Sr24* (McIntosh et al. 1977), and this linkage confers a high level of resistance to both leaf and stem rusts in India. Gene *Lr25* is effective against 10 important pathotypes of leaf rust in seedling stage (Sawhney and Goel 1983). The gene *Lr37* showed a high degree of resistance in adult-plant stage, and this resistance gene is linked with *Sr38* and *Yr17*, both providing high degree of resistance (Bariana and McIntosh 1993). The gene *Lr21* from *Ae. tauschii* confers a moderate degree of resistance to leaf rust at adult-plant stage. This gene was reported to be susceptible to most of the virulent pathotypes of leaf rust in seedling (Rajendra Kumar et al. 1988) but exhibited adult-plant resistance. The gene *SrAgi* is the only stem rust-resistance gene present in the partial amphidiploid TAF 46 (2n = 56) generated by Cauderon et al. (1973). *SrAgi* is highly effective against stem rust. Gene *Sr36* derived from *T. timopheevii* subsp. *timopheevii* and *SrAgi* conferred high degree of resistance, whereas *Sr30* from common wheat and *Sr37* derived from alien gene of *T. timopheevii* subsp. *timopheevii* was moderately resistant to stem rust. The genes *Sr26, Sr27, Sr31, Sr36*, and *SrAgi* confer a high degree of resistance to stem rust, and *Sr25, Sr30, Sr37*, and *Sr38* confer a moderate degree of resistance. Gene *Sr24* is completely ineffective to stem rust. *Sr26, Sr27*, and *Sr31* confer seedling resistance to 19 pathotypes occurring in India and effective in adult-plant stage as well (Sawhney and Goel 1981). Genes *Sr26, Sr27, Sr31, Sr32, Sr36*, and *SrAgi* confer a high degree of resistance, whereas *Sr25, Sr30*, *Sr33, Sr37,* and *Sr30* are moderately resistance. The genes *Sr24, Sr20*, and *Sr34* were reported to be ineffective (Menon and Tomar 2001).

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Development and use of molecular markers for wheat genomics and breeding.

Updating and construction of framework linkage map(s) using trait specific intervarietal RIL populations. Three framework linkage maps using three mapping populations are being prepared in our laboratory for QTL interval mapping of various agronomically important traits. These three mapping populations were originally prepared for the following three traits: (i) grain protein content (GPC), (ii) grain weight (GW), and (iii) preharvest sprouting tolerance (PHST).

Updating the framework linkage map of GPC population. We have prepared a framework linkage map for GPC population using 171 SSR markers (Prasad et al. 2003). 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, following two exercises were undertaken.

(a) The genotypic data used was on a set of 39 markers (including ISSR, SSR, and RAPD markers) recorded at NCL, Pune (India) under a network project, which allowed integration of 18 new markers to the available genetic map, giving a total of 189 markers on the map that is available with us at present.

(b) An additional set of 75 SSRs was used to study polymorphism between parents of GPC population (WL711 and PH132). Twenty-nine of the above 75 SSRs showed polymorphism. Genotyping of RILs with these 29 polymorphic markers is in progress, and the data generated will be used for filling the gaps in the available genetic map. Additional markers will be subsequently used to increase further the density of markers on the map.

Framework maps for GW population. A framework linkage map for four different chromosomes (1A, 2A, 2B, and 7A) was initially prepared using genotyping data for 453 molecular markers (34 SSR, 299 AFLP, and 120 SAMPL) on 100 RILs of GW population. Only 68 of the above 453 markers could be assigned to the above four chromosomes, and an average genetic distance of 13.37 cM to 19.74 cM between any two markers was observed (Kumar et al. 2006).

With a view of developing the whole-genome framework linkage map of GW population, an additional set of 259 SSRs was screened for polymorphism between the parents of GW (Rye Selection 111 and Chinese Spring) population. One hundred thirty (50.19 %) of the above 259 SSRs were found polymorphic. Genotyping of 100 RILs with a total of 53 of 130 polymorphic SSRs has already been completed and for the remaining 80 SSRs is in progress. As soon as the genotyping is complete, a framework map will be prepared and used for QTL interval mapping.

Framework maps for PHST population. A framework linkage map for a solitary chromosome (3A) was earlier prepared for PHST population, using genotyping data for 124 molecular markers (11 SSR, 76 AFLP and 37 SAMPL) on 100 RILs of the above population. Only 13 of the above 124 marker could be assigned to 3A, and an average genetic distance of 21.47 cM between any two markers was observed (Kulwal et al. 2005). A map of 3A was prepared for QTL interval mapping, since 3A was known to carry genes for PHST.

To develop the whole-genome framework linkage map of PHST population, additional 362 (149 gwm and 213 wmc) SSRs were screened for polymorphism between the parents of the PHST mapping population (HD2329 and SPR8198). One hundred thirty-four (37.02 %) SSRs of the above 362 SSRs were found to be polymorphic. Genotyping of 100 RILs with a total of 56 polymorphic SSRs has been completed and genotyping with the remaining 78 SSRs is underway. The genotypic data will be used for construction of a framework map for QTL interval mapping.

Single locus QTL analyses for growth and yield traits (using grain weight mapping population). QTL analysis for agronomically important traits in bread wheat was conducted following SMA, SIM, and CIM using an intervarietal RIL population derived from a cross between Rye Selection 111 (high GW) and CS (low GW). The parents and the above

RILs were grown in six different environments, and the data on different agronomic traits were recorded in each case. For conducting single-marker regression analysis, genotypic data of 419 markers (299 AFLP and 120 SAMPL) were used with phenotypic data for different agronomic traits recorded in each of the six different environments, and also with the data pooled over different environments (total seven environments). QTL interval mapping also was conducted using framework linkage maps prepared for chromosomes 1A, 2A, 2B, and 7A (see above for map details).

Single-marker analysis (*SMA*) *for growth and yield traits.* Using the intervarietal RIL population for GW, single-marker analysis was conducted for four growth related traits (days to heading (DH), days to maturity (DM), early growth habit (EGH), and plant height (PH)) and seven yield and yield-contributing traits (tillers/plant (TPP), biological yield (BY), grain yield (GY), harvest index (HI), spike length (SL), spikelets/spike (SPS), and grains/spike (GPS)). For three growth traits, 28 markers showed significant association (4 with DM, 7 with DH, and 17 with PH). Similarly, for yield traits, 38 markers showed significant association with five of the seven yield and yield-contributing traits (2 with BY, 3 with SL, 10 each with GY and TPP, and 13 with GPS), in at least four of the above seven environments. The PV explained by the associated markers for individual growth related traits ranged from 3.86–16.81%, and for yield and yield-contributing traits, it ranged from 3.90–14.53 %.

QTL interval mapping for growth related traits. A total of 64 QTL were detected following SIM and CIM, which included 24 QTL for four growth related traits (DH, DM, EGH, and PH) and 40 QTL for seven yield contributing traits (TPP, BY, GY, HI, SL, SPS, and GPS). All these QTL were detected above a threshold LOD of 2.00–4.50 following both SIM and CIM. The PV explained by an individual QTL ranged from 7.42–32.16%.

Two-locus QTL analysis for yield and yield-contributing traits.

Population for grain protein content (*GPC*). Two-locus QTL analysis was conducted (QTLNetwork V2.0) for seven different yield and yield contributing traits (TPP, BY, GY, HI, SL, SPS, and GPS) using phenotypic data of 100 RILs (GPC population) recorded at six different environments. As many as 35 QTL (including, main effect QTL (M-QTL) and interacting QTL (QE, QQ, and QQE)) were detected for five (TPP, BY, GY, HI, and SL) of the above seven yield and yield-contributing traits, with minimum and maximum number of QTL detected for TPP/HI and SL, respectively. Out of the above 35 QTL, 10 M-QTL were distributed on nine different chromosomes (1A, 1D, 2B, 4A, 5A, 6A, 6B, 7A, and 7B); four M-QTL were involved in 'Q x E' interactions. The remaining 25 QTL were E-QTL, which were either involved in digenic interactions (Q x Q) or digenic environmental interactions (Q x Q x E).

International Triticeae Mapping Initiative population (*ITMIpop*). ITMI population was also used for two-locus QTL analysis (QTLNetwork V2.0) using data for the above seven yield and yield-contributing traits, recorded at four different environments. As many as 41 QTL (including M-QTL and interacting QTL (QE, QQ, and QQE)) were detected for all the seven yield and yield-contributing traits, with a minimum number of QTL (one) detected for BY/HI and maximum number of QTL (four) detected for GY. Out of the above 41 QTL, 16 QTL were M-QTL distributed on seven different chromosomes (1A, 2A, 2D, 4A, 4B, 5A, and 6D); eight M-QTL were involved in 'Q x E' interactions. Twenty-eight of the above 41 QTL (including both M-QTL and E-QTL) were either involved in digenic interactions (Q x Q) or digenic environmental interactions (Q x Q x E).

High resolution mapping of the genomic regions containing important QTL for GPC and PHST.

QTL for high GPC (*QGpc.ccsu-2D.1*) *on 2DL.* A population of about 2,000 F_2 plants was derived from a cross between the two extreme RILs for high GPC versus low GPC. By analyzing the above population with markers flanking the QTL (*QGpc.ccsu-2D.1*) of interest 40 F_2/F_3 homozygous recombinants were identified.

In order to develop more markers to enrich the interval (11.4 cM) carrying *QGpc.ccsu-2D.1*, 64 AFLP primer combinations (8 *Eco* RI x 8 *Mse* I) were used, to identify chromosome arm (2DL)-specific AFLP markers (using nullisomic tetrasomic and ditelosomic lines of 2D), which could detect polymorphism among extreme RILs, representing parents of the above mapping population. Only seven AFLP markers specific to 2DL detected polymorphism among the parental genotypes and will be used for genotyping of the above 40 F_2/F_3 plants. An additional set of 960 AFLP primer combinations (unmapped) and 17 SSR primers (known to be mapped in the region of interest) are being used to identify an additional set of 2DL specific polymorphic markers. All these markers, identified as above, will be used for high resolution mapping of the region carrying the QTL of interest.

QTL for PHST (*QPhs.ccsu-3A.1*) *on 3AL.* A population of about 1,600 F_2 plants was derived from a cross between SPR8198 (PHS tolerant) and HD2329 (PHS susceptible), with the objective of enriching the region carrying the QTL of

interest (*QPhs.ccsu-3A.1*). The above population is being screened for the presence of recombinants using flanking markers of the region carrying *QPhs.ccsu-3A.1*. The recombinants identified as above will be genotyped using chromosome arm specific markers showing polymorphism between the genotypes representing parents of the above population. For this purpose, a set of 144 markers (19 SSRs and 125 STS) was developed using a chromosome arm (3AL)-specific genomic DNA library of bread wheat (see Gupta et al. 2005 for details). In addition to the above markers, a set of 1024 AFLP primer (16 *Eco* RI x 64 *Mse* I) combinations will be utilized to identify chromosome arm specific polymorphic markers.

Physical mapping of SSRs on 21 chromosomes of bread wheat. In bread wheat, a total of 485 SSRs including 325 gSSRs and 160 EST-SSRs were tried with 192 deletion lines, leading to successful mapping of 228 loci including 161 gSSR loci and 67 EST-SSR loci covering all the 21 chromosomes. A maximum number of 92 (40 %) loci were assigned to B genome followed by 68 (30 %) loci to A-genome and 68 (30 %) loci to D-genome. Except for eight discrepancies, a high degree of collinearity of gSSRs was observed between the physical and genetic maps. As many as 75 loci (including 32 gSSR and 43 EST-SSRs) were never used earlier for genetic mapping.

Marker-assisted selection for high GPC. In order to transfer a segment carrying a QTL for high GPC, 10 Indian cultivars were crossed with Yecora Rojo (seeds of Yecora Rojo was procured from J. Dubcovsky), a high grain protein content genotype. The F_1 plants were backcrossed with their corresponding recurrent parents to obtain BC_1 seeds during Rabi, 2004–05. The above BC_1 seed were used to raise BC_1F_1 population in phytotron (IARI, New Delhi) during summer of 2005. Genomic DNA was extracted from the above BC_1F_1 plants to perform three-step selection (see below) using molecular markers, which will give plants carrying desirable allele for high GPC along with a genomic background similar to their respective recurrent parents. Different steps involved in the selection process are as follows:

Step-one selection. Selection of BC_1F_1 plants was exercised using molecular markers (SSR (gwm193) and an allele specific amplification (ASA) marker) flanking the QTL of interest. Eleven BC_1F_1 plants showed the presence of the desirable alleles at both the marker loci that flank the QTL of interest.

Step-two selection. Background selection on the above, 11 BC_1F_1 plants was exercised using 20 SSR markers specific to chromosome 6B, carrying the QTL of interest. All 11 BC_1F_1 plants showed the presence of recipient parent alleles at 5 to 14 marker loci.

Step-three selection. All of the above 11 BC_1F_1 plants were subjected to the whole-genome background selection using 80 SSR markers, scattered throughout the genome. This selection identified seven of the above 11 BC_1F_1 plants that better represent the genomes of their recurrent parents. These plants were backcrossed with their recurrent parents and the backcross hybrid seeds were used for raising BC_2F_1 population in 2005–06.

Development and use of EST-SNPs in bread wheat. Under the aegis of the international Wheat SNP Consortium (WSC), we undertook discovery, validation, and genotyping of SNPs in a set of 48 wheat EST contigs (each having 20–89 EST from 2 to 11 different genotypes), assigned to our group. Contigs were classified into subcontigs belonging to three individual subgenomes (A, B, and D) of the hexaploid wheat, to avoid confusion between homoeologous sequence variants (HSVs) among related genomes and SNPs. As many as 230 putative SNPs were detected in 155 such subcontigs (representing homoeoloci) belonging to 42 EST contigs. STS primers were designed for the above 42 EST-contigs and were used to amplify genomic DNA from 30 elite wheat genotypes. Only 10 of the above 42 primers were used for resequencing and allowed validation of seven SNPs (1 SNP/520 bp) out of 30 putative SNPs detected *in silico* in the amplifiable region (amplicon) of the above 10 primers in corresponding EST contigs. Allele-specific primers also were designed for the seven validated SNPs and were used for genotyping of 50 elite wheat genotypes (including 30 genotypes used for validation of SNPs) to study the occurrence of these SNPs. Of the above seven validated SNPs, four belonged to a solitary locus (PKS37), thus allowing discrimination of haplotypes at this locus. Altogether, the results suggested that EST-SNPs constitute an important source of molecular markers and could be developed and used in large number for studies on wheat genomics.

Identification of natural variants of *Agp-L* gene through EcoTILLING. In order to identify variants of genes involved in starch biosynthesis and to develop functional markers (FMs) for early identification of desirable genotypes through MAS, we initiated an EcoTILLING program in bread wheat, involving large subunit of ADP-glucose pyrophosphorylase (*Agp-L*), a key enzyme in starch biosynthesis pathway. For this purpose, genome specific primers developed for B and D sub-genomes of bread wheat (Blake et al. 2004) are being used on a set of 52 elite wheat genotypes available with us.

Use of C_0t fractionation (CF) and methyl filtration (MF) for genomics research in bread wheat. Gene-enrichment strategies of methyl-filtration and reassociation kinetics were used to generate and analyze 2,000 hypomethylated (MF), 1,026 high C_0t (HC), and 1,253 reassociated DNA (RD) sequences of bread wheat, which together constituted 1.61 Mb of genomic sequences. Comparison of each of the above fractions with each of the other two fractions revealed large compositional/structural variations among the three groups of sequences. About 30 % of sequences from MF and 17 % of sequences from HC still represented repeat elements. SSRs also were detected in all the above three (MF, HC, and RD) fractions. A density of 1SSR/3.11 kb in MF was comparable to known SSR density in wheat genomic sequences. A density of 1SSR/2.27 kb in HC was comparable to that of SSRs in ESTs and a density of 1SSR/2.45 kb in RD was intermediate. In MF and RD sequences, the frequency of noncoding (nc) RNA genes was higher than that of protein coding genes but in HC sequences, the frequency of protein coding genes was relatively higher. Altogether, the frequencies of protein-coding genes relative to ncRNA genes varied from high to low in the following order HC→RD→MF, and those for ncRNA genes relative to protein coding genes varied in the following order RD→MF→HC. When matching was done with ESTs, large proportion of matching ESTs in the databases was found to represent transcripts encoded by transposable elements (TEs) and rRNA sequences; this was true with each of the three groups of sequences analyzed. Putative functions were also assigned to genes predicted from MF, HC and RD fractions. Genes encoding proteins conferring resistance against biotic stresses (mostly represented by gene families) were more frequent in MF sequences, and the genes encoding proteins involved in different metabolic pathways (perhaps housekeeping genes) were more frequent in HC sequences. However, the genes predicted in RD sequences largely matched proteins encoded by TEs. Matching with physically mapped wheat ESTs, allowed assignment of 58 MF sequences to 238 loci on 21 bread wheat chromosomes, of which 145 (60.9 %) loci reside in the distal halves of chromosomes. Also, while looking for synteny with rice sequences, synteny of 140 MF sequences was detected with rice genome sequences spread over all the 12 rice pseudochromosomes, with maximum number of loci on chromosome 3 and minimum number of loci on chromosome 12. A small proportion of MF and HC sequences also showed similarity with maize MF and HC sequences, suggesting that these sequences were conserved during evolution of cereals. Altogether, the above study suggests that the two gene-enriched fractions of wheat genome (MF, HC) differ significantly from each other and also differ from wheat ESTs, so that MF and HC sequences (along with wheat ESTs and RD sequences) should be used together to study the composition of wheat genome.

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The effect of sowing date on the interaction of loose smut and ear cockle in Indian wheat cultivars.

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Summary. All cultivars except WH896 and Raj 1555 were susceptible to loose smut having 17.71 to 43.33 % disease incidence. With delayed sowing, all cultivars had reduced disease incidence. Conversely, ear cockle incidence was drastically increased in HD2285 and Raj1555 from 28.35 to 48.88 % and 3.83 to 10.35 %, respectively.

Introduction. The simultaneous occurrence of *Ustilago segetum* var. *tritici* with *Anguina tritici* in wheat has been reported by various workers (Bedi et al. 1959; Pruthi and Gupta 1986). During the croping season of wheat, this type of association between *Anguina tritici* and *Ustilago segetum var tritici* has been observed in plant pathology research area. Such type of concomitant association of the fungus and nematode has different level of incidence on different wheat varieties cultivated in India and which among two predominant in different varieties. Therefore, an attempt has been made to study the effect of concomitant occurrence of loose smut and ear cockle on different varieties at different sowing date.

Materials and methods. A field experiment was conducted at Plant Pathology research area of CCSHAU-Hisar during 1997–2000 crop season. In each plot, 25 cultivars inoculated with loose smut spores in previous crop season were sown in 6 rows 2-m long. Each row received 10 nematode gall. Sowing dates of 25 November, 15 December, and 30 December were used for all treatments. Each cultivar has a subplot separated by 1 m distance by another one. Disease incidence was noticed on tiller basis in each cultivars. Tillers having both diseases were counted separately for both diseases.

Results and discussion. We noticed that two-thirds of the spikes constituting the lower part had almost been totally transformed into black sori of the loose smut fungus. The upper portion of this spike was infected by ear cockle nematode and black gall, which were clearly visible from distended glumes. All cultivars except WH896 and Raj 1555 were susceptible to loose smut with 17.71–43.33 % disease incidence. With a delay in sowing, all susceptible cultivars showed drastic reduction in disease expression (Table 1, p. 48). In the highly susceptible cultivar Sonalika, disease incidence was decreased from 43.33 to23.66%. A reduction in chlamydospore germination/mycelial inactivation along with fall in temperature may have caused this. Conversely, ear cockle incidence was drastically enhanced in HD2285 (from 28.35 to 48.88 %) and Raj 1555 (3.83 to 10.35 %). Sonalika and HD2285 had the maximum amount of disease.

A. tritici had more time for infection and prolonged germination time of seed along with fall in temperature. Pruthi and Gupta (1986) reported that the presence of a fungus with a nematode has an adverse effect on the number, motility, and development of larvae at the normal sowing time.

Table 1. The effect of three sowing dates on the interaction of loose smut (LS) and ear cockle (N) of wheat cultivars.

	25 November		15 December		30 December	
Cultivar	LS	N	LS	N	LS	N
C306	37.27	17.47	33.95	28.66	27.69	33.07
Sonalika	43.52	17.05	38.46	23.84	30.83	39.16
WH147	39.75	18.64	31.43	25.88	28.44	31.11
WH157	38.69	17.39	32.44	24.66	23.71	29.42
WH291	36.08	18.11	30.22	24.83	21.33	31.42
WH416	35.00	15.00	28.14	20.37	20.77	26.66
WH533	31.16	22.93	26.66	29.83	20.66	35.28
WH542	32.33	20.96	28.14	27.33	21.33	33.33
WH896	0.00	11.38	0.00	16.16	0.00	21.57
Sonak	31.66	22.77	24.33	30.16	18.83	38.83
HD2009	38.75	20.91	29.33	27.71	23.37	34.57
HD2285	36.48	24.83	26.83	30.83	19.77	41.33
HD 2329	30.00	18.33	22.22	24.77	16.66	30.96
HD2687	36.66	18.16	29.83	23.83	23.66	28.71
PBW175	31.42	18.77	26.83	26.42	21.66	31.88
PBW343	39.53	14.83	29.83	22.37	21.77	29.83
PBW373	33.33	18.66	26.71	24.16	20.16	30.57
PBW435	37.66	20.00	29.33	26.66	23.66	32.22
RAJ1555	0.00	14.28	0.00	18.22	0.00	23.33
RAJ3077	36.66	16.66	28.83	24.77	22.22	30.33
RAJ3765	34.44	18.16	27.66	23.71	21.33	29.33
RAJ3777	32.33	20.33	25.16	26.66	19.66	32.66
UP2338	33.83	19.14	26.57	25.66	20.44	31.33
UP2425	36.66	18.44	28.33	24.33	22.22	29.66
C.D. (0.05 %)	2.54	1.95	1.92	2.32	2.62	2.16

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Participatory varietal selection for high yield and faster spread of wheat genotypes in Indo-Gangetic plains of India.

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Introduction. Wheat is the leading grain crop in India and is cultivated under a wide range of climatic conditions. The most extensive production of wheat is in areas where the winters are cool and the summers are comparatively hot. The total area under wheat production in India is around 26 x 10^6 ha with total production hovering around 70 x 10^6 tons for the last decade. The bread wheat crop accounts for 84 % of the area; durum wheat occupies ~14 %. The productivity, duration, resistance, end product use, and suitability of bread wheat for the economically viable cropping systems of the farming community are some of the reasons that make durum wheat a second priority in the major wheat-growing zones of India. We now realize that yield gains in the Indo-Gangetic Plains area need to be further improved to meet the increased demand of wheat. Two feasible options are to improve yield potential of the genotypes and at the same time reduce the yield gaps between achieved and achievable. Researchers are making efforts to bridge yield gaps by advocating and demonstrating new technology, including cultivars, along with matching production technology in the farmers'

field. The concept, methodology, results, and future thrusts for making use of a participatory varietal selection (PVS) approach in the Indo-Gangetic Plains of India are discussed below.

The concept of PVS for yield improvement and adoption. Participatory varietal selection involves the selection of a nonsegregating, characterized product from plant breeding programs by farmers. Such material includes released cultivars, those in advanced stages of testing, and advanced nonsegregating lines. In contrast, participatory plant breeding (PPB) involves selecting genotypes from genetically variable, segregating material by the farmers. The difference between PVS and PPB may not appear to be great at first sight. However, PPB requires more resources than PVS, and PVS identifies material that can be adopted more rapidly by the formal seed sector. The majority of farmers in India, particularly in the eastern, far eastern, and warmer regions, are still growing very old cultivars, local types, or land races even four decades after the beginning of the green revolution and, hence, fail to reap the benefits of modern technologies such as new, improved cultivars and resource conservation technologies. The wheat crop area, which is nearly half a million hectares in the far eastern state, is believed to have the potential of producing about 3.5 t/ha under optimum conditions, provided suitable genotypes resistant to leaf blight and with a 100-day maturity time with recommended agronomic practice are available.

PVS in wheat for Indo-Gangetic plains of India. To deal with such issues as dominance of a single cultivar in a region, slow rate of cultivar replacement, or low yield, a farmer participatory research project entitled 'Participatory Research to Increase the Productivity and Sustainability of Wheat Cropping systems in the Eastern sub Continents of South Asia' funded by DFID has been initiated at the Directorate of Wheat Research, Karnal, through the South Asia Regional Office of CIMMYT in Kathmandu, Nepal, with objectives of increasing wheat productivity and sustainability in this region. The DWR Karnal was assigned to work on material development for PVS at the Shillongani and Ranchi centers under this project. The following activities were conducted during 2003–04 by DWR, Karnal, and the salient features of the progress under the period are given.

Design of PVS. PVS attempts to cover a large number of farmers, especially the resource-poor. Farmers who are risk-averse or limited due to small land holding can, therefore, still afford large plots. Being poor, they also may not have the capacity to use purchased inputs. PVS targets the existing environment to identify suitable cultivars, which means that the field designs have to be simple and adaptable. The project document specifies three approaches for PVS for farmer-managed participatory research (FAMPAR).

Mother trials. Under the PVS program, researcher-designed and farmer-managed trials having a single replication of mainly farmer-selected cultivars conducted by few farmers representing the target area. In such cases, these selected farmers also serve as replicates for data analysis. These trials also aim to produce quantitative data involving the selected farmers at each site. To evaluate and multiply, a set also was grown at the Research Station of DWR, Karnal. Based on the information generated from these trials, surveys, and opinion polls, ranking for the cultivars and traits of choice were estimated. These data will represent the adaptive research area for fine tuning the breeding program at large.

Baby trials. This set of trials was designed by researchers involved in the program but are managed by the farmers at their sites. These are single-entry trials, in which newly selected and proposed entries are grown alongside the farmer's check cultivar under similar management conditions. The individual farmer may serve as a replicate for analyzing the data from each site. For each site or location, the number of baby trials conducted cover the whole range of prevailing conditions of farmers' field in the target area. At each location, data are collected as perceptions of farmers covering that particular locality, and the results obtained again represent the adaptive area of research for future planning.

PVS as an approach. The PVS approach was thought to be a promising strategy of increasing the rate of adoption for new cultivars among farmers in this area. Under this approach a wide range of recently released, high yielding, short duration, modern cultivars are tested in the farmers' field. The step-wise implementation of the following interlinked activities at various sites improves the productivity of wheat in this area to supplement the ongoing wheat improvement program.

1. Planting promising cultivars in the farmers' field to identify need-based cultivars through PVS.
2. Popularizing the farmer's selected cultivars in the targeted area through demonstration.
3. Educating farmers, extension agencies, and nongovernmental organizations through training, field days, farmers' meals, and roving seminars creates awareness for new technology.
4. Conducting base line and impact assessment surveys to get the feedback on farmer perception and fine tuning the technology to come.

Material and methods. Under this program, we organized 8–9 one-acre sized, PVS demonstrations of improved wheat cultivars to convince and educate farmers about new technological advancements that now are available. Selected experimental sites were Darer, Janeshro (Karnal), Mathana, and Kishangarh (Kurukshtra). Eight mother trials consisting of eight cultivars, PBW 343, HD 2687, WH 711, WH 542, UP 2425, PBW 373, RAJ 3765, and UP2338, were sown in farmers' fields for participatory selection. These cultivars also were sown under different tillage options, such as no-till, raised bed, and conventional tillage. To popularize the cultivars other than PBW 343 in this area, eight 'Farmer Days' were organized in Mathana, Kishangarh, Janeshro, and Darer; four were organized in March 2004, before maturity, and four at maturity, in April 2004.

Results and discussion. The results of PVS experiments at the eight sites in two districts in the state of Haryana were analyzed and are presented in Tables 1 and 2. In addition to recording yield data at each site, the selected farmers were also asked to express their preferences. The economic importance of various parameters was assessed on a three-point continuum, very important (3), somewhat important (2), and not important (1) by the farmers in the Farmers Group Discussion mode. The characteristics-wise economic importance score of all the 18 parameters are given in Table 1.

The parameters assessed were germination, number of effective tillers, days to maturity, plant height, lodging resistance, insect and disease resistance, ear head length, grains per spike, grain yield, straw yield, and grain type. The two traits namely germination and grains/ spike with score three were the first priority of all the farmers surveyed. Days-to-flowering and maturity did not receive much attention as evident by the score less then two. Some yield contributing traits like number of effective tillers, grain type, and 1,000-kernel weight were preferred by the farmers and matter while selecting wheat genotype for commercial cultivation at these sites. This type of ranking also is practiced by the researchers and, hence, are in the similar order. During the farmers' days, the participants were briefed about the objectives of the DFID project. More than 1000 farmers participated in this program. However, for the purpose of perception a total 100 farmers were randomly selected from the adapted sites. O n the basis of farmers' responses, the varieties were ranked. All the cultivars sown were evaluated by individual farmers in the field before and at maturity on a three point continuum, very good (3), good (2), and not good (1). The matrix ranking along with the evaluation score of all the genotypes used for study were estimated and are given in Table 2.

Table 1. Economic importance score for 18 parameters (N = 100) for evaluating wheat cultivars under PVS.

Parameter	Score
Germination	3.00
Number of effective tillers	2.96
Days to flowering	1.88
Days to maturity	1.87
Plant height	2.72
Lodging resistance	2.84
Disease resistance	2.88
Insect resistance	2.31
Threshability	2.02
Grain colour	2.24
1,000-kernel weight	2.73
Cooking quality	2.07
Chapatti quality	2.35
Spike length	2.51
Grains / spike	3.00
Grain type	2.95
Grain yield	2.96
Straw yield	2.47

Table 2. Matrix ranking of different wheat cultivars for 18 parameters under PVS (N = 100). Figures in parentheses indicate the total score, where total score = 'mean economic importance score' x 'evaluation score of the same parameter'. The overall score = sum of the scores of all parameters of a cultivar.

Parameter	HD2687	PBW 343	PBW 373	RAJ 3765	UP 2338	UP2425	WH 542	WH 711
Germination	2 (7.89)	1 (8.76)	4 (7.53)	6 (6.81)	5 (7.08)	8 (6.24)	7 (6.66)	3 (7.80)
Effective tillers	2 (7.90)	1 (8.23)	6 (6.81)	7 (6.01)	4 (7.16)	8 (5.65)	6 (6.33)	3 (7.84)
Days to maturity	1 (4.96)	2 (4.92)	8 (4.81)	4 (4.90)	7 (4.84)	6 (4.86)	5 (4.88)	3 (4.92)
Plant height	3 (7.21)	1 (7.75)	4 (7.15)	8 (6.47)	5 (6.99)	6 (6.83)	7 (6.52)	2 (7.23)
Lodging resistance	2 (7.72)	1 (8.09)	5 (6.79)	8 (6.22)	6 (6.53)	4 (6.84)	7 (6.42)	2 (7.61)
Disease resistance	5 (6.22)	2 (6.83)	4 (6.39)	3 (6.42)	6 (6.22)	7 (6.11)	8 (5.73)	1 (7.03)
Insect resistance	4 (5.71)	1 (6.24)	5 (5.64)	6 (5.47)	3 (5.80)	7 (5.34)	8 (5.43)	2 (5.86)
Spike length	1 (6.80)	2 (6.80)	4 (6.25)	7 (5.37)	5 (6.17)	6 (6.12)	8 (5.25)	3 (6.73)
Grains/spike	3 (7.98)	1 (8.37)	4 (6.90)	6 (6.33)	5 (6.72)	7 (6.33)	8 (6.21)	2 (8.01)
Grain type	2 (7.85)	3 (7.67)	4 (6.96)	7 (6.11)	5 (6.76)	6 (6.76)	8 (5.96)	1 (8.05)
Grain yield	1 (8.58)	2 (8.55)	7 (5.65)	8 (5.39)	4 (6.48)	5 (5.74)	6 (5.74)	3 (7.87)
Straw yield	1 (7.21)	2 (6.92)	5 (5.06)	6 (5.04)	3 (6.64)	7 (4.45)	4 (5.29)	8 (4.32)
Rank and overall score	2 (86.03)	1 (89.13)	5 (75.94)	7 (70.54)	4 (77.40)	6 (71.27)	8 (70.42)	3 (83.38)

Matrix ranking of wheat cultivars on the basis of evaluation score and economic importance score of parameters. The cultivars were ranked on the basis of economic importance of the parameter and the evaluation score. Thereafter, the scores of all the parameters were summed for a cultivar to arrive at a composite score. On the basis of the composite score, PBW 343 ranked first, followed by HD 2687, WH 711, UP 2338, PBW 373, UP 2425, RAJ 3765, and WH 542.

Conclusion. The Participatory Varietal Selection programs in the high potential production system in India successfully identified new, nonrecommended cultivars that farmers preferred and adopted. The farmer participatory approach could be helpful in at least two ways. First, farmers would benefit by adopting new technologies and, second, a strong linkage would be established between researchers, farmers, and other sources of new technology such as the State Agriculture Department and seed certification agency, which, in turn, would increase production, productivity, and profitability of farmer and also help to meet our estimated demand of 109 x 10^6 t of wheat production by the year 2020.

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Effect of etherel on seed set, outcrossing, pollen sterility, and yield traits in wheat.

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Abstract. We studied the effect of etherel at different concentrations on various floral and yield traits, the crop growth stage for chemical spray, and sowing time for their possible use in development of wheat hybrids. Two genotypes, HD 2285 and Raj 3765, were included in the study and data were recorded on reduction in seed number/spike as % of control, outcrossing %, pollen sterility %, plant height (cm), spike length (cm), and spikelet length (mm). Etherel at 12,000 ppm was observed effective for maximum reduction in grain number/spike with increased pollen sterility and outcrosing (%). The reduction in plant height, spike length and spikelet length was observed due to phytotoxic effects of chemicals. Late sowing and chemical spray at early boot stage were found more effective for etherel treatment.

Introduction. Wheat is a strictly self-pollinated crop (Percival 1921). Conventional breeding methods have contributed significantly in increasing wheat production. We need to explore new approaches to break the yield barriers and make wheat cultivation more remunerative. Among the possible alternatives, an important approach has been to exploit hybrid vigor at commercial level. Hybrids in wheat may cause a quantum jump in production at the global level, but the main bottleneck is the floral structure of wheat, which has very small florets, necessitating hand emasculation and pollination,

labor oriented and tedious work, which ultimately results in higher cost for hybrid seed. The limitations of genetic and/or cytoplasmic male sterility, i.e., unstable nature, undesirable linkages, and need for use of maintainers, have prompted breeders to develop simple and more efficient methods to create male sterility by other means like use of chemical hybridizing agents (CHAs) and mutagens. Male sterility induced by CHAs (Moore 1950; Naylor 1950) is relatively more convenient to use because there is no need to maintain it (McRae 1985). These chemicals induce male sterility by inhibiting the early stages of sporogenous cell formation to the inhibition of anther dehiscence (McRae 1985). Law and Stoskopf (1973) and Hughes et al. (1974) suggested the use of etherel for creating male sterility in plants. The present investigation was aimed at the effect of different doses of etherel, the stage of crop for spray, and sowing time of genotypes on various floral and yield parameters.

Materials and methods. The wheat cultivars HD 2285 and Raj 3765 were used as experimental material. The field experiments were conducted in randomized block design with three replications during 1998–99 crop season at Agricultural Research Farm at Banaras Hindu University, Varanasi, India (25°18' N latitude and 82°03' longitude), which falls under semiarid to subhumid climate. The annual average rainfall is 1,081.4 mm, and mean relative humidity is 62 %. The maximum and minimum temperatures range between 23.2–46.4°C and 9.3–24.5°C, respectively. Wheat cultivars were sown on two dates to evaluate timely and late-sown conditions. Each plot had six 2.5-m rows with inter- and intrarow spacing of 25 cm and 10 cm, respectively. The inner two rows were treated as females and the outer four rows as males. A gap of 1 week was kept between the male and female rows to synchronize the pollen release and stigma receptivity; female rows were sown first. Etherel (6,000, 9,000, and 12,000 ppm) was sprayed at two crop growth stages. First spraying was done when spike length was 11–13 mm and was still inside the whorl. This stage of spike length was achieved at around 35 days after germination when the plant height was slightly less than one foot and the second at boot stage prior to spike emergence. Control plants were sprayed with water. Chemicals were sprayed in the evening to give sufficient time for their absorption by the wheat plant. At flowering, the male rows were shaken with the help of a rope pulled across the field. Control plants were also grown and sprayed with water. The data was recorded on reduction in

Table 3. Analysis of variance (ANOVA) for various traits following a spray of etherel in wheat. * and ** indicate significance at the 0.05 and 0.01 levels, respectively.

Source	d.f.	Reduction in grain #/spike (%)	Outcrossing (%)	Pollen sterility (%)	Plant height (cm)	Spike length (cm)	Spikelet length (mm)
Replication	2	0.061	1.894*	0.538	0.303*	0.002	0.002
Treatment	31	4,672.097**	352.992**	4,540.879**	582.965**	2.310**	16.997**
Factor A (sowing date)	1	16.129**	45.128**	0.461	36.236**	0.776**	5.120**
Factor B (spray)	1	2.145**	1.092	0.210	3.977**	0.173**	1.443**
AB (sowing date x spray)	1	0.137*	0.007	0.002	0.078	0.002	0.003
Factor C (genotype)	1	14.750**	142.301**	3.701**	167.059**	0.159**	0.178**
AC (sowing date x genotype)	1	0.010	1.260	0.790*	1.972**	0.071**	0.410**
BC (spray x genotype)	1	0.069	0.186	0.077	0.002	0.015	0.098**
ABC (sowing date x spray x genotype)	1	0.011	0.182	0.007	0.096	0.005	0.001
Factor D (Concentration)	3	48,262.271**	3,553.475**	46,916.510**	5,940.677**	22.667**	169.326**
AD (sowing date x concentration)	3	2.341**	4.792**	0.410	2.706**	0.049**	0.382**
BD (spray x concentration)	3	0.344**	0.674	0.184	0.638**	0.018**	0.086**
ABD (sowing date x spray x concentration)	3	0.072*	0.167	0.406	0.022	0.006	0.005
CD (Genotype x concentration)	3	1.923**	22.078**	2.733**	9.579**	0.669**	3.336**
ACD (sowing date x genotype x concentration)	3	0.051	2.459**	0.296	0.419**	0.048**	0.062**
BCD (spray x genotype x concentration)	3	0.167**	0.455	0.110	0.095	0.012	0.010
ABCD (Sowing date x spray x genotype x concentration)	3	0.082**	0.105	0.017	0.034	0.003	0.008
Error	62	0.020	0.596	0.183	0.076	0.006	0.008
Total	95						

grain number/ spike as percent of control, out crossing (%), pollen sterility (%), plant height (cm), spike length (cm), and spikelet length (mm). The data were recorded as per the procedure followed by Mahajan et al. (1997). Analysis of variance was done using factorial randomized block design analysis. The computer program INDOSTAT was used for this purpose.

Table 4. The effect of different doses of etherel on various traits in wheat. SD1 = Timely sown conditions and SD2 = Late-sown conditions; S1 = crop stage when spike is 11–13 mm long (about 35 days after sowing) and S2 = early boot stage.

Sowing date	Spray stage	HD 2285				Raj 3765			
		Control	6,000	9,000	12,000	Control	6,000	9,000	12,000
Reduction in seed set (%)									
SD1	S1	0.00	85.04	89.28	93.18	0.00	84.27	88.32	91.99
	S2	0.00	86.16	89.78	93.37	0.00	84.40	89.01	92.38
SD2	S1	0.00	86.64	90.77	93.69	0.00	85.32	89.98	92.87
	S2	0.00	87.28	90.92	93.91	0.00	85.75	90.07	93.12
		SE ± 0.08				CD (5 %) = 0.16			
Outcrossing (%)									
SD1	S1	1.53	23.69	27.43	28.60	1.41	20.87	22.43	25.89
	S2	1.63	23.88	27.56	27.40	1.35	21.28	21.67	25.50
SD2	S1	1.58	25.51	29.16	29.29	1.37	21.87	25.05	28.42
	S2	1.61	25.52	28.56	28.72	1.35	21.90	24.63	28.62
		SE ± 0.45				CD (5 %) = 0.90			
Pollen sterility (%)									
SD1	S1	8.24	95.85	96.00	97.01	7.54	93.98	96.17	97.27
	S2	8.10	95.53	95.67	97.55	7.47	93.92	95.33	97.67
SD2	S1	7.72	95.52	95.88	97.70	7.54	94.60	96.49	97.64
	S2	7.77	95.45	96.10	97.46	7.39	94.58	96.22	97.45
		SE ± 0.25				CD (5 %) = 0.50			
Plant height (cm)									
SD1	S1	75.01	45.47	43.45	40.80	70.60	44.80	41.05	38.65
	S2	75.01	44.80	42.80	40.50	70.72	44.20	40.80	38.20
SD2	S1	74.48	44.35	41.90	40.20	70.27	42.80	38.95	37.50
	S2	74.52	43.75	41.20	39.90	70.17	41.60	38.50	37.10
		SE ± 0.16				CD (5 %) = 0.32			
Spike length (cm)									
SD1	S1	8.70	7.53	7.10	6.25	8.63	7.25	6.90	6.75
	S2	8.75	7.35	6.80	6.15	8.62	7.15	6.85	6.70
SD2	S1	8.65	7.25	6.55	6.10	8.55	7.05	6.80	6.65
	S2	8.60	7.15	6.40	6.05	8.49	6.95	6.75	6.60
		SE ± 0.04				CD (5 %) = 0.08			
Spikelet length (mm)									
SD1	S1	13.83	11.37	9.45	8.40	14.70	10.25	9.05	8.65
	S2	13.70	10.90	9.10	8.10	14.63	9.87	8.95	8.40
SD2	S1	13.57	10.30	8.90	7.90	14.60	9.65	8.80	8.20
	S2	13.50	9.85	8.60	7.50	14.50	9.45	8.65	8.00
		SE ± 0.05				CD (5 %) = 0.10			

Results and discussion. The ANOVA (Table 3, p. 52) revealed that variation in sowing dates, genotypes, chemical concentrations, and spray stages were highly significant for the traits of reduction in grain number/ spike (%), plant height (cm), spike length (cm), and spikelet length (mm). Out crossing (%) and pollen sterility (%) had highly significant differences due to genotype and chemical concentrations, indicating that these two traits were unaffected due to change in sowing time as well as spray of chemical in different stages.

Effect on seed set, out crossing, and pollen sterility. The results (Table 4) indicated that the seed setting in the genotype HD 2285 was more adversely affected due to etherel treatment as it showed more than 93 % reduction in seed setting compared to control at higher concentrations. Maximum reduction (93.91 %) was observed at 12,000 ppm concentration in HD 2285 when etherel was sprayed at boot stage in late sown crop. A similar trend also was observed in the Raj 3765. The range of out crossing in the control (untreated) in both the genotypes was 1.35 to 1.63 %. An increase in the outcrossing percent was noticed when these genotypes were treated with etherel and was higher with

increased concentration. More than 28 % outcrossing was observed at higher concentrations in both the genotypes. Significant differences were observed between various combinations of sowing time and spray stage within the genotype. Both the genotype showed about 7–8 % pollen sterility in the untreated population. Because etherel works as chemical hybridizing agent that causes male sterility in plant system, it induced more than 97 % pollen sterility in both the genotypes. More pollen sterility at high concentrations may be a probable reason for poor seed set in these genotypes.

Table 5. The effect of sowing date on various traits at different doses of etherel in wheat. SD1 = Timely sown conditions and SD2 = Late-sown conditions.

Sowing time	HD 2285				Raj 3765			
	Control	6,000	9,000	12,000	Control	6,000	9,000	12,000
Reduction in seed set (%)								
SD1	0.00	85.60	89.53	93.28	0.00	84.34	88.67	92.19
SD2	0.00	86.96	90.84	93.80	0.00	85.53	90.02	92.99
	SE = ±0.06				CD (5 %) = 0.12			
Outcrossing (%)								
SD1	1.58	23.79	27.50	28.00	1.38	21.08	22.05	25.70
SD2	1.89	25.52	28.86	29.16	1.36	21.89	24.84	28.52
	SE = ±0.32				CD (5 %) = 0.64			
Pollen sterility (%)								
SD1	8.17	95.69	95.83	97.28	7.51	93.95	95.75	97.47
SD2	7.75	95.48	95.99	97.58	7.47	94.59	96.36	97.55
	SE = ±0.18				CD (5 %) = 0.36			
Plant height (cm)								
SD1	75.01	45.13	43.13	40.65	70.66	44.50	40.93	38.43
SD2	74.50	44.05	41.55	40.05	70.22	42.20	38.73	37.30
	SE = ±0.11				CD (5 %) = 0.22			
Spike length (cm)								
SD1	8.72	7.44	6.95	6.20	8.62	7.20	6.88	6.73
SD2	8.63	7.20	6.48	6.08	8.52	7.00	6.78	6.63
	SE = ±0.03				CD (5 %) = 0.06			
Spikelet length (mm)								
SD1	13.77	11.14	9.28	8.25	14.67	10.09	9.00	8.53
SD2	13.53	10.08	8.75	7.70	14.55	9.55	8.73	8.10
	SE =±0.04				CD (5 %) = 0.08			

Effect on yield traits (plant height, spike length, and spikelet length). Plant height, spike length, and spikelet length are the traits that significantly contribute to yield. A drastic reduction was noticed in these traits due to etherel treatment in both the genotypes (Table 4, p. 53). In Raj 3765, more than a 47 % reduction in plant height was observed at 12,000 ppm, whereas it was little less in HD 2285 (46.46 %). This reduction was particularly due to phytotoxic effects of the etherel that reduced internode length. Reduction in plant height due to etherel also was observed by Rathgeb et al. (1982), Barbosa et al. (1987), Savchenko et al. (1989), and Zhao et al. (1993). Spike length was less affected in Raj 3765 compared to HD 2285. At 12,000 ppm, maximum reduction (29.71 %) in spike length was observed in timely sown treatment of HD 2285 when spraying was done at early boot stage. In Raj 3765 about 22 % reduction was recorded at highest concentration. The spikelet length was ranged from 7.50–11.37 mm in treated populations. The quantum of reduction in spikelet length was more than 44 % in both the genotypes compared to untreated control population when late sown crop was sprayed with 12,000 ppm etherel at early boot stage.

Effect of sowing date and crop stage. The effect of sowing date and crop stage for etherel spray on various traits in wheat genotypes was studied. The effect of chemical spray on various traits was observed in timely as well as late sown condition and the results indicated more reduction in seed setting in late sown genotypes (Table 5). The late-sown crop was more responsive to the etherel treatment for increasing out crossing rate. In late-sown conditions, the outcrossing rate was 5.66–8.39 % more when compared to timely sown crop. A significant increase in outcrossing was observed in Raj 3765 with increased concentrations. Pollen sterility % was similar in timely and late-sown conditions, which also was indicated from the ANOVA. Plant height, spike length, and spikelet length showed more reduction in late-sown conditions. These findings indicated that the late sown crop was more responsive to CHA treatment for induction of male sterility, enhanced out crossing rate and reduced seed setting in selfed spikes (Mahajan et al. 1997; Singh et al.

2000), but the extent of phytotoxic effects in terms of reduction in plant height, spike length, and spikelet length should be considered because significant reduction in these traits was observed compared to timely sown crop.

The effect of etherel on these two genotypes was observed in relation to crop growth stage for spray of the chemical (Table 6). Spray at early boot stage showed more reduction in seed setting than the spray when spike length was 11–13 mm. Outcrossing rate and pollen sterility were almost similar in both the cases and these traits are not affected by the crop stage for spray. Plant height, spike length, and spikelet length were the traits that are more adversely affected by the chemical spray at early boot stage. These have relatively less reduction when etherel was sprayed at stage when spike length was 11–13 mm. From these findings, early boot stage might be the appropriate stage of chemical spray provided the chemicals has less phytotoxic effects at the proper concentration for complete pollen sterility.

Table 6. The effect of spray stage on various traits at different doses of etherel in wheat. S1 = crop stage when spike is 11–13 mm long (about 35 days after sowing) and S2 = early boot stage.

Sowing time	HD 2285				Raj 3765			
	Control	6,000	9,000	12,000	Control	6,000	9,000	12,000
Reduction in seed set (%)								
S1	0.00	85.84	90.02	93.44	0.00	84.80	89.15	92.43
S2	0.00	86.72	90.35	93.64	0.00	85.07	89.54	92.75
	SE ± 0.06				CD (5 %) = 0.12			
Outcrossing (%)								
S1	1.75	24.60	28.30	29.10	1.39	21.37	23.74	27.15
S2	1.72	24.70	28.06	28.06	1.35	21.59	23.15	27.06
	SE ± 0.32				CD (5 %) = 0.64			
Pollen sterility (%)								
S1	7.98	95.68	95.94	97.35	7.54	94.29	96.33	97.46
S2	7.94	95.49	95.88	97.50	7.43	94.25	95.78	97.56
	SE ± 0.18				CD (5 %) = 0.36			
Plant height (cm)								
S1	74.74	44.91	42.68	40.50	70.44	43.80	40.00	38.08
S2	74.76	44.28	42.00	40.20	70.45	42.90	39.65	37.65
	SE ± 0.11				CD (5 %) = 0.22			
Spike length (cm)								
S1	8.68	7.39	6.83	6.18	8.59	7.15	6.85	6.70
S2	8.68	7.25	6.60	6.10	8.55	7.05	6.80	6.65
	SE ± 0.03				CD (5 %) = 0.06			
Spikelet length (mm)								
S1	13.70	10.84	9.12	8.15	14.65	9.95	8.93	8.43
S2	13.60	10.38	8.85	7.80	14.57	9.66	8.80	8.20
	SE ± 0.04				CD (5 %) = 0.08			

From the above findings and discussion, we concluded that the etherel at higher concentrations may create perfect male sterility. Spraying at early boot stage is advantageous in late sown conditions for getting more sterility. In the future, the chemical that causes 100 % male sterility at lower concentration with minimum phytotoxic effects will make hybrid wheat a success.

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Determining the optimum row ratio for hybrid seed production in wheat.

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Determining the optimum male:female row ratio is important for having economically viable, hybrid seed production program. An optimum row ratio not only reduces the cost of production of hybrid seed but also helps in better utilization of the available resources. This experiment determined the optimum row ratio (male and female) for hybrid seed production in wheat.

Four cultivars, HD2285, HD2329, HUW 234, and HUW 206, were used as experimental material. HD 2285 and HD 2329 were female parents and HUW 234 and HUW 206 were males. The female and male rows (3-m long) were sown in at 1:1, 2:1, and 3:1 ratios in a randomized block design with three replications at the Agri Research Farm, Banaras Hindu University, Varanasi, India. Recommended practices were adopted for raising a good crop. The inter- and intrarow spacings were 25 cm and 10 cm, respectively. Etherel was sprayed in the female rows at 7,000 ppm at the stage when spike was about to emerge out of the leaf sheath to induce male sterility in those rows. This concentration created more than 90 % male sterility. A rope was pulled across the row at flowering for three consecutive days to promote outcrossing. At maturity, all female rows were harvested and the yield/female row was calculated. The data was subjected to two-factor factorial randomized block design analysis. Factors A and B were row ratio and crosses, respectively. To test significance, the calculated F values were compared with Table F values at an error d.f. of 5 % and 1 % level of significance.

Yield levels were measured at three male:female ratios, 1:1, 1:2, and 1:3. The ANOVA showed that treatments and crosses differed significantly (Table 7). However, ANOVA did not indicate a significant difference for the row ratios, indicating that all the row ratios are comparable. The mean values of yield/female row in variable row ratios (male:female) of four crosses have been shown in Table 8. Comparing yield of individual crosses at variable row ratios, the results indicated that 1:1 was significantly superior to 1:2 and 1:3 ratios in 50

Table 7. Analysis of variance (ANOVA) for yield/female row (g) in wheat (** indicates significance at the 1 % level).

Source	d.f.	Mean square
Replication	2	33.94
Treatment	11	172.15**
Factor A (Row ratio)	2	90.11
Factor B (crosses)	3	559.59**
AB (Row ratio x crosses)	6	5.78
Error	22	27.91
Total	35	

Table 8. Grain yield/row (g) of female parent in different male:female ratios of four wheat crosses (C.D. 1 %; row ratio = 4.31; crosses = 4.98).

	Yield / female row		
Cross	1:1	1:2	1:3
HD2285 / HUW234	37.38	30.83	31.66
HD2285 / HUW206	39.37	34.67	33.21
HD2329 / HUW234	52.33	48.00	46.11
HD2329 / HUW206	32.44	32.17	29.44

% of the cases. Thus, the results in general have indications for the superiority of 1:1 row ratio than the other two ratios. In the cross 'HD2285/HUW234', a 1:3 ratio yielded more than a 1:2 ratio. Among the cross combinations, 'HD2329/HUW234' had maximum yield/female row in the entire row ratios followed by 'HD2285/HUW206' and 'HD2285/HUW234'. However, all row ratios were comparable in the cross 'HD2329/HUW206'. Earlier studies in row ratio are lacking, but these also suggest comparable performance at 1:1, 1:2 and 1:3 row ratios (Wilson 1968; Miller and Lucken 1976; Briganti et al. 1981; Warner 1985). From the results it is concluded that all the row ratios were comparable from yield point of view. Although the highest yield was obtained from 1:1 male:female ratio, 1:3 male:female ratio can be utilized for economic seed production.

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Prebreeding to pyramid genes for yield and quality component traits in Indian wheats.

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Wheat occupies an area of nearly 27 million ha in India and now stands second next to China at the global level. During the last three decades, wheat production has continued to increase at a rate of about 1.0 % per annum. However, this is not enough to feed the ever increasing population of India, which will need around 109 x 10^6 t of wheat by 2020 AD. From the onset of the Green Revolution in India, the program has had diverse material and cultivars were released for different agro-climatic and production conditions. Now, the yield potential of modern cultivars has not shown expected increases after the release of a very popular cultivar PBW 343, probably due to exhausting genetic diversity. We now need the proper gene combinations responsible for higher yields and end-product quality. Because genetic variability is directly linked with selection efficiency not only for yield but for biotic and abiotic factors, efforts were initiated about a decade ago to mobilize the genes from unconventional sources such as synthetic wheats, buitre types, and wild species . Long spike buitre material developed by Ricardo Rodriguez has a robust stem, a long spike, more spikelets and grains/spike, a large leaf area, and broad leaves. A large number of synthetic hexaploids developed at CIMMYT (Mujeeb Kazi 1996) are endowed with genetic richness for high grain weight, delayed senescence (stay green), HMW-glutenin content, and resistance to KB and yellow rust. However, this germ plasm had certain inherent limitations, such as susceptibility to rust diseases and seed shriveling in buitre types, hard threshing, red grain color, and delayed heading and maturity. Several selections of recombination and mild selection may be required to develop a gene pool that adequately will allow further progress using wild relatives. Prebreeding efforts in using the wild species is very essential.

Donor lines were identified for major economic traits such as tillering, spike length, grain size, protein content, and b-carotene content. A number of crosses involving these lines were attempted with promising released cultivars (Table 9).

Table 9. Crosses attempted with wild relatives and F_2 seeds available.

Wild species	Promising cultivars	# F_2 seed obtained
Ae. peregrina	Raj 1555, HI 8498, PBW 343	1–2
T. urartu	HI 8498, Gulab, PDW 233	2
Ae. speltoides	Raj 1555, HI 8498	3
Ae. tauschii	HI 8498	3
Ae. cylindrica	PDW 233	10
Long ear buitre type	HI 8498, C306, Raj 1555	5
T. turgidum subsp. *polonicum*	PBW 343, HI 8498	Seeds with deformed embryo

The F_1 seed was sown, but only a few germinated. In some cross combinations no seed was set, whereas in others a few seeds were obtained. Cytological observations revealed a large number of cells showed aneuploidy and asynapsis between the chromosomes of the two different genomes resulting in sterile pollen. A few plants survived and set seed in the F_2 generation and are in advanced generations. Some plants from these crosses had good spike length with more spikelets/spike (Table 10). Plants from the cross *'Ae. kotchyii* / HI 8498' had a spike length of 17.2 cm compared to 9.2 cm for the durum wheat check. Similarly, progeny of *'Ae peregrina* / Exo 48' also have a very long spike. These lines have been back crossed with recurrent parent.

Table 10. Wide crosses showing promising traits in advanced generations.

Genotype	Ear length (cm)	Tillers/plant	Spikelets/ spike
T. urartu / WH 542	14.2–15.4	9.5	20
Ae. kotschyi / HI 8498	15.8–17.2	8.0	24
Ae peregrina / Exo 48	15.0–16.3	8.0	23
HI 8498 (d)	8.5–9.2	6.0	21

To widen the adaptability to various stress conditions, synthetic lines involving *Ae. tauschii* in their pedigree are being used in our hybridizing program with promising cultivars such as WH 542, PBW 343, and HD 2687.

Crosses attempted using synthetics are listed below:

68112 / Ward / *Ae. tauschii* / WH542
PBW114 /*Ae. tauschii* / PBW343
68112 / Ward / *Ae. tauschii* / PBW343
PBW114 / *Ae. tauschii* / HD2687
CROC-1 / *Ae. tauschii* / WH542
Gan / *Ae. tauschii* / PBW343
CROC-1 / *Ae. tauschii* / HD2687
Gan / *Ae. tauschii* / WH542

Segregating lines have shown improvement in tillering (up to 43 %), spike length (27 %), and grain size (23 %) compared to PBW 343, PDW 233, PBW 34, HD 2687, and C 306.

The β-carotene (~6 ppm) and protein content (~12%) in promising cultivars are comparatively low and, therefore, some donors possessing high β-carotene (> 9 ppm) and protein content (> 15 %) were identified and crossed with well-adapted modern cultivars to improve their end-product quality (Table 11). As a result, improvement for these characters was very apparent. We recorded increase for these two traits up to 14 ppm and 18 %, for β-carotene and protein content, respectively. This material is now in advanced stages (F_5, F_6, and F_7) of testing and also is being shared with active wheat-breeding centers in India. Some lines were even better than the best check for β-carotene and test weight and comparable with the check for heading and grain yield. One such genotype, DDW 06, which was evaluated at the national level, was in the first nonsignificant group in the Peninsular Zone and is being used for further improvement with respect to disease resistance, particularly black rust. Identified sources and promising cultivars used are in Table 12.

Table 11. Trait-specific parents and characteristics identified for quality improvement of Indian wheat cultivars.

Characteristic	Stock parent	Low-value parent
β-carotene	NGSN 6, DDW 01	PBW 34, HD 4502
1,000-kernel weight	Bawaji, CDW 03	PDW 233
Protein	Winter durums	PDW 233

Table 12. Identified sources for certain traits and promising cultivars used for improvement.

Trait	Sources
β-carotene (>9 ppm)	DDW 01, NGSN 6, NGSN 7, DBP 01-16
Protein content (>14 %)	SABIL, Terter, NP 404
Kernel size (>55 g /TG)	Bawaji, DDW 02, CDW 03
Elite cultivars to be improved	HD4502, PDW233, HI8498, A-9-30-1

We also have noticed that some of the lines coming out of crosses made with synthetics need improvement in threshability and duration. Backcrossing with an agronomically useful parent is being attempted. In crosses involving

wide sources, the negative effect of grain shriveling, which might be due to asynapsis, is being complemented by manipulating the *ph* locus. This scheme has helped develop and identify sources of economic and quality traits and also to widen the genetic base to some extent. Utilizing unconventional sources for improving these traits seems a very viable option to achieve the anticipated yield gains in wheat crop.

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Screening of wheat genotypes for root aphid (Rhopalosiphum rufiabdominalis) resistance.

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At present, in the IPR system the emphasis in the Indian wheat program is on creating new genetic variability through unexploited germ plasm, such as long-spike buitre plant types, synthetic hexaploids, Chinese subcompact ear germ plasm, and wild relatives. The long-spike Buitre material developed by Rodriguez Ricardo has a robust stem, a long spike, more spikelets and grains per spike, a large leaf area, and broad leaves. A large number of synthetic hexaploids developed at CIMMYT by Mujeeb Kazi are genetically rich for high grain weight, delayed senescence (stay green), HMW glutenins, and resistance to KB and yellow rust. The subcompact Chinese germ plasm has a robust stem, more grains/spike, and is a new source of yellow rust resistance genes. However, these synthetic hexaploid lines have certain inherent limitations, such as susceptibility to rust and seed shriveling in the Buitre types, hard threshing, red grain color, and delayed heading and maturity. Likewise, the very soft grains in the Chinese germ plasm are very prone to insect damage.

Cereal aphid infestation of the wheat crop has not been dealt with in detail in India so far because of their limited importance in wheat production. But changes in the environment and new crop production practices are changing the pest spectrum. Of the four major species of aphids reported in India, the rice root aphid (*Rhopalosiphum rufiabdominalis*) is becoming a regular pest in northwestern plains on wheat during the last 3 years (Fig. 1). The rice root aphid remained an obscure species in the Indian wheat program because of its limited occurrence in central India until now. The activity of root aphid starts during first fortnight of December and continues until temperatures are slightly warmer, sometime up to the first week of January.

Fig. 1. *Rhopalosiphum rufiabdominalis*, the rice root aphid, infesting a wheat crop.

Although little work has assessed the impact of this pest on yield and yield-contributing characteristics, Kindler et al. (2003) suggested it will cause economic damage and transfer BYDV. Keeping this in view, we screened wheat genotypes selected from various national and international nurseries having good agronomic background and disease resistance against rice root aphid.

Material and methods. Thirty-nine wheat genotypes which were found resistance to rust diseases and having good grain strength and better performance for various yield traits were taken for the study (Table 13). These genotypes were planted in the field in a double row plot of 3.0 m length during two consecutive crop seasons, Rabi 2004–05 and 2005–06. These genotypes were grown in two replications, and 30 random plants were selected for screening under natural conditions against root aphids. The standard screening procedure of the All India Coordinated Wheat and Barley Improvement Project was followed to screen these genotypes (Table 14).

Results and discussion. The genotypes screened against root aphid represented diverse groups. Grown in natural conditions, no insect control measures were used. Among the genotypes, six were highly resistant (PB03-16, PB03-17, PB03-23, PB03-24, PB03-34, and PB03-39), which included indigenously developed material and exotic lines that have BABAX, PRL, SITE, and MILAN in their pedigrees. Similarly, four synthetic hexaploid genotypes selected from various international nurseries were found to be resistant (4PB03-20, PB03-28, PB03-35, and PB 03-36).

None of the genotype was immune to the root aphid, whereas the remainder of the genotypes had aphid populations of more than 11 insects/plant and were categorized as susceptible. The genotypes with resistant reactions may be utilized in wheat improvement programs when the need arises.

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Table 13. Genotypes screened for resistance to the rice root aphid (*Rhopalosiphum rufiabdominalis*) at Karnal, India, during the 2004–05 and 2005–06 rabi seasons.

Genotype	Parentage
PB03-1	VS1065/PBW 343
PB03-2	VS 433/RAJ 3777
PB03-3	HTWYT6/ESWYT 38
PB03-4	VS 433/RAJ 3777
PB03-5	NTWYT 6/ESWYT 38
PB03-6	PBW 343/HE 1/5XCN079BM95
PB03-7	PBW 343/HE 1/5XCN079BM95
PB03-8	VS 433/RAJ 3777
PB03-9	FASAN/2*TEPOCA/3/CHEN/*Ae. tauschii*//BCN
PB03-10	DL 321
PB03-11	PGW 21
PB03-12	KYZ 0144
PB03-13	PBW 343/FIOS 1
PB03-14	PSN/BOW//SITTA/3/RDWG
PB03-15	RAJ 3765/K9107/JOB 79
PB03-16	RAJ 3765/K9107/JOB 79
PB03-17	F3BMESTE 57
PB03-18	CHIL/PRL
PB03-19	CMH83.2517/GW 190
PB03-20	CHEN/*Ae. tauschii*//FCT/3/3
PB03-21	WR 783
PB03-22	LONG 94 444/WH542
PB03-23	LOK BOLD
PB03-24	SGH 15
PB03-25	SGH 30
PB03-26	MUNIA/CHTO/3/PFAU/BOW/VEE#9/4/CHEN/…
PB03-27	CROC_1/*Ae. tauschii* (213)//PGO/3/CMH81.38/…
PB03-28	CROC_1/*Ae. tauschii* (213)//PGO/3/CMH81.38/…
PB03-29	CROC_1/*Ae. tauschii* (213)//PGO/3/CMH81.38/…
PB03-30	ATTILA/3*BCN
PB03-31	XIANG 82.2661/2*KAUZ
PB03-32	YUMAI 13 / 2*KAUZ
PB03-33	BCN/CROC 1/*Ae. tauschii* (662)
PB03-34	BABAX*2/PRL
PB03-35	ALTAR 84/*Ae. tauschii* (219)//SERI
PB03-36	ALTAR 84/*Ae. tauschii* (219)//2*LOXIA/3/KAUZ
PB03-37	CHEN/*Ae. tauschii*//BCN/3/KAUZ
PB03-38	BOW//BUC/3/WEAVER/4/STAR
PB03-39	SITE/MO/MILAN

Table 14. Criteria for scoring of resistance against root aphid.

Category	No. of root aphids/plant
Immune	0
Highly resistant	1–5
Resistant	6–10
Susceptible	> 11

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Genetic diversity among bread wheat germ plasm for yield and its attributes.

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Introduction. Knowledge of genetic divergence, geographic diversity, and ancestory of parents is important for initiating a breeding strategy. The degree of heterosis as a result of hybridization is generally believed to be correlated with genetic divergence between the parents used (Ramanujam et al. 1974). The use of diverse parents in breeding program to obtain transgressive segregants has been emphasized (Jatsara and Paroda 1983; Cox and Murphy 1990). Geographical diversity and place of origin do not favor that the selected plants are necessarily genetically diverse (Murty and Arunachalam 1966; Lee and Kaltsikes 1972; Garg and Gautam 1988). The characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound D^2 statistics. Mahalanobis' (1936) generalized distance has been successfully and extensively used to cluster genotypes in different group based on morphological characters in crop plants (Jatasara and Paroda 1978; Joshi and Singh 1979; Rao 1952). In this study, an attempt was made to evaluate 90 genotypes of bread wheat to identify genetically diverse and suitable parents for crossing program through the dispersion in different groups/clusters.

Materials and methods. Ninety genotypes of bread wheat from the Indian wheat program and those of exotic origin were used. These genotypes were grown in randomized block design with three replications at the Research Farm of Indian Agricultural Research Institute, New Delhi, during Rabi 2003–04, to assess genetic divergence using Mahalanobis' D^2 statistics. Each genotype was sown in paired rows 3.0-m long with a between row distance of 23 cm and seed-to-seed spacing of 10 cm. The recommended amount of fertilizer and other inputs were applied to raise a successful crop. Five randomly selected plants from each plot were selected for recording observation on nine quantitative traits, days-to-heading, days-to-maturity, plant height, tiller number/plant, grains/spike, grain weight/ear, 1,000-kernel weight, total biomass, and grain yield/plant. Mahalanaobis' D^2 statistics were used to assess the genetic diversity. Genotypes were grouped on the basis of minimum generalized distance/minimum generalized closeness using Tocher's method as described by Rao (1952).

Results and discussion. Genetic divergence among 90 wheat genotypes was worked out on basis of nine morphological characters. Based on the similarity of characters, the genotypes grouped into eight clusters (Table 1). Considerable genetic diversity in germ plasm exists for the characters studied as the number of genotypes varied from two to nineteen in these clusters. No similar pattern of characters was observed if two or more clusters were considered together. These genotypes seem to have been developed at different national wheat research centers. The exchange of wheat germ plasm

Table 1. Distribution pattern of 90 genotypes of wheat into eight clusters.

Cluster No.	No. of genotypes	Genotype name
I	19	HW2002A, HP1731, HD2258, HD2428, CIANO F67, DL932, SERI-82, RAJ4016, WH741, HW2046, HW2044, J492, WH712, HW2045, WH737, UP2586, LOK45, Super X, UP2425
II	10	HUW327, DW1133, J908, HD2646, WH739, DW1182, HW2031, HD2705, HD2772, Kalyansona
III	17	HD2270, HD2285, HD2307, RAJ3765, HD2877, J1316, HD2631, HD2637, HD2643, DL69, UP2338, HD2402, PBW343, NIAW34, LOK45, HI977, DWR162
IV	14	Kavkaz, Nainari 60, DW1062, HD2687, HD2760, HD2733, HD2735, HW2002, HD2590, K9453, WR180, Triumph, CPAN1436, PBW502
V	9	DL-784-3, Pavan, UP2504, RAJ4004, HD2670, HD2849, NP852, Mexipak, HD2160
VI	16	Chil, PDW299, DW1192, K9704, HUW206, K9107, Parula 'S', HD2329, WH542, Siete Cerros, CPAN 3004, WR1038, DL50, Girija, C306, C217
VII	3	DL-788-2, NI 8289, CPAN 1517

as a result of international cooperation has played a very important role in the genetic amelioration of this crop. Genotypes used were developed at CIMMYT (Mexico), Australia, Canada, the U.S., Pakistan, and Brazil. The genotypes of different breeding centers grouped together in the same cluster. Genotypes from one place, HD, WR, DL, and DW (Delhi); UP (Pantnagar); WH (Hisar); HUW (Varanasi); PBW (Ludhiana); Triumph, Maxipak, Super X, and Sietecerros (Mexico); and the Raj series (Rajasthan) were scattered in different clusters with cultivars of different geographical regions/origin indicating that pattern of clustering of genotypes was independent of their geographical region. These findings are in accordance with those of Murty and Arunachalam (1966), Bhatt (1970), Sethi et al. (1992), and Garg and Gautam (1988).

Divergence is an outcome of several factors namely genetic drift and selection intensity over the time that have resulted to cause genetic diversity rather than their geographical distance among genotypes. Any cultivars/genotypes may have a common place of development, but breeders may have used diverse germ plasm derived originally from widely separated geographical regions. No relationship between genetic diversity and place of origin of the genotypes could be ascertained. Somayajulu et al. (1970), Upadhyay and Murty (1970), Jatsra and Paroda (1978) also support this conclusion. The distribution of genotypes into different clusters was independent, because of the lack of relationship between the pedigree of genotypes and genetic divergence between them. Wheat genotypes with a common pedigree were grouped into different clusters having cultivars with different parentages. For example, Super X, Kalyansona, Mexipak, and Siete Cerros are derived from the cross II-8156 with the common pedigree 'Penjaino 'S'/Gabo55)' and were grouped in clusters I, II, V, and VI, respectively. Similarly PBW343, UP2338, PBW502, HD2687, HD2733, and HUW206 were derived from a Vee 'S' cross with T1B·1R were dispersed in clusters III, V, and VI. This substantiates the fact that these genotypes have become varying genetically different due to recombination and selection for traits in segregating generations. Furthermore, most of the genotypes grouped in cluster III were suitable for late-sowing conditions and were developed by different wheat research centers. Dependence on directional selection pressure that lead to the mechanism may favor accumulation of desired traits resulting in indiscriminate clustering (Redhu et al. 1993).

Grain yield shows the highest contribution towards genetic divergences followed by biological yield, tiller number, and grain/spike. Biological yield and harvest index cannot be considered as independent characters because their main component is through the economic yield, i.e., grain yield. In this study, the major characters contributing to genetic divergence are grain yield and tiller number with a moderate contribution from grain/spike, 1,000-kernel weight, and plant height. Jagshoran and Tandon (1995) observed grain yield, biological yield, and 1,000-kernel weight contributed more towards genetic divergence in winter wheat. Tillers/plant and grain yield have sizeable individual contribution (Kumar and Singh 1997). Mean values of nine morphological characters indicated considerable difference among mean values for all the characters and between the clusters (Table 2). Cluster III had the highest grain weight/spike (2.63 gm), 1,000-kernel weight (42.39 gm), and grain yield/plant (40.8 gm), whereas Cluster I had the maximum number of grain/spike (53.47) and biological yield (99.13 gm). The greatest number of tillers/plant were observed in Cluster IV (19.32). The three major yield-contributing traits, 1,000-kernel weight, grain/spike, and tillers/plant were dispersed in genotypes of clusters III and IV. If these traits are brought together through crossing, novel recombinants are possible in the succeeding generations.

Table 2. Mean values of different clusters for nine characters in bread wheat.

Cluster	Days to heading	Days to maturity	Plant height (cm)	Tillers/ plant	Grains/ spike	Grain weight/ spike (gm)	1,000-kernel weight (gm)	Biomass (gm)	Grain yield/ plant (gm)
I	86.95	127.26	96.43	19.27	53.47	2.32	39.36	99.13	36.79
II	90.00	123.57	97.83	16.84	51.35	2.13	39.73	83.27	37.37
III	85.30	118.42	103.57	18.74	53.27	2.63	42.39	93.16	40.89
IV	90.32	129.32	100.37	19.32	49.79	2.24	40.34	90.89	36.38
V	85.43	127.42	88.37	17.69	52.79	2.01	36.73	80.78	33.27
VI	84.43	131.57	90.57	16.65	51.73	2.17	38.17	63.41	36.78
VII	84.23	130.72	115.37	15.89	51.32	2.53	41.32	78.57	34.83
VIII	85.00	126.82	133.67	17.40	50.70	1.98	37.31	73.10	30.13
GM	86.45	126.88	103.27	17.72	51.80	2.25	39.41	82.78	35.80
SE (M)±	1.21	1.73	2.11	–1.32	2.44	0.18	2.01	4.01	2.11

Genotypes of one cluster are considered similar in respect to the combine effects of the characters studied. Cluster means and coefficients of variation provide information on the nature of diversity. The highest intercluster distance indicated greater diversity whereas minimum distance indicated less diversity or close relationship. The parent for a crossing program should be selected from a diverse cluster characterized by large intercluster distance. The better performing genotypes among the different clusters, HD2329 (VI), HD2160 (V), Lok 45 (III), Raj3765 (III), PBW343 (III), CPAN 3004 (VI), WR180 (IV), DL69 (III), and DL784-3 (V), were picked for their use in a crossing program aimed at obtaining superior segregants, because these parents possessed diverse yield.

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A rust-resistant, high-yielding bread wheat cultivar HD 2833 (Pusa wheat-105) released for Peninsular India likely to improve farm economy.

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An early maturing wheat cultivar HD 2833 (Pusa wheat-105) developed jointly by IARI, RS, Wellington, and the Division of Genetics, IARI, New Delhi; exhibiting a high degree of resistance to all the Indian leaf rust pathotypes with best chapati-making quality recently was released for commercial cultivation by the CVIRC. This cultivar has been released for irrigated, late-sown situations occurring in the Peninsular Zone of India.

The area under late-sown conditions in Peninsular Zone has increased. The sowing of wheat now extends until mid-December. Because of the short duration of winter, farmers need early maturing cultivars that can withstand high temperatures at the time of anthesis and maturity. Thus, the Peninsular Zone demands early maturing and thermotolerant cultivars. The Peninsular Zone is an established route for uredospore transport to central India. The prominent pathotypes of stem rust in the Peninsular Zone are 40A, 40-1, and 122. Prominent leaf rust pathotypes are 77-5, 104-2, and 104B. *Puccinia* pathotypes could be interrupted by diversification of cultivars having different genetic composition of rust resistance genes in this epidemiological important zone. Because HD 2833 has a high degree of seedling and adult-plant resistance to the prevalent pathotypes of all the three rusts, cultivation would consequently avert the likelihood occurrence of epidemic(s).

HD 2833 has shown superior performance over all the checks and qualifying cultivars. HD 2833 was in the top nonsignificant group in all years of testing. The cultivar has a high degree of adult-plant resistance to all the three rusts and also is listed as resistant in the seedling stage to brown and block rusts. Yield response of HD 2833 in agronomic trials is higher than that of the check and qualifying cultivars under late and very late sown conditions. Thus, HD 2833 fulfils all the requirements of a successful late-sown wheat cultivar for Peninsular Zone.

HD 2833 recorded the highest grain yield of 34.5 q/ha and 31.2 q/ha under late-sown and very late sown conditions, respectively. These yields were superior to the checks and other cultivars. The data clearly demonstrate the agronomic superiority of HD 2833 under varying production conditions. HD 2833 produces lustrous grains with a higher appearance score than those of the check and other qualifying cultivars. The average hectoliter weight of HD 2833 is higher (80.9) than those of the checks HI 977 (78.0), NIAW 34 (79.3), and LOK 45 (76.0).

During quality testing in 2002–03 and 2004–05, HD 2833 was identified as one of the best cultivars for chapati making characteristics (Score >8/10) and was nutritionally rich with >13 % protein. This cultivar will have definite market preference, because this part of the world consumes the majority of wheat in the form of chapati and will play active roll in addressing the malnutrition problem as well.

With good grain appearance, high hectoliter weight, a high chapati-making score, and a desirable protein content, we expect that HD 2833 will become the consumer's preference. Rust resistance and good yield performance under late and very late sowing conditions will help farmers adopt HD 2833. For future wheat export, this cultivar will be one of the best choices, because it meets maximum quality parameters for both bread- and chapati-making quality with high protein content (13.12 %).

One of the parents involved in the pedigree has rust-resistance genes. A high degree of rust resistance is likely due to the presence of an alien segment. HD 2833 is postulated to have *Sr2*+gene(s), which provide durable resistance to stem rust. The Peninsular Zone is prone to have stem rust infections. HD 2833 is likely to occupy more area in near future even under nontraditional wheat belts in the Southern Hill Plains (in the states of Karnataka and Tamilnadu), where a sizable area is farmed by resource-poor farmers. Thus, this cultivar is likely to improve the livelihood of farmers and their farm economy.

Genetic enhancement and diversity of genetic composition in wheat cultivars by introgression of rust-resistance genes into popular Indian bread wheat cultivars.

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Introduction. Yield loss caused by various rust diseases (stem, leaf, and stripe) are reported by several workers from time to time. To combat the disease, using the available genetic sources in wheat-improvement programs and developing rust-resistant wheats are the most effective means of control worldwide. The effective leaf rust genes *Lr19*, *Lr24*, *Lr28*, *Lr32*, and *Lr37*, and stem rust genes *Sr24*, *Sr25*, *Sr31*, and *Sr38*, have already been utilized by various workers world-wide and at IARI, Wellington (a hot-spot for rust and other foliar diseases), in particular. We have already initiated the process to utilize the newer rust-resistance gene sources.

Introgression of newer rust-resistance genes. Wheat is cultivated on about 26 x 10^6 ha in India with present day wheat production of 72 x 10^6 tons. The wheat crop is grown in various macro- and microclimatic zones and production

Table 1. A comprehensive back cross program for transfer of newer effective rust resistance genes at IARI, Regional Station, Wellington. An * indicates newer genes used in the program.

Disease	Genes used	Source	Chromosomal location
Leaf rust	*Lr19+Sr25*	*A. elongatum*	7DL
	Lr24+Sr24	*A. elongatum*	3DL
	Lr28	*Ae. speltoides*	4AL
	Lr32	*Ae. tauschii*	3D
	*Lr35**	*Ae. speltoides*	2B
	Lr37+Sr38+Yr17	*Ae. ventricosa*	2AS
	*Lr39**	*Ae. tauschii*	2DS
	*Lr40**	*Ae. tauschii*	1D
	*Lr41**	*Ae. tauschii*	2DS
	*Lr42**	*Ae. tauschii*	1D
	*Lr44**	*T. aestivum* subsp. *spelta* 7831	1BL
	*Lr45**	*S. cereale*	2AS
	*Lr48**	CSP44	
	*Lr49**	VL404	
Stem rust	*Sr24*, *Sr25*, *Sr38*		
	*Sr26**	*A. elongatum*	6AL
	*Sr27**	Imperial rye	3A
	*Sr31+Lr26+Yr9+Pm8**	Petkus rye	T1BL·1RS
	*Sr36**	*T. timopheevii* subsp. *timopheevii*	3AL
Stripe rust	*Yr6**	Heines Kolben	7BS
	*Yr10**	Moro	1BS
	*Yr15**	Dippes, Triumph, *T. turgidum* subsp. *dicoccoides*	1BL
	*Yr16**	Capelle-Desprez	2DS
	Yr17	*Ae. ventricosa*	2AS
Powdery mildew	*Pm6**		
	*Pm8**	Petkus rye	T1BL·1RS

conditions. The entire region is under the threat of stem and leaf rust epidemics, and yellow rust also is a problem in the North Western and Hill Regions. The scientific and systematic management of the wheat program in India has not allowed a rust epidemic in the recent past because of diversification of gene sources for rust resistance and releasing such cultivars for commercial cultivation. To avoid further epidemics, one has to deploy new cultivars with diverse genetic sources to curtail the evolution and spread of new rust pathotypes. We are making a continuous effort to introgress newer rust-resistance genes in several popular bread wheat cultivars that were carefully chosen from each zone and production conditions (see Table 1). The developed NILs and lines developed by hybridization will play a very effective roll in combating rust in India. Introgression and selection are made under natural epiphytotic conditions at Wellington and further confirmed on seedlings by using differentials at DWR, Regional Station, Shimla. We also use MAS by developing markers that are then used for further confirmation in a network with IARI, New Delhi, and DWR, Karnal. Similar work already has been done for *Lr19*, *Lr24*, *Lr28*, *Lr32*, *Lr37*, *Sr24*, *Sr25*, and *Sr31*.

Wheat cultivars used in the program include C 306, Sonalika, Kalyansona, WL 711, WH147, HD 2285, HD 2329, HD2402, HD2687, HS240, HUW234, K9107, Lok1, Lok bold, Lok-45, Lok 50, Lok 55, .MACS 2496, NI 5439, PBW226, PBW 343, WH542, HD2733, NIAW34, UP262, UP2338, HI1077, HI977, RAJ3077, PBN54, KRL99, and HD2009. The transfer and introgression of newer genes is now in at BC_3, and material will be available from 2007 rabi onwards.

Traits associated with some of alien rust-resistance genes based on our field observation rather than effectiveness. *Lr19 + Sr25*. Yellow pigmentation in the endosperm. We used a mutant devoid of it developed by Knott and Sharma, Cook 19, and Sunstar. Strongly associated with slow leaf senescence, *Lr19 + Lr25* gives a significant yield advantage, however, new virulence for this gene was reported recently in India.

Lr24 + Sr24. Tightly linked genes. *Sr24* is not effective in India (40-1). No yield loss has been observed on the lines with this gene. We used an amber grain derivative.

Lr28. A very effective gene but associated with fast stem rusting. In combination with *Sr31*, *Lr28* gives a 5–10 % yield

advantage over the recurrent parent (needs further investigation). An increased number of tillers and spikelets/spike are seen in this combination (results are in press). Lines with *Lr28* are less susceptible to powdery mildew.

Lr32. A very effective gene but associated with fast rusting to stem rust. In combination with *Sr31* gives 5–10 % yield advantage over recurrent parent (needs further investigation). Increased tillers and spikelets/spike is seen in this combination (results to be published).

Sr31+Lr26+Yr9+Pm8. Slow leaf senescence and a 10 % yield advantage, but linked to slight red tinge in the grain, and increased susceptibility to powdery mildew.

Lr37. Thermosensitive gene under increased minimum temperature shows susceptibility to brown rust in the seedling stage and under certain background gives susceptibility to yellow rust. Associated with lower incidence of powdery mildew.

Lr44. Fast rusting to stem rust.

Lr45. Tightly linked to pink awn (phenotypical marker) and waxiness in the spike, peduncle, stem, and leaf

Sr27. Tightly linked to the apical claw or club tip to the spike (phenotypic marker). Careful selection for *Sr27* results in lines with significant yield potential over the recurrent parents.

HW 1095 Pusa dwarf dicoccum has high yield performance across the Indian zones.

K.A. Nayeem and M. Sivasamy.

To improve the lodging resistance in high yielding *T. tugidum* subsp. *dicoccum*, an exhaustive program was undertaken at IARI, Wellington, in collaboration with Bhabha Atomic Research Institute, Mumbai. One semidwarf plant with profuse tillering in the M_2 was selected and designated as HW 1095.

HW 1095 (Filler) was tested with *T. turgidum* subsp. *dicoccum* lines DDK 1025, DDK 1028, DDK 1029, DDK 1030, MACS 2956, MACS 2947, MACS 2961 NP 200 and DDK 1009 using MACS 2846 (*T. turgidum* subsp. *durum*) and MACS 2496 (*T. aestivum* subsp. *aestivum*) as checks. The results are presented in the Table 2. Across all locations,

Table 2. Summary of disease resistance and agronomic characteristic data for the dwarf dicoccum line HW 1095 (Filler) grown in the Peninsular Zone of India during the Rabi season 2004–05. Trial 0407-SPL-IR-TS-DIC. Data from Progress Report (2004–05) Crop Improvement, AICWP, Directorate of Wheat, Karnal (India); ancillary data from Ugar, Dharwad, Karad, Arabhavi, Pune, and Kolhapur Centers; lodging data reported from Karad and Pune centers. C denotes a check cultivar.

	Rust reaction		Agronomic characteristics							Grain characteristics			
Line	Black	Brown	Days to heading (range)	Days to heading (mean)	Days to maturity (range)	Days to maturity (mean)	Height (range)	Height (mean)	Lodging (range)	Thr	Color	Texture	1,000-kernel wt. (range)	1,000-kernel wt. (mean)
DDK 1025	20MR	5MR	58–65	62	99–110	104	78–96	88	35–90	H	R	SH	36–46	41
DDK 1028	5MR	20MR	60–65	63	99–108	103	76–97	86	0–95	H	R	SH	29–42	37
DDK 1029	5MR	10MR	60–65	63	100–110	105	71–91	81	0–90	H	R	SH	37–45	40
DDK 1030	10MR	10MR	61–68	64	98–108	102	71–91	82	0–80	EY	R	SH	34–43	38
MACS 2956	5MR	5MR	58–64	62	97–110	104	81–104	89	30–90	EY	R	SH	36–44	39
MACS 2947	5MR	5MR	60–65	62	92–109	102	78–102	90	20–90	EY	R	SH	35–46	39
MACS 2961	10S	20MR	62–68	64	97–108	102	74–97	86	0–80	EY–M	R	SH	27–39	34
HW 1095 (Filler)	5MR	5MR	62–72	67	98–111	105	74–95	84	0–10	H	R	H	35–48	42
NP 200 (C)	10MR	5MR	62–68	64	96–107	103	77–97	86	0–90	H	R	SH	36–47	39
DDK 1009 (C)	5MR	5MR	62–68	65	98–108	102	73–94	84	0–60	EY	R	SH	33–43	38
MACS 2846 (C)	5MR	5MR	56–60	58	90–112	102	79–97	88	0–35	M	A	H	45–54	50
MACS 2496 (C)	5MR	80S	61–69	64	96–110	102	74–96	83	0	EY	A	SH	30–42	36

MACS 2496 (bread wheat) ranked first, followed by HW 1095 (Filler) 40 q/ha. Both lines constituted the first nonsignificant group of entries. The new type HW 1095, MACS 2961, and DDK 1029 were significantly superior to the dicoccum check DDK 1009 at the national level. HW 1095 (Filler) gave the highest grain yield and was first in Karnataka and Maharashtra with 43.3 and 49.1 q/ha, respectively (Table 3). HW 1095 ranked fourth in Gujarat with 29.0 q/ha compared to the dicoccum check DDK 1009 (23.5 q/ha). In Tamil Nadu, HW 1095 yielded 21.6 q/ha. Considering the overall average from three zones, Central, Peninsular, and South, HW 1095 ranked second (40.0 q/ha) and surpassed all dicoccum and durum checks and was equal to the bread wheat check MACS 2496 (40.4 q/ha). The results clearly indicate a high yielding ability with resistance to black (5MS) and brown rust (tMS).

Table 3. State and Zonal means (Q/Ha) for yield performance for high-yielding *T. turgidum* subsp. *dicoccum* lines during the Rabi season 2004–05 across different regions of India. Gujarat (GUJ), Karnataka (KAR), Maharashtra (MAH), Tamil Nadu (TN), and Peninsular Zone (PEN).

	GUJ		KAR		MAH		TN		PEN		All Zones		
Line	Yield	Rank	Yield	Rank	Yield	Rank	Yield	Rank	Yield	Rank	Yield	Rank	G
DDK – 1025*	21.7	12	42.5	3	39.4	11	31.8	2	44.1	6	36.3	7	0
DDK – 1028	22.7	10	37.8	11	37.9	12	22.1	6	37.6	12	33.2	11	0
DDK – 1029	31.5	3	41.4	4	46.5	3	10.9	11	43.5	3	37.9	4	0
DDK – 1030	23.5	8	39.7	7	41.2	7	7.2	12	40.3	7	33.6	10	0
MACS – 2956	25.4	7	40.0	5	39.6	10	35.9	1	39.7	9	36.6	6	0
MACS – 2947	26.8	5	39.5	8	40.9	8	27.2	4	40.0	8	36.2	8	0
MACS – 2961	26.8	5	42.7	2	46.0	5	23.4	5	44.1	2	38.6	3	0
HW 1095 (Filler)	29.0	4	43.3	1	49.1	1	21.6	7	45.8	1	40.0	2	1
NP - 200#	22.6	11	34.4	12	42.7	6	20.6	8	37.9	11	33.2	11	0
DDK – 1009#	23.5	8	38.5	10	40.2	9	29.4	3	39.2	10	35.1	9	0
MACS – 2846#	34.7	2	38.6	9	46.4	4	12.4	10	41.8	5	37.5	5	0
MACS – 2496#	45.3	1	40.0	5	47.0	2	12.5	9	43.2	4	40.4	1	1
Std Error (M) =	0.637		0.655		1.084		0.436		0.439				
CD =	1.8		1.8		3.0		1.3		1.2				

Table 4. Seedling and adult-plant reaction at Directorate of Wheat Research, Shimla, to different wheat rusts.

	Brown rust isolates				Black rust isolates				Yellow rust isolates		
	1RS	42.1R 63-1	21R 31-1	21R 55	62G29	62G29-1	37G79	7G11	46S103	46S 119	46S10
Sonalika	1P3	3+	1P0; 1P3	1P0; 1P2	2+	2	X	2^-	3+	3C	—
HW 2001	1P2	0;	0;	0;	3+	3+	3	2^-	3+	3C	—
HW 2001A	0;	;	;	0;					3^+	3^+	;
Sr24 + Lr24	0;	;	;1	0;	2^-	2^-	0;	2^-	3+	3+	—

			Reaction to rust		
Recurrent parent/backcross line	New line	Gene(s) present	Brown	Black	Yellow
Sonalika	—	—	80S	60S	60S
Sonalika*5//TR 380-14*7/3 Ag#14	HW 2001	*Sr24 + Lr24*	F	40S	60S

Two Sonalika recombinant lines confirmed transfer of rust-resistance genes Sr24 and Lr24.

K.A. Nayeem and M. Sivasamy.

In 2001, Menon and Tomar successfully transferred the tightly liked genes *Sr24 + Lr24* from *A. elongatum* into several Indian cultivars by the backcross method. The presence of the genes was confirmed at DWR, Flowerdale, Shimla. Two recombinant lines, HW 2001 and HW 2001-A, were inoculated with all the virulent pathotypes of black, brown, and yellow rust. We postulated total resistance to leaf rust for the tightly linked genes, however the most virulent races of black rust, 62G29, 62G29-1, and 37G79, were virulent on *Sr24* (Table 4, p. 67). Thus, only *Lr24* is very effective for brown rus in our investigation. HW 2001 and HW 2001-A are sister lines differing only in glume color (Table 5). HW 2001 is brown and HW 2001-A is white glumed. HW 2001 has been released as the cultivar **Sonak** for the state of Haryana.

Table 5. Characterization and evaluation information of HW 2001 and HW 2001A (Sonalika*5//TR 380-14*7/3 Ag#14).

	HW2001	HW2001 A	Sonalika (check)
Days to heading	64 days	60 days	59 days
Days to maturity	114	111	112
Plant height	76.6	84.2	72.0
Length of spike	8.7 cm	6.6 cm	7.8 cm
Spikelet/spike	13.4	12.6	13.2
Seed/spike	26.8	27.2	29.2
Flag leaf length	21.42 cm	21.88 cm	22.7 cm
Flag leaf breadth	1.02 cm	2.92 cm	0.98 cm
1,000-kernel weight	32.0 gm	26.4 gm	27.4 gm
Protein content	11.94	11.56	13.21
Plant growth habit	Erect	Erect	Semierect
Coleoptile pigmentation	Green	Green	Green
Auricle color	Colorless	Colorless	Colorless
Auricle pubescence	Nonpubescent	Amber	Nonpubescent
Flag leave angle	Semicurve	Semicurved	Semicurved
Waxiness	Peduncle	Peduncle	Peduncle
Foliage color	Green	Green	Green
Spike color	Brown	White	White
Spike shape	Parallel	Parallel	Parallel
Spike density	Intermediate	Lax	Intermediate
Spike length	Short	Short	Short
Awn length	Short	Short	Short
Awn color	White	White	White
Outer glume shoulder shape	Round	Round	Square
Outer glume pubescence	Nonpubescent	Nonpubescent	Pubescent
Glume beak length	Medium	Medium	Short
Glume beak curvature	Medium	Short	Medium
Grain color	White	White	Amber
Grain shape	Elliptical	Elliptical	Elliptical
Grain texture	Semi hard	Semi hard	Hard
Grain size	Bold	Bold	Medium
Brush hair length	Short	Long	Short
Brush hair profile	Pointed	Pointed	Blunt
Germ width	Wide	Medium	Medium
Grain crease	Shallow	Medium wide	Shallow

ITEMS FROM IRAN

ABRII — AGRICULTURAL BIOTECHNOLOGY RESEARCH INSTITUTE OF IRAN
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QTL mapping of Fusarium head blight resistance genes in wheat.

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QTL mapping of Fusarium head blight resistance genes in wheat in Iran began in 2002 by with scientific cooperation projects between Iran and Austria. Different types of mapping populations and DNA markers were used for QTL mapping of FHB resistance. The preliminary QTL analysis results identified one consistent QTL for FHB resistance on chromosome arm 3BS in both Wangshuibai and Sumai 3 mapping populations. Three consistent QTL for FHB resistance on chromosome arms 1BL, 3AL, and 7AS were detected in Frontana mapping populations.

Functional genomics of wheat: development of PCR-based molecular markers for candidate Fusarium resistance genes.

M. Mardi, M.R. Ghaffari, G. Adam, H. Buerstmayr, and B. Ghareyazie.

Strong emphasis was placed on mapping candidate genes (*PDR5*-like, *RP1*) and ESTs putatively involved in FHB resistance. The preliminary, single-marker analyses indicated that gene-specific markers for *PDR5*-like and *RP1* genes had significant negative effects on FHB severity in derived mapping populations.

Wheat genomics: molecular response of wheat to Fusarium head blight Infection.

M. Mardi, M.R. Ghaffari, A. Sadeghi, S.G.H. Salekdeh, H. Buerstmayr, and B. Ghareyazie.

Identifying specific FHB infection responsive genes/proteins using transcriptome (cDNA-AFLP) and two-dimensional gel electrophoresis (2D–GE) analyses in our developed RILs and NILs are in progress.

Publications.

Mardi M, Pazouki L, Delavar H, Kazemi MB, Ghareyazie B, Steiner B, Nolz R, Lemmens M, and Buerstmayr H. 2006. QTL analysis of resistance to Fusarium head blight in wheat using a 'Frontana' derived population. Plant Breed (In press).

Mardi M, Buerstmayr H, Ghareyazie B, Lemmens M, Mohammadi SA, Nolz R, and Ruckenbauer P. 2005. QTL analysis of resistance to Fusarium head blight in wheat using a 'Wangshuibai' derived population. Plant Breed 124:329-333.

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ITEMS FROM ITALY

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Ancient and modern wheats: a comparison of biochemical, nutritional, and technological features of selected lines grown in southern Italy.

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Recently, farmers, consumers, and researchers have been giving attention to the so-called 'ancient wheats' emmer (*T. turgidum* subsp. *dicoccum*), spelt, and oriental wheat or khorasan (*T. turgidum* subsp. *turanicum*). As a consequence, a niche market has developed around them. Today, scarce and controversial information is found in literature about the agronomic, biochemical, nutritional, and technological characteristics of these crop species. For this reason, we made a comparison between selected emmer, spelt, and oriental wheat using a multidisciplinary approach. Two modern cultivars, one each for durum and bread wheat, were included in the study as references.

The material was tested in an experimental field in southern Italy, a geographic area devoted to the wheat cultivation. A total of fifteen parameters, including the main nutritional and technological indices, were determined on both whole and refined meal obtained from the tested lines. Meal obtained from the three ancient wheats were characterized by a protein ash content superior to those of modern cultivars. Differences among the species were detected relative to some parameters such as β-carotene and some macro- and microelements. In general, the nutritional traits of oriental wheat were more similar to those of the tested durum wheat cultivar Norba than to those of the emmer cultivar Farvento. Bread-making trials compared the quality of the final product. The bread quality, good loaf volume, and sensory properties recorded for the oriental and spelt cultivars were comparable to those of the common and durum wheats.

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Reaction of 33 cultivars of durum wheat to cereal soilborne mosaic virus during 2004–05.

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Cereal soilborne mosaic virus is widespread in northern and central Italy where it causes severe losses on both common and durum wheat crops. Yield losses of 70 % have been recorded on susceptible cultivars of durum wheat. CSBMV

Table 1. Symptom severity, ELISA values, grain yield, 1,000-kernel weight, test weight, plant height, and days to heading for 33 durum wheat cultivars grown in a field with CSBMV near Bologna, Italy, during 2004–05.

Cultivar	Symptom score (1–4)	ELISA value	Grain yield (t/ha)	1,000-kernel weight (g)	Test weight (kg/hl)	Plant height (cm)	Days to heading (from 1 April)
Anco Marzio	2.9 ab	1.285 ae	3.94 gi	34.6 l	74.6 ad	64 ij	44 be
Avispa	1.1 ei	0.124 km	5.64 ag	42.7 ch	69.9 ce	74 ai	41 gj
Canion	1.3 eh	0.270 jm	5.85 ae	42.5 ch	73.0 ae	78 ad	40 ij
Ciccio	2.4 bc	1.738 a	3.77 hi	35.2 kl	74.4 ad	53 k	39 j
Claudio	3.1 ab	0.963 dh	1.92 j	40.0 fl	75.7 ac	52 k	47 ab
Colorado	1.2 eh	0.240 jm	5.99 ad	41.4 dj	77.0 ab	78 ae	46 ad
Duetto	1.5 dg	0.849 ei	5.33 bh	52.9 a	75.9 ac	79 ac	47 a
Duilio	0.9 gi	0.319 im	4.54 ci	43.7 cg	68.4 de	73 ai	42 ei
Dylan	0.3 i	0.460 hm	5.63 ag	40.3 fk	71.2 ae	82 a	43 dg
Fiore	1.0 fi	0.216 jm	7.06 a	42.1 ci	75.9 ac	77 af	43 dg
Giove	2.3 bd	1.141 cg	4.98 ci	41.1 ej	72.3 ae	66 gj	40 ij
Giusto	0.6 hi	0.187 jm	4.07 fi	39.8 fl	67.0 e	81 a	44 cf
Grazia	3.1 ab	1.472 ad	3.40 i	34.5 l	77.4 ab	65 hj	44 be
Grecale	1.7 cf	0.302 jm	5.31 bh	37.1 hl	70.7 be	73 ai	41 gj
Ionio	0.8 gi	0.278 jm	5.64 ag	43.6 cg	73.9 ad	73 ai	40 hj
Iride	0.4 hi	0.230 jm	5.14 ch	41.3 dj	76.5 ac	71 bi	40 hj
Levante	1.2 eh	0.246 jm	6.19 ac	45.2 bf	76.3 ac	82 a	41 fj
Meridiano	0.3 i	0.059 m	6.85 ab	47.4 bc	77.7 a	79 ac	41 fj
Neodur	0.7 hi	0.242 jm	4.80 ci	42.3 ch	75.2 ac	77 af	46 ac
Normanno	1.1 ei	0.691 fj	4.93 ci	42.1 ci	70.8 be	74 ah	42 ei
Orobel	2.5 bc	1.663 ac	3.97 fi	39.7 fl	71.0 ae	69 dj	46 ad
Portorico	2.5 bc	1.582 ac	5.70 af	43.7 cg	76.6 ac	66 gj	44 be
Prometeo	3.4 a	1.174 bf	4.16 ei	35.8 jl	75.3 ac	60 jk	42 ej
Provenzal	0.5 hi	0.075 lm	—	—	—	—	—
Simeto	2.3 bd	1.621 ac	4.71 ci	47.0 bd	73.9 ad	60 jk	42 ei
Sorrento	2.3 bc	0.691 fj	3.98 fi	36.5 il	75.8 ac	73 ai	41 gj
Sorriso	2.6 bc	1.679 ab	4.47 ci	50.2 ab	74.7 ad	65 hj	40 hj
Tiziana	1.2 eh	0.624 gl	4.63 ci	46.6 be	75.5 ac	76 af	44 cf
Torrebianca	1.5 dg	0.470 hm	4.93 ci	43.7 cg	72.2 ae	80 ab	42 ej
Valerio	0.8 gi	0.083 lm	4.62 ci	43.0 cg	71.4 ae	75 ag	42 ej
Vendetta	1.2 eh	0.680 fk	5.24 bh	43.7 cg	71.9 ae	70 ci	43 dg
Vinci	2.4 bc	1.775 a	4.35 di	38.8 gl	74.1 ad	68 ej	43 eh
Virgilio	1.9 ce	0.728 fj	4.77 ci	41.4 dj	72.9 ae	68 fj	42 ei
MEAN	**1.6**	**0.732**	**4.91**	**41.9**	**73.8**	**71**	**43**

also is present in a number of farms in southern Italy and in Sicily. During the 2004-05 season, 33 durum wheat cultivars were assayed in a severely CSBMV-infested field situated near Cadriano (Bologna). The cultivars were grown in 10 m^2 plots distributed in the field according to a randomized block design with three replicates. Resistance was evaluated on the basis of DAS-ELISA readings (on two dates), symptom severity (on four dates, using a 0–4 scale), and agronomic performance (Table 1, p. 71). Because seed of cultivar Provenzal germinated poorly, agronomic performance was not evaluated for this entry. Cultivars Anco Marzio, Giove, Sorrento, Sorriso, Vendetta, and Vinci, all assayed for the first time, proved susceptible. Simple correlation coefficients between the agronomic data, ELISA values, and symptom scores were relatively high and mostly statistically significant (Table 2). Regression analysis indicated that cultivars with disease scores higher than 3.0 suffered grain yield, kernel weight, and plant height reductions of about 48 %, 18 % and 29 %, respectively.

Table 2. Correlation coefficients between symptom scores, ELISA values, and agronomic characters for 32 durum wheat cultivars grown in field with cereal soilborne mosaic virus near Bologna in 2004–05.

	Symptoms	ELISA
ELISA value	0.819 **	
Grain yield	0.633 **	0.519 **
Kernel weight	0.399 *	0.196 ns
Test weight	0.272 ns	0.200 ns
Plant height	0.782 **	0.732 **
Heading	0.116 ns	0.108 ns

Reaction of 35 cultivars of common wheat to cereal soilborne mosaic virus during 2004–05.

V. Vallega and C. Rubies-Autonell, A. Pisi, and C. Ratti (Dipartimento di Scienze e Tecnologie Agroalimentari, Area di Patologia Vegetale, Università di Bologna, Italy).

Thirty-five cultivars of common wheat were grown in a severely CSBMV-infested field near Cadriano (Bologna) during the 2004–05 season. Entries were grown in 10 m^2 plots distributed in the field according to a randomized block design with three replicates. Resistance was evaluated on the basis of DAS-ELISA readings (on two dates), symptom severity, (on three dates, using a 0–4 scale), and agronomic performance. Cultivars Africa, Albachiara, Avorio and Serpico, assayed for the first time, proved susceptible to CSBMV (Table 3, p. 73). As in previous trials, symptoms were milder than those observed on durum wheat cultivars grown in an adjacent field. ELISA values, symptom scores, and agronomic data were significantly correlated with each other (Table 4). Regression analysis indicated that cultivars with disease scores higher than 3.0 suffered grain yield and plant height reductions of about 38 % and 10 %, respectively. Yield reductions as high as 50 % had been recorded in previous trials.

Table 4. Correlation coefficients between symptom scores, ELISA values, and agronomic characters for 35 common wheat cultivars grown in field with cereal soilborne mosaic virus near Bologna in 2004–05.

	Symptoms	ELISA
ELISA value	0.856 **	
Grain yield	0.722 **	0.656 **
Kernel weight	0.125 ns	0.195 ns
Test weight	0.017 ns	0.007 ns
Plant height	0.463 **	0.399 *
Heading	0.113 ns	0.210 ns

Table 3. Symptom severity, ELISA values, grain yield, 1,000-kernel weight, test weight, plant height, and days to heading for 35 common wheat cultivars grown in a field with CSBMV near Bologna, Italy, during 2004–05.

Cultivar	Symptom score (1–4)	ELISA value	Grain yield (t/ha)	1,000-kernel weight (g)	Test weight (kg/hl)	Plant height (cm)	Days to heading (from 1 April)
A416	0.1 l	0.118 h	6.24 dg	46.4 a	77.0 di	77 cj	45 fj
Africa	1.7 cd	1.142 ac	6.29 cg	38.0 dh	76.0 hk	69 km	47 ce
Agadir	0.5 hl	0.229 fh	8.05 a	42.3 bc	78.7 bg	92 a	48 bd
Albachiara	2.2 ac	1.319 ac	4.59 i	39.0 ch	74.6 jm	68 km	43 ko
Alcione	0.6 hl	0.463 dh	6.61 bg	32.1 jk	73.2 m	72 hm	43 ko
Amarok	1.6 ce	1.093 ac	6.66 ag	34.9 hj	75.8 hk	70 km	48 bd
Apache	0.9 fi	0.800 bf	7.68 ac	38.9 ch	78.8 bf	88 ab	49 ab
Artico	0.1 l	0.077 h	7.13 ae	37.7 dh	75.0 im	78 ch	44 gk
Aster	1.1 eh	0.940 ae	4.78 hi	44.0 ab	78.9 bf	78 ci	42 mq
Aubusson	0.4 hl	1.172 ac	6.29 cg	37.0 fh	77.0 di	78 ch	46 eg
Avorio	1.8 ad	1.406 ab	5.50 fi	35.6 gj	77.7 ch	73 fk	42 lp
Bilancia	1.7 bd	1.574 a	5.38 gi	34.9 hj	75.9 hk	65 mn	40 q
Blasco	0.1 kl	0.197 fh	6.08 eh	34.7 hj	81.3 a	82 ce	41 pq
Bologna	0.6 hl	0.461 dh	6.52 cg	29.1 k	78.0 ch	75 ek	44 gk
Bramante	0.7 gk	0.980 ad	6.16 eg	32.2 ik	77.3 di	73 fk	44 gk
Carisma	0.9 fh	0.446 dh	6.22 dg	37.2 fh	78.0 ch	75 dk	46 eh
Colfiorito	0.0 l	0.068 h	6.87 af	38.0 dh	77.7 ch	78 ch	41 nq
Esperia	0.0 l	0.071 h	6.88 af	39.9 bg	76.9 ej	75 ek	41 oq
Geppetto	0.1 l	0.089 h	7.13 ae	35.8 gj	75.6 hl	72 gl	48 bc
Geronimo	2.3 ab	1.161 ac	5.40 gi	37.7 dh	79.4 ad	74 ek	44 il
Granbel	0.1 l	0.077 h	6.97 ae	41.6 be	76.4 gj	75 ek	45 fj
Greina	0.1 l	0.135 gh	6.31 cg	35.0 hj	80.8 ab	82 bd	43 ko
Guarni	0.8 gj	0.424 dh	7.65 ad	37.6 dh	75.2 im	80 cf	43 kn
Isengrain	0.9 fh	0.447 dh	6.57 cg	37.0 fh	77.9 ch	78 ci	46 eh
Kalango	0.3 il	0.325 eh	6.21 eg	38.2 ch	79.3 ae	70 jm	46 df
Nomade	1.3 dg	1.089 ac	5.80 ei	37.2 fh	75.1 im	73 fk	44 hl
Palesio	0.8 gi	1.223 ac	6.27 cg	37.3 eh	77.7 ch	73 fk	41 oq
Palladio	0.1 l	0.092 h	6.46 cg	36.4 fi	76.6 fj	83 bc	43 jm
PR22R58	0.0 l	0.080 h	8.04 a	40.5 bf	77.8 ch	70 jm	47 ce
Quality	0.1 jl	0.072 h	6.79 ag	36.4 fi	73.7 km	70 jm	44 il
Serpico	2.4 a	1.021 ad	4.58 i	39.6 cg	79.8 ac	71 im	44 hl
Tremie	0.0 l	0.054 h	7.99 ab	41.9 bd	73.4 lm	79 cg	45 ei
Trofeo	2.3 ab	1.335 ac	3.18 j	37.9 dh	76.3 gj	66.ln	44 gk
Victo	0.5 hl	0.070 h	6.80 ag	37.8 dh	76.5 fj	69 km	51 a
Zena	1.5 df	0.759 cg	4.79 hi	32.1 jk	75.2 im	62 n	41 oq
MEAN	**0.8**	**0.600**	**6.31**	**37.5**	**77.0**	**75**	**44**

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Reaction of 111 cultivars of durum wheat of various origins to cereal soilborne mosaic virus.

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One hundred eleven old and modern durum wheat cultivars representative of a large portion of the genetic diversity present in the world's improved durum wheat gene pool were grown for two seasons in a field near Bologna (Italy) with natural inoculum sources of cereal soilborne mosaic virus (CSBMV) and evaluated for resistance on the basis of symptom severity expression and CSBMV concentration in leaves using DAS (Double Antibody Sandwich) ELISA. Entries were sown in plots consisting of three 122-cm long, solid-seeded rows, distributed according to a randomized block design with two replicates. Symptom severity was scored on three dates in 2003 and on four dates in 2004 using a 0–4 scale. Virus concentration was determined on extracts from leaves collected on three dates in 2003 and on two dates in 2004. Extracts were from a bulk of the apical half of the second and third youngest leaves of 10 randomly chosen plants/plot. Bulked leaf samples from each plot were processed separately. Symptom scores were significantly correlated ($P \leq 0.01$) with ELISA values in both seasons ($r = 0.827$ in 2003 and $r = 0.890$ in 2004). Interyear correlations too were highly significant for both ELISA values ($r = 0.911$) and symptom scores ($r = 0.848$). The cultivars analyzed manifested a wide range of reactions to CSBMV (Table 1, pp. 74-76), but none remained symptomless in both seasons nor were clearly devoid of CSBMV. Thirty-five cultivars consistently showed low ELISA values, and 21 had mean ELISA values higher than that of the susceptible control

Table 1. Mean ELISA values and mean symptom scores for 111 durum wheat cultivars grown in a field with cereal soilborne mosaic virus near Bologna, Italy, during 2002–03 and 2003–04.

Cultivar	Mean ELISA value		Mean symptom score	
	2003	2004	2003	2004
Acalou	1.103 ai	1.684 ad	2.1 ai	2.5 ai
AC Avonlea	0.080 q	0.033 r	0.8 is	0.2 vy
AC Melita	0.035 q	0.131 qr	0.5 ns	0.5 ry
AC Morse	0.051 q	0.051 r	0.5 ns	1.0 ny
AC Navigator	0.248 nq	0.435 lr	1.1 es	1.0 ny
AC Pathfinder	0.261 nq	0.995 fk	0.1 s	1.3 kx
Agridur	1.464 af	1.699 ad	2.8 ad	2.9 ad
Altar 84	0.998 cj	1.674 ad	2.5 ad	3.0 ad
Anton	0.066 q	0.085 qr	0.6 ms	1.3 kx
Appio	0.737 ho	0.440 lr	1.2 es	1.0 ny
Appulo	0.778 hn	1.156 di	1.0 gs	1.3 kx
Aramon	1.574 ab	1.424 af	2.4 ae	3.2 ac
Arcalis	1.143 ai	1.209 bh	1.5 dq	2.4 bl
Arcangelo	1.343 ag	1.597 ae	1.0 gs	1.9 dp
Arcobaleno	1.397 af	1.693 ad	2.3 af	3.3 ab
Ardente	0.215 oq	0.491 kr	0.3 ps	1.3 jx
Arstar	1.255 ah	1.661 ad	2.2 ag	3.3 ab
Auroch	0.091 q	0.573 jr	0.8 is	0.8 oy
Belikh 2	0.137 q	0.099 qr	0.4 os	1.0 ny
Belzer	0.928 fl	1.681 ad	2.3 af	3.3 ab
Ben	0.036 q	0.071 qr	0.8 is	0.6 qy
Bravadur	0.064 q	0.060 qr	0.9 hs	1.1 ny
Brindur	0.245 nq	0.240 or	0.5 ns	0.6 qy
Bronte	1.343 ag	1.737 ac	1.7 bo	2.9 ae
Capeiti 8	0.817 gm	1.192 ch	0.5 ns	0.9 ny
Cappelli	0.304 mq	0.746 hp	0.4 os	1.4 iw
Ciccio	1.487 ae	1.641 ad	1.6 cp	2.8 af
Colorado	0.068 q	0.069 qr	0.3 qs	0.7 py
Colosseo	0.257 nq	0.953 fl	1.7 bn	2.0 co
Cortez	1.229 ai	1.764 ab	1.5 dr	3.0 ad
Creso	0.498 jq	1.304 ag	1.2 es	3.0 ad
Don Pedro	0.066 q	0.066 qr	0.2 rs	0.6 qy
Duilio	0.026 q	0.094 qr	0.5 ns	1.5 hu
Duraking	0.084 q	0.040 r	0.2 rs	0.8 py
Durex	0.692 ip	0.095 qr	0.7 ls	1.2 ly
Durfort	0.263 nq	0.075 qr	0.4 os	0.5 sy
Duriac	1.605 ab	1.799 a	1.7 bn	2.4 ak
Edmore	0.053 q	0.172 qr	1.2 es	0.8 oy
Excalibur	1.509 ad	1.760 ab	2.1 ah	3.3 ab
Extradur	1.397 af	1.695 ad	1.2 es	2.7 ag
Flavio	0.426 lq	0.110 qr	0.4 os	1.6 gt
Fortore	1.526 ac	1.674 ad	1.8 am	3.1 ac
Frankodur	1.131 ai	1.730 ac	1.2 es	3.1 ad
Galadur	0.056 q	0.047 r	0.2 s	0.5 sy
Gargano	1.196 ai	1.765 ab	1.2 es	2.5 ai
Goldur	0.055 q	0.105 qr	0.2 rs	0.1 xy
Grandur	0.374 mq	0.937 fm	0.6 ms	1.6 fs
Grazia	1.342 ag	1.729 ac	2.6 ad	3.1 ad

Table 1 (continued). Mean ELISA values and mean symptom scores for 111 durum wheat cultivars grown in a field with cereal soilborne mosaic virus near Bologna, Italy, during 2002–03 and 2003–04.

Cultivar	Mean ELISA value		Mean symptom score	
	2003	2004	2003	2004
Heider	1.523 ac	1.753 ac	2.0 ak	2.7 ah
Helidur	0.233 nq	0.510 kr	0.2 rs	1.1 ny
Hercules	0.049 q	0.057 qr	0.7 ls	0.0 y
Ionio = Ares	0.102 q	0.054 r	0.4 os	1.5 iu
Iride	0.040 q	0.314 nr	0.2 rs	1.2 ly
Italo	0.079 q	0.846 gn	0.6 ms	0.8 oy
Ixos	0.970 dj	1.693 ad	1.7 bo	3.2 ac
Jabato	1.386 af	1.770 ab	2.2 ag	3.1 ac
Kabir	0.091 q	0.487 kr	0.7 ks	2.5 aj
Kamilaroi	0.124 q	0.440 lr	0.7 ks	1.3 jx
Karel	1.563 ab	1.636 ad	1.9 al	2.8 af
Korifla (Cham 3)	0.090 q	0.098 qr	0.7 ls	1.9 dp
Kronos	1.074 bi	1.742 ac	2.7 ad	3.4 ab
Kyle	0.045 q	0.168 qr	0.6 ms	1.1 my
L 35	0.083 q	0.148 qr	0.6 ms	0.7 py
Lakota	0.061 q	0.071 qr	0.6 ms	0.4 ty
Langdon	0.276 nq	0.233 or	0.1 s	0.7 py
Latino	0.350 mq	0.165 qr	1.0 gs	1.4 iw
Lira	0.139 q	1.545 ae	0.2 rs	2.1 cn
Lloyd	0.037 q	0.274 or	0.6 ms	1.1 ny
Maier	0.089 q	0.235 or	1.0 gs	0.9 ny
Messapia	1.651 a	1.737 ac	2.2 ag	3.0 ad
Mexicali 75	0.323 mq	0.503 kr	0.4 os	0.8 py
Mindum	0.316 mq	0.404 mr	0.0 s	0.7 py
Mohawk	0.067 q	0.453 kr	0.5 ns	0.6 qy
Munich	0.349 mq	0.058 qr	1.2 es	0.6 qy
Nefer	0.079 q	0.046 r	0.7 ls	0.6 qy
Neodur	0.033 q	0.042 r	0.6 ms	0.4 ty
Ofanto	1.509 ad	1.794 a	2.0 ak	2.3 bm
Orjaune	0.055 q	0.243 or	0.5 ns	0.9 ny
Platani	0.265 nq	0.949 fm	1.0 gs	1.5 iu
Plaza	0.035 q	0.082 qr	1.0 fs	1.4 iw
Plenty	0.032 q	0.121 qr	1.0 gs	0.7 py
Plinio	1.164 ai	1.708 ad	2.0 aj	2.3 bm
Primadur	1.317 ag	1.753 ac	1.0 gs	2.4 ak
Produra	1.474 af	1.687 ad	2.9 ab	2.7 ag
Renville	0.046 q	0.065 qr	0.2 s	1.0 ny
Reva	0.035 q	0.111 qr	0.6 ms	1.2 ly
Roqueño	1.324 ag	1.757 ab	3.0 a	3.3 ab
Rugby	0.447 kq	1.079 ej	0.2 rs	0.9 ny
Russello SG7	0.952 ek	0.770 go	1.1 fs	1.4 iv
San Carlo	0.060 q	0.159 qr	1.0 gs	0.9 ny
Saragolla	0.036 q	0.037 r	0.1 s	0.5 ry
Sceptre	0.070 q	0.628 iq	0.3 ps	0.8 oy
Semperdur	0.200 oq	0.096 qr	0.3 ps	0.2 xy
Simeto	1.230 ai	1.752 ac	2.1 ai	2.8 af
Solex	0.071 q	0.274 or	0.0 s	0.3 uy

cultivar Grazia. The resistant entries identified included the cultivar Edmore and twelve Edmore-derivatives independently bred in Canada, France, Italy, and the U.S., suggesting that this cultivar has one or few major genes for CSBMV resistance. Studies have been undertaken to identify markers associated with the CSBMV-resistance gene(s) present in cultivar Edmore and in some of the other, unrelated, CSBMV-resistant cultivars identified in the study. Because of their extreme reactions to CSBMV and their wide adaptability, a number of the cultivars assayed should prove useful for investigating the existence of CSBMV pathotypes and/or pathogenic differences between CSBMV, wheat soilborne mosaic virus, and Chinese wheat mosaic virus.

Reaction of UK winter wheat varieties to CSBMV and WSSMV in France, Italy, and the U.K.

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In Europe, cereal soilborne mosaic virus is widely distributed, whereas wheat spindle streak mosaic virus, often found infecting wheat in combination with CSBMV, thus far, was identified only in France, Germany, and Italy. Twenty U.K.-recommended winter wheat cultivars (Aardvark, Biscay, Buchan, Buster, Charger, Claire, Cockpit, Consort, Deben, Eclipse, Equinox, Hereward, Madrigal, Malacca, Napier, Reaper, Rialto, Riband, Savannah, Shamrock, and Xi19) were grown at six sites with a history of viral infection by CSBMV and/or WSSMV in France (Chambon sur Cisse and Landes Le Gaulois) , Italy (Minerbio, Ozzano and Rome), and the U.K. (Wiltshire). Eleven trials were conducted over three seasons. Local varieties of known reaction to both viruses (Aztec, Cezanne, Tremie, Grazia, and Valnova) also were planted at each site as controls. Cultivar responses to CSBMV and WSSMV were evaluated on the basis of symptom severity, ELISA values, grain yield, stem height at harvest, and 1,000-kernel weight. Severe symptoms of CSBMV were seen in the

Table 1 (continued). Mean ELISA values and mean symptom scores for 111 durum wheat cultivars grown in a field with cereal soilborne mosaic virus near Bologna, Italy, during 2002–03 and 2003–04.

Cultivar	Mean ELISA value		Mean symptom score	
	2003	2004	2003	2004
Svevo	0.080 q	0.206 pr	0.3 ps	1.7 er
Tacna	1.487 ae	1.765 ab	1.8 am	3.6 a
Tetradur	0.312 mq	0.088 qr	0.5 ns	0.6 qy
Topdur	0.305 mq	0.050 r	0.0 s	0.4 ty
Trinakria	1.053 bi	1.230 ah	1.1 es	1.8 eq
Valbelice	1.547 ac	1.759 ab	1.7 an	2.3 bl
Valforte	1.450 af	1.645 ad	2.6 ad	3.6 a
Valnova	1.558 ab	1.781 a	3.0 a	3.2 ac
Varano	1.459 af	1.789 a	2.2 ag	3.0 ad
Vic	0.079 q	0.049 r	1.2 es	1.3 kx
Waha	1.571 ab	1.787 a	2.9 ac	3.1 ac
Wallaroi	0.315 mq	0.107 qr	0.8 js	0.6 qy
WB 881	0.717 ho	0.255 or	0.5 ns	0.8 oy
WB Turbo	0.075 q	0.118 qr	0.8 is	1.0 ny
Yallaroi	0.154 pq	0.096 qr	0.6 ms	1.0 ny
Yuma	0.071 q	0.227 or	0.0 s	0.2 wy
Mean	0.593	0.792	1.1	1.6
Minimum value	0.026	0.033	0.0	0.0
Maximum value	1.651	1.799	3.0	3.6

majority of the cultivars assayed. Little or no symptoms were seen in the cultivars Aardvark, Charger, Claire, Hereward, and Xi 19. WSSMV was not detected in the leaves or roots of any U.K. cultivars, suggesting, the varieties tested were immune.

Studies on the occurrence of pathotypes in the Furuvirus genus.

C. Rubies-Autonell and C. Ratti, U. Kastirr (Federal Centre for Breeding Research on Cultivated Plants, Institute of Resistance Research and Pathogen Diagnostics, Aschersleben, Germany), and V. Vallega (C.R.A., Istituto Sperimentale per la Cerealicoltura, Rome, Italy).

Fourteen cultivars of durum wheat from Italy and from other countries were grown in a field with CSBMV near Bologna, Italy (Table 2), as part of a collaborative study to determine the presence of pathotypes within CSBMV and of pathogenic differences between CSBMV, wheat soilborne mosaic virus and Chinese wheat mosaic virus. The same cultivars are being assayed against CSBMV and WSBMV in Germany, both under controlled environmental conditions and in field trials.

Sixth IWGPVFV symposium and proceedings

The Sixth Symposium of the International Working Group on Plant Viruses with Fungal Vectors was held in Bologna, Italy, from 5-7 September 2005 (local organizers C. Rubies-Autonell and V. Vallega). Scientists from twenty-three countries attended the symposium. Eighteen communications dealt with viral diseases of wheat. The Sessions were chaired by Tetsuo Tamada, Lesley Torrance, Frank Ordon, Claude Bragard, Michael J. Adams, Charlie Rush, and Thomas Kühne. The proceedings (edited by C.M. Rush and U. Merz) will be published in late 2005 or early 2006. In the meantime, the program and the abstracts of the communications presented can be accessed at www.rothamsted.bbsrc.ac.uk/ppi/Iwgpvfv/Bologna.html. The next meeting is planned to be held in Quedlinburg, Germany in 2008 (local organizer, Dr Thomas Kühne, (t.kuehne@bafz.de). The present IWGPVFV Committee is comprized of Ueli Merz, Charles M. Rush, and Michael J. Adams.

Table 2. Reaction of 14 cultivars of durum wheat grown in a field with cereal soilborne mosaic virus near Bologna, Italy, during 2004–05.

Cultivar	Symptom score	ELISA value
Caesar	0.2	0.034
Durabon	1.3	0.797
Heradur	3.4	1.378
Prowidur	3.1	1.230
Soldur	0.7	0.139
Superdur	1.8	1.706
Windur	2.9	0.894
Yukon	1.4	1.047
Grazia	2.9	1.588
Nefer	1.0	0.046
Colorado	0.7	0.110
Neodur	0.3	0.045
Ciccio	2.0	1.572
Cirillo	3.1	1.515

ITEMS FROM JAPAN

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Nobuyoshi Watanabe.

The occurrence and inheritance of a brittle rachis phenotype in Italian durum wheat cultivars.

Italian and Tunisian durum wheats from different eras of breeding were assessed for the presence of a gene for brittle rachis. Nine of 15 Italian durum landraces had brittle rachides. Strampelli's achievement was the release of the well-known variety, Senatore Cappelli, which was derived from a Tunisian landrace, Jenah Rhettifah, which has a brittle rachis. Rachides of two Tunisian landraces were also brittle. Since the 1950s, 16 accessions were released as selections from crosses or mutagenesis involving Senatore Cappelli. Seven of these accessions have brittle rachides. F_2 segregation in intercrosses of Senatore Cappelli with other durum accessions with brittle rachides indicated a common allele for brittle rachis. The gene for brittle rachis of Senatore Cappelli was allelic to the brittle allele of the *Br-B1* locus on chromosome 3B. Senatore Cappelli was presumably the only source of brittle rachis used in Italian breeding programs. The genes for brittle rachis have been retained in the gene pool of durum wheat, suggesting that the brittle rachis character does is not seem to be associated with an appreciable yield loss in modern farming systems in Mediterranean environments.

Genetic mapping of the genes for glaucous leaf and tough rachis in Aegilops tauschii.

Glaucous leaf and tough rachis phenotypes were rare in *Ae. tauschii*, the D-genome donor to bread wheat. The genes for glaucous leaf and tough rachis were mapped using microsatellite probes in *Ae. tauschii*. The glaucous phenotype was suppressed by the inhibitor $W2^I$ located on chromosome 2DS. The gene $W2^I$ was mapped to the distal part of 2DS, and was unlinked to the centromere. This suggests that the distance of the $W2^I$ locus from the centromere was maintained during the establishment of hexaploid wheat from its diploid progenitors as the inhibitor gene is at the same position in *Ae. tauschii* and modern bread wheat. The Br^t (*Brittle rachis of Ae. tauschii*) locus was located on the short arm of chromosome 3D and was linked to the centromeric marker *Xgdm72* (19.7 cM). It is noted that Br^t causes breakage of the spike at the nodes, thus creating barrel-shaped spikelets, whereas *Br1* in hexaploid wheat causes breakage above the junction of the rachilla with the rachis such that a fragment of rachis is attached below each spikelet.

Personnel.

Nobuyoshi Watanabe is now a professor at Ibaraki University since1 December 2005.

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Quality evaluations of flour yield and flour particle size distribution for Japanese commercial and waxy wheats.

Hiro Nakamura.

Introduction. The evaluation method for Japanese hexaploid wheat flour hardness was developed by the Ministry of Agriculture and Forestry (1968) in coöperation with other National Institutes related to wheat. Few studies have been reported on Japanese wheat quality (Nagao 1976, 1977; National Food Research Institute 1984; Takada 1987; Toyokawa 1989a, b). However, the most important characteristic of wheat quality acceptability is wheat flour hardness related to flour yield. There is a little information about the most important quality factors of flour hardness in Japan (Yamashita 1994). However, by the late 1980s, the particle size parameters in wheat flour by laser beam diffractometry method was being used for most flour particle size analyses in the U.S., the AACC technical committee in quality tests for wheat and flour initiated a collaborative study on the determination of wheat flour particle size parameters by the laser beam instrumental method (McDonald 1994). Wu et al. (1990) found that the size distributions of flours measured by sieving and air classification. Devaux et al. (1998) also reported that the detailed particle size distributions can be easily determined by using a laser light apparatus. Flour yield is a main factor affect in wheat bread and noodle quality (Yamashita 1994). Yamazaki and Donelson (1983) reported previously that particle size index for the soft wheat was significantly associated with the break flour yield obtained in milling the common wheat. Particle size in wheat flour is significantly related to the degree of the hardness in the wheat kernel, and hardness is an important factor in flour functionality in wheat food products (Obuchowski and Bushuk 1980). Therefore, it would be of interest to reveal that relationship between flour hardness or flour yield and flour particle size distribution by using laser light diffraction apparatus.

In Japan, a major objective of wheat breeders is to develop new, high flour yielding cultivars with improved bread or Japanese soft noodle-making quality. Wheat for making bread or Japanese soft noodles must have certain minimum standard levels of flour yield and protein content. At the Wheat Breeding Institute, a greater effort is being placed on the improvement of protein quality in the Japanese breeding program (Nakamura 1999, 2000a, b, c). Waxy (amylose-free) wheats have been produced in Japan (Nakamura et al. 1995). Amylose content plays an important role in the quality of wheat since it affects starch properties (Yamamori and Quynh 2000). Therefore, the flour yield of Japanese waxy commercial wheat varieties is greatly important in wheat breeding programs in Japan.

It is well known that as well as being of great importance nutritionally flour hardness plays a fundamental part in food processing, for instance, in the manufacture of bread, biscuits, breakfast cereals, pasta, and Japanese soft-noodle (Udon) products. The aim of this study was to find which flour particle size or flour particle size distribution may be the new flour hardness index instead of glassy kernel ratio (%) in Japan and to find flour particle size distribution most affect flour yield between soft and hard in Japanese wheats.

Flour hardness of breeding or commercial hexaploid wheat from the northern Japan, was related to mean flour particle size and particle size distribution determined by laser diffraction. Hard and soft wheat differed in mean flour particle size and flour particle size distribution patterns from air classification of flour. Hard wheat appeared to differ from soft wheat in mean flour particle size > 64 μm fraction from air classification of flour. Thus, > 64 μm from air classification or screening of flour distinguishes hard wheat, and < 64 μm from air classification or screening of flour

distinguishes soft wheat in this study. Hard and soft wheat also were distinctly different in flour particle size distribution patterns from air classification of flour. The two peak particle distribution patterns (pattern II) was shown in soft wheat variety Nebarigoshi, it could be associated to a higher flour yield of soft wheat line. This result suggest that flour particle size distribution pattern II (with two peak patterns) seems to be affected a higher flour yield than that of soft wheat (with only a lower one peak; pattern I) in Japanese wheat.

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ITEMS FROM LEBANON

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Sui-Kwong Yau and Jacqueline Pridham, and Martin Entz (University of Manitoba, Department of Plant Sciences, Winnipeg, Canada).

Root weight differences between Canadian wheat cultivars under organic farming management.

A field experiment comprising 15 bread wheat entries (four Canadian bread wheat cultivars and all their combinations) in four replicates was set up at a certified organic site near Carman in 2005 under organic management. The broad objectives of the experiment were to find out whether old cultivars would perform better than new cultivars under

organic farming, and whether mixtures will perform better than pure lines. In this report, only results on root weight are presented.

Red Fife and Marquis were the two old cultivars used, and the two new cultivars were AC Barrie and BW297. Red Fife was first introduced in Manitoba in 1870. Marquis was developed later by Dr. Charles Saunders from a cross between Red Fife and an early ripening HRSW from India. AC Barrie became the most widely grown wheat cultivar just 2 years after certified seed sale in 1995. BW297, yet to be officially named, was developed by Proven Seed and its breeding partner AgriPro Wheat. BW297 has exhibited high yield and protein levels with a high level of Fusarium head blight and rust tolerance.

Roots were sampled after heading on 22 July, 2005. Two soil cores of 90-cm depth taken the day earlier showed that roots were no more than 20 cm deep. In order to take bigger samples in a shorter time, samples were collected manually with a circular root sampler instead of using the Giddings soil sampler. The root sampler was 15-cm tall with a diameter of 7 cm (lower side). A '21 x 21 cm' square covering two planted rows was sampled randomly within the area where shoot samples were harvested 3 days before. This meant that nine (3 x 3) scoops of soil, six from the two planted-rows and three from within the two planted-rows, were taken. Samples were stored at 3°C before washing and after washing before drying.

Cylindrical root washers, which remove the soil particles with water and compressed air coming out from the base of the cylinders, were used to clean the roots from the samples. After cleaning, seminal and basal roots were cut and collected manually. Roots coming out from the first node and from occasional weeds were not collected. Root dry weight was recorded after drying at 65°C for 72 hr.

Analysis of variances showed that there were significant differences in root dry weight among entries (Table 1). One of the old cultivar, Red Fife, and one of the new cultivar, AC Berrie, had >30 % root dry weight than the other two cultivars: Marquis and BW297. Two mixtures (Red Fife with AC Berrie; and Red Fife, AC Berrie, with Marquis) gave the highest root dry weight (>30.0 g/m^2), and significantly higher than BW297, Marquis, the mixture of BW297, Marquis, and Red Fife, and the mixture of Marquis with Red Fife.

Table 1. Root dry weight (g/m^2) of four bread wheat cultivars and some mixtures (l SD = 8.74 g/m^2).

	Red Fife	Marquis	AC Barrie	BW297
	22.3	16.9	25.7	16.0
Marquis	21.3			
AC Barrie	31.5	22.0		
BW297	23.0	23.8	21.5	
Marquis & AC Barrie	30.4			
Marquis & BW297	17.8			
AC Barrie & BW297	24.0	25.4		
Marquis, AC Barrie, & BW297	23.4			

The unusual high rainfall of the growing season caused widespread flooding in Manitoba, and ditches needed to be dug around the experiment to lead water away from the plot. Thus, cultivar differences in root weight found in this study may not hold under normal or dry years.

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Evaluation of high quality elite genotypes of bread wheat for resistance to Karnal bunt.

Guillermo Fuentes-Dávila and Javier Ireta-Moreno.

Introduction. Karnal bunt occurs naturally on bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). Infected grains are in general partially affected, but sometimes completely infected grains can also be found (Bedi et al. 1949; Chona 1961; Mitra 1935). The susceptibility of bread wheat to Karnal bunt has been well documented (Fuentes-Dávila et al. 1992, 1993) reaching infection levels greater than 50 % under artificial inoculations; therefore, it is important to continue evaluating new advanced lines and cultivars, as a measure to avoid economic problems, which could derive from the release of susceptible cultivar for commercial use.

Materials and methods. Seventy, high-quality, elite bread wheat genotypes were evaluated for resistance to Karnal bunt during the agricultural season autumn-winter 2001–02 in the Yaqui valley, Sonora, Mexico. Planting dates were 8 and 20 November, 2001, using approximately 10 g of seed on 1-m beds with two rows. A mist-irrigation system was used 3 to 5 times a day during 15 each time, to provide high relative humidity in the experimental area. Inoculations were made by injecting 1 ml of an allantoid sporidial suspension (10,000/ml) during the boot stage on 10 heads/genotype. Harvest was done manually, and the counting of healthy and infected grains was done by visual inspection. Genotypes evaluated were various advanced wheat lines generated by the CIMMYT–INIFAP collaborative breeding program.

Results and discussion. The range of infection for the first planting date was 0 to 65.48 %, with and average of 27.27 %; within this group, only two lines showed infection levels below 5 % (Fig. 1). The range of infection for the second planting date was 1.59 to 75.79 %, with and average of 34.10 %; three lines showed infection levels below 5 %. Only four sister lines showed consistently infection levels below 6.91 % (SKAUZ/2*STAR, 3KBY; 4KBY; 5KBY; 8KBY) (Table 1, p. 82) (lines that show less than 5 % infection are considered as resistant (Fuentes-Dávila and Rajaram 1994). The susceptible check WL-711 had an infection level of 86.09 %. In general, the group of lines evaluated showed a high level of infection, reaching 75.79 % (BOW//BUC/BUL/3/WEAVER/4/STAR, Table 2, p. 82). These results indicate the predominant susceptible reaction in this particular group of bread wheats, and the difficulty to generate wheats that combine quality, yield, resistance to leaf rust and to Karnal bunt. Although bread wheat cultivars Arivechi M92 (Camacho-Casas et al. 1992) and INIFAP M97 and TOBARITO M97 (Camacho-Casas et al. 1998) partly were released because they are resistant to Karnal bunt, they

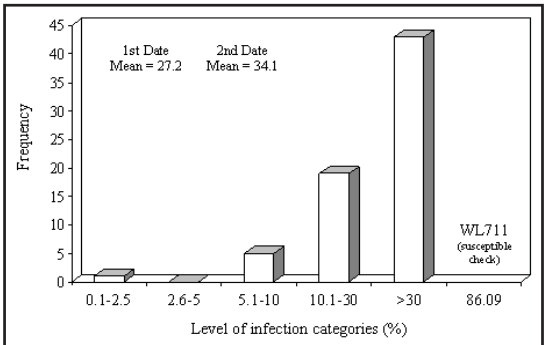

Fig. 1. Results of artificial field inoculations of 70 elite, high-quality bread wheat genotypes with Karnal bunt on two planting dates in the Yaqui Valley, Sonora, Mexico, during the agricultural cycel autumn–winter 2001–02. The level of infection of the check WL 711 is the average of the three highest levels.

are not being cultivated commercially, because they do not comply with the quality requirements by the milling industry. Joint efforts between INIFAP and CIMMYT continue to assure acceptable resistance levels to Karnal bunt in the new and promising lines of bread wheat so that a commercial and viable crop can be produced for the farmers in northwest Mexico, and that also complies with the industry's quality standards.

Table 1. High-quality, elite, bread wheat genotypes with infection levels below 10 %, after artificial field inoculation with Karnal bunt on two planting dates, during the agricultural cycle autumn-winter 2001–02 in the Yaqui Valley, Sonora, Mexico.

Genotype No.	Pedigree
	< 5 %
7	SKAUZ/2*STAR CMBW91MO3009M-0TOPY-20M-010Y-010M-010Y-2Y-OM-4KBY-OY
	< 10 %
6	SKAUZ/2*STAR CMBW91MO3009M-0TOPY-20M-010Y-010M-010Y-2Y-OM-3KBY-OY
8	SKAUZ/2*STAR CMBW91MO3009M-0TOPY-20M-010Y-010M-010Y-2Y-OM-5KBY-OY
10	SKAUZ/2*STAR CMBW91MO3009M-0TOPY-20M-010Y-010M-010Y-2Y-OM-8KBY-OY
18	KEA/TAN/4/TSH/3/KAL/BB/TQFN/5/WL7168/6/SNB CMSS92Y01398T-22Y-010M-010Y-10M-0Y-3KBY-0Y
27	Irena//CMH76.173/2*GEN/3/SNB/4/BORL95 CMSS92MO2911T-015M-OY-OY-050M-8Y-3M-OY

Table 2. High-quality, elite, bread wheat genotypes with infection levels greater than 50 %, after artificial field inoculation with Karnal bunt on two planting dates, during the agricultural cycle autumn-winter 2001–02 in the Yaqui Valley, Sonora, Mexico.

Genotype No.	Pedigree
3	Pastor CM85295-0101TOPY-2M-OM-112Y-OB
13	BORL95/RABE CMBW91MO4347S-7M-010Y-03M-OY-6M-0Y
24	VEE/TRAP#1//Angra/3/Pastor CMSS92MO2657T-015M-OY-OY-050M-18Y-3M-OY
30	BOW//BUC/BUL/3/Weaver/4/Star CMSS93YO2898T-55Y-010Y-010M-010Y-7M-OY
31	Pastor/3/KAUZ*2/Opata//KAUZ CMSS93BOO308S-29Y-010M-010Y-010M-9Y-0M
43	Huites/4/CS/TH.SC//3*PVN/3/Mirlo/BUC CMSS94Y00476S-0300M-0100Y-0100M-17Y-4M-OY
49	CMH82A.1294/2*KAUZ//Munia/CHTO/3/Milan CMSS94Y02249T-030Y-0300M-0100Y-0100M-4Y-8M-0Y
50	Weaver//VEE/PJN/3/Milan CMSS94Y02337T-030Y-0300M-0100Y-0100M-10Y-6M-0Y
59	VEE/PJN//2/TUI/3/WH576 CMSS95Y00795S-0100Y-114DH-OB
61	RABE/6/WRM/3*TH//K58/2*N/3/AUS-6869/5/Pelotas-Arthur/7/2*RABE/8/Irena CMSS95Y01330S-0100Y-79DH-OB

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Production of allantoid secondary esporidia of Tilletia indica in vitro by teliospores isolated from bread and durum wheat infected under natural conditions.

Irazema Fuentes-Bueno and Guillermo Fuentes-Dávila.

Introduction. Karnal bunt is a floral-infecting organism (Mundkur 1943) that partially infects seed of bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). *Tilletia indica* is a fungus that upon teliospore germination, produces a promycelium or promycelia, and primary sporidia at the apex; primary sporidia germinate directly or indirectly; in the latter case, giving rise to allantoid secondary sporidia on sterigmata from which they are forcibly discharged. These in turn, germinate directly or by repetition (Krishna and Singh 1983; Fuentes-Davila and Duran 1986). Chona et al. (1961) evaluated several inoculation methods in the field, indicating that injection during the boot stage of wheat using sporidial suspensions produced the highest levels of infection. Singh and Krishna (1982) evaluated the injection technique at several phenologic stages of the wheat plant from panicle initiation to milky stage using sporidial suspensions, and reported that the most susceptible stage for inoculation was when awns were just emerging (stage 49, Zadoks et al. 1974) (84 % infected grain as compared to boot with 75 %, heading with 4 %, and 6 % at flowering). Field inoculations have required the use of more specific propagules of the fungus, as it has been with the allantoid secondary sporidia, in order to obtain consistent high levels of infection (Singh et al. 1988; Fuentes-Dávila et al. 1993). In this report, we present results of production of allantoid secondary sporidia *in vitro*, derived from teliospores obtained from grain of durum wheat and bread wheat infected under natural conditions.

Materials and methods. Infected grains from cultivars Baviacora M92 and Altar C84 were obtained from commercial fields in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn-winter 2002–03.

Teliospore isolation and germination. Teliospores were scraped off infected grains with a dissecting needle and kept in a water-Tween 20 solution for 24 h, then the suspension was filtered through a 60 μm nylon sieve and centrifuged at 3,000 rpm. After discarding the supernatant, sodium hypochlorite 0.5 % a.i. was used to disinfect teliospores for 2 min while centrifuging again. Teliospores were then rinsed twice with sterile distilled water while centrifuging. Teliospores were resuspended in sterile distilled water in the centrifuge tube and 1 ml of the teliospore suspension was spread on Petri plates with 2 % water-agar (AA), which were incubated at 20˚C in darkness. After 6 to 9 days, teliospore germination was evaluated using a compound microscope at 10X.

Inoculum multiplication. Pieces of AA with germinated teliospore were removed and placed upside down on the lid of Petri plates containing potato-dextrose-agar (PDA). After 10 to 14 days, 2 to 3 ml of sterile distilled water were added to the plates and the colonies were scraped gently using a sterile spatula. Hyphae and sporidia were inoculated onto other plates with PDA using a sterile syringe, and the plates were incubated at 20˚C in darkness for about 9 days.

Production of allantoid secondary sporidia. After incubation, pieces of PDA with the different fungal propagules were transferred and placed upside down on the lids of sterile glass Petri plates, in order to induce production of allantoid secondary sporidia (Dhaliwal and Singh 1989; Fuentes-Dávila et al. 1993). Three ml of sterile distilled water were added to the bottom of the plates. Plates with fungal propagules derived from teliospores produced on Altar C84 and Baviacora M92 were kept separately and incubated under two regimes: a) within an incubator at 20˚C in darkness and b) at room temperature (range 23–28˚C, mean 26.4˚C) with a 14 h photoperiod. There were four plates (replicates) per fungal culture-cultivar, and the evaluation was carried out six times (groups). Water from the plates was collected every

two days in order to do sporidia counts; water collection and sporidia counts were repeated five times. Sporidia were counted using a hemocytometer.

Results and discussion. Sporidia counts from teliospores obtained from Altar C84 and incubated at 20˚C in darkness had a minimum of 615 allantoid secondary sporidia and a maximum of 2,064 with an average of 1,541.16 (Fig. 2). The range of sporidia from cultures incubated at room temperature was 980–2,665 with an average of 2,148.16. Sporidia counts from teliospores obtained from Baviacora M92 and incubated at 20˚C in darkness had a minimum of 57 allantoid secondary sporidia and a maximum of 2,187 with an average of 642 (Fig. 3). The range of sporidia from cultures incubated at room temperature was 182–1,297 with an average of 693.66. Production of sporidia at room temperature which fluctuated from 23 to 28˚C and with a 14 h photoperiod, was greater than at 20˚C in darkness in all groups from teliospores obtained from cv. Altar C84 and in four from Baviacora M92; in the first cv. the minimum and maximum difference in sporidia production was 37 and 1,433, respectively, with and average of 607, whereas in the latter, it was 57 and 800, respectively, with an average of 436. In Baviacora M92, the minimum and maximum difference in sporidia production in the two groups with greater production at 20˚C in darkness was 376 and 1,058, respectively, with an average of 717. Overall production of allantoid secondary sporidia was greater by teliospores obtained from Altar C84 than from Baviacora M92.

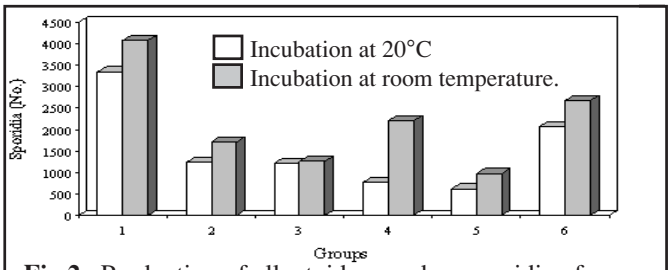

Fig 2. Production of allantoid secondary sporidia of *Tilletia indica* under two different icubation regimes (at 20°C in the dark and at 23–28°C with a 14-h photoperiod) by teliospores obtained from durum wheat cultivar Altar C84 and infeceted under natural conditions in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2002–2003.

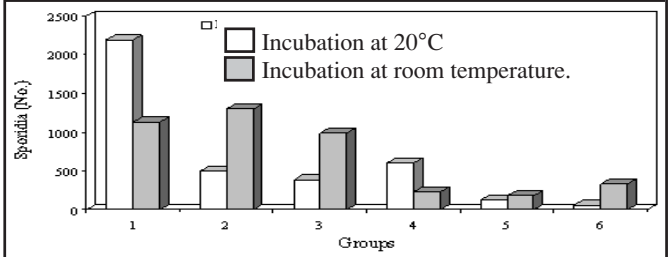

Fig 3. Production of allantoid secondary sporidia of *Tilletia indica* under two different icubation regimes (at 20°C in the dark and at 23–28°C with a 14-h photoperiod) by teliospores obtained from bread wheat cultivar Baviacora M92 and infeceted under natural conditions in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2002–2003.

This preliminary evaluation of sporidia production *in vitro*, indicates that although optimum temperature for teliospore germination is 15–25˚C, diminishing considerably below 5 and over 30˚C (Mitra 1935; Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1985), optimum temperature for sporidia production is between 24 and 26˚C (Smilanick et al. 1989). More experimentation is needed to determine: a) the effect of light on sporidia production, as Krishna and Singh (1982) and Zhang et al. (1984) have reported that light has a stimulatory germination effect on teliospores; and b) if the difference in sporidia production can be attributed to physiologic forms of *T. indica*.

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Evaluation of elite durum wheat genotypes for resistance to Karnal bunt under artificial field inoculation in the Yaqui valley, Sonora, Mexico, during the crop cycle 2004–05.

Guillermo Fuentes-Dávila and Karim Ammar.

Introduction. Karnal bunt occurs naturally on bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). Affected kernels are usually partially infected and completely infected ones are rare (Mitra 1935; Bedi et al. 1949; Chona et al. 1961). Durum wheat cultivars and advanced lines with resistance to Karnal bunt under artificial inoculations have been reported by Bedi et al. (1949) and Fuentes-Davila et al. (1992, 1993). Currently, durum wheat is the most important crop for the autumn-winter crop cycle in the southern part of Sonora state, Mexico; therefore, new elite lines and cultivars from the INIFAP-CIMMYT collaborative program should be evaluated for resistance to *T. indica*, in order to avoid possible economic problems for farmers by the release of a susceptible cultivar.

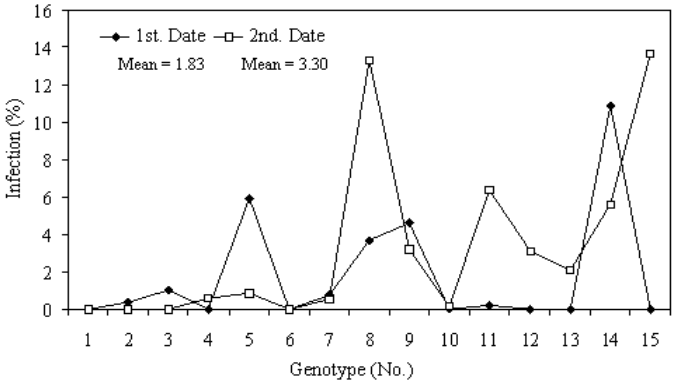

Fig. 4. Percentage of infection with Karnal bunt (*Tilletia indica*) of 15 durum wheat genotypes artificially inoculated in the field during the crop cycle 2004–05 on two dates in the Yaqui Valley, Sonora, Mexico.

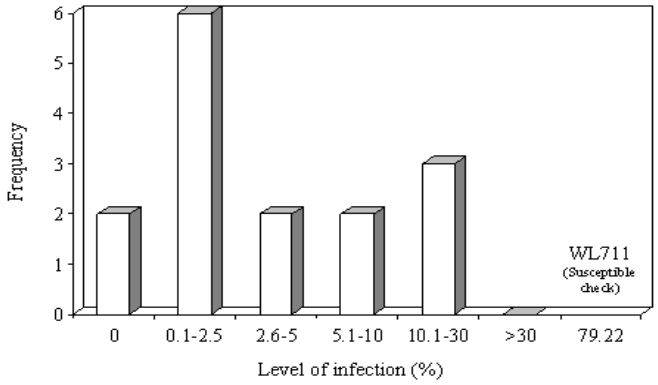

Fig. 5, Results of artificial field inoculation on two dates with Karnal bunt (*Tilletia indica*) of 15 durum wheat genotypes in the Yaqui Valley, Sonora, Mexico, during the crop cycle 2004–05. The level of infection of WL 711 is the mean of the three highest infection scores.

Materials and methods. Fourteen elite, durum wheat advanced genotypes and the cultivar Samayoa C2004 (pedigree: SOMAT_4/INTER_8; selection history: CDSS95B00181S-0M-1Y-0B-1Y-0B-0Y-0B-14EY-0Y) were evaluated for reaction to Karnal bunt during the crop cycle 2004–05. Planting dates were 10 and 28 November, 2004, using approximately 10 g of seed for a bed with two 1-m rows. A mist-irrigation system was used 3–5 times/day during 15 min each time to provide a humid environment in the experimental area. Inoculation was done by injection during the boot stage applying 1 ml of an allantoid sporidial suspension (10,000/ml) to ten spikes for each genotype. Harvest was done manually, and the evaluation and counting of healthy and infected kernels was by visual inspection.

Results and discussion. The range of infection for the first planting date was 0–10.85, with a

Table 3. Durum wheat genotypes with infection levels below 5 % of infected grain after artificial field inoculation with Karnal bunt in two planting dates, during the crop cycle autumn–winter 2004–05 in the Yaqui Valley, Sonora, Mexico.

Genotype No.	Pedigree
Lines with no infected grain	
1	Ajaia_12/F3Local(SEL.Ethio.135.85)//Plata_13/3/Somat_3/4/Sooty_9/Rascon_37 CDSS97Y00729S-0TOPM-2Y-0M-0Y-0B-0B-2Y-0BLR-2Y-0B
6	Ranco//CIT71/CII/3/COMDK/4/TCHO//SHWA/MALD/3/CREX/5/SN TURK MI83-84 375/ Nigris_5//Tantlo_1 CDSS97Y00614S-1Y-0M-0Y-0B-0B-5Y-0BLR-2Y-0B
Lines with 0–2.5 % infection	
2	CNDO/Primadur//HAI-OU_17/3/SN TURK MI83-84 375/Nigris_5//Tantlo_1 CDSS96Y01373T-0TOPM-2Y-0M-0Y-2B-0Y-0B-0B-0BLR-1Y-0B
3	Malmuk_1//Lotus_5/F3Local(SEL.Ethio.135.85) CDSS97B00455S-0M-4Y-0M-0Y-0B-0Y-0BLR-4Y-0B
4	Plata_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13 /8/THKNEE_11/9 CHEN/Altar 84/3/HUI/POC//BUB/RUFO/4/FNFOOT CDSS97Y01080T-0TOPM-3Y-0M-0Y-0B-0B-4Y-0BLR-3Y-0B
7	ROLA_5/3/Ajaia_12/F3Local(SEL.Ethio.135.85)//Plata_13/4/Malmuk_1/Serrator_1 CDSS97Y00966S-0TOPM-2Y-0M-0Y-0B-0B-1Y-0BLR-1Y-0B
10	1A.1D 5+10-6/2*WB881//1A.1D 5+10-6/3*MOJO/3/BISU_1/Patka_3 CDSS96B00540S-1M-0Y-3B-0Y-0B-0B-4Y-0M-0Y
13	USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/Ardente/7/HUI/YAV79/8/POD_9 CDSS96Y00484S-2Y-0M-0Y-2B-0Y-0B-0B-0BLR-2Y-0B
Lines with 2.6–5.0 % infection	
9	VanRikse_6.2//1A-1D 2+12-5/3*WB881 CDSS98Y00665S-0M-5Y-0M-0Y-0BLR-1Y-0B
12	Tarro_1/Yuan_1//Tarro_1/3/SN TURK MI83-84 375/Nigris_5//Tantlo_1 /5/CHEN_11/POC/ Tantlo/4/ENTE/MEXI_2//HUI/3/YAV_1/Gediz CDSS97Y01222T-0TOPM-2Y-0M-0Y-0B-0B-1Y-0BLR-1Y-0B

mean of 1.83; five lines did not have any infected grain (Fig. 4, p. 85). The range of infection for the second planting date was 0–13.66 with a mean of 3.30; four lines did not show any infected grains. The difference between the mean percent infection of the first and second planting dates and the mean of the three highest levels of infection of the susceptible check WL711 (79.22 %) was 77.39 and 75.92, respectively. Genotypes 1 and 6 did not show any infection in both planting dates (Table 3). Lines with less than 5 % infection are considered resistant (Fuentes-Dávila and Rajaram, 1994). Six lines had infection levels in category 0.1–2.5 %, two in 2.6–5.0 %, two in 5.1–10.0 %, and three in category 10.1–30.0 % (Fig. 5, p. 85). The cultivar Samayoa C84 had a range of infection of 3.71–13.31 with a mean of 8.51% (Fig. 4, genotype No. 8, p. 85). Although, results indicate that the high level of resistance to KB in durum wheat has been maintained in the new elite germ plasm coming out of the CIMMYT program, some genotypes are moderately susceptible, like cultivar Samayoa C84. Collaborative efforts between INIFAP and CIMMYT are continuing to ensure adequate levels of KB resistance in new promising material of durum wheat, in order to provide a commercially viable crop for the growers in the state of Sonora and maximize their access to export markets.

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Effect of Prothioconazole on seed germination from treated plots of the bread wheat cultivar Bacanora T88 after foliar application.

Irazema Fuentes-Bueno and Guillermo Fuentes-Dávila.

Introduction. Karnal bunt or partial bunt of wheat which is caused by the fungus *T. indica* and is an important disease of wheat seed and grain in the southern part of Sonora state, Mexico (Fuentes-Dávila 1997). Wheat is the most important crop in that region during the crop cycle autumn–winter, occupying approximately 200,000 ha with an average yield of 5 t/ha. Karnal bunt causes economic losses due to the effect on quality of seed, grain, and flour (Peña et al. 1992); quarantine regulations also have negative economic effects on farmers, seed producers, and the industry (Brennan et al. 1990). Because no commercial wheat cultivars are immune to the disease, the application of fungicides is an important component of the integrated control management. Based on the life cycle of the pathogen, application of fungicides during heading-flowering-anthesis provides good control of the disease that under certain conditions also is feasible economically (Salazar-Huerta et al. 1997). Fungicides reported to significantly control the disease include benomyl (Benlate), carbendazim (Bavistin), mancozeb (Dithane-M45), and fentin hydroxide (Duter) (Singh and Prasad 1980); triadimenol (Baytan) and triadimefon (Bayleton) (Singh and Singh 1985); propiconazole (Tilt), etaconazole (Vangard), mancozeb (Manzate), and copper hydroxide (Kocide) (Smilanick et al. 1987); propiconazole (Figueroa and Valdés 1991; Salazar-Huerta et al. 1997); propiconazole and epoxyconazole (Opus) (Figueroa-López and Alvarez-Zamorano 2000); and tebuconazole (Folicur) and propiconazole (Fuentes-Dávila et al. 2005).

Prothioconazole (Proline 250 EW or 480 SC) is a fungicide that belongs to the group that inhibits sterol biosynthesis, which is an effective tool for control of plant diseases (Kuck 2004). This product has been evaluated for Karnal bunt control in the collaborative INIFAP-CIMMYT Karnal bunt research program in the Yaqui Valley, Sonora, Mexico. A component of this project was to determine the effect of Prothioconazole on seed germination from treated plots of bread wheat after foliar application.

Materials and methods. The experiment was carried out in the Yaqui Valley, during the crop cycle Fall-Winter 2004-2005. Treatments (Table 4) were applied on bread wheat cultivar Bacanora T88, under a randomized complete block design with four replications (experimental unit was four beds with two rows each 3 x 0.80 m). Bacanora T88 is a susceptible cultivar to Karnal bunt. Inoculation was done by injection of 1 ml of a sporidial suspension of 10,000/ml during the boot stage (stage 49, Zadoks et al. 1974), on 20 spikes/replication. Fungicides were applied with a motorized Robin RS450 sprayer with four nozzles. During applications (2) (10 and 20 days after inoculation), 4 x 4-m plastic pieces were used to avoid carry over of product to other plots. After collection of inoculated spikes and spikes from the experimental plots for yield assessment, seed from the latter was used to evaluate germination twelve months after fungicide application. The seed was kept at room temperature during that period of time. For germination tests, five rows with five seeds (25) were placed on wet paper towel within plastic bags,

Table 4. Formulation and rates of Prothioconazole applied during flowering-anthesis on bread wheat (*Triticum aestivum*) cultivar Bacanora T88 for the control of karnal bunt (*Tilletia indica*) in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2004–05.

	Treatment	Formulation	Rate (g a.i./ha)
1	Prothioconazole	250 EW	100
2	"	250 EW	125
3	"	250 EW	150
4	"	480 SC	100
5	"	480 SC	125
6	"	480 SC	150
7	Propiconazole	250 EC	125
8	Untreated check		

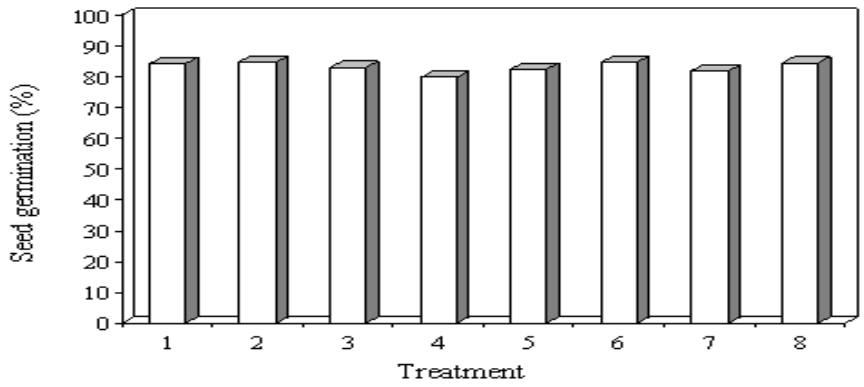

Fig. 6. Percent germination of seed from the bread wheat cultivar Bacanora T88 11 months after treatment with Prothioconazole (treatments 1–3: Prothioconazole 250 EW at 100, 125, and 150 g.a.i./ha, respectively; treatments 4–6: Prothioconazole 480 SC at 100, 125, and 150, respectively); Propicanazole 250 EC at 125; and an untreated check. Plants were grown during the 2004–05 crop cycle in the Yaqui Valley, Sonora, Mexico.

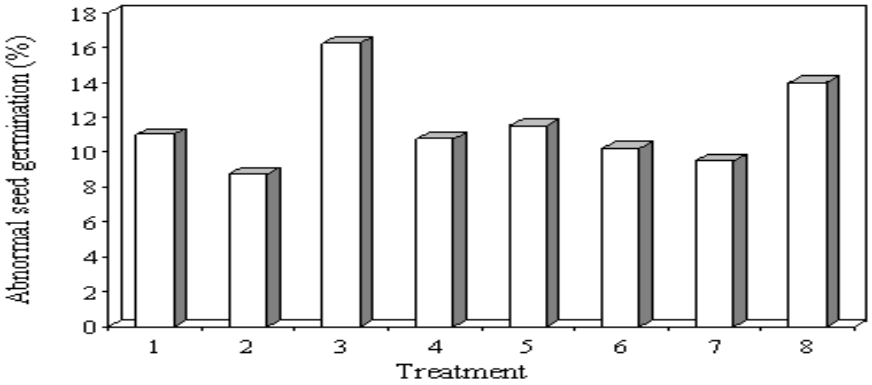

Fig. 7. Percent abnormal germination of seed from the bread wheat cultivar Bacanora T88 11 months after treatment with Prothioconazole (treatments 1–3: Prothioconazole 250 EW at 100, 125, and 150 g.a.i./ha, respectively; treatments 4–6: Prothioconazole 480 SC at 100, 125, and 150, respectively); Propicanazole 250 EC at 125; and an untreated check. Plants were grown during the 2004–05 crop cycle in the Yaqui Valley, Sonora, Mexico.

and incubated at room temperature (23–28˚C) with a 14-h photoperiod. Four replications were made per treatment. After 5 days, seed germination was evaluated by visual inspection, considering the initial growth of coleoptile and seminal roots as germinated. Abnormal seed germination was also registered as a possible indicator of negative effects of the fungicide on seed.

Results and discussion. The range of the average seed germination was 79.75–84.75 % with a mean of 83.15 % (Fig. 6). The untreated check had an average of 84.5 %, and the difference between the check and the various treatments was 0.25, 0.25 (Prothioconazole 250 EW, 125 g a.i./ha), 1.5, 4.75, 2, 0.25 (Prothioconazole 480 SC, 150 g a.i./ha), and 2.75 for treatments 1-7, respectively. The range of the average abnormal seed germination was 8.75–16.25 % with a mean of 11.50 % (Fig. 7). The untreated check had an average of 14 %, and the difference between the check and the various treatments was 3, 5.25, 2.25, 3.25, 2.5, 3.75, and 4.50 for treatments 1-7, respectively. Treatment 3 (Prothioconazole 250 EW, 150 g a.i./ha), which had the highest rate of the product in the EW formulation, showed the highest percentage of abnormal seed germination. This preliminary report indicates that Prothioconazole might have a negative effect on seed germination at high rates when applied as foliar spray and even after a long period of time after application and that plots for wheat seed production treated with other fungicides as foliar sprays should be evaluated for seed germination.

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Evaluation of elite triticale (X Triticosecale) genotypes for resistance to Karnal bunt under artificial field inoculation in the Yaqui valley, Sonora, Mexico, during the 2004–05 crop cycle.

Guillermo Fuentes-Dávila and Karim Ammar.

Introduction. The Karnal bunt fungus *T. indica* occurs naturally on bread wheat (Mitra 1931), durum wheat, and triticale (X *Triticosecale*; Agarwal et al. 1977). Affected kernels are usually partially infected and completely infected ones are rare (Mitra 1935; Bedi et al. 1949; Chona et al. 1961). Since the early 1980s, resistance and inmunity in triticale cultivars and experimental advanced lines under artificial inoculations were reported (Meeta et al. 1980; Fuentes-Davila et al. 1992). Advanced lines were selected primarily for their resistance to a new race of yellow rust that appeared in Central Mexico and to which most CIMMYT triticales are susceptible (Hede et al. 2002). Sources of resistance to this race also include progenies from crosses with either bread or durum wheat. The objective of this work was to evaluate twenty elite triticale genotypes for resistance to Karnal bunt.

Materials and methods. Twenty elite, advanced triticale genotypes were evaluated for Karnal bunt resistance during the 2004–05 crop cycle. Planting dates were 10, 18, and 26 November, 2004 using approximately 10 g of seed for a bed with two 1-m rows. A mist-irrigation system was used 3–5 times/day during 15 min each time to provide a humid environment in the experimental area. Inoculation was by injection during the boot stage applying 1 ml of an allantoid sporidial suspension (10,000/ml) to 10 heads/genotype. Harvest was done manually, and the evaluation and counting of healthy and infected kernels was by visual inspection. Tested genotypes included the long term yield check POLLMER TCL 2003, recently released as feed grain cultivar in the state of Sonora, and two new candidates for commercial release in the same state. These three genotypes are susceptible to yellow rust in central Mexico. The remaining 17 genotypes are new advanced lines selected for their resistance to yellow rust in the central Mexican highlands and internationally, representing the genotypic variability available in the current feed and forage triticale germ plasm of the CIMMYT program.

Results and discussion. The range of infection for the first planting date was 0–0.56, with a mean of 0.046. Eighteen lines did not have any infected kernels (Fig. 8, p, 90). No infected grains were obtained in the second date. For the third planting date the range of infection was 0–0.21 with a mean of 0.017. Eighteen lines did not show any infected grain. The difference between the mean percent infection of the first, second, and third planting dates and the mean of the three highest levels of infection of the susceptible check WL711 (79.22 %) was 79.17, 79.22, and 79.20 %, respectively. Only the lines SUSI_2/5/Tapir/Yougi_1//2*MUSX/3/Erizo_7/4/ Faras_1/6/Varsa_2/7/754.3/ IBEX//BUF_2 (CTSS98Y00367S-0M-4Y-0M-0Y-9B-2Y-0B), 804/BAT/3/MUSX/ LYNX//STIER_12-3/4/Varsa_3-1/5/Fahad_8-1*2//

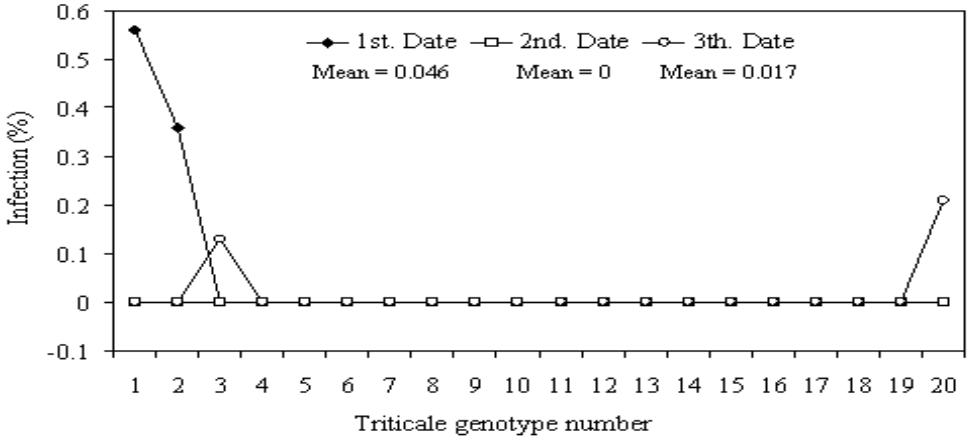

Fig. 8. Percentage of infection with Karnal bunt of 20 triticale (X Triticosecale) genotypes artificially inoculated on three dates during in the field during the 2004–05 crop cycle in the Yaqui Valley, Sonora, Mexico.

HARE_263/ Civet (CTSS98Y00236S-0M-1Y-0M-0Y-8B-1Y-0B), BAT*2/BCN//CAAL/3/ Erizo _7/Bagal_2// Faras_1 (CTSS99Y00246S-1Y-0M-0Y-5B-1Y-0B), and T1505_WG//Erizo_10/ BULL_1-1/3/Erizo_10/ BULL_1-1/4/COPI_1/5/ ARDI_1/TOPO1419// Erizo_9/3/SUSI_2 (CTSS00Y00759T-0TOPB-8Y-7M-1Y-3M-3Y-3M-6Y) fell within the 0–2.5 % infection category. Lines with less than 5 % infection are considered resistant (Fuentes-Dávila and Rajaram 1994). Sixteen lines did not have any infected kernels in the three evaluations (Table 5, p. 91). Genotypes 10, 11, and 12 did not have any infected kernels in previous evaluations (Fuentes-Dávila and Ammar 2005). These results indicate that the high level of resistance to KB in triticale has been maintained in the new elite germ plasm coming out of the CIMMYT program. Collaborative efforts between INIFAP and CIMMYT to ensure adequate levels of KB resistance in new promising material is being continued in order to provide a sound, safe, and commercially viable feed grain option for the growers in the State of Sonora.

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Evaluation of elite bread wheat lines and synthetic hexaploid wheat derivatives (T. turgidum subsp. turgidum/Aegilops tauschii//T. aestivum subsp. aestivum) for resistance to Karnal bunt.

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Introduction. *Tilletia indica* is the causal agent of Karnal bunt of wheat (Mitra 1931). Control of this pathogen is difficult because teliospores are resistant to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1988). Chemical control can be accomplished by applying fungicides during flowering (Fuentes-Dávila et al. 2005). However, this measure is not feasible when quarantine does not allow tolerance levels for seed production.

Table 5. Triticale genotypes that did not show any infected kernels after artificial field inoculation with Karnal bunt (*Tilletia indica*) on three planting dates, during the 2004–05 crop cycle in the Yaqui valley, Sonora, Mexico.

Genotype No.	Pedigree
4	T1502_WG/Moloc_4//Rhino_3/BULL_1-1/3/Pollmer_3/FOCA_2-1 CTSS99Y00231S-1Y-0M-0Y-5B-1Y-0B
5	GAUR_2/HARE_3//JLO 97/Civet/5/DISB5/3/SPHD/PVN//Yogui_6/4/KER_3/6/150.83//2*Tesmo_1/MUSX 603/7/GAUR_2/HARE_3//JLO 97/Civet CTSS99B00185S-0M-7Y-10M-1Y-0M
6	Dahbi_6/3/ARDI_1/TOPO 1419//Erizo_9/4/2*Zebra 79/LYNX*2//Fahad_1 CTSS99B00862M-0TOPY-0M-3Y-7M-1Y-0M
7	Erizo_10/2*BULL_1-1//CAAL/4/2*PACA_2/COPI_1-1/3/ARDI_1/TOPO 1419/Erizo_9 CTSS99B00872M-0TOPY-0M-5Y-1M-1Y-0M
8	Pollmer_2.2.1*2//Faras/CMH84.4414 CTSS99B00990F-0TOPY-0M-2Y-10M-1Y-0M
9	Sonni_3*2//Faras/CMH84.4414 CTSS99B00998F-0TOPY-0M-1Y-12M-2Y-0M
10	Presto//2*Tesmo_1/MUSX 603/4/ARDI_1/TOPO 1419//Erizo_9/3/SUSI_2 CTSS94Y00465T-C-2M-0Y-0B-1Y-0B-2B-0Y
11	Pollmer_2.1.1 CTY88.547-22RES-1M-0Y-2M-1Y-0M-1B-0Y
12	Liron_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/Manati_1 CTSS94Y00486T-E-1M-0Y-0B-1Y-0B-4B-0Y
13	ARDI_1/TOPO 1419//Erizo_9/3/Liron_1-1/4/Fahad_4/Faras_1 CTSS95B00243S-19M-0Y-0B-0Y-0B-7B-0Y-7B-0Y
14	Presto//2*Tesmo_1/MUSX 603/4/ARDI_1/TOPO 1419//Erizo_9/3/SUSI_2/5AR/SNP6//Tarasca 87_2/C,S10/3/Porsas_4-1/4/Chacal_3-2 CTSS01Y00150S-4Y-010M-6Y-2M-5Y
15	Dahbi_6/3/ARDI_1/TOPO 1419//Erizo_9/4/Dagro/IBEX//Civet#2/5/Fahad_5/Pollmer_3 CTSS01Y00519T-0TOPB-20Y-010M-3Y-8M-6Y
16	Dahbi_6/3/ARDI_1/TOPO 1419//Erizo_9/4/Rondo/BANT_5//Anoas_2/5/LAD 622.81/Porsas_4-1/3/ARDI_1/TOPO 1419//Erizo_9 CTSS00B00426T-0TOPY-0M-5Y-010M-3Y-1M-5Y
17	Faras_2*2/Walrus_1-3//Pollmer_3.5.1/3/Erizo_7/Bagal_2//Faras_1 CTSS99Y00738T-0TOPB-0Y-0M-4Y-5M-4Y-6M-5Y
18	GAUR_2/HARE_3//JLO 97/Civet/5/DIS B5/3/SPHD/PVN//Yogui_6/ 4/KER_3/6/150.83//2*Tesmo_1/MUSX 603/7/Fahad_8-2*2//PTR/PND-T/8/Pollmer_3/FOCA_2-1 CTSS00Y00766T-0TOPB-9Y-13M-2Y-5M-2Y-6M-6Y
19	Dahbi/Coati_1//Erizo_11*2/Milan/3/Pollmer_2//Erizo_11/Yogui_3 CTSS00Y00939T-0TOPB-4Y-3M-1Y-5M-4Y-1M-5Y

The susceptibility of bread wheat has been documented (Fuentes-Dávila et al. 1992, 1993) reaching infection levels above 50 % under artificial inoculation. However, bread wheats that have consistently shown low infection levels are known to occur (Fuentes-Dávila and Rajaram 1994). Resistance sources are also known in durum wheat and triticale germplasm under natural and artificially inoculated conditions (Bedi et al. 1949; Fuentes-Davila et al. 1992). Villareal et al. (1994) reported that 49 % of the synthetic hexaploids (SH) evaluated during three crop cycles under artificial inoculation, were immune to the disease. Villareal et al. (1996) registered four SHs as immune sources. The resistant reaction appears to be conferred by the genetic base of *Ae*. *tauschii* and *T*. *turgidum* subsp. *turdigum*. The objective of this work was to evaluate elite bread wheat lines, synthetic hexaploid wheat derivatives, commercial cultivars, and candidates for release for resistance to Karnal bunt under artificial inoculation.

Materials and methods. One hundred and two elite bread wheat lines and synthetic hexaploid wheat derivatives, four commercial cultivars, and two candidates for release were evaluated for resistance to Karnal bunt during the 2004–05

autumn–winter crop cycle in the Yaqui valley, Sonora, Mexico. Planting dates were 10 and 28 November, 2004, using approximately 10 g of seed on 1-m beds with two rows. A mist-irrigation system was used 3 to 5 times each day for 15 min each time to provide high relative humidity in the experimental area. Inoculations were carried out by injecting 1 ml of an allantoid sporidial suspension (10,000/mL) during the boot stage on 10 heads/line. Only lines, cultivars, and candidates for release that had 5 % infection or less were evaluated on the second planting date. Harvest was done manually, and the counting of healthy and infected grains was by visual inspection to calculate the percentage of infection (infected grains).

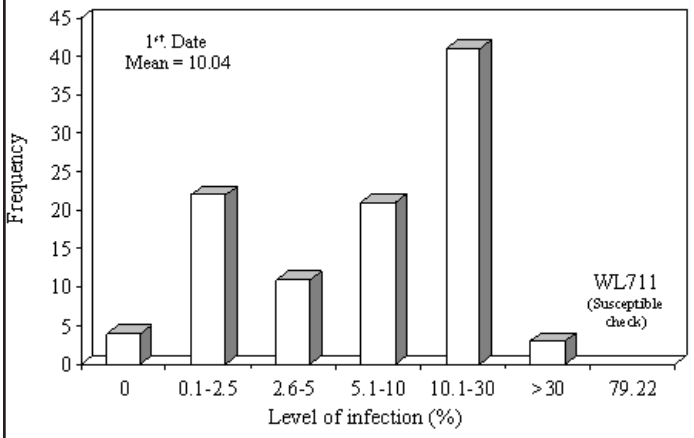

Fig. 9. Results of artificial field inoculation with Karnal bunt at the first planting date (10 November) of 102 elite, bread wheat lines and synthetic hexaploid whet derivatives (*T. turgidum* subsp. *turgidum*/*Ae*. *tauschii*//*T. aestivum* subsp. *aestivum*) in the Yaqui Valley, Sonora, Mexico, during the 2004–05 crop cycle. The level of infection of WL 711 is the mean of the three highest infeciton scores.

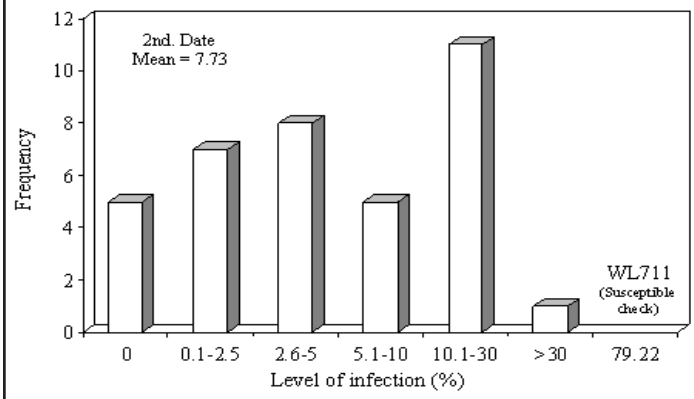

Fig. 10. Results of artificial field inoculation with Karnal bunt at the second planting date (28 November) of 102 elite, bread wheat lines and synthetic hexaploid whet derivatives (*T. turgidum* subsp. *turgidum*/*Ae*. *tauschii*//*T. aestivum* subsp. *aestivum*) in the Yaqui Valley, Sonora, Mexico, during the 2004–05 crop cycle. The level of infection of WL 711 is the mean of the three highest infeciton scores.

Results and discussion. The range of infection for the first planting date was 0–45.48 %, with a mean of 10.04 %. Four lines did not have infected grain (Fig. 9). Twenty-two lines were within the category of 0.1–2.5 % infection, 11 in 2.6–5.0 %, 21 in 5.1–10.0 %, 41 in 10.1–30 %, and 3 had more than 30 % infection. The susceptible check had 79.22 % infection. Thirty-seven lines with 5 % infection or less were evaluated in the second planting date. The range of infection was 0–41.73 % with a mean of 7.73. Five lines did not have infected grain, 7 were within the 0.1–2.5 % infection category, 8 were 2.6–5.0 %, 5 were 5.1–10.0 %, 11 were 10.1–30 %, and one had more than 30 % infected grain (Fig. 10). Fifty-four percent of the lines originally classified as resistant were resistant in the second planting date (Fuentes-Dávila and Rajaram 1994), which emphasizes the importance of several planting dates in order to avoid escapes (Fuentes-Davila 1997). Only the line, CROC_1/*Ae*. *tauschii* (205)//KAUZ/3/Attila (CMSS93Y01031S-13Y-5KBY-010M-010Y-8M-0KBY-0M), did not have infected grain on both dates (Table 6, p. 93). Seven lines (five are sister lines of CROC_1/*Ae*. *tauschii* (205)//KAUZ/3/Attila) had 0.1-2.5% infection levels and eleven 2.6–5.0 % (seven of these lines have *Ae*. *tauschii* in the pedigree). Cultivars Tacupeto F2003, Tarachi F2000, and Wheatear, a candidate for release, had 26.45, 18.37, and 19.86 % infection, respectively, in the first planting date and were not further evaluated. Only the cultivar Kronstad F2003 showed levels of infection below 5 % on both dates with a mean of 2.68 %, whereas Rayon F89 and Berkut, another candidate for release, had 8.94 and 28.51 % infection, respectively, on the second planting date. Our results show that synthetic-derived bread wheats provide a new level of resistance, almost immunity to Karnal bunt.

Table 6. Bread wheat lines and synthetic hexaploid wheat derivatives (*T. turgidum* subsp. *turgidum*/*Ae. tauschii*//*T. aestivum* subsp. *aestivum*) with infection levels below 5 % after artificial field inoculation with Karnal bunt (*Tilletia indica*) at two planting dates during the 2004–05 autumn–winter crop cycle in the Yaqui Valley, Sonora, Mexico.

Line No.	Pedigree
Lines that did not show any infected grain.	
27	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-13Y-5KBY-010M-010Y-8M-0KBY-0M
Lines with 0.1–2.5 % infection.	
23	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-13Y-5KBY-010M-010Y-5M-0KBY-0M-4KBY-0Y-0KBY
24	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-13Y-5KBY-010M-010Y-5M-0KBY-0M-9KBY-0Y-0KBY
26	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-13Y-5KBY-010M-010Y-6M-0KBY-0M-0KBY-0M-0KBY
28	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-13Y-5KBY-010M-010Y-9M-0KBY-0M
29	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-13Y-5KBY-010M-010Y-9M-0KBY-0M-0KBY
70	INIF97/SW91.4903//Weaver CMSS96M05066T-040Y-050M-040Y-0100M-020Y-9M-0Y-3M-0Y
82	SARA/THB//VEE/3/VEE/PJN//2*KAUZ CMSS97Y00594S-040Y-050M-020Y-030M-16Y-2M-0Y
Lines with 2.6–5.0 % infection.	
14	Bonasa CMSS92GH00064M-13GH-3B-5KBY-1KBY-010M-5Y-3M-0KBY-0M-4KBY-0KBY-0M-0KBY
16	CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/Weaver/5/Picus CMSS93Y00854S-14Y-2KBY-010M-010Y-10M-0KBY-0M-6KBY-0Y-0KBY
20	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Sasia CMSS93Y01001S-12Y-1KBY-010M-010Y-1M-0KBY-0M-12KBY-0Y-0KBY
22	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Sasia CMSS93Y01001S-12Y-1KBY-010M-010Y-9M-0KBY-0M-10KBY-0Y-0KBY
32	CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila CMSS93Y01031S-14Y-3KBY-010M-010Y-6M-0KBY-0M-7KBY-0Y-0KBY
33	PASTOR/3/VORONA/CNO79//KAUZ CMSS93B00303S-6Y-010M-010Y-010M-5Y-0M
40	CROC_1/*Ae. tauschii* (205)//BORL95/3/2*Milan CMSS93B01879M-040Y-1Y-010M-010Y-010M-7Y-0M-0KBY
42	Pastor//TRAP#1/BOW/3/CHEN/*Ae. tauschii* (TAUS)//BCN CMSS94Y02321T-030Y-0300M-0100Y-0100M-9Y-6M-0Y-0KBY
45	CHEN/*Ae. tauschii* (TAUS)//BCN/3/BAV92 CMSS95Y00539S-3Y-010M-010Y-010M-39Y-0Y-1M-0Y
47	HAHN/2*Weaver/4/BOW/CROW//BUC/PVN/3/2*VEE#10 CMSS95Y00630S-0100Y-0200M-12Y-010M-7Y-0Y-1M-0Y
83	SARA/THB//VEE/3/VEE/PJN//2*KAUZ CMSS97Y00594S-040Y-050M-020Y-030M-18Y-2M-0Y

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