III. CONTRIBUTIONS

PRIVATE COMPANIES

AGRIPRO WHEAT – SOUTHEASTERN USA
P.O. Box 2365, Jonesboro, AR 72402-2365, U.S.A.
www.agriprowheat.com

J. Barton Fogleman, Michael Montgomery, and Christopher DeArmond.

We expanded our research station at Jonesboro, AR, by adding a new greenhouse, a new equipment shed, additional office space, and an ocean-going container (for seed fumigation and storage) in 2003.

A new SRWW cultivar, **AgriPro Savage**, was released to midsouth wheat producers in the autumn. AgriPro Savage has midseason maturity and is resistant/moderately resistant to the soil virus complex (SBMV–WSSMV) and to the current races of leaf and stripe rust. Savage also has very good test weight. Savage is a good complement to our 2002 release, AgriPro Natchez, which is becoming popular with midsouth wheat producers due to its overall strong disease resistance package.

We are continuing our efforts to develop Clearfield wheats in coöperation with BASF. Although AP112CL was withdrawn due to stripe rust susceptibility and lack of performance, several new candidates were identified and our Clearfield wheat testing continues.

We also have been active the past 3 years in attempting to establish Identity Preserved wheat programs in Alabama and Georgia that would pay wheat producers premium incentives to grow a specific wheat variety for a specific customer. Progress is slow, but we are aware that changes of this type are difficult and we are persistent and committed.

DAKOTA GROWERS PASTA COMPANY
One Pasta Avenue, P.O. Box 21, Carrington ND 58421, U.S.A.

James Quick and Brad Miller.

Dakota Growers Pasta Company launched its durum breeding program in 2003. DGPC has been working with Quick and WestBred, LLC to conduct field trials, including research on FHB resistance, which has been causing durum quality and grain-yield problems. DGPC is developing durum wheats with specialized quality to fill niche or identity-preserved markets. The company already has pasta customers that request specialized semolina. DGPC's breeding program hopes to develop further collaboration with the durum breeding programs at North Dakota State University and elsewhere. Organized in 1991 as a coöperative of durum wheat growers, Dakota Growers Pasta is the third largest producer of dry pasta products in North America and is the leading supplier of retail store brand pasta and a leader in the foodservice and ingredient pasta markets.

The breeding and agronomy program conducted trials at six locations in ND in 2003, and will evaluate early generation materials at northern and southern locations. The greenhouse is used for crossing and single-seed descent programs during the winter. Several sources of resistance to FHB are contributing genes for pyramiding. Quality and FHB-resistance tests are contracted with public and private agencies. The company will launch its first durum variety, **Primo Doro**, with Westbred, LLC in 2004.

OR SEED BREEDING CO.
Rua João Battisti, 71 – Paso Fundo, RS–CEP, 99050-380, Brazil.

A. Rosa, O.S. Rosa and O. Rosa-Filho.

Wheat production in Brazil almost doubled in 2003 compared to 2002. The increase to more than 5 x 10^6 tons of production is explained mostly by excellent weather conditions but also is due to a small increase in acreage and the availability of responsive technology. Even though Brazil continues to be a big wheat importer, it exported about 1 x 10^6 tons in 2003–04. Exporting wheat was an important achievement that allowed production to continue to be economically attractive at a production range of 5–6 x 10^6 tons.

A wheat leaf rust laboratory for the identification of races and virulence was recently installed to supply information to the OR breeding program. The emphasis is on durable resistance.

OR has released four cultivars in the last 2 years. In 2003, **Pampeano** and **Safira** were released for the state of Rio Grande do Sul and, in 2004, **Supera** and **Vanguarda** were released for the state of Paraná. The release of Pampeano (ORL91274/ORL93807//ORL95711's' (ORL95711's' = BR35//BR14*2/Sumai#3/OR1)) has been expected by farmers since 2000, when it showed excellent resistance to scab. Safira (PF9099/OR1//Granito) is an important improvement in terms of yield over currently grown cultivars such as Rubi and Ônix while maintaining the bread-making quality of these two cultivars. Supera's (PF9099/OR1) main attribute is its excellent yield performance. Vanguarda is an OR1 backcross and replacement, offering advantages over OR1 in grain quality and various agronomic attributes.

The cultivar Ônix (CEP24/Rubi), released in 2001 for cultivation in Rio Grande do Sul and Paraná, has performed well from southern Argentina (37°S) to central Brazil (Cerrado; 15°S). In 2003, Ônix became one of the most cultivated materials in Rio Grande do Sul (28°S). Currently, about 20 % of Brazilian wheat production is based on OR cultivars.

ITEMS FROM ARGENTINA

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

Bread-making quality in wheat lines after six cycles of recurrent selection.

Z. Gaido and M.E. Dubois.

For the second year, we have evaluated the effects in wheat lines of six cycles (C_0 to C_6) of recurrent selection on bread-making quality of 12 commercial bread wheat cultivars. No significant differences were observed in the bread-making quality between derivatives of C_0 and C_6 lines (Table 1, p. 18). The contrast among the value means of the C_6 cycle and that of the commercial cultivars was significant in three of the four analyzed variables, the C_6 values being superior in all cases (Table 1).

Mixograph dough development time (MDDT) of the 96 analyzed genotypes (12 for each cycle) are presented in the Table 2 (p. 18). For the best interval MDDT (3.5–5.5), a proportion of the 75 % is observed in the C_6, proportion only overcome by the wheat commercial cultivars (83 %).

Of the results corresponding to baking-quality parameters, we observed that after six cycles of recurrent selection, quality did not suffer significant changes. Coincident results were obtained after two cycles (Dubois et al. 1998) and three cycles (Gaido et al. 2000) of recurrent selection. We are planning, however, to recycle agronomic and qualitatively superior genotypes, such as improving the qualitative profile of the germ plasm subject to improvement genetics.

Table 1. Parameters of bread-making quality during 2002 after six cycles of recurrent selection and for wheat commercial cultivars.

Cycles of recurrent selection	Grain protein (%)	Gluten (%)	High mixograph (unid)	Mixograph dough developement time (min)
C_0	12.30 bc	28.72 bc	6.55 b	5.26 bc
C_1	12.55 b	28.51 bc	6.51 b	5.63 c
C_2	12.27 bc	29.37 bc	6.76 b	4.80 bc
C_3	11.75 c	26.76 c	6.43 b	5.16 bc
C_4	12.39 bc	31.33 ab	7.39 b	3.60 a
C_5	12.10 bc	28.38 bc	6.83 b	5.20 bc
C_6	12.19 bc	27.70 c	6.60 b	5.12 bc
commercial cultivars	13.51 a	33.21 a	7.68 a	4.,05 ab

a–c: Different letters denote means statistically different at $P < 0.05$ according Duncan's Test.

Table 2. Mixograph dough development time (MDDT) after six cycles of recurrent selection and for commercial wheat cultivars.

Cycles of recurrent selection	MDDT < 3.5	3.5 > MDDT < 5.5	MDDT > 5.5
C_0	2	5	5
C_1	1	7	4
C_2	2	7	3
C_3	0	8	4
C_4	5	7	0
C_5	1	7	4
C_6	0	9	3
commercial cultivars	2	10	0

References.

Dubois ME, Gaido ZA, Manera GA, and Maich RH. 1998. Evaluación del efecto de dos ciclos de selección recurrente por rendimiento en semilla sobre la calidad panadera en trigos (*Triticum aestivum* L.) aptos para la región semiárida del centro de Argentina. Phyton **62**(1/2):167-174 (In Spanish).

Gaido ZA, Maich RH, and Dubois ME. 2000. Calidad panadera en líneas de trigo pan con crecientes rendimientos potenciales en semilla. Phyton **69**:85-90 (In Spanish).

Effect of a compost suspension extract on imbibition in wheat seed on initial seedling vigor.

R. Maich, I.M. Lorello, L.E. Torres, R. Rolando, and L. Torres.

Compost contains organic matter in an intermediate state of decomposition with respect to the humus and, likewise, it improves the biological, chemical, and physical properties of amended soils. The objective of this study was to measure the effects of several extracts obtained from compost suspensions on the development of wheat seedlings. The compost was obtained from the leaves of deciduous trees (*Populus* spp.) collected in the city of Córdoba. Seeds of the wheat cultivar Baguette 10 were imbibed in a compost suspension extract with and without a heat treatment. Seedlings derived from treated seeds possessed a longer first leaf. The seminal root number was higher in those seedlings derived from seeds imbibed in a 1:5 compost:water extract without a heat treatment. The length of the first leaf of the seedlings and of the main seminal root derived from artificially aged seeds increased when the seeds were immersed in a compost extract. These results will help to establish the real relationship between early vigor and grain yield related characters.

Publication.

Maich R, Lorello IM, Torres LE, Rolando R, and Torres L. 2003. Efecto de la imbibición de semillas de trigo en extracto de suspensión de compost maduro sobre el vigor inicial de las plántulas. Agriscientia **XX**:89-94 (In Spanish).

The effects of plant breeding on the number of floret primordia and fertile florets and morphological characteristics of the flag leaves in bread wheat.

S.P. Gil, R.H. Maich, and M.M. Cerana.

Currently, we are working with six cycles (C_0 to C_6) of recurrent selection in order to evaluate the effects of plant breeding on the number of floret primordia and fertile florets and three morphological characteristics of flag leaves, i.e., length, width, and area. The plants were grown at the Experimental Farm of the College of Agriculture (31°29' S and 64°00' W), Córdoba, Argentina, during 2002.

We compared the following cycles: C_0 (initial); C_1, C_2, C_3, C_4, and C_5 (intermediate); and C_6 (more evolved). Five spikes of the main shoot were divided into thirds (lower third, spikelets 4 and 5; middle third, spikelets 9 and 10; and upper third, subterminal spikelet), and five flag leaves from each of 12 S-derived families/populations were studied. Data were evaluated with ANOVA and Duncan's Multiple Range Test.

The results indicated that the C_4 mean values were higher than the other cycles except for the floret primordia and fertile florets in the lower third, regardless of the degree of significance. Plants from the more evolved cycle (C_6) did not perform better than those from other cycles.

A new, experimental wheat line.

R. Maich, D. Ortega, G. Astolfi, R. Argenti, and G. Manera.

We investigated the existence of trait variability between genotypes and estimated to what extent the new genotypes are better than standard cultivars. The different traits that influence yield were investigated using nine wheat breeding lines and cultivars (genotypes). The experiment was set in a randomized, complete-block design with four replications on a basic plot of 5 m^2 in 2003. Grain yield and its components were measured for each experimental unit. The results showed considerable variation for all measured traits and are very promising if we compare the new genotype C3-00-42 and four Argentinian cultivars. For example, a significant increase of 16 % was achieved for grain yield, and a similar tendency was observed for biological yield and grain number/m. These results are for the first year of a 3-year study. Simultaneously, we will evaluate the new genotype C3-00-42 under conditions in the farmers' field.

Publications.

Gil SP, Cerana MM, and Maich RH. 2003. Efecto de un programa de selección recurrente en trigo sobre el número de flores por espiga. Boletín de la Sociedad Argentina de Botánica **38**:289 (Abstract, in Spanish).

Gil SP, Manera G, Dubois ME, and Maich RH. 2003. Spike changes associated to six cycles of recurrent selection in bread wheat (*Triticum aestivum* L.) Agriscientia **XX**:95-98.

Maich R and Ordoñez A. 2003. Improved meiotic index in hexaploid triticale (*Triticosecale* Wittmack). Cytolologia **68**:303- 306.

Maich R, Torres LE, Manera GA, and Dubois ME. 2003. Grain yield improvement in bread wheat after three cycles of recurrent selection. J Genet Breed **57**:in press.

Ortega D, Chaves G, Astolfi G, and Maich R. 2003. Cambios en la espiga de trigo (*Triticum aestivum* L.) asociados a seis ciclos de selección recurrente. Basic Appl Genet **XV**(2):120 (Abstract, in Spanish).

Evaluating two criteria for selecting S_0 progenies in bread wheat and triticale.

G. Chaves, M.C. Coraglio, B. Costero, L.E. Torres, and R. Maich.

The objective of this research was to evaluate the actual grain yield advances in bread wheat and hexaploid triticale using two selection indices.

18-character selection index. For each trait measured at the plot or sample level and taking into account the direction of selection, the progeny mean value was compared to the corresponding 131 C_2S_0 (hexaploid triticale) or 121 C_5S_0 (bread wheat) sample mean values with respect to the controls. One (morphological) or two (physiological and physical) points were assigned when the performance of the progeny was agronomically superior to that for the reference mean value. An additional point was assigned if the frequency of superior progenies with respect to the reference mean value was less than 25 %. The score/S_0 progeny was estimated and disruptive selection intensities of 7.6 % (triticale) and 8.3 % (bread wheat) were applied in each sense for the selection index variable.

11-character selection index. For each trait measured at plot level, the progeny mean value was compared to the corresponding 142 C_3S_0 (hexaploid triticale) or 89 C_6S_0 (bread wheat) sample mean values (=100). The score/S_0 progeny was obtained as the sum of the 11 percentages (positives and negatives). A disruptive selection intensity of 7.0 % (triticale) and 11.2 % (bread wheat) was applied in each sense for the selection index variable.

For both indices, 20 S_1 triticale families (10/group) and 20 S_1 bread wheat families (10/group) were evaluated under rainfed conditions at the Experimental Farm of the College of Agriculture. Complete, randomized designs with two replications were used. The characters measured on a plot basis were grain and above-ground biological yield (g/m^2), spike number/m^2, 1,000-kernel weight (g), harvest index (%), and grain number/m^2. For each trait, the differential (ds) and the response to selection (RS) were estimated from the S_0 progenies and S_1-derived families, respectively, as the mean difference (in percent) between higher and lower (=100) selection index groups. Two over six (triticale) and four over six (bread wheat) RS and ds coincidences were observed for the 18-character selection index**;** whereas, six over six RS and ds coincidences were observed in both species for the 11-character selection index**.**

Taking into account the results of multiple trait selection in triticale and bread wheat, we propose to reduce the number of traits included in the selection index in order to obtain more equilibrate multiple trait response.

Effects of Azospirillum brasilense inoculation on agronomic performance in wheat.

L. Dubini, R. Maich, and A. Abril.

Many microorganisms are capable of N_2 fixation. Some are free-living organisms such as bacteria and cyanobacteria. One of the nonsymbiotic associations involves grasses and nitrogen-fixing bacteria of the genus *Azospirillum*. *Azospirillum* spp. are interesting plant growth promoting rhizobacteria. We determined the effect of an *A. brasilense* inoculant on grain yield and its principal component grain number/m^2. Nine genotypes of bread wheat with different biological cycles (early and late heading) were inoculated. Preliminary results show a significant, negative relationship between the seeding–heading interval in days and a difference between inoculated and uninoculated (= 100) material. Rainfed conditions and the occurrence of a terminal drought stress probably are responsible for the specific and positive association between *A. brasilense* and earlier heading wheat genotypes.

ITEMS FROM AUSTRALIA

QUEENSLAND

CENTRE FOR RURAL & ENVIRONMENTAL BIOTECHNOLOGY
Faculty of Sciences, University of Southern Queensland, Toowoomba, QLD 4350, Australia.
www.usq.edu.au/creb/

Generation and evaluation of transgenic wheat for frost tolerance.

Grant Daggard, Joan Vickers, Mark Sutherland, and Rob Learmonth.

Frost damage is a significant but unpredictable threat to spring wheat grown in Australia. Reducing frost risk by delaying planting reduces yields by up to 10 % annually. Conventional approaches to breeding for increased resistance have yet to be successful. This project, funded by Grains Research and Development Corporation (GRDC), aims at using a genetic approach to provide frost resistance via the introduction of novel genes that inhibit ice formation and/or ameliorate its effects on the wheat plant during flowering. Initial *in vitro* tests of transformed plants indicate a potential for improved frost tolerance that will be further evaluated by whole-plant testing.

Black point: marker development and gene isolation.

Grant Daggard, Yihua Chen, Anke Lehmensiek, Mark Sutherland, Peter Williamson, and Miram Michalowitz.

Black point results in the discoloration of the embryo end of the grain and is associated with elevated humidity during grain development. A significant problem in most Australian wheat-growing areas, black point can cause losses of up to $50 x 10^6 annually. This GRDC-funded project between the University of Southern Queensland and the Leslie Research Centre aims to locate molecular markers associated with black point resistance/susceptibility, which would allow rapid and reliable screening in breeding programs throughout Australia. A second objective is to obtain information on the actual genes involved in the symptoms of black point via use of ESTs for a better understanding of the underlying causes of the disease and to identify candidate genes.

Molecular markers for wheat quality attributes and disease resistance.

Mark Sutherland, Bert Collard, Anke Lehmensiek, Grant Daggard, and G. Wildermuth.

This project will develop molecular markers for use in commercial breeding programs. Attributes of particular interest are those for whom phenotypic screening is expensive, time consuming, and strongly influenced by G x E interactions. Quality attributes of particular interest are milling yield, flour color and color stability, preharvest sprouting tolerance, water absorption, and extensibility. As part of our research into quality QTL, we are analyzing and refining wheat maps and phenotypic data sets accumulated within the Australian Winter Cereals Molecular Marker Programme.

Crown rot is a major constraint on wheat, barley, and durum production in the Northern Region grains belt. We recently have made major advances in identifying QTL that are linked to partial disease resistance in some hexaploid wheat sources. QTL from these different sources are being pyramided in an attempt to develop lines possessing improved resistance for commercial breeding.

Publications.

Chalmers KJ, Campbell AW, Kretschmer J, Karakousis A, Henschke PH, Pierens S, Harker N, Pallota M, Cornish GB, Shariflou MR, Rampling LR, McLauchlan A, Daggard G, Sharp PJ, Holton TA, Sutherland MW, Appels R, and Langridge P. 2001. Construction of three linkage maps in bread wheat, *Triticum aestivum*. Aus J Agric Res **52**:1089-1119.

Chen Y, Weining S, and Daggard G. 2003. Preparation of total RNA from a very small wheat embryo suitable for differential display. Ann Appl Biol **143**(2):261-264.

Daggard G and Appels R. 2002. Parental chromosome inheritance in wheat DH's. **In:** Proc 12th Aus Plant Breed Conf, Perth, Australia. Pp. 691-695.

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Kammholz SJ, Campbell AW, Sutherland MW, Hollamby GJ, Martin PJ, Eastwood RF, Barclay I, Wilson RE, Brennan PS, and Sheppard JA. 2001. Establishment and characterisation of Wheat Genetic Mapping Populations. Aus J Agric Res **52**:1079-1088.

Khanna HK and Daggard GE. 2001. Enhanced shoot regeneration in nine Australian wheat cultivars by spermidine and water stress treatments. Aus J Plant Physiol **28**:1243-1247.

<u>SOUTH AUSTRALIA</u>

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

Research Interests.

Daryl Mares, Kolumbina Mrva, Robert Asenstorfer, Richard Leach, and Anuja Kumaratilake.

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. Our research aims to identify the environmental factors that trigger development of grain defects; identify tolerant genotypes and QTL/genes associated with tolerance; develop a better understanding of the mechanisms involved in tolerance; devise accurate and more effective phenotyping procedures based on field, controlled-environment, and biochemical screening; develop and validate molecular markers for tolerance; introgress tolerance into elite, locally adapted germ plasm; assist wheat breeders to incorporate new traits into breeding programs; and provide reliable information on wheat cultivars to wheat growers.

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, and lipoxygenase), nutritive aspects of cereal xanthophylls (lutein and lutein esters). This research aims to identify and quantify the biochemical constituents, enzymes and interactions that influence quality, specifically color, and, hence, the marketability of noodles; develop efficient, small-scale screening technologies for color and color constituents; identify QTL/genes associated with control of color components; develop and validate molecular markers for critical traits; and exploit available genetic variation, mutations, and synthetic wheats to develop wheat genotypes with improved or novel characteristics.

Preharvest sprouting tolerance.

Daryl Mares and Kolumbina Mrva.

Preharvest sprouting periodically causes massive losses to the Australian wheat industry and affects all states, albeit with different frequency. Cultivar improvement, using dormancy from older white-grained genotypes introduced from South Africa and, more recently, landraces from China, has proven to be quite difficult due to inefficient screening techniques, strong environmental effects, a complex mode of inheritance, and a need for extensive capital and labor infrastructure. Despite these obstacles, parental germ plasm has now been developed that combines sprouting tolerance (tolerance equivalent to the South African parental genotype AUS1408) with black point tolerance, absence of LMA, and low polyphenol oxidase in a locally adapted, semidwarf background. A major QTL associated with dormancy in this germ plasm corresponded to a QTL on chromosome 4A previously identified in the partially dormant Australian white wheat Halberd, and in some dormant red-grained cultivars overseas. The 4A QTL and its association with grain dormancy has now been confirmed in populations involving the Chinese sources of dormancy and in a population involving a dormant, single-gene red wheat. Eight SSR and two STS markers have been located within 110 cM with two SSR markers flanking the highest likelihood ratio statistic position.

Late maturity α-amylase in wheat.

Kolumbina Mrva and Daryl Mares.

Genetic control of LMA and the interaction with semidwarfing genes was investigated in wheat populations involving a number of the different LMA sources present in Australian and CIMMYT germ plasm (Spica, Seri, BD159, Kennedy, Cleo-Inia, Cranbrook, and RAC655) combined with different height reducing genes (*Rht1, Rht2,* and *Rht1+Rht2*) or the T1BL·1RS translocation. Cool temperature treatment of detached tillers was used to induce expression of LMA in lines carrying the defect. Preliminary results indicated that the QTL on the chromosome 7B and 3B, previously identified as controlling the expression of LMA in the cross 'Cranbrook/Halberd' also were associated with the high amylase phenotype in the crosses 'Spica/Maringa (*Rht1*)', 'Spica/Maringa (*Rht2*)', and 'Janz/BD159'. These QTL were independently effective and additive with the QTL on 7B having a greater effect than the QTL on 3B. *Rht1* or *Rht2* reduced the effects associated with each QTL, whereas LMA was extremely difficult to stimulate in lines containing *Rht1+Rht2*. In contrast to the Spica and BD159 populations, only the 3B region appeared to be associated with high amylase in the 'Hartog (no LMA, *Rht2*)/Seri (LMA, *Rht1*)' cross. This observation was unexpected since Seri produces very high levels of α-amylase despite the presence of *Rht1*. Regions on 3A and 7A homoeologous to 7B and 3B currently are being examined. When the 'Hartog/Seri' progeny were typed for T1BL·1RS, it was apparent that most lines with extremely high levels of α-amylase activity also possessed the T1BL·1RS translocation. Further investigation of the interactions between LMA QTL, *Rht* genes, and T1BL·1RS are in progress.

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.

BRS Umbu – a new wheat cultivar for the southern Brazil.

Leo J.A. Del Duca, Cantídio N.A. Sousa, Aroldo G. Linhares, Pedro L. Scheeren, Márcio Sóe Silva, Alfredo Nascimento Júnior, Renato S. Fontaneli, Osmar Rodrigues, Gilberto R. Cunha, Eliana M. Guarienti, Martha Z. Miranda, Leila M. Costamilan, Maria Imaculada P.M. Lima, Márcia S. Chaves, and Ariano M. Prestes.

In order to provide alternatives that will diversify sowing times and cycles and with the aim of minimizing the risks associated with wheat culture, the wheat cultivar **BRS Umbu** was released in 2003 for the state of Rio Grande do Sul (RS) and in 2004 for south central Paraná (PR). Developed by Embrapa Trigo, BRS Umbu was derived from the single cross 'Century/B 35'. BRS Umbu has semilate cycle after early sowing (the cultivar was selected while looking for a late-early cycle with an emergency-heading period longer than the conventional early cultivars) and medium stature. The cultivar is moderately resistant in the field to powdery mildew under natural infection and moderately resistant to glume blotch and scab under artificial inoculation. In spite of its seedling susceptibility to the group of leaf rust races, BRS Umbu has been resistant with low severity under field conditions consistently over the years under high inoculum pressure. Seedling reaction under both greenhouse and field conditions is evidence that the cultivar shows adult plant-resistance. BRS Umbu is resistant to natural dehiscence of the spike and moderately resistant to soil aluminum toxicity and lodging under normal soil fertility conditions. Tested in early sowings and under double purpose use (forage production and grain) in Rio Grande do Sul and south central Paraná between 1999 and 2002, BRS Umbu produced 1,448 kg/ha of dry matter with one clipping, 27 % greater than that of the common black oat (dry matter check), when averaged over different locations that varied according to the year (Passo Fundo, Cruz Alta, Vacaria, São Borja, and Uruguaiana in RS and Guarapuava, Ponta Grossa, and Castro in PR). In these same tests, grain-yield averages were 3,806 kg/ha and 3,011 kg/ha for treatments without and with one clipping, respectively. These averages were 27 % (without clipping) and 39 % (one clipping) greater than the average of two of the better, early wheat checks (among BR 23, BR 35, CEP 24, CEP 27, and OCEPAR 21), which varied for location and year. BRS Umbu is classified as a soft wheat, to be used for crackers, cookies, sweet shop products, pizzas, fresh pasta, and in mixes with wheat for bread and/ or domestic use. Dry matter and grain-yield trials and validation activities with this cultivar were through a partnership between Embrapa Trigo, Fundação Pró-Sementes, Fundação Agrária, and Fundação ABC in RS and PR.

Brazilian wheat production and grain yield – the 2003 crop and perspectives.

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

Brazil has 175 x 10^6 inhabitants that consume nearly 1 x 10^9 tons of wheat annually. With the opening of the Brazilian economy in the 1990s, a proimport policy and a large Argentinian surplus discouraged local wheat production. Beginning in 1999 with changes in the policy favoring exports and hindering imports, the price parity of imported wheat started to influence domestic prices. Thus, attractive prices in the national production had positive influence in Brazilian agribusiness. The 2003 Brazilian wheat production exceeded 5 x 10^6 tons and clearly showed an reversal in the behavior of farmers (P.M. Rabelo, http://conab.gov.br). The 2003 national wheat crop (5,552.2 tons) represents an increase of 90 % when compared to previous crops (Table 1, p. 25). Such production is the result of a 20 % increase in the cultivated area and a notable productivity gain of 49.5 % in relation to the previous year. Farmers were stimulated by favorable prices from 2002 business and industrial partnerships. This progress was due to the confidence in research recommendations and favorable weather conditions, a decisive factor for yield and quality of the crop. This is the largest production registered in a free-market context after deregulation in the wheat sector in 1990. The 6 x 10^6 tons recorded in 1987 were obtained by artificially maintaining prices, not considering international competition, and not allowing the farmer to evaluate his capacity and efficiency.

Table 1. Production and grain yield of the Brazilian wheat crop for the 2001–02 and 2002–03 seasons. Source: CONAB (December 2002 and December 2003); http://conab.gov.br.

	Production (1,000 t)		Grain yield (kg/ha)	
State	2001–02	2002–03	2001–02	2002–03
Paraná	1,621.6	2,829.9	1,435	2,395
Santa Catarina	82.2	141.0	1,550	1,900
Rio Grande do Sul	977.6	2,189.9	1,300	2,100
Total for southern Brazil	2,681.4	5,160.8	1,386	2,245
Minas Gerais	26.7	30.1	4,450	4,300
São Paulo	59.5	104.7	1,700	2,200
Total for southeastern Brazil	86.2	134.8	2,102	2,469
Mato Grosso do Sul	78.8	184.1	860	1,980
Goiás	45.1	67.0	2,200	3,990
Distrito Federal	2.3	5.5	4,535	4,600
Total for west central Brazil	126.2	256.6	1,121	2,312
Total for all Brazil	2,893.8	5,552.2	1,386	2,253

Progress in productivity and quality is expected in the states with larger wheat production, Rio Grande do Sul and Paraná. Because of greater production, offer concentration, and pressure exercised by the imported product, trading in these states has been difficult for the producers. High purchases in external markets during the initial stage of national crop circumvented the expected follow-up. Thus, the federal government introduced business-regulating mechanisms, announced credit and favorable instruments, and auctioned contracts of option of sale of 800,000 tons of wheat. The intent was to decrease offer pressure, allowing the producer to compensate for the inevitable elevation of the prices, up to mid-2004.

The juncture for the wheat sector is more promising at present, because a pool of coöperatives in RS and PR, in a pioneer initiative in Brazil, began to export wheat to Europe and Asia. Thus, because of the quality in this crop and the reduction in world wheat offer, Brazil stepped into the international market, exporting about 500,000 tons of wheat.

Wheat production in southern Brazilian, despite efforts of the producers and research progress, critically depends on the climate, which is not restricted to Brazil. In addition to production losses, elevating costs identify wheat as a high-risk crop. Such circumstances must be considered when planning any increase in Brazilian production in an attempt to alleviate national expenses with imports. Research has shown promising results, and farmers have followed technical recommendations. However, to achieve a balance in commercial conditions, adjusting internal tariffs in relation to the subsidized imports as well as the tariffs for the imported inputs used in production is necessary (M. Júnior, http://conab.gov.br). West central Brazil confirmed its potential for incrementing wheat production. The southern states of RS and PR, responsible for more than 90 % of national wheat production, a crop with increments of 98 % and 87 %, respectively, was obtained. Brazil advanced the goal of producing more than half of total consumption of wheat in the country, reducing the demand for imported product mainly from Argentina, where the tendency to speculate on prices was due to a probable crop reduction in 2003. In this scenario, increasing interest in Brazilian wheat is assumed, making good trading conditions for producers, encouraging the next winter crop, and relieving expenses with imports. The 2003 Brazilian wheat crop can be a mark for the sustained growth of production in Brazil. The entire chain of production, in order to maintain such growth and elevate domestic consumption of wheat and derived products, needs to reach a higher position in the world scenario, which is showing fundamental signs of future changes (http://conab.gov.br/download/safra/safra 20032004Lev02.pdf).

Main Brazilian wheat cultivars sown in the 2001–02 season.

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

During the 2001–02 wheat season in Brazil, each of the 23 cultivars listed in Table 2 (p. 26) made up more than 1 % of the total seed available. Information about the pedigree and industrial quality of the cultivars is provided.

Considering the industrial quality of these cultivars, only seven are classified as soft wheats (BRS 179, Fundacep 30, CEP 27-Missões, BRS 120, Trigo BR 23, CD 105, and Fundacep 32). The remaining genotypes, including

CD 104, IPR 85, and Embrapa 42 (strong gluten), are considered to be of good bread-making quality. Nearly 53 % of seed production is in only eight cultivars, IAPAR 78, CD 104, BRS 49, BRS 179, Rubi, Fundacep 30, CEP 24-Industrial, and OR 1 (each cultivar with more than 4 % of the total seed available) out of 67 cultivars used in all the Brazilian states.

A more diverse number of cultivars is desirable considering the extent of the Brazilian wheat-cropping area in 2001–02 (nearly 2.09 million ha) and great ecological diversity. Because the Brazilian wheat crop is highly dependent on the climatic variations, which contributes to crop failure every 3–4 years (FNP Consultoria & Trade Ltda., Agrianual 2002), genotype diversification could reduce risk.

Seed of IAPAR 78 was in greater availability in Brazil for the 2001–02 crop (10.5 %). Cultivars CD 104, BRS 49, BRS 179, Rubi, Fundacep 30, CEP 24-Industrial, and OR 1 also were available with 4.30–9.27 % of the Brazilian seed.

Table 2. Seed availability and quality of the prevalent wheat cultivars grown in Brazil in 2001–02. Source of seed availability data is MAPA/Embrapa/ABRASEM, Embrapa-SNT.

Rank	Cultivar	Cross	Seed availability (tons)	%	Industrial quality in Brazil[1]
1	IAPAR 78	VEE SIB/BOW SIB	25,823.08	10.50	bread
2	CD 104	PFAU SIB/IAPAR 17	24,565.40	9.27	strong
3	BRS 49	BR 35/PF 83619//PF 858/PF 8550	20,741.82	7.83	bread
4	BRS 179	BR 35/PF 8596/3/PF 772003*2/PF 813// PF 83899	17,728.11	6. 69	soft
5	Rubi	PF 869107/Klein H 3450 C 3131	14,599.32	5.51	bread
6	Fundacep 30	BR 32/CEP 21//Ciano 79	12,042.36	4.54	soft
7	CEP 24-Industrial	BR 3/CEP 7887//CEP 7775/CEP 11	11,448.52	4.32	bread
8	OR 1	EMBRAPA 27/Bagula SIB	11,390.55	4.30	bread
9	CEP 27-Missões	CEP 8057/Butuí//CEP 8324	10,381.35	3.92	soft
10	IAPAR 53	Sulino/IA 7929	9,405.46	3.55	bread
11	Alcover	Ocepar 16/EMBRAPA 27//Ocepar 16	8,633.75	3.26	bread
12	BR 18-Terena	D6301/NAI60//Weique/Red Mace/3/CIA*2/ Chris=ALD45 SEL	8,315.65	3.14	bread
13	BRS 120	PF 83899/PF 813//F 27141	6,865.32	2.59	soft
14	Trigo BR 23	CC/ALD SIB/3/IAS 54-20/COP//CNT 8	6,719.50	2.54	soft
15	IPR 84	ANA 75/PF 7455/PF 72556/3/Pamir SIB/ ALD SIB//KAVKO SIB	5,383.02	2.03	bread
16	CD 105	PFAU SIB/2*Ocepar 14//IAPAR 41	4,672.32	1.76	soft
17	IPR 85	IAPAR 30/BR 18	4,454.14	1.68	strong
18	Granito	PF 869107/Klein H 3450 C 3131	4,416.57	1.67	bread
19	Avante	PF 89232/2*OR 1	4,306.44	1.63	bread
20	BRS 208	CPAC 89118/3/BR 23//CEP 19/PF 85490	3,219.96	1.22	bread
21	Fundacep 32	CEP 85155/3/CEP 7780*2//H499.71A/ 4*JUP 73/4/BR 23	3,199.47	1.21	soft
22	Embrapa 42	LAP 689/MS 7936	3,038.40	1.15	strong
23	Fundacep 31	BR 8//PVN/ANI SIB	2,744.02	1.04	bread
Other cultivars[2]			38,883.05	14.67	
Total			264,977.58	100.00	

[1] Wheat Industrial quality values (W) are from the alveograph method, the deformation energy of the dough, where soft (W ≥ 50 < 180); bread (W ≥ 180 < 300); and strong (W ≥ 300).
[2] Different cultivars (44) with less than 1 % of the seed availability are not listed.

Distribution by state of the main Brazilian wheat cultivars sown in the 2001–02 season.

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

The most important wheat cultivars of each Brazilian state are listed in Table 3. Additional information regarding the pedigree of the genotype and its industrial quality classification also is presented. The states of Paraná and Rio Grande do Sul are responsible for most Brazilian wheat production. The Brazilian wheat-producing area is widespread, covering many different growing conditions in the different states, including rainfed or irrigated fields, presence or absence of aluminum toxicity in the soil, and high or low soil fertility levels. Of the three cultivars with the greatest seed availability in each state, the most widely seeded Brazilian wheat cultivars in 2001–02 season were BRS 179 and Rubi, outstanding in Rio Grande do Sul and Santa Catarina; BRS 49 in Santa Catarina and Paraná; IAPAR 78 in Paraná and Mato Grosso do Sul; Embrapa 22 in Minas Gerais and Goiás; and BR 18-Terena in São Paulo, Mato Grosso do Sul, and Goiás.

Table 3. Seed availability of the most grown wheat cultivars in the Brazilian wheat-producing states in 2001–02.

State[1]	Cultivar	Pedigree	Quality in Brazil[2]	Available seed[3]	% for state[4]
RS	BRS 179	BR 35/PF 8596/3/PF 772003*2/PF 813// PF 83899	soft	15,870.47	16.67
	FUNDACEP 30	BR 32/CEP 21//CIANO 79	soft	12,042.36	12.65
	Rubi	PF869107/KL H 3450 C 3131	bread	10,568.59	11.10
SC	Rubi	PF 869107/KL H 3450 C 3131	bread	2.284.86	26.41
	BRS 179	BR 35/PF 8596/3/PF 772003*2/PF 813// PF 83899	soft	1,812.84	20.95
	BRS 49	BR 35/PF 83619//PF 858/PF 8550	bread	1,180.00	13.64
PR	IAPAR 78	VEE SIB/BOW SIB	bread	27,772.98	18.24
	CD 104	PFAU SIB/IAPAR 17	strong	24,565.40	16.14
	BRS 49	BR 35/PF 83619//PF 858/PF 8550	bread	11,104.50	7.29
SP	IAC 350-Giuapa	2109-36/SERI	bread	1,614.44	45.5
	IAC 24-Tucuruí	IAS 51/IRN 597-70	strong	987.08	27.83
	BR 18-Terena	D6301/NAI60//Weique/Red Mace/3/CIA*2/ CHR=ALD45 SEL	bread	799.24	22.53
MS	BR 18-Terena	D6301/NAI60//Weique/Red Mace/3/CIA*2/ CHR=ALD45 SEL	bread	740.41	84.51
	BR 17-Caiuá	Tezanos Pinto Precoz//IRN 46/Ciano/3/ II-64-27	strong	85.65	9.78
	IAPAR 78	VEE SIB/BOW SIB	bread	50.10	5.72
MG	Embrapa 22	VEE SIB/3/KLTO SIB/PAT 19//MO/JUP	bread	136.85	100.00
GO	Embrapa 42	LAP 689/MS 7936	strong	3,038.40	70.30
	BR 18-Terena	D6301/NAI60//Weique/Red Mace/3/CIA*2/ CHR=ALD45 SEL	bread	561.60	12.99
	Embrapa 22		bread	434.00	6.66

[1] Brazilian states listed are RS (Rio Grande do Sul), SC (Santa Catarina), PR (Paraná), SP (São Paulo), MS (Mato Grosso do Sul), MG (Minas Gerais), and GO (Goiás).
[2] Wheat industrial quality are alveograph values (W), the deformation energy of dough, where soft (W ≥ 50 < 180), bread (W ≥ 180 < 300), and strong (W ≥ 300).
[3] Seed availability expressed as tons available for the 2001–02 season.
[4] Percentage for state is the most used cultivars ranked by state. Information concerning Mato Grosso and Distrito Federal are not available for the 2001–02 season.
Source of seed availability data is MAPA/Embrapa/ABRASEM; Embrapa-SNT.

CERÉALES, OLÉOPROTÉAGINEUX, ET MAIS — CEROM
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Development of a Fusarium head blight-resistant spring wheat.

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Efforts to develop germ plasm and cultivars resistant to FHB were initiated in 1979 in Quebec. After a long struggle with the genetic complexity of the problem, those efforts are now yielding results. Crosses initiated by Dr. Jean-Pierre Dubuc at AAFC Ste-Foy and selected with the help of Dr. Luc Couture (Ste-Foy) and Alain Devaux (MAPAQ) led to lines that were confirmed as resistant in the hands of scientists from ECORC, CRC, and CEROM. Among the examples of recent success, one must quote a line that was supported for registration in 2002, CRGB-O-623.4. This line embodies a good package of valuable traits, but is very susceptible to rusts and powdery mildew. The FHB resistance is about midway between that of AC Barrie and Sumai 3, and the yield is quite adequate in the province of Quebec.

The pedigree of the line is 'AC Pollet/QW539.8//QW526.17/QW530.2'. The expanded pedigree is 'Frontana LF320//Concorde/Opal/3/Glenlea/Minaret/4/Ciano79/Anza//Ciano79/82Pch794/3/unknown QW line/Nobeoka Bouzu'. The intermediate line QW530.2 was derived from the cross of an unknown QW line to Nobeoka Bouzu. The presence of an unknown QW line is due to the former use of a composite cross approach for germ plasm development, whenever the probability of success was considered low. This method reduces the number of accessions to be handled, but causes a loss of precise pedigree information. However, the unknown QW line was probably not a significant source of FHB resistance. The line QW530.2 was verified to possess approximately twice the number of infected spikelets (28 % versus 14 %) when compared to Nyu Bai, a resistant line that is genetically very similar to Nobeoka Bouzu. In the same trials, the susceptible check Roblin had 43 % infected spikelets and the susceptible check Max, 64 %. Thus, QW530.2 had approximately half of the resistance of a very resistant parent from Japan. The end result, however, which is CRGB-O-623.4, now appears to be quite close to Nyu Bai in terms of resistance. Nyu Bai is still more resistant, but the difference is not statistically significant based on the current data set (seven test sites). We therefore hypothesize that CRGB-O-623.4 has integrated other genes of FHB resistance from the other possible sources.

Among possible resistance sources, Frontana LF 320 is noteworthy; a Frontana reselection obtained by Alain Devaux circa 1980. This reselection has been widely used in Canada and, perhaps, elsewhere, labeled simply as 'Frontana'. Scientists in Brazil have confirmed that Frontana itself is a F_4-derived line in which genetic biodiversity is still present (Cantidio de Sousa, pers comm). The same comment applied to many Brazilian cultivars and, especially, to the older ones.

Frontana LF 320 is a well-documented source of type 1 resistance (to infection) to FHB. The line also is capable of degrading trichothecenes, according to Miller and Arnison (1986). Nobeoka Bouzu is a source of type-II resistance (to spread). The use of sources of type-II resistance often leads to problems of low biomass, low root biomass, and low yield. That trend has been verified repeatedly but never properly explained. Germ plasm that has BYDV tolerance shows the contrary trend, since BYDV tolerance is associated with high biomass, high root biomass, and high yield if the lodging is not severe. One parent of CRGB-O-623.4 is a Ste-Foy BYDV-tolerant line based on CIMMYT germ plasm (QW526.17, derived from 'Ciano79/Anza//Ciano79/82Pch794'). Verifying whether BYDV tolerance could offset the biomass problems of type-II, FHB-resistant wheats thus becomes an interesting research avenue, currently explored in a collaborative effort at some Canadian research centers.

Creating usable derivatives of Nobeoka Bouzu is not easy. Because QW530.2 proved to be a valuable parental line, 12-year-old seed of QW530.2 was retrieved. The original seed had only 0.1 % germination, thus, it will need to be increased before being sent to the Canadian germ plasm bank (Plant Gene Resources, Saskatoon). Efforts to diversify the sources of FHB resistance also are under way with the help of CEROM and many AAFC Centres (Winnipeg, Swift Current, Lethbridge, Ottawa, and Charlottetown). Most sources of FHB resistance prior to 2001 were all very susceptible to BYDV and Pythium root rot. Sources that offer FHB resistance together with resistance to other diseases have been identified in Brazilian wheats, i.e., EMBRAPA 27 and BRS 177. However, these two cultivars carry genes that reduce bread-making quality. Attempts to introgress genes from interspecific origin also are under way. We hope the current success can serve as a basis for further progress.

ITEMS FROM CROATIA

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Analysis of the variability in some quantitative traits of Bc winter wheat cultivars.

Rade Mlinar and Ivica Ikic.

Introduction. Past investigations on the productive value of a wheat cultivar focused primarily on proving productivity. To get a clear picture of the entire economic value of a cultivar, investigating stability of certain traits and adaptability to different growing conditions is a necessity (Vasilj and Milas 1981; Surlan-Momirovic et al. 1990). The Bc Institute regularly investigates crucial traits contributing to wheat yield under different environments, such as cultural practices, fertilizer application and rate, protection planting date and rate. We wanted to determine the variability of some important quantitative traits of the Bc wheat cultivars in comparison with Zitarka, the standard cultivar, and to identify superior genotypes with wide adaptability.

Materials and Methods. Investigations were conducted in field trials in 2000–01, 2001–02, and 2002–03 at Aagreb (Botinec). In all 3 years, plants was completed by the second half of October at a planting rate of 750 viable kernels/m^2. Cultivars from different selection cycles were planted in five replications following a random block design with a basic plot size of 5 m^2. Trials were conducted under production conditions and total fertilizer application was 155 kg/ha N, 100 kg/ha P_2O_5, and 150 kg/ha K_2O. Table 1 lists the winter wheat cultivars tested.

Table 1. Winter wheat cultivars tested by the Bc Institute in field trial between 2000 and 2003.

Cultivar	Developed by	Year of registration	Pedigree
Sana	Bc Institut d.d.	1983	Mura x CI14123 X BC-2413/72
Zitarka	Poljop. Inst. Osijek	1985	OSK-6.30/20 x Slavonka x H-68 OSK-154/19 x Kavkaz
Marija	Bc Institut d.d.	1988	Bc-4527/68 x Kavkaz x Bc-1971/70
Tina	Bc Institut d.d.	1993	Sana x Gala
Patria	Bc Institut d.d.	1994	Odesskaya-51 x ZG IPK 82 10 x GK-32-82
Mihelca	Bc Institut d.d.	1995	Bc-1325/78 x SO-1065
Zdenka	Bc Institut d.d.	1996	Beauchamp x BC-2557/83
Liberta	Bc Institut d.d.	1997	M-441-1 X Drina x Bc-167/86
Aura	Bc Institut d.d.	1997	434 K-4CM x 7903-93-1
Concordia	Bc Institut d.d.	1998	Bc-186/82 x Castan

Results and Discussion. Grain yield. The average yield for all cultivars during 3 years of investigation was 5,796 kg/ha. The highest average yield was obtained in 2001 (7,254 kg/ha), a year which favored wheat growth, and the lowest yield (3,088 kg/ha) in the extremely dry environment in 2003. Range of variation was 4,166 kg. The highest yield of all cultivars was Liberta (8,239 kg/ha), which was the highest yielding cultivar on average (6,217 kg/ha; coefficient of variation was 32.3). Liberta was followed by Mihelca (5,943; 34.3), Tina (6,053; 35.5, Marija (6,023; 30.0), Patria (6,012; 28.2), Sana (5,985; 35.5), Zdenka (5,943; 35.0), Aura (5,842; 32.4), Zitarka (4,928; 36.9), and Concordia (4,866; 34.7). These results show that there are genetic differences in yield potential among the tested lines. Relative variability indicates more clearly the differences among the cultivars; the highest value for all 3 years was for the check cultivar Zitarka. Patria, Marija, and Liberta all had low relative variability, but stand out with regards to their high productivity and stability, making them suitable for growing under different production conditions. Because of their performance during our trails, we believe that Mihelca and Tina can successfully only be grown under conditions that do not differ substantially from those in Botinec.

1,000-kernel weight. Greatly influenced by environment, 1,000-kernel weight averaged 39.58 g over all cultivars and years, the range between years was 9.63 g. The 1,000-kernel weight of all cultivars were sensitive to agroecological factors. Mihelca had the highest 1,000-kernel weight at 46.12 g, followed by Liberta (42.66 g) and Tina (42.48 g). Tina and Mihelca also had low relative variabilities of 7.95 and 9.79, respectively, unlike Liberta with a relative variability of 15.07 for 1,000-kernel weight.

Plant height. Because tall cultivars are more prone to lodging, height is an important characteristic. Plant height determines agroecological conditions suitable for an individual cultivar. We discovered considerable differences in plant height among the tested cultivars and over years. The overall average was 75 cm; the variation between years was 39 cm. Mihelca and Patria were the tallest (80 cm), followed by Liberta (78 cm) and Aura (76 cm). The height of the other lines was similar to that of the check Zitarka (70 cm). Variability among repetitions was highest for Tina and Liberty and lowest for Zdenka.

Sedimentation. As an indirect index of wheat baking property, the sedimentation value was lowest in 2001 at 30 ml. This year saw the highest yields. A higher value, 38 ml, was measured for the 2002 and 2003 test years, giving a range of 8 ml. The difference between the cultivar with the highest sedimentation value, Zdenka (54 ml), and the lowest, Patria (24 ml), was 30 ml. A high sedimentation value also was found in Aura (51 ml). Zdenka and Aura were developed in a more recent cycle of wheat breeding at the Bc Institute. During the 3-year period, Zitarka and Sana has the lowest variability; Concordia the greatest (24.3).

Conclusion. Based on obtained yields and variability parameters, development of wheat cultivars that can meet both criteria of yield capacity and stability seems to be possible.

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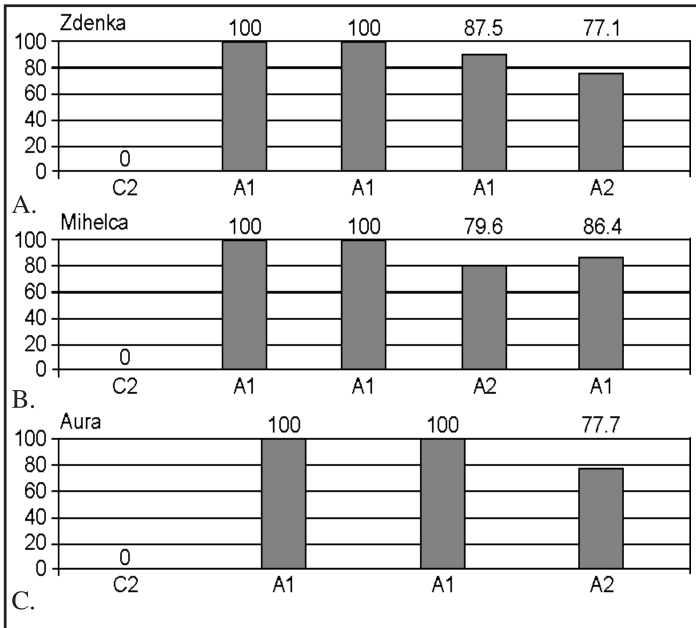

Fig. 1. Quality values for cultivars Zdenka, Mihelca, and Aura.

Results of quality testing of Bc winter wheat cultivars.

Slobodan Tomasovic, Rade Milnar, Ivica Ikic, and Kristijan Puskaric.

Winter wheat breeding at the Bc Institute in Zagreb is based on developing high-yielding genotypes with wide adaptability and high plasticity under different agroecological conditions. In addition to developing a highly productive and stable geno-

Table 2. Milling and baking quality tests for the cultivar Zdenka, 2001–02.

		Farinogram					Extensogram					
Company	Wet gluten (%)	Absorption (%)	Elasticity (min)	Stability (min)	Resistance (min)	Softness (FJ)	Quality No.	Quality group	Energy (cm)	Elasticity (mm)	Resistance (FJ)	E/R
PIK Vinkovci	31.4	69.9	2.3	12.7	15.0	0	100.0	A1	135	173	350	2.02
Ljudevit Posavski	33.2	65.0	2.8	7.0	9.8	25	87.5	A1	141	191	345	1.81
Podravka	27.2	61.3	2.5	3.0	5.5	20	77.1	A2	146	165	436	2.70

Table 3. Milling and baking quality tests for the cultivar Mihelca, 2001–02.

		Farinogram					Extensogram					
Company	Wet gluten (%)	Absorption (%)	Elasticity (min)	Stability (min)	Resistance (min)	Softness (FJ)	Quality No.	Quality group	Energy (cm)	Elasticity (mm)	Resistance (FJ)	E/R
PIK Vinkovci	26.5	62.5	3.0	12.0	15.0	0	100.0	A1	114	156	360	2.30
Ljudevit Posavski	29.3	58.1	5.5	2.5	8.0	40	79.6	A2	120	185	290	1.57
Podravka	25.6	56.8	1.7	8.8	10.5	5	86.4	A1	114	168	316	1.90

Table 4. Milling and baking quality tests for the cultivar Aura, 2001–02.

		Farinogram					Extensogram					
Company	Wet gluten (%)	Absorption (%)	Elasticity (min)	Stability (min)	Resistance (min)	Softness (FJ)	Quality No.	Quality group	Energy (cm)	Elasticity (mm)	Resistance (FJ)	E/R
PIK Vinkovci	33.1	62.5	2.3	12.7	15.0	0	100.0	A1	137	166	430	2.59
Ljudevit Posavski	35.3	61.5	2.5	1.7	4.2	30	77.7	A2	167	180	390	2.17

types, improved quality of grain and flour also have been incorporated. This work has resulted in the winter wheat cultivars Zdenka, Mihelca, and Aura.

Rheological analyses were conducted by the companies of PIK Vinkovci d.d., Ljudevit Posavski d.d. Sisak, and Podravka d.d. Koprivnica in 2002. The results prove that these are high-quality winter wheat cultivars that fully meet the needs of the milling and baking industry. Farinogram and extensogram values are given for each of the three cultivars; Zdenka (Table 2 and Fig. 1A (p. 30)), Mihelca (Table 3 and Fig. 1B (p. 30)), and Aura (Table 4 and Fig. 1C (p. 30)). These three winter wheats are first quality class and belong to the A1 and A2 quality groups. These results indicate that with the well-conceived breeding work at the Bc Institute, the new cultivars meet or surpass the quality level of foreign improvers.

ITEMS FROM THE CZECH REPUBLIC

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Evaluation of winter triticale collection in 2003.

Z. Stehno and L. Cejka.

Triticale growing in the Czech Republic has stabilized recently between 35 and 55 x 10^3 ha (Table 1). Grain yield did not vary much (3.52–3.87 t/ha). At present, 12 triticale cultivars are registered in the Czech Republic. Among them, only Gabo is a spring cultivar. A set of winter cultivars contains the original Czech cultivar Kolor bred by Selgen. Three cultivars, Kitaro, Lamberto, and Ticino, were registered in 2003.

Table 1. Growing area and average yield of triticale in the Czech Republic between 2000–03.

Year	Growing area (ha)	Yield (t/ha)
2000	37,001	3.74
2001	49,499	3.87
2002	53,093	3.77
2003	45,970	3.52

Evaluating the triticale collection continues regularly under the framework of plant genetic activities of the Gene Bank Department of the RICP. For comparing results from different years, Kolor, winter triticale; Samanta, a winter wheat; Albedo, a winter rye; and Apart, a hybrid winter rye were used as check cultivars. Overwintering, plant height, and resistance to lodging, powdery mildew, leaf rust, and Septoria were emphasized during evaluation.

The highest level of overwintering among check cultivars was detected in the triticale Kolor and in the rye Albedo (Table 2, p. 33). Within the tested set of triticale cultivars, the winter hardiness of Pinokio is the highest. The number of days from 1 January till heading has indicated that all triticale accessions are intermediate (143–151 days) when compared with rye (136–138) and wheat (151 days). Plant height of the triticale cultivars was intermediate and ranged between the winter wheat Samanta (90 cm) and the rye cultivars Apart and Albedo (135 and 138 cm, respectively). Only the triticale Trado was shorter (88 cm) than Samanta.

All the triticales were more resistant to powdery mildew than Samanta (score of 2) or the winter ryes (Apart, 3; Albedo, 7). The triticale cultivars also were more resistant to Septoria than the wheat check and equal to or better than the resistant as rye cultivars. Greater differences were observed in the response to leaf rust infection.

Grain yield of the winter triticale Pronto (11.59 t/ha) and registered Disco (11.53 t/ha) were higher than the yields of the rye cultivars Albedo and Apart (11.51 and 10.77 t/ha, respectively).

Table 2. Evaluation of winter triticales, 2002–03. Over wintering and resistance to lodging and to the powdery mildew, Septoria, and leaf rust pathogens were rated on a scale of 1 (resistant) to 9 (susceptible).

					Resistance to						
Cultivar	Over wintering	Days to heading (from 1 Jan)	Plant height (cm)	Spike number (per m^2)	Powdery mildew	Septoria	Leaf rust	Days to maturity (from 1 Jan)	Lodging	Grain yield (t/ha)	1,000-kernel weight (g)
Samanta (winter wheat)											
	8	151	90	764	2	3	7	206	6	6.06	32.59
Albedo (winter rye)											
	9	136	138	568	3	5	7	203	9	11.51	41.98
Apart (hybrid winter rye)											
	8	138	135	732	7	6	4	204	6	10.77	34.12
Kolor (check)											
	9	147	110	596	9	7	5	209	8	10.45	47.92
Pronto	8	145	106	808	8	7	9	207	9	11.59	36.50
Disco	8	146	118	580	9	6	5	209	8	11.53	45.42
Janus	6	148	105	612	7	6	9	206	9	10.14	39.12
Pinokio	9	151	97	568	7	6	4	215	9	9.95	47.46
Polego	8	144	113	672	8	6	9	205	9	9.85	42.47
Kitaro	9	145	108	704	8	6	4	205	9	9.80	43.60
Lupus	7	150	115	532	8	7	4	210	8	9.69	36.65
Passus	6	149	95	672	7	6	9	209	8	9.45	41.13
Trimaran	8	145	107	732	7	6	9	204	9	9.39	41.15
Prader	7	144	95	684	8	5	5	208	9	9.03	39.86
Lamberto	8	146	112	744	7	6	3	209	9	9.01	38.35
Bogo	8	147	111	728	8	7	9	208	7	8.96	32.37
Timbo	7	144	97	632	7	6	4	205	9	8.86	40.18
Marko	7	147	117	640	8	6	3	206	5	8.64	36.48
Presto	8	143	125	852	8	7	5	211	3	8.11	37.91
Sekundo	7	147	120	656	7	6	3	205	4	8.02	40.99
Tricolor	7	146	112	784	6	6	8	210	8	7.93	38.68
Modus	8	145	116	748	8	7	6	207	3	7.85	37.72
Vitalis	8	143	115	676	8	7	3	204	9	7.69	41.77
Ticino	4	147	106	584	8	7	8	213	9	7.65	42.57
Donatus	6	145	96	480	8	7	4	206	9	7.61	37.46
Vihren	6	144	101	520	7	5	9	206	6	6.55	41.72
Trado	4	144	88	384	8	7	9	205	9	5.92	44.71
Persenk	4	144	98	436	7	5	9	205	9	5.89	45.19
Marval	3	144	102	392	8	6	5	204	9	4.97	49.34

ITEMS FROM ESTONIA

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Allelic variation of Glu-1-encoded, HMW-glutenin subunits of spring wheat hybrid lines of Scandinavian origin.

Maimu Tohver.

Success in breeding depends mostly on heritable traits and methods to identify the quality of grain in early hybrid generations. Identification of storage protein subunits is used widely in wheat-breeding programs. Prolamin gene electrophoresis is the usual method of identifying economically important characters and properties of common wheat. The HMW-glutenin subunits encoded by the *Glu-1* gene are used in wheat breeding for selecting the alleles that correlate with quality.

Cultivars and breeding lines from Nordic countries are suitable for the Estonian climate and soil conditions. Many cultivars and hybrid lines are tested each year. The aim of this study was to use SDS–PAGE to identify the diversity of the glutenin proteins in hybrid lines of spring wheat originating from Scandinavia, and grown in Estonia during 2000–01. Grain stocks were obtained from the Jõgeva Plant Breeding Institute. One hundred twenty-one hybrid lines were analyzed to determine the different allelic forms of HMW glutenins. Proteins were extracted from a single kernel and electrophoresis was performed using the procedures described in D'Ovidio et al. (1996) and Tohver et al. (2001). To determine the alleles observed, the spring wheat cultivars Courtot, Chinese Spring, Marquis, and Kadett were used as standards for the HMW-glutenin subunits. The HMW-glutenin subunit banding patterns were assigned the corresponding Payne and Lawrence (1983) and UPOV (1994). Theoretical quality scores were calculated based on those assignments.

Results. A total of 13 alleles coding for 12 HMW-glutenin subunits were identified from analysis of the hybrid lines (Table 1). The greatest polymorphism was observed on chromosome 1B, with five allelic forms at the *Glu-B1* locus. The most frequent alleles at the *Glu-B1* locus were *c*, coding for subunits 7+9 (53 %, quality score (QS) 2), and *b*, coding for subunits 7+8 (38.6 %, QS 3). At the *Glu-A1* locus, the most frequent alleles were *b*, coding subunit 2* (42.2 %, QS 3), and *c* (null allele) (40.9 %, QS 1). Allele *d* prevails at the *Glu-D1* locus and codes for subunits 5+10 (75.6 %, QS 4). The frequent occurrence of glutenin subunits 7+8 and 7+9 encoded at the *Glu-B1* locus has been reported in several European collections (Sontag-Strohm et al. 1986; Igrejas et al. 1999). We found heterogeneity in some lines with up to four different electrophoretic variants/line.

Table 1. HMW-glutenin subunits present in hybrid lines analyzed. QS = quality score.

Glu-A1	Protein	*Glu-B1*	Proteins	*Glu-D1*	Proteins
QS = 10 was observed in 10.8 % of cases with HMW-glutenin subunit compositions					
b	2*	*b*	7+8	*d*	5+10
a	1	*b*	7+8	*d*	5+10
QS = 9 was observed in 30.1 % of cases with HMW-glutenin subunit compositions					
a	1	*c*	7+9	*d*	5+10
b	2*	*c*	7+9	*d*	5+10
QS = 8 was observed in 24.1 % of cases with HMW-glutenin subunit compositions					
b	2*	*b*	7+8	*a*	2+12
a	1	*d*	6+8	*d*	5+10
c	—	*b*	7+8	*d*	5+10
b	2*	*a*	7	*d*	5+10
c	—	*f*	13+16	*d*	5+10
QS = 7 was observed in 22.9 % of cases with HMW-glutenin subunit composition					
b	2*	*c*	7+9	*a*	2+12
c	—	*c*	7+9	*d*	5+10
QS = 6 was observed in 12.0 % of cases with HMW-glutenin subunit composition					
c	—	*a*	7	*d*	5+10
c	—	*b*	7+8	*a*	2+12

The HMW-glutenin subunits influence the baking properties of wheat and triticale, but have a lesser effect in rye. Payne and Lawrence (1983) have worked out a scoring system based on HMW-glutenin subunits, and this system was used to estimate the value of breeding lines. The maximum quality score was observed 10, and the minium was 6. A large number of alleles for bread-making quality have been designated, however, only few alleles currently are in use in commercial cultivars. For that reason, novel sources of unknown alleles are needed.

From this study, we observed that breeding lines do not vary widely in HMW-glutenin subunit groups. Previously, Sontag et al. (1986) already had shown that the range and distribution of HMW-glutenin subunits found in Finnish bread wheats is very limited compared to cultivars grown elsewhere in Europe. A third of the Finnish cultivars contained one of two HMW compositions: 1, 7+9 , 5+10 or 2*, 7+9, 2+12. In Swedish wheats, the most common compositions were 2*, 6+8 or 7+9, and 2+12. Rarely have the subunits 13+16, 14+15, and 17+18 been found in Swedish wheat lines (Johansson et al. 1995). In Norwegian breeding lines, the HMW-glutenin subunit combinations 2*, 7+8, 5+10, and 2*, 13+16, 5+10 were prevalent (Uhlen 1990) and 20, 17+18 and 7 were rare subunits. From this data, the most occurring alleles in Scandinavian wheats are *b* at locus *Glu-1A* encoding subunit 2*, *c* at locus *Glu-B1* encoding subunits 7+9, and *a* and *d* at locus *Glu-D1* encoding subunits 2+12 and 5+10, respectively. Other investigators (Payne et al. 1981, 1983, 1987; Lukow et al. 1989) have shown that a positive correlation exists between high bread-making quality and the presence of the HMW-glutenin subunits 1 or 2* of *Glu-A1*; 7+8, 7+9, 17+18, 14+15, or 13+16 of *Glu-B1*, and 5+10 of *Glu-D1*. The low quality glutenin subunits are null of *Glu-A1*; 7 and 20 of *Glu-B1*, and 2+12 of *Glu-D1*. Incorporation of new subunits and their combinations could increase variation in breeding lines. Introducing the subunits 17+18 and 13+16 into Scandinavian cultivars would be necessary to widen the genetic diversity because of their correlation with good bread-making qualities.

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Salt tolerance.

Three hundred fifty-nine spring wheat accessions and 210 winter wheat accessions were tested for salt tolerance at the germination stage. Three different NaCl solutions (1 %, 1.5 %, and 2 %) and a distilled water control were used to determine the tolerance against salt stress. Spring wheat accessions from the Himalaja region of Asia have shown a high tolerance. Accessions from the northern part of Africa (Tunisia and Libya) also showed a high tolerance. In general, winter wheat possesses a higher salt tolerance in comparison to spring wheat, but no geographical connections were found.

Morphological characters of the spike are less suitable for the selection of genotypes tolerant to salt stress. A slight effect of awn length was found. Accessions with short awns reacted more tolerant than accessions with long awns.

Several control plants of tolerant and sensitive accessions selected from the germination test were further analyzed in a greenhouse experiment. The plants were transferred in pots with a soil mixture (sand and peat moss in a 2:1 ratio) and treated in three variants (water, 4 g NaCl/L, and 8 g NaCl/L) until maturity. The average yield reduction in the tolerant accessions was 30–50 % at 4g NaCl/L and 80–90 % at 8g NaCl/L. The decrease in yield at 4g NaCl/L for sensitive accessions was more than 75 %. The sensitive wheat completely failed to develop spikes in the 8g NaCl/L treatment. The number of the tillers obviously influenced the reaction to salt stress. Plants with a high number of tillers in the control treatment tended to show a more sensitive reaction under salt stress conditions. The reaction in the germination stage was not equal to the reaction in the adult-plant stage in all cases. Therefore, germination tests are not enough to assess salt tolerance during the whole life cycle of a plant.

In addition, a set of *T. aestivum*/*Ae. tauschii* introgression lines developed at IPK was tested in order to localize chromosomal regions that affect salt tolerance. The test was carried out in the same manner as described for the screening of the wheat accessions. Interesting segments in respect to the germination in a saline environment were found on chromosome 3D, 4D, and 7D.

Post-anthesis drought tolerance.

Post-anthesis drought stress is a common problem in wheat productions. The wheat stem can function as both a source and sink for assimilates. Soluble carbohydrates usually accumulate in cereal stems and other vegetative tissues from the time of spike emergence until shortly after anthesis. Stem reserves are a major resource providing carbohydrates and nitrogen for grain filling when the transient photosynthetic source is inhibited by stress. Stem reserve mobilization was reported to be associated with post-anthesis drought tolerance. Previous studies have shown that some chemical desiccants and senescing agents, when applied to adequately watered cereals 10 to 14 days after anthesis, can be used to select lines with stable grain size (kernel weight) under post-anthesis water deficit. The present study evaluated the potential of one of these chemicals, potassium iodide (KI), to select for this character and to identify and map QTL associated with post-anthesis drought tolerance in hexaploid wheat. Quantitative trait loci analysis was carried out with a set of 114 RILs from the International Triticeae Mapping Initiative population (ITMI) of synthetic wheat 'W7984, tolerant/Mexican wheat Opata 85, sensitive' to identify the genomic regions controlling traits related to post-anthesis drought tolerance (PADT). In one experiment in Gatersleben, the amount of dry matter stored and mobilized was estimated by measuring changes in 1,000-kernel weight after a chemical desiccation treatment. The reduction in final grain weight ranged between 35.35 % and 99.77 %. We have determined the chromosomal locations of QTL affecting grain yield under drought stress on chromosomes 1B, 2D, 5D, and 7D. Also, using phenotypic data obtained after spray treatment with KI, QTL for six grain characters, i.e., area, length, width, circumference, roundness, and density, were mapped on chromosomes 1B, 2D, 5A, 7A, 3D, 4D, 5D, 2B, and 7B.

Copper tolerance.

Fifty-three recombinant inbred lines originated from the crossing of the hexaploid wheat Opata 85 and the synthetic hexaploid wheat W7984 were screened in the greenhouse for copper tolerance, and QTL mapping of the copper tolerance traits was performed. QTL with a great significant effect were found on the chromosomes 5DL and 7DS and with smaller effect on the chromosomes 1AL, 4AL, 2DS, 2AL, and 5BL. The role of the chromosomes 5D and 7D for Cu tolerance was reported in earlier testing of substitution lines. These results suggest that copper tolerance is under the control of more than one chromosome, indicating the polygenic character of Cu tolerance. QTL influencing the shoot Cu, Fe, Mn, and Zn concentrations in control and a Cu-treated environment also were determined

Preharvest sprouting / dormancy.

A set of 114 RILs of the ITMI mapping population was grown under field conditions in Gatersleben. The lines were evaluated for the domestication traits preharvest sprouting and dormancy (germinability). Main QTL could be localized for preharvest sprouting on chromosome 4AL and for dormancy on chromosome 3AL. But preharvest sprouting and dormancy in wheat are complex, involving multiple physiological risks and multiple interactions between genetic and environmental factors. Therefore, we need to retry the evaluation under constant greenhouse conditions in the coming season to eliminate the influence of weather and verify the detected QTL. Also wheat–*Ae. tauschii* introgression lines will be tested to discover the influence of the D genome on preharvest sprouting and dormancy.

Genetic diversity.

Using microsatellite markers, samples of cultivated wheat collected in intervals of 40 to 50 years in four geographical regions of Europe and Asia (Albania, Austria, North India, and Nepal) were analyzed. No significant differences in either the total number of alleles per locus or in the PIC values were detected by comparing material from repeated collection missions in all four regions analyzed. About two-thirds of the alleles were common for both collection periods. One-third, however, represented collection mission-specific alleles. These findings demonstrate that allele flow took place during the adaptation of traditional agriculture to modern systems, whereas the level of genetic diversity was not influenced significantly. The data clearly demonstrate that in a certain period of cultivation a certain amount of unique alleles is present, which may have consequences for the conservation of plant genetic resources. The exploitation of the whole range of allelic variation makes it necessary both to maintain the already existing *ex situ* collections but also to collect new material.

Mapping wheat microsatellite markers in rye.

For wheat, more than 1,000 GWM (Gatersleben Wheat Microsatellite) markers have been developed at IPK Gatersleben or TraitGenetics GmbH, Gatersleben, of which 651 were screened for their usability for rye mapping, regardless of whether they represent microsatellites or STS markers. In total, 81 primer pairs (12.4 %) amplified PCR products of a good quality in the rye genome; 56 amplified 70 loci either polymorphic in one of the four mapping populations (60) or located on particular chromosomes using the set of wheat–rye addition lines (10). Comparing the locations of *Xgwm* loci amplified by the same primer pairs in wheat and rye genomes, we showed that 44 out of 60 *Xgwm* loci mapped in orthologous positions, by considering the multiple evolutionary translocations in the rye genome relative to those of hexaploid wheat and the other Triticeae species. The identification of cross-amplifying microsatellite (STS) loci is important for their further application in comparative studies among wheat and rye or even other cereals.

Transferability and comparative mapping of barley microsatellite markers into wheat.

Rajeev K. Varshney, Nils Stein, and Andreas Graner.

In the context of developing microsatellite markers in barley, a set of 111,090 barley ESTs (corresponding to 55.9 Mb) was employed for the searching of microsatellites or SSRs. With the help of a PERL5 script (MISA, http://pgrc.ipk-gatersleben.de/misa/; Thiel et al. 2003), a total of 9,564 microsatellites (EST–SSRs) were identified in 8,766 ESTs (SSR–ESTs). Cluster-analysis revealed 2,823 nonredundant SSR–ESTs (see Varshney et al. 2002). A set of 756 primer pairs for EST-derived SSRs (EST–SSRs) was analyzed in a set of seven barley genotypes (including parents of three mapping populations), and a total of 190 EST–SSRs were placed onto the barley genetic map.

Of the 165 barley microsatellites examined, 74 % showed amplification in wheat. *In silico* analysis of 190 barley SSR–ESTs (corresponding to mapped barley EST–SSRs) against 502,868 wheat ESTs showed the presence of homologues of 93 % barley SSR–ESTs in wheat. Furthermore, the sequences of all 190 mapped barley SSR–ESTs were compared (BLASTN) to 90 genetically mapped wheat SSR–ESTs (Mark Sorrells, personal communication). A total of 11 barley SSR–ESTs showed a significant match (< $1E^{-10}$) to wheat SSR–ESTs that were located in corresponding homoeologous linkage groups. The sequences of the same set of barley SSR–ESTs was compared further to 4,840 wheat ESTs that have been physically assigned to wheat chromosomes via deletion mapping (http://wheat.pw.usda.gov/NSF/progress_ mapping.html). Twenty-seven barley SSR–ESTs had significant homology with 23 wheat ESTs physically mapped on the corresponding homoeologous linkage groups in wheat. Altogether, 38 barley SSR–ESTs (20 %) showed the best sequence homology to 34 wheat ESTs mapped genetically or physically on homoeologous linkage groups (Table 1). Out of 38 barley SSR–ESTs, four were found to be derived from the same gene after redundancy analysis, though the EST–SSR markers were derived for different microsatellites.

In order to determine the occurrence of conserved microsatellite motifs in putatively orthologous loci between barley and wheat, *in silico* sequence analysis was performed on EST-contig/EST sequences of wheat. A total of 14 of 34 (41.2 %) wheat contig/ESTs contained microsatellites. However, similar SSR repeat motifs, as in barley, were present only in 12 (35.3 %) contig/ESTs (Table 1).

The above analysis indicates the potential of gene-derived microsatellite markers of barley to be transferred to wheat. However, despite the high level of transferability, the conservation of the individual microsatellite motifs is low between the two species.

Table 1. Homology of barley SSR–ESTs with wheat ESTs

Barley chromosome	Number of barley markers	Hit with wheat ESTs [1]	Wheat ESTs mapped [1]		Conservation of orthologous SSR repeat motif
			Genetically	Physically	
1H	26	7	1 (1*)	6 (1)	2 (28.9 %)
2H	33	5	1 (1)	4 (0)	1 (20.0 %)
3H	36	13	2 (2)	7** (1)	3 (23.1 %)
4H	26	2	1 (0)	1 (1)	1 (50.0 %)
5H	22	3	1 (1)	2 (0)	1 (33.0 %)
6H	25	3	3 (2)	0 (0)	2 (66.7 %)
7H	22	5	2 (2)	3 (0)	2 (40.0 %)
Total	**190**	**38**	**11 (9)**	**23 (3)**	**12 (35.3 %)**

[1] Barley markers that gave significant hit (< $1E^{-10}$) with wheat ESTs, mapped genetically (by M. Sorrells' group, Cornell University, USA) or physically (http://wheat.pw.usda.gov/NSF/) on homoeologous linkage groups.
* Number of wheat ESTs containing similar SSR-repeat motif as of barley is given in parenthesis.
** Two of seven wheat EST showed significant homology with more than one barley SSR–ESTs .

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ITEMS FROM HUNGARY

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Wheat season. During a colder than average winter, the winter durum and winter barley cultivars, which had poor frost resistance, were killed, but the winter wheat suffered little damage. Spring and summer were warmer than average and exceptionally dry. Because of the drought, which began in April and lasted up to harvest, the wheat yield was only 2.63 t/ha, less than 50 % of that expected in a favorable year.

Breeding.

Z. Bedö, L. Láng, O. Veisz, G. Vida, I. Karsai, K. Mészáros, M. Rakszegi, P. Szücs, K. Puskás, C. Kuti, M. Megyeri, S. Bence, M. Cséplö, D. Láng, and J. Bányai.

Breeding. Seven new winter wheat cultivars were registered in 2003.

Mv Toborzó (Mv 05-2001) is the earliest maturing winter wheat ever bred at Martonvásár. Despite its earliness, this cultivar has good frost resistance and a yield potential that is competitive with that of cultivars with longer vegetation periods. Mv Toborzó is moderately resistant to powdery mildew and resistant to the local races of leaf and stem rust. Mv Toborzó is a good quality bread wheat, with high gluten content and good gluten quality.

Mv Piroska (Mv 06-2001) is an extremely high-yielding cultivar originating from the Open/Recital combination. Mv Piroska has moderate winter hardiness, good resistance to powdery mildew and stem rust, and excellent resistance to leaf rust. Although protein content is relatively low, the quality is good. This cultivar is recommended for production under intensive conditions in regions with mild winters.

Mv Matyó (Mv 07-2001) is an early, high-yielding cultivar with moderate frost resistance. The pedigree is 'Mv-Magma/GK-Kalaka//Mv-Magma/Ilona'. The cultivar has excellent disease resistance to powdery mildew, leaf rust, and stem rust and good production traits. Mv Matyó has a low wet gluten content of around 22–25 % and a farinograph quality of B1–B2.

Mv Garmada (Mv 08-2001) is a mid-early bread wheat with the pedigree 'Mv-Magdalena/F2098'. Mv Garmada has good field disease resistance and competitive yield potential. Mv Garmada is a good quality bread wheat with average protein content and above-average protein quality.

Mv Béres (Mv 14-2001) is a mid-early wheat cultivar with excellent quality and extremely good agronomic properties. This cultivar has excellent frost resistance and is resistant to powdery mildew, leaf rust, and stem rust. The pedigree of Mv Béres is 'Eryth352/Mv-Magdalena'. Mv Béres has a wet gluten content of 34–36 % with excellent gluten quality.

Mv Mazurka (Mv 20-2001) is the latest-maturing Martonvásár cultivar, heading 11 days later than Mv Toborzó. Good frost resistance and moderate disease resistance allow an average yield level to be achieved. Mv Mazurka has an extremely high gluten content and a farinograph quality of A1.

Mv Walzer (Mv 22-2001) is a late-maturing wheat with good frost resistance. Mv Walzer has average yield potential and disease resistance, but excellent quality. With a high wet gluten content of 33–36 %, Mv Walzer has optimum gluten elasticity and extensibility.

Storage proteins. Bánkúti 1201, an old Hungarian wheat cultivar with special quality traits, was analyzed to determine the relationships between its storage-protein composition and superior quality attributes for bread making. Based on the storage-protein composition, the cultivar appears to have the nature of a population, containing several genotypes with different gluten protein alleles. Using molecular markers, a new, mutant, x-type HMW-glutenin allele was identified that contains an extra cystein residue and shows a moderate, positive effect on gluten properties. In lines possessing subunits Bx7 + By8, the overexpression of the Bx-type subunit could be detected, resulting in a higher unextractable polymeric protein (UPP) content and increased dough strength. We found that the presence or absence of subunit Bx7 has an equilibrating effect on the dough extensibility, which is generally characteristic of the Bánkúti 120 population. The complex good bread-making quality of the cultivar, which has strong but highly extensible dough, is probably due to the balance between lines which express subunit Bx7 and those that do not.

Plant regeneration from embryos. A tissue-culture method for regeneration of plants from immature embryos of elite Hungarian winter wheat cultivars was established. The influence of growth regulators and the concentration of macroelements in the regeneration medium and of the incubation temperature and light intensity on regeneration frequency were investigated. The most noticeable effect on regeneration frequency was achieved by simultaneously reducing both the incubation temperature to 23°C and the concentration of macroelements in the regeneration medium to half-strength. This modification increased the average regeneration frequency from about 10 % to 78 %. Changes in the light intensity and temperature gave an average plant regeneration frequency of 83 %.

Durum wheat breeding. The main aim in winter durum wheat breeding continues to be the improvement of cold tolerance, winter hardiness, pasta quality, and productivity. Four high-yielding, cold-tolerant Martonvásár lines with good technological quality traits are now being tested in official state trials.

Winter durum wheat genotypes have been selected on the basis of the yellow color of the semolina since 1995. During this period, a total of 1,324 winter durum wheat cultivars and advanced lines has been tested for their yellow index using a Minolta CR-300 chromameter. Selection has resulted in a substantial increase in the yellow index of the winter durum wheat lines intended for inclusion in state trials. Compared with the control, the mean yellow index of these lines was 99.2 % prior to selection, but reached 113.2 % by 2000. The yellow index of the best Martonvásár lines exceeds that of the control cultivar, Parus, by over 30 %, whereas the proportion of lines with a yellow index lower than that of the control has dropped from 60 % to 5 %.

Disease resistance studies. The stem rust infection of genotypes with known resistance genes was tested in an artificially infected nursery. In 2003, cultivars with genes *Sr5*, *Sr11*, *Sr24*, *Sr31*, and *Sr32* exhibited little infection and those with gene *Sr36* none at all.

With molecular marker-assisted selection, genes for leaf rust resistance (*Lr9*, *Lr24*, *Lr25*, and *Lr29*) were identified and traced in the progeny populations of crosses made between four Martonvásár cultivars and sources carrying the resistance genes.

Race composition, degree of virulence, and efficiency of the known resistance genes were determined under controlled conditions in the greenhouse for the naturally occurring powdery mildew population found in Martonvásár. The dominant races of wheat powdery mildew (and their frequency) in 2003 were as follows: 63 (17.7 %), 77 (17.7 %), 51 (10.8 %), 76 (10.8 %), and 72 (10.1 %). The average number of virulence genes in the pathogen population was 4.81. Almost complete protection against the wheat powdery mildew pathotypes was provided by the resistance gene *Pm4a+* (Khapli). Only varieties with genes *Pm2+Mld* and *Pm3d* became infected, with an infection percentage of less than 40 %.

The FHB resistance of Martonvásár wheat cultivars and advanced lines was tested in an irrigated nursery. In 2003, an extremely severe infection was noted on plots treated with isolates of *F. graminearum* and *F. culmorum*, with a significant quantity of early spikelet mortality and grain infection even in the majority of exotic resistance sources. On the basis of the 2003 tests, the cultivars Bánkúti 1201, Mv Emese, and Mandolin had outstanding resistance. Testing has begun both in the field and in the greenhouse on the spread of Fusarium in the spike (type-II resistance). In the field experiment, the wheat genotypes were more severely infected than in the greenhouse. Considerable differences could be observed between cultivars in the intensity of infection.

Abiotic stress resistance studies. As part of our work on cold tolerance, we studied changes in the activity of antioxidant enzymes. Significant differences were detected in the antioxidant enzyme activity of cultivars and substitution lines even without cold treatment. Glutathione reductase (GR) activity measured in the tillering nodes of the plants was found to be correlated with the frost resistance of the genotypes and with the duration of hardening. Motto had the best frost resistance of all the cultivars, and the donor cultivar Cheyenne had better resistance than any of the substitution lines, irrespective of the length of the hardening period. Glutathion reductase enzyme activity also was the greatest in plants of these cultivars hardened for the same length of time, whereas the lowest enzyme activity was recorded for the winter oat Gerald, which had the poorest frost resistance, and the winter barley Hardy, which also had poor frost resistance. In all the cultivars, the activity of the GR enzyme increased as the hardening period progressed, whereas in the substitution lines, little change or a slight decrease was observed as in Cheyenne.

Within the framework of environment protection research, work on the effect of global climate changes involved experiments carried out in the phytotron at various atmospheric CO_2 concentrations. Wheat plants grown at double the present CO_2 level produced more biomass (25–35 %) and yield (9–38 %) than those grown at the normal level. Considerable differences in yield quality were observed at increased CO_2 concentration; in some cultivars there was a reduction in the protein and wet gluten content of the flour, whereas in others, the quality remained at the normal level. In plants grown at increased CO_2 concentration, nutrient requirements increased because of a greater uptake of CO_2; the optimum level of nitrogen supplies in the soil was also higher. As the result of heat shock at heading, a 19–35 % yield loss was observed, but this could be counteracted to a considerable extent by doubling the CO_2 concentration. Grain quality, however, was poorest in plants raised at increased CO_2 level and subjected to heat shock. The gluten index was 9–39 % lower than that recorded at normal CO_2 and temperature levels.

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Cell Biology Department

B. Barnabás, M. Molnár-Láng, É. Darkó, G. Linc, É. Szakács, E.D. Nagy, I. Takács, F. Bakos, K. Jäger, I. Molnár, H. Ambrus, A. Schneider, and I. Timár.

Physiological response of aluminium-tolerant wheat DH lines selected *in vitro* from microspores. The influence of Al on plant growth and mineral nutrition was investigated in Al-sensitive and Al-tolerant plants selected and regenerated from microspores. In the Al-sensitive genotype, increasing aluminium concentrations increased the accumulation of Al in the roots, causing a high reduction in root growth. A tight correlation was found between the increase of Al and the decrease of Ba, Cu, Mg, and Mn contents of the roots, indicating that Al inhibits the uptake of these elements. However, Al increased Fe and P accumulation in the roots. Aluminium accumulation and the phytotoxic effects of Al were lower in the Al-tolerant plants, suggesting an Al-exclusion mechanism was operating in the resistant lines.

The formation of reactive oxygen species induced by Al stress also was investigated in the selected lines. The roots of Al-tolerant plants were found to exhibit more intensive root growth, whereas accumulating less Al^{3+} and reactive oxygen species than Al-sensitive plants under Al-stress conditions. Aluminium accumulation was found chiefly in the root apex, although the formation of superoxides and peroxides was detected mainly in the elongation zone. Among the superoxide dismutase, ascorbate peroxidase, catalase, and glutathione-S-tranferase enzymes induced by Al stress, catalase and glutathione-S-tranferase may play an important role in the detoxification of reactive oxygen species in Al-tolerant plants, because they were found to have higher activity than in the Al-sensitive plants.

Effect of parental genotypes and colchicine treatment on the androgenic response of wheat F_1 hybrids. The effect of parental genotypes and colchicine treatment on the androgenic response of wheat F_1 hybrids was studied. Anthers from three F_1 hybrids and their parents were cultured on W14 initiation medium and W14 supplemented with 0.03 % colchicine. The number of responding anthers, microspore-derived structures/100 anthers, green plants/embryos cultured, green plants/100 anthers, and albino plants/100 anthers were recorded. The traits were genetically controlled and genotype dependent . In both treatments, the cultivar Kavkaz had a significantly higher percentage of responding anthers, microspore-derived structures, and green plants/100 anthers than the other genotypes. On the other hand, the cultivar Myconos also demonstrated high microspore-derived structure production and green-plant regeneration when treated with colchicine. The good response observed in these two wheats indicates the importance of colchicine treatment only for certain genotypes. The green plant-production capacity of the hybrids was intermediate to that of the parental genotypes. Because one parent with a high or even an intermediate response to anther culture could lead to the production of sufficient (for breeding purposes) green plants form the F_1 hybrids, we concluded that screening inbred lines for the response to anther culture with and without colchicine treatment could contribute to utilization of breeding material with a low response to anther culture via the proper hybrid combinations.

Wheat/barley hybridization and molecular cytogenetic identification of the derivatives. New winter wheat/winter barley hybrids were produced in Martonvásár using six-rowed, Ukrainian winter barley cultivars Manas and Osnova. Because the hybrids were sterile, they were multiplied in tissue culture and more than 100 regenerants were produced from the 'Asakaze komugi/Manas' combination. *In vitro* multiplication was repeated three times, because no backcross seeds were obtained even on the regenerants. Backcross seed finally was developed after the third *in vitro* multiplication cycle.

The chromosome constitution of the regenerated hybrids was analyzed using genomic *in situ* hybridization after each *in vitro* multiplication cycle to check that the barley chromosomes had not been eliminated. The seven barley chromosomes were present even after the third *in vitro* multiplication cycle, but abnormalities were observed. The pairing frequency between wheat and barley chromosomes increased, chromosome breakages occurred, the number of barley telocentrics and the number of amphidiploid cells increased, and wheat–barley translocations were detected.

Monosomic wheat–barley additions were developed by twice backcrossing Chinese Spring wheat with Betzes barley hybrids with the winter wheat genotypes Asakaze komugi and Martonvásári 9 *krl*. One 44-chromosome, disomic addition line was found among the selfed progeny of the 43-chromosome plants. By pollinating other 43-chromosome plants with maize, dihaploids were developed that were found to include one disomic addition line. Using total barley genomic DNA as a probe, the barley chromosomes were identified in the disomic addition lines by means of GISH. Barley chromosomes 2H and 6H were identified in the various lines using Giemsa C-banding. The effect of the barley chromosomes on the fertility and morphological traits of the plants was studied, and the stability of the lines was analyzed.

Production and identification of wheat–*Aegilops biuncialis* addition lines using FISH. FISH using two repetitive DNA clones (pSc119.2 and pAs1) on *Ae. biuncialis* (2n = 4x = 28, UUMM) and its two diploid progenitor species (*Ae. umbellulata* and *Ae. comosa*) was used to detect chromosome polymorphism. Differences in the hybridization patterns of all chromosomes except 5U and 5M were observed between the *Ae. umbellulata*, *Ae. comosa*, and *Ae. biuncialis* species. The differences in the hybridization patterns of the wheat and *Ae. biuncialis* parents analyzed after FISH using different repetitive DNA clones facilitated the exact identification of the *Ae. biuncialis* chromosomes in the wheat–*Ae. biuncialis* disomic additions produced in Martonvásár. Disomic addition lines for chromosomes 2M, 3M, 7M, and 3U have been selected, and two more lines still need to be characterized.

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Genetic and physiological studies.

G. Galiba, G. Kocsy, T. Janda, G. Kovács, J. Sutka, E. Páldi, G. Szalai, A. Vágújfalvy, B. Tóth, E. Horváth, A.F. Bálint, M. Pál, and V. Szilágyi.

Mapping genes affecting flowering time and frost resistance on chromosome 5B of wheat. Two populations of single-chromosome recombinant lines were used to map genes controlling flowering time on chromosome 5B of wheat, and one of the populations also was used to map a new frost resistance gene. Genetic maps were developed, mainly using microsatellite markers, and QTL analysis was applied to phenotypic data on the performance of each population collected from growth-chamber tests of flowering time and frost tolerance. Using a RSL mapping population derived from a cross between the substitution line Chinese Spring (Cheyenne 5B) and Chinese Spring, the gene *Vrn-B1*, affecting vernalization response, an earliness *per se* locus, *Eps-5BL1*, and the gene *Fr-B1* affecting frost resistance, were mapped. Using a 'Hobbit' sib' (Chinese Spring 5BL)/Hobbit' sib' RSL mapping population, the earliness *per se* locus *Eps-5BL2* was mapped. The *Vrn-B1* locus was mapped on the distal portion of the long arm of chromosome 5B to a region syntenous with the segments of chromosomes 5A and 5D containing *Vrn-A1* and *Vrn-D1* loci, respectively. The two E*ps-5BL* loci were mapped close to the centromere at a distance of 16 cM, which is in agreement with the position of a homoeologous locus previously mapped on chromosome 5H of barley and suggested by the response of Chinese Spring deletion lines. *Fr-B1* was mapped on the long arm of chromosome 5B, 40 cM from the centromeric marker. Previous comparative mapping data with rice chromosome 9 suggests that this gene could be orthologous to the other *Fr* genes mapped previously by us on chromosomes 5A or 5D of wheat, although in a more proximal position. This study completes the mapping of the homoeoallelic series of vernalization-requirement genes and frost-resistance genes on the chromosomes of the homoeologous group 5 in wheat.

Changes in the content of modified nucleotides in wheat rRNA during greening. The modified nucleotide content of ribosomal RNAs in wheat is greatly influenced by light. The rRNAs of etiolated seedlings contain far fewer derivatives. The modified nucleotide composition characteristic of green plants develops gradually as a result of irradiation. In the course of our experiments, changes in the state of modification of the 5.8S and 18S rRNAs were examined during the greening of etiolated wheat seedlings. Three types of minor nucleotides, O^2-methyladenosine, O^2-methylguanosine, and pseudouridine, were found in the 5.8S rRNA of green wheat leaves, none of which was detected in etiolated wheat. The minor nucleotides appeared in the 5.8S rRNA only 48 h after irradiation. The sequences of 5.8 rDNA, ITS1, ITS2, and 18S rDNA also were determined, and the presence of the hyper-modified nucleotide 1-methyl-3-(α-amino-α-carboxyropyl)-pseudoiridine was detected in green wheat 18S rRNA. This minor component was not demonstrable in etiolated wheat 18S rRNA but appeared after irradiation for 48 h.

Comparative study of frost tolerance and antioxidant activity in cereals. We investigated the correlation between the frost tolerance of cereals and their antioxidant capacity. Frost-tolerant and frost-sensitive cereal species, including wheat, barley, rye, durum wheat, and oat cultivars and wheat chromosome substitution lines, were cold-hardened at low, gradually decreasing temperature for 7 weeks. Control, unhardened plants were grown at a constant temperature of 17/

16°C. Changes in the activity of antioxidant enzymes/catalase, ascorbate peroxidase, guaiacol peroxidase (GPx), glutathione-S-transferase, and glutathione reductase in the crown and leaves were determined in the control and in hardened plants. The glutathione-S-transferase in the crown and leaf and the ascorbate peroxidase and GPx in the leaf were significantly higher in the hardened plants than in the controls. Catalase activity in the leaves was lower in the hardened plants. The highest correlation between the enzyme activity and frost tolerance was found for GPx and ascorbate peroxidase from hardened leaves. Enzyme activities in the crown and in unhardened leaves showed no significant positive correlation.

Effect of vernalization on the methylation level of DNA. We examined the changes in the 5-methylcytosine content of the DNA during vernalization in the winter wheat cultivar Mv 15, with a short vernalization requirement. The results indicated that low temperature treatment reduced the level of DNA methylation to a similar extent as the treatment with 50 mM 5-azacytidine (5-azaC), a compound causing demethylation. Illumination had no substantial influence on the quantity of methylated derivatives. The combined effect of vernalization and 5-azaC treatment caused a substantial reduction in the quantity of methylated cytosine. The data also proved that although the 5-azaC treatment reduced the methylation rate of the DNA in unvernalized plants, this in itself was not sufficient to induce flowering. Demethylation appears to be an important part of the vernalization; a factor induced by cold also is required.

Genetic resources. The growing interest in emmer and einkorn cultivation has no doubt been stimulated by the increasing demand for traditional foods with an image of naturalness, especially in the organic market. This new economic situation could stimulate breeding and production of emmer and einkorn as the source of an especially valuable foodstuff. The task of breeders is to produce cultivars that can survive without serious damage even the hardest winter occurring in the targeted cultivation area. The best sources for improving winter hardiness are probably emmer and einkorn genetic resources stored in gene banks. Unfortunately, no public data are available on the frost tolerance and winter hardiness of the various gene bank accessions. In our recent research, the frost tolerance and winter hardiness of 92 winter emmer and 46 einkorn gene bank accessions were studied under nursery and phytotronic conditions. The results suggest that the majority of the emmer populations studied are frost-sensitive, and only few landraces have an acceptable level of winter hardiness and frost resistance. Most of the einkorn accessions, however, showed a relatively high level of frost tolerance and winter hardiness. Based on a field experiment, 10 landraces from each species showing acceptable agronomic performance were selected to initiate an organic breeding program.

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The crop year 2002–03 was very special in Hungary, especially in the plains area where the Karcag Research Institute is located. Timely planting with good soil moisture led to excellent stand establishment, autumn growth, and spring recovery. However, high temperatures in the spring and drought stress during spring and summer reduced yield considerably and increased the expression of yield differences among the cultivars in both trials and large-scale production.

Recently released Karcag cultivars did quite well compared to other wheats coming from moist areas. We had only 4.1 mm precipitation in April, 26.2 mm in May, and 3.2 mm in the first 10 days of June.

Significant differences between the drought-tolerant and intolerant genotypes were observed. We had a good chance to select new entries for further advancement.

Currently, we have one early maturing (Kg Magor), four medium maturing (Kondor, Alex, Hunor, and Rona), and one medium-late (Kg Kunhalom) cultivars. These lines did well in both foundation seed increase and state-wide trials. The breeders seed and first reproduction sold completely.

At the same time, we advanced a large number of experimental lines for further testing and also put many of them in the statutory trials. One of our projects is to develop new cultivars for the unfavorable ecological conditions of the Plains area; another is the development of drought-tolerant cultivars. Both projects were successful in the last 2 years. We have had a chance to select genotypes and test the experimental lines in replicated trials.

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ITEMS FROM INDIA

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Combining quality traits with durable rust-resistance genes and molecular studies in Indian wheat.

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

Improving wheat quality by combining desirable HMW-glutenin subunits and durable rust-resistance genes in a high-yielding background is in progress. Single-plant selections made in the F_3 generation are being evaluated for their agronomic characters.

Wheat–rye translocations have been widely used by breeders worldwide. Translocations involving the short arm of chromosome 1 (1RS) of rye significantly influence wheat cultivar performance, because 1RS has genes for resistance to pathogenic fungi and insect pests and also influences dough quality and agronomic traits. The reciprocal translocation involving wheat chromosome 1BS is designated as T1BL·1RS. In a study of genetic diversity among Indian wheat cultivars using RAPD markers, a 1.1-kb band was found only among cultivars lacking T1BL·1RS. Of 49 cultivars, 35 cultivars lacking T1BL·1RS amplified this band. A close link between this band and the region of 1BS involved in the translocation was postulated. An F_2 population from a cross involving one parent with T1BL·1RS was analyzed. The 1.1-kb band segregated in 3:1 ratio. Segregation between the T1BL·1RS translocation and the 1.1-kb marker indicated that the new marker will be useful in identifying homozygous individuals for T1BL·1RS in early generations. The marker is being developed into SCAR a marker.

Crosses were made between Indian and Australian cultivars for genetics and breeding objectives. F_2 populations were grown. These populations will be used to develop molecular marker(s) and transfer useful gene(s) to Indian cultivar backgrounds.

Internal transcribed spacer region variation in bread wheat.

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Variation in the internal transcribed spacer (ITS) region was detected using PCR–RFLP in the cultivars Kalyansona and Sonalika. An F_2 population of 150 plants resulting from a cross between these two genotypes was analyzed. Segregation for the Kalyansona variant was observed to fit a 3:1 ratio (X^2, P = 0.2–0.3). The ITS variant was mapped on chromosome 1B at a distance of 26.8 cM from the *Glu-1B* locus.

A radiation-induced mutant in wheat.

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

Radiation-induced mutants can be useful in genetic studies. A genetic stock with the sphaerococcum character was subjected to gamma-ray treatment. A mutant with a lax spike was isolated and stabilized into a true-breeding condition. The parent had a spike length of 5.22 ± 0.11 cm with 3.14 ± 0.07 spikelets/cm. In the mutant, the spike length was 6.8 ± 0.15 with 2.06 ± 0.07 spikelets/cm. The mutant showed a 30.2 % increase in spike length and a 34.4 % reduction in spikelets/cm. An F_2 population from a cross between the mutant and parent showed segregation for lax intermediate and compact spikes. Initial results indicated monogenic inheritance of the lax spike mutation.

Image analysis of wheat grains.

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Grain morphology is important in assessing wheat grain quality and in visual cultivar identification. Computer-based, image analysis can measure morphometric parameters accurately and, thus, has a potential for use in the assessment and identification. Grain size and shape is influenced by environment. We designed experiments to study how computer-based, image analysis can be used to deal with environmental and genotypic variation. Three cultivars were sown on three different dates in the field at Trombay in a replicated experiment. Grain samples were collected at maturity and image analysis was made on each replicate separately. Images were grabbed using a scanner and analyzed with Comprehensive Image Analysis Software (CIPS). About 45 size- and shape-related parameters were used based on the variation. Euclidean distances were calculated. Euclidean distances for samples of the same cultivar sown at different times were smaller, indicating a greater resemblance between them than compared to samples of different cultivars. The results indicate that image analysis has the potential to overcome problems of environmental variation to a certain extent.

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Breeding for rust resistance and seed-storage proteins in bread wheat.

V.R.K. Reddy and G. Kalaiselvi.

Eight stem rust-resistance genes (*Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr28*, *Sr31*, *Sr36*, and *Sr38*), four leaf rust-resistance genes (*Lr19*, *Lr24*, *Lr26*, and *Lr37*), and two stripe rust-resistance genes (*Yr9* and *Yr17*), present singly or in combination (in linked condition), were transferred from alien hexaploid wheat stocks into three Indian hexaploid wheat cultivars (HW 2034, HW 4001, and K 8962). Gene transfer was confirmed with biochemical markers. Changes in the enzymatic activity of peroxidase, polyphenol oxidase, catalase, esterase, and lipoxygenase in the leaves of 25-day-old plants of rust-susceptible wheat parents and rust-resistant NILs inoculated with the respective rust pathogen showed altered activity.

The constituted lines showed higher peroxidase activity compared to the healthy controls 2–7 days postinoculation. Polyphenol oxidase activity increased in all NILs 3–7 days postinoculation, whereas a decrease in activity was observed in the susceptible parents. Catalase activity was higher in susceptible wheat parents than in the resistant NILs. Lipoxygenase activity increased in both the susceptible wheat parents and their NILs 2 days after inoculation, but subsequently decreased 7 days after inoculation in resistant plants. A consistent increase was noticed in the susceptible parents. Esterase activity increased in all the NILs 3–7 days after inoculation but decreased in activity in the susceptible wheat parents. The total lipid content of the leaves increased in both susceptible and rust-resistant NILs 2 days after inoculation but subsequently decreased as the postinoculation time increased. 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 subsequently decreased towards later stages of infection. The percent decrease was greater in susceptible lines 7 days after inoculation.

SDS–PAGE analysis of the soluble proteins did not show any major qualitative difference in the protein profiles in the leaves of either healthy or inoculated susceptible parents and their resistant NILs 1 and 7 days after inoculation with rust spores, and most of the protein bands were common in all the lanes. However, quantitative changes were observed as seen from the intensity of the banding pattern. Some of the major protein bands were found to increase in intensity in the leaves 24 hours after inoculation in both susceptible and resistant plants. The increase was greater in the resistant plants. The intensity of the major protein bands decreased in the leaves of susceptible and resistant plants 7 days after inoculation. The decrease was greater in the susceptible plants.

The specific activity of ribonuclease-I and combined ribonuclease-II and nuclease-I was high at the 15-day stage compared to that at the 10th day in both susceptible and resistant lines. Resistant NILs had a relatively higher chlorophyll content than the susceptible wheat parents. Free amino-acid content increased up to the 8 days after inoculation in both susceptible and resistant wheat lines. After 8 days, a slight reduction was seem in both cases.

Respiration rate increased to a greater extent in resistant NILs compared to their susceptible wheat parents. By the 3rd day after inoculation, the reduction in respiration rate in the susceptible parents was dynamic, whereas in the resistant NILs, the level was more or less constant. A significant increase in total free phenols and tannin content was observed in the NILs over their respective recurrent wheat parents. The NILs had a significantly higher nuclear DNA content than their respective susceptible wheat parents. Resistant NILs accumulated proline at a more rapid rate and at higher level as a result of infection than did the susceptible wheat parents.

High-molecular-weight glutenin subunit composition in wheat.

V.R.K. Reddy and G. Kalaiselvi.

Twenty *T. aestivum* cultivars were analyzed for their allelic variations of HMW-glutenin subunits by SDS–PAGE. A total of 10 alleles were identified, three (a, b, and c) at the *Glu-A1* locus, four (a, b, c, and d) at the *Glu-B1* locus, and three (a, b, and d) at the *Glu-D1* locus. The most frequent HMW-glutenin subunits were 2* at *Glu-A1*, 7 at *Glu-B1*, and 2+12 at *Glu-D1*. The most frequent protein combinations are 2*, 7+8, 2+12 and 2*, 7, 5+10. The *Glu-1* quality score ranged from 5–10. The *Glu-1* quality score 8 is present in a large number of cultivars. We predict that those cultivars that possess a high *Glu*-1 score have good bread-making quality, i.e., above 8, and those with a *Glu-1* score below 7 are of very poor bread-making quality.

The relationship between gliadin bands and wheat quality.

V.R.K. Reddy and G. Kalaiselvi.

Gliadins from 10 common wheat cultivars were extracted and separated by SDS–PAGE. The cultivars were classified into two groups based on the presence or absence of two bands (designated as 40 and 43.5 according to their mobility) in their electrophoregrams. Cultivars of group 1 had prominent band 40 and lack band 43.5, whereas cultivars comprising group 2 showed the strong band 43.5 and lacked band 40. The cultivars containing band 43.5 possess stronger gluten properties than the cultivars containing band 40. Bands 40 and 43.5 could be gliadin components typical of bread wheats, coded by the locus on homologous chromosome group 1D. In view of the important effects of bands 40 and 43.5 on gluten properties, a better understanding of genetic aspects of these bands could be of considerable value in the qualitative breeding of common wheats.

Incorporation of leaf rust-resistance genes and their confirmation through molecular markers.

V.R.K. Reddy and M. Binumol.

We introgressed five leaf rust-resistance genes (*Lr19*, *Lr24*, *Lr28*, *Lr32*, and *Lr37*), four stem rust-resistance genes (*Sr24*, *Sr25*, *Sr34*, and *Sr38*), and two stripe rust-resistance genes (*Yr8* and *Yr17*) into three Indian wheat cultivars C 306, UP 2338, and HP 1205 in a backcross breeding program. Near-isogenic wheat lines were constituted either in the BC_2F_5 and/or the BC_5F_5. Gene transfers were confirmed with molecular markers. Isogenic lines with leaf rust-resistance gene *Lr24* were used this purpose. The primers J09/1 and J09/2 gave a specific band for the resistant lines 1, 3, 5, and 7, whereas it was absent in the susceptible lines. The amplification product size was 4,000 bp. The presence of this band only in the donor parent and its resistant derivatives indicates that this fragment originated from the donor parent.

Eight RAPD primers, OPB–07, OPB–16, OPB–03, OPJ–09, OPB–18, OPB–11, OPB–06, and OPR–11, also were used to identify bands specifically present in only the resistant lines of C-306, HP1205, and UP 2338. They gave amplification products ranging from 400–1,200 bp, whereas several other bands generated by the RAPD primers were identical in both susceptible and resistant NILs.

Hybrid necrosis and chlorosis in some hexaploid and tetraploid wheats.

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Fifteen *T. aestivum* and 15 *T. turgidum* subsp. *dicoccum* wheat cultivars were crossed with four tester *T. aestivum* cultivars C 306 (*Ne1 ne2 ch1 Ch2*), Sujatha (*ne1 Ne2 Ch1 ch2*), Klein Lucero (*ne1 Ne2 ch1 Ch2*), and Kharkof (*ne1 Ne2 Ch1 ch2*). All hexaploid and tetraploid wheat genotypes were crossed separately with each of the testers. The genotypes of the wheat cultivars for hybrid necrosis and hybrid chlorosis were determined from the phenotype of their F_1 hybrids. Observations on the degree of hybrid necrosis and hybrid chlorosis were taken periodically at different stages of plant growth. Six out of 15 hexalpoid wheats produced normal hybrids without any necrosis when crossed with testers C 306 and Sujatha, whereas the same cultivars produced necrotic hybrids with Klein Lucero and Kharkof indicating the presence of *Ne2* in these wheats. The remaining nine wheats produced necrotic hybrids with C 306 and Sujatha, suggesting that they are carriers of *Ne2*. They produced normal hybrids with the other two testers. On the other hand, all 15 hexaploid wheats produced normal hybrids without any chlorosis with C 306 and Klein Lucero and chlorotic hybrids with Sujatha (except HI 667 and HI 687), also indicating that all of them are the carriers of *Ch2*. HI 667 and HI 687 produced normal hybrids without any chlorosis with the other two testers suggesting that they do not carry any dominant chlorotic genes.

In the dicoccum wheats, all 15 cultivars produced normal hybrids without any necrosis with C 306 and Sujatha. These lines carry *Ne1*. The fact that 10 out of 15 wheats produced necrotic hybrids with

Table 1. Genotypes of the hexaploid and tetraploid wheats and the necrosis and chlorosis genes present.

Hexaploid wheats: Cultivar	Genotype	Tetraploid wheats: Cultivar	Genotype
HD 2009	*ne1* $Ne2^m$ *ch1* $Ch2^w$	Azar	$Ne1^w$ *ne2* $Ch1^s$ *ch2*
HD 2021	*ne1* $Ne2^m$ *ch1* $Ch2^w$	Farmer K 6413	$Ne1^w$ *ne2* $Ch1^s$ *ch2*
HD 2028	*ne1 Ne2s ch1* $Ch2^w$	Felted Khapli	$Ne1^w$ *ne2* $Ch1^s$*s ch2*
HD 2068	*ne1 Ne2s ch1* $Ch2^w$	Khapli	$Ne1^w$ *ne2* $Ch1^m$ *ch2*
HP 741	*Ne1s ne2 ch1* $Ch2^w$	Khapli PI 33	$Ne1^m$ *ne2* $Ch1^m$ *ch2*
HW 515	$Ne1^m$ *ne2 ch1* $Ch2^w$	Khapli Pink 508	$Ne1^w$ *ne2* $Ch1^m$ *ch2*
MP 113	$Ne1^s$ *ne2 ch1* $Ch2^w$	Khapli 101 Yellow	$Ne1^w$ *ne2* $Ch1^s$ *ch2*
MP 114	$Ne1^s$ *ne2 ch1* $Ch2^w$	Swan 248	$Ne1^w$ *ne2* $Ch1^s$ *ch2*
HI 667	*ne1 ne2 ch1 ch2*	WDL 26	$Ne1^w$ *ne2* $Ch1^s$ *ch2*
HUW 12	*ne1* $Ne2^m$ *ch1* $Ch2^m$	WDL 27	$Ne1^w$ *ne2* $Ch1^m$ *ch2*
HUW 91	*ne1* $Ne2^s$ *ch1* $Ch2^m$	NP 201	*ne1 ne2 ch1 ch2*
HW 558	*ne1* $Ne2^s$ *ch1* $Ch2^m$	NP 202	*ne1 ne2 ch1 ch2*
HW 600	*ne1* $Ne2^m$ *ch1* $Ch2^m$	HW 65	*ne1 ne2 ch1 ch2*
HW 601	*ne1* $Ne2^s$ *ch1* $Ch2^m$	V 585	*ne1 ne2 ch1 ch2*
HI 687	*ne1 ne1 ch1 ch2*	V 604	*ne1 ne2 ch1 ch2*

Klein Lucero and Kharkof also supports this conclusion. The remaining five tetraploid wheats produced normal hybrids without necrosis with the other two testers, indicating that they carry recessive necrotic alleles. All 15 dicoccum wheats produced normal hybrids without chlorosis with Sujatha and Kharkof indicating the presence of *Ch1* alleles in all these cultivars. Five of the 15 tetraploid wheats also produced normal hybrids without any symptoms of chlorosis with C 306 and Klein Lucero, suggesting that they carry recessive chlorotic alleles. The genotypes of the hexalpoid and tetraploid wheats with reference to necrosis and chlorosis genes present are given in Table 1 (p. 51).

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Development and use of molecular markers for wheat genomics.

QTL analysis for different traits using the International Triticeae Mapping Initiative population and a trait-specific population.

QTL analysis for grain-protein content (GPC) using two populations (an intervarietal population and the International Triticeae Mapping Initiative population (ITMI pop).

Genetic dissection of GPC followed single-locus and two-locus QTL analyses, with the particular objective of studying QTL x QTL (QQ), QTL x environment (QE), and the QTL x QTL x environment interaction (QQE) for this trait. Two different mapping populations were utilized. Population I was derived from a cross between two Indian cultivars (WL711/PH132), and population II was the ITMIpop. Each population was grown in 4–5 different environments. A total of 14 QTL (spread over eight different chromosomes; 1A, 2B, 2D, 4A, 5B, 6D, 7A, and 7D) in population I and 12 QTL (spread over following eight chromosomes; 1A, 1B, 1D, 2A, 2D, 3B, 5D, and 7A) in the ITIMIpop were detected following two-locus analyses (QTLMapper), as opposed to 10 and 7 QTL detected in Population I and the ITMIpop, respectively, following a single-locus CIM (QTL Cartographer). Ten M-QTL (main effect QTL) were detected in the two populations; five in each population. The M-QTL accounted for 7.24 % of the total variation in Population I and 7.22 % variation in the ITMIpop. In both the mapping populations, major QTL were detected on chromosome 2D. In Population I, four E-QTL (epistatic QTL), and in the ITMIpop, six E-QTL, were detected, which accounted for a mere 2.68 % and 6.04 % of the phenotypic variation, respectively. Contrary to the small proportion of variation contributed by M-QTL and E-QTL for GPC, QE and QQE contributed a substantial proportion of variation in Population I (25.91 %) and in the ITMIpop (47.99 %). The importance of using more than one diverse mapping population for detecting many more QTL and using two-locus analysis in detecting interactions has been documented in this study. This work has been submitted for publication to Plant Physiology.

QTL analysis for preharvest sprouting tolerance (PHST) using the ITMI pop.

QTL interval mapping for preharvest-sprouting tolerance (PHST) with the ITMIpop used single-locus and two-locus analyses. For this trait, 110 RILs of the ITMIpop were evaluated in four different environments comprising three different locations. At physiological maturity, data on PHST were recorded on each of the 110 RILs (in each of the four environments) on a scale of 1–9 with a score of 1 for genotypes with complete resistance to preharvest sprouting and a score of 9 for the genotypes with complete sprouting. Marker genotyping data of 521 mapped molecular markers was retrieved from GrainGenes for QTL analysis. A wide range of variability for PHST among the RILs as opposed to the narrow range of variability between the parents (W7984 and Opata85) of the ITMIpop encouraged us to conduct QTL interval mapping using single-locus analysis followed by composite-interval mapping (CIM). We identified five QTL on four chromosomes, 2B, 2D, 3B, and 3D. A two-locus analysis using QTLMapper resolved a total of 14 QTL including eight M-QTL, eight E-QTL, and five QTL involved in QE or QQE interactions. Four of the five QTL detected following CIM were common to the 14 QTL detected following two-locus analysis. We observed that more than three-fourths (76.68 %) of the variation for PHST is due to M-QTL (47.95 %) and E-QTL (28.73 %) as opposed to a very small fraction (3.24 %) that is due to QE and QQE. Two QTL detected above the threshold LOD score and in more than one environment were located on 3BL and 3DL, presumably in the vicinity of dormancy gene *TaVp1*. Another QTL located on 3BL was in close proximity to the R gene for red grain color. Thus, PHST differs from GPC in its genetic control. PHST is mainly controlled by M-QTL and E-QTL, whereas GPC is mainly controlled by QE and QQE interactions. This study on PHST has been published in *Functional & Integrated Genomics*.

QTL analysis of PHST and grain weight (GW) using trait-specific, intervarietal mapping populations.
Two mapping populations consisting of 100 RILs each, one derived from the cross 'SPR8198 (PHS tolerant)/HD2329 (PHS susceptible)' and the other from the cross 'Rye selection (high GW)/Chinese Spring (low GW)' are available. Phenotypic data on PHST and GW were recorded at three different locations for 2 years for a total of six environments. Genotyping of both populations of 100 RILs was made using AFLP, SAMPL, and SSR markers. AFLP and SAMPL genotyping used fluorescent primers and an ABI 377 sequencer and GeneScan/Genotyper software. SSR analysis used the conventional method of silver staining. Marker genotyping data for a total of 320 and 466 markers (including a combination of AFLP, SAMPL, and SSR markers) for the PHST and GW mapping populations, respectively, were available. This data was used to prepare framework linkage maps of these mapping populations. Using this genotyping data, and the phenotypic data recorded in six environments (and also that averaged over environments), single-marker regression analysis was conducted for PHST. A total of 63 markers were found to be associated significantly to QTL that contribute to variation for PHST, with an R^2 ranging from 4.09 % to 29.03 %. Marker gwm155, which was earlier mapped on 3AL, exhibited the highest R^2 (29.03 %). For GW, 79 markers were found to be associated with QTL that contribute significantly to variation for PHST, with R^2 ranging from 3.96 % to 11.89 %.

Monosomic analysis for GPC. Continuing our earlier studies, an F_2 monosomic analysis was used to identify chromosomes that carry genes/QTL for GPC. The crosses involved a high GPC (14.82 %) wheat genotype, PH132, which also is a parent of an intervarietal mapping population we used for QTL analysis for GPC and a monosomic series in Chinese Spring. Ten different chromosomes (2A, 1B, 2B, 3B, 4B, 5B, 6B, 7B, 1D, and 2D) were identified to carry genes/QTL for GPC.

The results of monosomic analysis were compared with those from our recent studies on QTL analyses conducted for eight different environments. We detected QTL for GPC on 16 different chromosomes of bread wheat using CIM by QTL Cartographer and by conducting two-locus analysis by QTLMapper, which detects QTL with main effect, epistatic effects, and 'QTL x environment' interaction. The 16 chromosomes with QTL included 9 out of the 10 different chromosomes identified by monosomic analysis. From these results, we concluded that the QTL analysis detected QTL for GPC on seven more chromosomes than were identified following monosomic analysis. Similarly, none of the QTL for GPC detected following QTL analysis could be assigned to 1D, which was one of the 10 chromosomes that were identified to carry genes/QTL for GPC following monosomic analysis. Failure to detect genes/QTL on 1D through QTL analysis should be due to unavailability of an adequate number of mapped markers on this chromosome. In the future when more markers are used, QTL analysis also should be able to detect QTL for GPC on 1D.

Development and use of EST–SSRs and EST–SNPs (using wEST).
Development of EST–SSRs from wheat EST databases.
We have extended our study on the development of wheat EST–SSRs to increase the density of SSRs in the expressed region of the wheat genome. For this purpose, we screened ~415,000 wESTs for the presence of SSRs and discovered 10,415 nonredundant (nr) SSRs giving a density of one SSR/20.15 kb. Trinucleotide repeats (TNRs) were the most frequent. Primers also were designed for 380 nrEST–SSRs. The above SSR–ESTs also were annotated and divided into 16 classes based on their putative function predicted by a BLAST similarity search.

Transferability of wheat EST–SSRs and genomic SSRs in 18 alien species of Triticeae. Sixty-four functional EST–SSR primers developed previously that we used to study polymorphism, transferability (against oats, maize, rice, rye, and barley), and genetic diversity among 52 elite wheat genotypes (Gupta et al. 2003) also were used to study transferability to 18 alien species of Triticeae possessing different genomes (A, B, D, M, N, and U) and ploidy levels (2x, 4x, and 6x). The results were summarized in Bandopadhyay et al. 2004. In-gel hybridization and PCR-based approaches also were used earlier to study interspecific SSR polymorphism among 14 species of *Triticum–Aegilops* group (Sharma et al. 2002).

Development of EST-SNPs and estimation of LD. Massive databases of ESTs and gDNA clones derived from libraries enriched for genes already have been developed and are being further improved for bread wheat. To exploit these resources and reduce duplication of efforts between laboratories, a wheat SNP consortium was established. This consortium assembled all available wESTs into 40,000 contigs. From the above set of 40,000 contigs, 9,346 contained ≥ 8 ESTs (exploitable for SNP mining) and were considered suitable for detecting SNPs. These contigs also were allocated to different members of the consortium. Each member partner received 48 contigs. From the set of 48 contigs, we were able to detect 462 HSVs (homoeologue-specific variations) and 231 SNPs, giving a density of one SNP/273.4 bp. Of these SNPs, 53.5 % represent transitions and 46.5% represent transversions. Primers also were designed and synthesized for 43 SNP containing contigs.

LD was also estimated electronically, using the above data. From the study of a few EST contigs/genes, we found that in wheat (like *Arabidopsis* and rice), relative to maize, LD persists for much longer distances. These results confirm the belief that LD persists for longer distances in wheat like other autogamous crops.

Physical mapping of SSRs on all 21 chromosomes of bread wheat. Approximately 1,500 SSRs have been genetically mapped in bread wheat (D. Sommers, personal communication; Sourdille et al. 2004). Only Sourdille et al. has physically mapped of some of the SSRs that they independently genetically mapped. Thus, a large number of genetically mapped SSRs still remain physically unmapped. In the present study, using two nullisomic-tetrasomic lines and two ditelocentric lines for each of the 21 wheat chromosomes and a total of 300 terminal deletion stocks, we tried to physically map as many as 590 SSRs (wmc, gwm, psp, cfa, and cfd). Of these, 413 markers were physically mapped. The remaining 177 of the above 590 genetically mapped SSRs could not be mapped physically, because the homoeoloci for these markers were monomorphic. A comparison of the physical maps of individual chromosomes with their genetic maps (D. Sommers, personal communication; Sourdille et al. 2004) revealed that the linear order of 95 % of the marker loci did not differ in genetic and physical maps, but the distances between the markers differed greatly in genetic and physical maps.

High-resolution mapping of genomic regions containing important QTL for GPC. Two major QTL for GPC located on chromosome arms 2DL and 7AS, identified in our earlier studies (Prasad et al. 2002), were selected for high density mapping of the genomic regions containing these QTL. For this purpose, a large F_2 population was derived from crosses between two RILs, one containing both the high-GPC alleles and the other containing low-GPC alleles for the selected QTL. DNA has been isolated from about 2,000 individual plants that is being genotyped to identify recombinants.

Future Plan of Work. *High-density mapping.* Individual F_2 plants will be screened using markers flanking the genomic region containing the desired QTL for GPC and the recombinants for the markers flanking the QTL will be selected. Genotyping of recombinant F_2 plants will be carried out using SAMPL, AFLP, STS, and SSR markers to saturate the regions of our interest. Wheat EST markers already mapped in the genomic region containing QTL of our interest and those mapped in the syntenic regions in other grasses also will be used for saturation mapping of the selected regions.

Study of organization of SSRs in repetitive and unique fractions of genomic DNA (using Cot fractionation and methyl filtration). In order to study the organization of SSRs separately in repetitive and unique fractions of genomic DNA of wheat, we separated repetitive and nonrepetitive fractions from total genomic DNA of Chinese Spring wheat using hydroxyapetite column chromatography. Repetitive DNA (low Cot fraction) in the range of 500–1,500 bp was selected for genomic library construction. A genomic library was constructed in the pUC18 (*Sma*I/dephosphorylated) vector. Blue–white screening was used to check transformed (with an insert) and nontransformed cells using IPTG and X-gal. About 2,000 white colonies were transferred to Hybond (N+) membrane and screened for clones representing highly repetitive DNA, using sheared genomic Chinese Spring DNA as a probe. After the first round of screening, we selected about 500 clones (clones that gave strong signals) assuming that these clones contain repetitive DNA. These clones will be used for secondary and tertiary screening. Nonredundant, positive repetitive DNA clones will be sequenced to identify the clones containing SSRs and study the organization of sequences containing SSRs. The sequence data of different clones will also be compared with wheat/Triticeae repetitive DNA sequences data available in the database. Nonredundant, repetitive DNA clones containing SSRs also will be used as probes in Southern hybridization to study the genomic organization of SSR containing repetitive DNA sequences in wheat. Physical distribution of the cloned repetitive DNA–SSRs in wheat also will be studied using FISH in mitotic metaphase chromosomes.

The single-stranded nonrepetitive DNA as separated above, will be converted to double-stranded form. The double-stranded fragments will then be size-selected over an agarose gel and cloned into the PCR4 TOPO vector. This library will be enriched for low-copy sequences like genes, and clones containing SSRs will be identified and sequenced. The information generated will be used for a study of the organization of SSRs in the unique DNA sequences.

We also propose to use methyl filtration for separation of repetitive and nonrepetitive fractions of wheat genomic DNA. Repetitive DNA is often more highly methylated than low-copy DNA. The methylated and unmethylated DNA will be separated using either methylation-sensitive restriction enzyme or bacterial host strains that preferentially restrict methylated DNA. The sequences of as many as 1,000 clones representing a sample of hypomethylated fraction of wheat genomic DNA also will be procured from Orion Genomics and used for a study of the organization of SSRs in this hypomethylated fraction of genomic DNA.

Marker-assisted selection (MAS) for high GPC and PHST. The high-GPC gene already has been transferred from *T. turgidum* subsp. *dicoccoides* into durum and hexaploid backgrounds, which is a valuable resource for increasing GPC. We have one of the high-GPC hexaploid lines Yecora Rojo (16–17 % GPC), which was procured from Jorge Dubcovsky, University of California, Davis, USA. Using Yecora Rojo and SPR8198 as donor parents for GPC and PHST, respectively, we are conducting a backcrossing program for the introgression of high GPC and PHST QTL into low-GPC and preharvest sprouting susceptible elite Indian wheat genotypes.

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Mapping of soil mycoflora in wheat based cotton-wheat sequence.

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Soil is a reservoir of microflora that fluctuates with soil type, cropping system, and the prevailing environmental condition. Soilborne mycoflora were mapped and monitored in a cotton–wheat rotation in two wheat breeding research plots during the 1997–2001 crop seasons. The plots were '25 x 10 m' and 2 m apart. Randomly collected soil samples from the rhizosphere from the cotton (cultivar HS-6) and wheat (cultivar WH 147) crops were analyzed in order to map soil biology and pest dynamics in the different cropping systems and observe changes in the soil mycoflora populations and buildup of either pathogenic or nonpathogenic inoculum. Two treatments were used. An herbicide was applied to one plot. The other plot did not receive any herbicide in the wheat or cotton. Isoproturon was used in the wheat plot, and Stomp was used to know its effect on soil mycoflora in the cropping sequence. Soil samples were taken at three stages, at sowing, at flowering, and at harvest in cotton; and five stages in wheat, before field preparation, at sowing, 30 days after sowing, at flowering, and at maturity.

From the cotton field, 10 fungal species were isolated; 12 fungal species were isolated from the wheat field. The data are presented in Tables 1 and 2 (p. 57). *Aspergillus niger*, *Fusarium spp*., and *Helminthosporium spp*. were found in the soil environment of both crops. These were nonpathogenic but perpetuating. Similar observations were made by Pathak (2000) and Singh et al. (2000) in soybean–wheat and rice–wheat systems at Sagar and Faizabad, respectively, which confirm our study.

Table 1. Soil mycoflora of a cotton crop under a cotton–wheat rotation. Frequencies (number of colonies/gm of soil x 10^{10}). Treatment one (T1) is with hand weeding and treatment two (T2) is with an herbicide application.

	Sowing		Flowering		Harvest	
Fungi isolated	T1	T2	T1	T2	T1	T2
Alternaria alernata	2.10	11.50	15.00	12.75	8.75	6.50
Aspergillus flavus	2.00	1.50	2.75	2.25	4.25	3.75
Aspergillis niger	2.90	2.25	2.75	2.50	6.50	5.25
Cladosporium spp.	4.00	3.75	4.50	3.75	5.00	4.75
Curvularia lunata	—	—	4.10	3.90	8.90	6.50
Fusarium spp.	6.90	6.10	9.00	7.90	7.50	7.00
Helmithosporium spp.	3.25	12.00	16.75	15.01	12.90	11.00
Mucor spp.	3.25	2.00	3.75	2.50	3.50	2.25
Penicillum spp.	—	—	3.10	2.25	2.90	2.75
Rhizopus spp.	10.00	9.40	19.50	17.90	15.25	11.75

Table 2. Soil mycoflora in wheat under a cotton–wheat rotation. Frequencies (number of colonies/gm of soil x 10^{10}). Treatment one (T1) is with hand weeding and treatment two (T2) is with the herbicide Stomp applied.

	Before field preparation	At sowing	30 days after sowing		Flowering		Harvest	
			T1	T2	T1	T2	T1	T2
Alternaria alternata	5.25	5.80	10.50	10.00	15.75	12.25	10.75	8.50
Aspergillus flavus	2.50	2.00	4.75	3.75	4.25	4.00	5.50	4.80
Aspergillus niger	2.75	3.00	3.00	2.25	3.50	3.00	5.75	4.90
Aspergillus nidulans	3.25	3.00	5.75	5.25	6.00	5.10	6.25	5.75
Aspergillus terreus	2.25	3.25	3.10	2.75	3.00	2.90	3.50	3.10
Aspergillus sydowi	2.25	2.75	3.50	2.75	3.10	2.50	3.25	2.80
Fusarium spp.	3.20	3.50	5.00	4.80	8.90	8.75	7.25	7.10
Helmithosporium spp.	—	—	2.00	1.25	3.25	2.50	4.10	3.50
Penicillum spp.	9.25	8.75	12.50	11.50	15.10	12.50	12.75	0.50
Rhizopus nigricans	10.00	9.75	16.25	15.50	20.75	18.75	16.75	10.80
Trichoderma spp.	1.50	2.70	5.10	4.80	5.20	4.90	4.20	4.00
Trichoderma viridae	1.50	2.50	5.00	4.50	5.00	4.70	4.20	4.00

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Exploiting diversity in wheat: synthetic wheats as potential donors for some economic traits for the Indian subcontinent.

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Summary. Wheat is the life line in a country like India where the population is around 100 crores. Wheat researchers will not only have to maintain the present growth rate in wheat productivity but also need to further accelerate the pace in productivity per year. In India, all efforts are being made to create and harness variability, which is a ladder for all crop-improvement programs. With this in mind, efforts were made to enhance the genetic diversity in wheat for economic traits, particularly yield attributes. A set of 90 synthetics obtained from CIMMYT–Mexico was evaluated in an augmented design for assessing genetic variability in yield-contributing traits. We observed that most of the synthetic lines had more tillers/m^2 and better spike and grain size compared to the best *T. aestivum* (PBW 343) and *T. durum* (HI 8498) checks. The top 10 lines were selected for each character and these have been crossed with promising indigenous cultivars to pyramid genes for these traits. Although they produce material that is of low threshability and red grained, two to three backcrosses seem to improve such type of undesired traits. Many of the synthetics possess resistance to many diseases particularly leaf blight and rusts. In general, these synthetics also possess tolerance to abiotic stresses, namely heat and drought but have long duration. Our research deals with the variability for various economic traits in synthetics, their use as potential donors for specific traits, and the problems associated with their use in wheat improvement programs in the Indian subcontinent.

Introduction. Wheat has been linked with the development of both agriculture and civilization in many for countries in the world. Presently, wheat is the staple food of above 40 % human population across the globe. In India, wheat along with rice contributes over 40 % of the total food grain reserves, thus, reducing the need to import wheat even during poor monsoon years. Estimates predict that the population of India will be more than 1.3 billion by the year 2020. To make 180 g of wheat/capita/day available, India will need 109 x 10^6 tons of wheat. Because a marginal increase in area under wheat is unlikely, to achieve this target no option exists but to increase the yield potential of new wheat cultivars to a greater extent. An increase of 1 %/year in production has been achieved through the higher-yielding ability of wheat cultivars during the last 30 years.

In order to strengthen and make the wheat-breeding program vibrant, the availability of diverse material is very important. Alien genetic resources are not routinely used in a breeding program. These wild species are the reservoir of various useful biotic and abiotic traits and have remained largely untapped for economically important traits such as high seed weight, protein content, high tiller number, long spikes, and disease resistance (Kerber and Dyck 1979; Ma et al. 1995; Villareal et al. 1994a, b). Most of the diversity derived from wild relatives has been from the secondary gene pool species, which needs some effort to incorporate them into the background of primary gene pool species. The synthetic hexaploid wheats may emerge as the potential resource to break the yield barrier.

Material and Methods. A set of 90 synthetic lines was procured from Wheat Genetic Resources Unit, CIMMYT, Mexico, during 1998–99 for evaluation and utilization in the Indian wheat program. These synthetic lines, which are hexaploid in nature, were originally developed at CIMMYT–Mexico by crossing durum (4x) wheats with *Ae. tauschii* (2x) and then making the F_1s into dihaploids (6x). During the 2001–02 season, 90 synthetic lines, along with local cultivars as checks, were planted in an augmented design. For each genotype, a 3-m, six-row plot was planted with a 23 cm row-to-row distance. Normal agronomic practices were followed to raise a good crop. Data on various traits were recorded on five, randomly selected plants and then means were calculated. The tillers/m were counted from the middle two rows by randomly selecting one meter row distance at two places. Spike length was taken on the 10 different spikes of the main tiller and then averaged. Other data also were taken on the main tiller of each selected plant. Statistical analysis for testing the significance (t-test) of various traits was carried out following the approach suggested by Panse and Sukhatme (1967).

Results and Discussion. The data recorded on various agronomic traits in 90 synthetic wheat lines showed a wide range of variation for yield-component characters (Table 1, p. 59). The highest coefficient of variation (CV) was noted in tillers/meter (31.34) followed by seeds/spike (24.25), and 1,000-kernel weight (20.61 g). The smallest CV was estimated

Table 1. Extent of variability for yield traits in synthetic wheats from CIMMYT–Mexico.

Parameter	Spike length (cm)	Spikelets /spike	Seeds /spike	Tillers /meter	1000-kernel weight (g)
	Character				
Range	9.0–15.8	13.8–24.6	11.4–64.0	50–222	20–50.4
Mean	12.73	17.79	35.03	125.36	38.44
Standard deviation	1.68	1.89	8.49	39.28	7.92
Coefficient of variation	13.24	10.67	24.25	31.34	20.61
Mean of best check	11.62	19.12	45.99	70	41.45
Minimum selection criterion used	> 14	> 20	> 45	> 160	> 46
Number of elite lines selected	14	9	7	13	14

for spikelets/spike (10.67). For efficient and effective selection in any breeding program, the high standard deviation (SD) and high CV are the prerequisites and not actually the mean per se. For CV values in the high range, disruptive selection for higher values can be performed that will result in a higher mean in the selected population. In this study, we made a disruptive selection for three characters, tillers/meter, spike length, and 1,000-kernel weight. For effective utilization, we took the mean of the check as the minimum limit for selection. The top-ranking lines for each of the three traits, along with other agronomic characters are presented in Tables 2 (tillers/m), 3 (spike length; p. 60), and 4 (1,000-kernel weight; p. 60).

Tillers/meter. The number of effective tillers/unit area directly contributes to yield potential. In the synthetic lines, 222 tillers/m were recorded in lines 88 and 93 in compassion to the PBW 343 check (Table 2). These lines, however, were late flowering and late in maturity. Some of the synthetics had good kernel size and spike length.

Table 2. Promising synthetic entries selected for high tiller number/meter when grown under field conditions at Karnal, India, during 2001–02. Lines marked with an * are significant at a probability level of 5 %.

Synthetic and Pedigree	Tillers /meter	Days to heading	Days to maturity	Spike length (cm)	Spikelets /spike	1,000-kernel weight (g)
	Character					
88 (CPI/GEDIZ/3/GOOJO 69/CRA/4/*Ae. tauschii*)	222*	112	141	12.9	15.8	31.1
93 (DEVERD 2/*Ae. tauschii*)	222*	118	150	13.1	17.2	42.5
57 (LCK 59.61/*Ae. tauschii*)	214*	107	147	14.8	21.5	32.7
66 (BOTNO/*Ae. tauschii*)	210*	122	160	15.8	17.0	34.4
3 (Altar 84/*Ae. tauschii*)	200*	119	152	11.6	18.0	44.7
55 (GAN/*Ae. tauschii*)	200*	107	147	13.2	19.8	46.5
98 (DOY/*Ae. tauschii*)	186*	116	152	9.8	17.0	46.0
27 (GARZA/BOY//*Ae. tauschii*)	170*	111	146	12.8	16.8	45.5
HI 8498 (Check)	72	96	132	9.8	17.0	46.0
PBW 343 (Check)	87	95	130	12.0	18.0	37.0

Spike length. Synthetic lines were selected with ~15-cm spikes compared to the best bread wheat check PBW 343. No apparent increase in the number of spikelets/spike was observed, which means that the spike were of the lax type. Synthetic line 66 showed high tillering with a maximum spike length of 15 cm, but it flowered late and produced smaller kernels (Table 3).

Table 3. Promising synthetic entries selected for increased spike length when grown under field conditions at Karnal, India, during 2001–02. Lines marked with an * are significant at a probability level of 5 %.

	Character					
Synthetic and Pedigree	Spike length	Days to heading	Days to maturity	Tillers /m	Spikelets /spike	1,000-kernel weight (g)
64 (BOTNO/*Ae. tauschii*)	15.8*	122	160	210	17.0	34.4
66 (BOTNO/*Ae. tauschii*)	15.8*	122	160	210	17.0	34.4
98 (DOY1/*Ae. tauschii*)	15.7*	116	152	186	21.2	42.5
8 (CPI/GEDIZ/3/GOOJO 69/CRA/4/*Ae. tauschii*)	15.5*	111	146	112	18.3	45.0
49 (68-111/RGB-U//WARD /3/FGO/4/RABI /5/*Ae. tauschii*)	15.5*	111	149	68	19.8	29.2
45 (68-111/RGB-U//WARD /3/FGO/4/RABI /5/*Ae. tauschii*)	15.1*	111	144	116	17.4	43.5
97 (RASCON/*Ae. tauschii*)	15.1*	119	156	134	16.4	45.1
7 (Altar 84/*Ae. tauschi*)	15.0*	114	148	50	20.2	21.0
40 (68-111/RGB-U//WARD RESEL/3/ STIL/4/*Ae. tauschii*)	15.0*	114	147	52	18.8	44.3
44 (68-111/RGB-U//WARD /3/FGO/4/RABI /5/*Ae. tauschii*)	15.0*	106	144	96	17.4	50.0
HI 8498 (Check)	9.8	96	132	72	17.0	46.0
PBW 343 (Check)	12.0	95	130	87	18.0	37.0

1,000-kernel weight. Selections were made on the basis of higher kernel weight. About eight synthetic lines were selected based on a 1,000-kernel weight greater than 47 g (Table 4). Lines, 31, 33, and 38, are high tillering with good spike length, but flowered 12 days later then the check PBW 343.

Table 4. Promising synthetic entries selected for increased 1,000-kernel weight when grown under field conditions at Karnal, India, during 2001–02. Lines marked with an * are significant at a probability level of 5 %.

	Character					
Synthetic and Pedigree	1,000-kernel weight (g)	Spike length	Days to heading	Days to maturity	Tillers /m	Spikelets /spike
38 (FGO/USA 2111//*Ae. tauschii*)	48.7	114	147	156	13.0	18.2
31 (68112/wARD//*Ae. tauschii*)	48.1	111	146	160	13.5	16.8
36 (DOY 1/*Ae. tauschii*)	48.0	114	151	90	12.0	14.4
6 (CROC 1/*Ae. tauschii*)	47.2	114	147	102	14.0	18.0
44 (68.111/RGB-U//WARD/3/FGO/4/RABI/ 5/*Ae. tauschii*)	50.0*	106	144	96	15.0	17.4
50 (CROC 1/*Ae. tauschii*)	50.4*	101	139	100	11.0	16.8
51 (PBW 114/*Ae. tauschii*)	49.1*	100	145	122	12.5	16.4
72 (GAN/*Ae. tauschii*)	50.0*	113	147	76	14.6	18.0
HI 8498 (Check)	45.0	96	132	72	9.8	17.0

Table 5. Some selected cross combinations involving CIMMYT synthetic wheats along with traits improved. The populations were obtained primarily from simple crosses and are being advanced following a modified spike-to-row progeny method.

Cross combination	Traits improved
HI 8498/ Synthetic 44//HI 8498	Spike length, 1,000-kernel weight, grains/spike
PBW 34/Synthetic 93//PDW 233	Tillers/m, grain appearance, grain/spike
PBW 343/Synthetic 88//PBW 343	Tillers/m, powdery mildew resistance
C 306/Synthetic 55	Rust resistance, tillers/m, lodging resistance
K 9107/Synthetic 57	Leaf blight resistance, tillers/m
HUW 234//Synthetic 72	Leaf blight resistance, rust resistance, spike length
K 9006/Synthetic 66	Leaf blight resistance, tillers/m
WH 542/Synthetic 55	Tillers/m, grain/spike, 1,000-kernel weight
WH 542/ Synthetic 44	Spike length, 1,000-kernel weight
A-9-30-1/ Synthetic 3	Tillers/m, drought and heat resistance

Improving economic traits utilizing synthetic wheats. The promising synthetics identified from the present study cannot be released as cultivars, but they can serve as genetic stocks for many yield-contributing characters and as such might prove useful in a crossing program (Rasmusson 1996). In general, the synthetics have been observed to be late flowering, hard threshing, and red grained, traits that are not acceptable to Indian consumers. On the other hand, these are stocks are resistant to disease and biotic stresses. Promising released cultivars that are lacking a few important economic traits were selected and crossed with the elite synthetics in order to incorporate these traits (Table 5). In the segregating generations, we generally observed that the threshability is hard and a few grains were red in color, even with poor grain appearance. In a few cases, a backcross to the wheat cultivar parent was tried to improve desirable traits. We noticed that by making a few backcrosses, the population improved for such traits. We concluded from the study that the use of synthetics for improving some economic traits in wheat has potential only if the recipient parents are selected carefully and the material is advanced by judicious backcrossing, thereby eliminating undesirable traits. We expect that this type of crossing program also may break the negative linkages between important traits, thus pyramiding the positive genes in a good agronomic background.

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A new wheat cultivar for hot-humid agro-ecosystem of eastern India.

B.S. Malik, A.P. Sethi, V. Tiwari, R.K. Sharma, S. Chaudhary, and V.C. Sinha.

In Eastern India, the wheat growing area of approximately 8.9 x 10^6 ha covers the states of eastern Uttar Pradesh, Bihar, Jharkhand, W.Bengal, Orissa, the plains of Assam, and other far eastern states. Wheat is one of the major cereal crops of this cold region and comprises an important component of rice–wheat cropping sequence. The difference between the yield and production of wheat in western and eastern parts of the country is big. The western part averages productivity of 3.8 t/ha, whereas the eastern region averages 2.7 t/ha. Low productivity in eastern region is due to delayed wheat sowing caused mainly by limitations of the rice–wheat cropping system. Rice is grown mainly in rainfed areas. A short winter, heat stress in both early and late growth stages, high disease pressure particularly from leaf rust and blight, and edaphic problems are other limiting factors causing a reduction in productivity of wheat in eastern India.

One cultivar that has shown great promise for increasing productivity in hot-humid conditions of eastern India is Poorva, which was released by the Central Sub-Committee on Crop Standard, Notification and Release of Varieties in November 2003 for cultivation under irrigated, timely sown conditions. Poorva was tested under the name HD2824 in coördinated evaluation experiments conducted under the auspices of All India Coordinated Wheat Improvement Project for 3 years from 2000–01 to 2002–03.

HD2824 was developed by the pedigree method from the cross ‘PTO/CNO79/PRL/GAA//HD1951’, which involves Mexican and Indian wheats. In multilocation trials conducted over 3 years to evaluate yield ability, HD2824 exhibited an average increase of 5 to 14 % over the check cultivars PBW343, HUW468, HD2733, and K9107. The cultivar gave an average yield of 46 t/ha and a potential yield level of 6.5 t/ha (Figs. 1 and 2). HD2824 also has shown plasticity for delayed sowings, which meets the agronomic requirements of the predominantly adopted rice-wheat cropping system in eastern India.

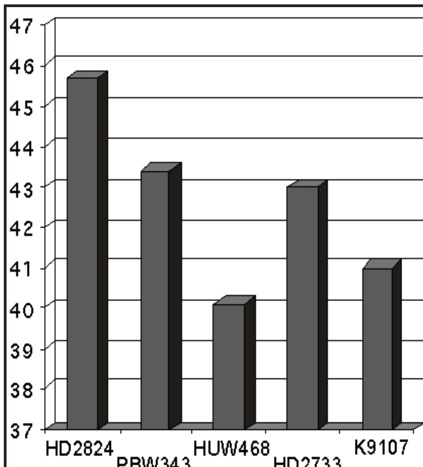

Fig. 1. Comparative mean yield of HD2824 (q/ha).

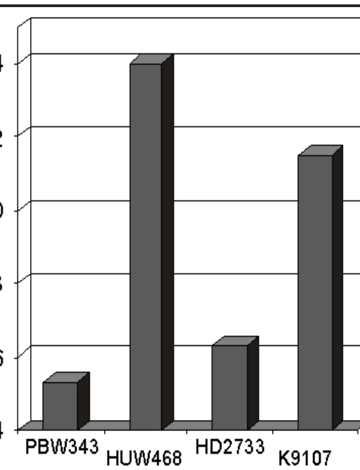

Fig. 2. Percent yield superiority of HD2824 over the checks (t/ha).

HD2824 has a new gene, *Lr23*, for resistance against leaf rust. *Lr23* will help to contain the spread of virulent and prevalent pathotypes of the group 77. The postulated resistance genes in the variety are *Sr31* + *Lr23* + *Lr26*, and *Yr9*, which give durable resistance to rust. For leaf blight, which is the major disease of the area, HD2824 is moderately resistant to resistant under natural and artificial conditions.

The characteristic features of HD2824 are a semispreading growth habit; a plant height of 85–90 cm; waxy, dark-green, semierect leaves; white tapering ears with nonpubescent glumes; and a maturity of 120–125 days. The grains are amber, hard, and lustrous with a 1,000-kernel weight of 41 g. HD2824 makes excellent unleavened bread that is preferred by people of the region.

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Two wheat cultivars developed for introduciton into the nontraditional areas of southern India.

M. Sivasamy, A.J. Prabakaran, K.A. Nayeen, and R.N. Brahma.

Introduction. Until high-yielding, paddy cultivars were introduced, the major cereal crops cultivated in the nontraditional areas (areas adjoining the Southern Hills in the states of Tamilnadu, Karnataka, and Andhra Pradesh) were sorghum followed by pearl millet; ragi; minor millets like Varagu and Pani Varagu, and foxtail millets; and dicoccum wheat. These areas are in the plains, where ever cooler weather conditions prevail in isolated packets. Over time, they slowly were replaced by cotton and vegetable crops. Today, some pockets exist where farmers cultivate dicoccum wheat. Although the climate is favorable and soil types suitable in these areas and the adjoining hills, farmers did not prefer wheat, because they were growing rice and other remunerative vegetable crops. Because of the lack of frequent monsoons and a shortage of irrigation water, farmers now are looking for a alternate, viable cereal crops.

Several reasons demand the introduction of wheat. The availability of suitable wheat strains (developed at IARI, Regional Station, Wellington) that are adaptable to these regions with high per day productivity. Recently, extensive research has lead to developing and identifying genotypes suitable for cultivation in the warmer areas that possess resistance to biotic stress (rusts and Fusarium root rot). A collaborative research program with Tamilnadu Agricultural University, Coimbatore, and the IARI Regional Station, Wellington, was initiated in the year 1997–98 Rabi to identify genotypes tolerant/resistant to biotic and abiotic stresses. Initially, cultivars for the plains area were selected. Five years of intensive research lead to the identification of the genotypes HW 3070, HW 3094, DWR 162, MACS 2496, and HD 2285, which possess resistance to Fusarium root rot and are consistent performers under the conditions at the test locations. Common to this region is a short winter of approximately 90 days from October to February with a few periods of high temperature and high humidity. Typical winter temperature variation for this area appear in Fig. 1. This climate facilitates severe inci-

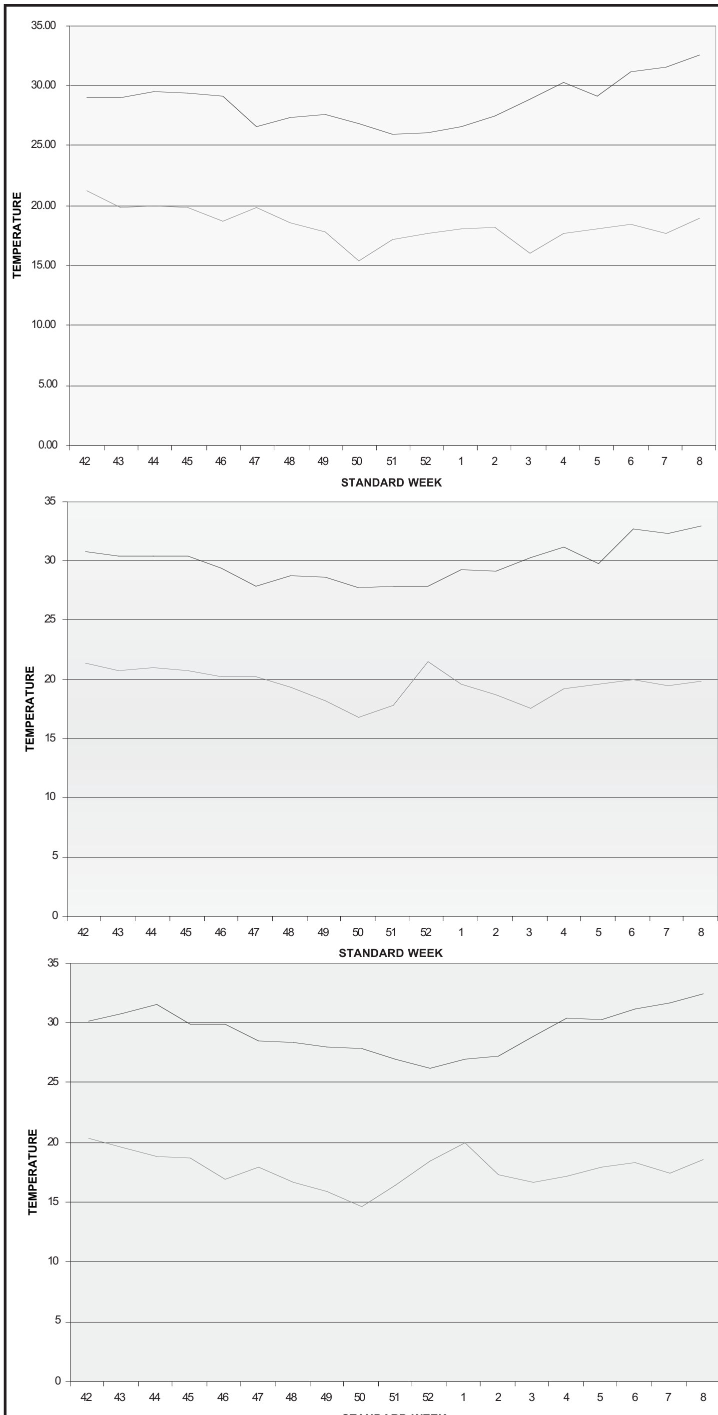

Fig. 1. Typical winter temperatures for the years 1999–2002 for the nontraditional wheat-growing areas of the Southern Hills in the states of Tamilnadu, Karnataka, and Andhra Pradesh. A. Karnataka, B. Coimbatore, C. Dharmapuri, D. Vellore, and E. Madurai (Figure is continued on p. 64).

dences of Fusarium root rot. Of the selected cultivars, subsequent station trials and agricultural research trials in 12 districts revealed that HW 3070 and HW 3094 were capable of producing consistent higher yields (1.5–2.0 tons/ha) over the others and have remarkable resistance to foliar diseases and Fusarium wilt. These cultivars mature in about 90 days and per day productivity is far higher than in the conventional areas.

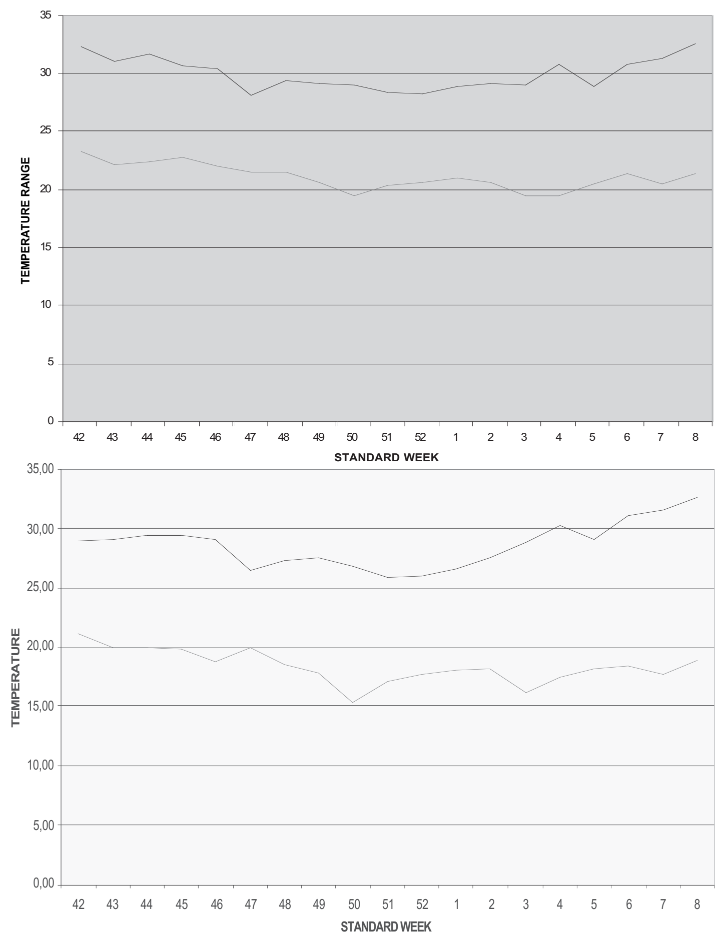

Fig. 1 (continued). Typical winter temperatures for the years 1999–2002 for the nontraditional wheat-growing areas of the Southern Hills in the states of Tamilnadu, Karnataka, and Andhra Pradesh. A. Karnataka, B. Coimbatore, C. Dharmapuri, D. Vellore, and E. Madurai.

Findings of the expert team include

1. Bread and dicoccum wheat can be successfully cultivated with 5-6 irrigations in various districts of Tamilnadu and Karnataka in the areas adjoining hills.
2. The area is prone to water logging and not suitable for wheat.
3. Intercropping with coconut and tapioca plantations with better drainage can be used.
4. In many districts, the time of sowing was found to be crucial. Any delay in sowing beyond 15 November can result in a yield loss. The best suited planting time is 15 October to 15 November.
5. Spacing between rows should be 20 cm rather than 23 cm, which we normally recommend, with no seed-to-seed spacing. Wider spacing results in poor stands with poor tillering. From our observations, closer spacing clearly altered the microenvironment, which facilitated better tillering under the regions climatic conditions (very short winter spell with intermittent high temperature ranges).
6. Study to standardize different agrotechniques should be initiated.

To take advantage of favorable weather conditions prevalent in this part of the country, the hilly areas in southern India are highly suitable for cultivation of wheat all through the year. The main seasons, kharif and rabi, can be followed either under rainfed or restricted irrigated conditions. In the Lower Hills and areas adjoining them, the weather conditions are highly favorable for cultivation of wheat between October and February. However, planting should not be delayed past 15 November except in areas where there is a longer winter. In these areas, cultivars with a longer growth cycle can be grown if sowing is made during the last week of October. The optimal temperatures for wheat growth are day temperatures below 30°C and night temperatures below 20°C, particularly during grain filling.

The demand for wheat has increased because of changes in eating habits. Thanks to the promotional effort of government and nongovernmental agencies about the need for a balanced diet, changes in the eating habits of people in southern India have increased the demand for wheat. Today, families who do not use wheat in their weekly diet are hard to find. Needless to say, 80 % of the wheat processing industries are situated in southern India and, hence, the demand for wheat has grown manyfold. In the Southern Hills, because of lower tea sales and the high cost of production of commercial crops, farmers are slowly switching to a cropping system that includes wheat as one of the food crops. Evidenced by the recent upward revision of area under wheat (in Kharif and Rabi seasons), in the Southern Hills.

The wheat crop ensures food grain for the family and fodder for the cattle. Wheat is amenable for intercropping or mixed cropping During 2003–04, experimental crops of wheat as an intercrop with tapioca under rainfed (October sown) was very successful in the Kalrayan Hills. Farmers in this region are looking for a viable, alternative crop. Traditional crops like cotton, vegetables, paddy, and other cereals have failed in the recent past because of infrequent monsoons. The availability of water is scarce until and beyond the Rabi season. In this situation, wheat has proven to be a viable, alternative cereal crop.

The advantages of cultivating wheat in these regions include

1. Wheat requires less water. Wheat requires 5 to 6 irrigations during its critical growth stages, the first immediately after sowing (life irrigation), a second on the 15th day after sowing, a third during the crown root-initiation stage (30–35 days) with one weeding and top dressing, a fourth during boot stage, and a fifth during milk stage (60–65 days). One or two irrigation can be skipped if there is any precipitation during this period.
2. Wheat is a short duration crop. Research has indicated that in the Lower Hills and adjoining areas, the wheat crop matures in about 85–90 days.
3. No major pests or diseases occur. The recommended cultivars have rust-resistant genes. Except for termites towards maturity, which can be controlled effectively by application Neem cake or Lindane during top dressing (around day 35–40).
4. Domestic requirement of wheat grains is met.
5. Bread wheat is easy to thresh.
6. A successful wheat crop gives high profitability with the minimum yield of 1,000 kg/acre in about just 90 days. The per day productivity is far better than any other wheat cultivating area in the country. Wheat is amenable to intercropping and mixed cropping. Wheat can be sold locally and purchase by flour-mills ensures marketing. Wheat flour can be made at the local iron mills. Wheat seeds can be stored up to 3 years in the plains under the ambient conditions. Cultivation of the nutritionally rich, dicoccum wheat ensures high remuneration.

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Nature of stripe rust-resistance genes against race 46S119 in exotic bread wheats from the Indian subcontinent.

The prevalence of strip rust race 46S119 having virulence on the gene *Yr9* originating from *S. cereale* is responsible for the break down of stripe rust resistance of some high-yielding cultivars in the Indian subcontinent. Incorporating genes for resistance against this race in the development of cultivars for use in the cooler, northern states of India is, therefore, a priority. Because quantitatively inherited, nonhypersensitive genes for slow-rusting resistance provide long-lasting resistance, their use seems to be the best approach for development of cultivars. Based on multirace tests conducted at Punjab Agricultural University, 18 bread wheats were identified as putative carriers of diverse genes conferring such resistance. These wheats were crossed with the two susceptible Indian cultivars Agra Local and WL711 to examine the nature and number of genes conferring nonhypersensitive resistance in each of these wheats. Observations on seedling infection types and field reaction of the 18 parental lines and their F_1s with susceptible cultivars to race 46S119 are given in Table 1 (p. 66). All cultivars except VL404 were susceptible to race 46S119, indicating that all these cultivars except VL404 have adult-plant resistance to this race. The F_1s from all crosses, except those with the cultivar Dove, were more susceptible than the resistant parent indicating that both resistance alleles are essential for producing the parental phenotype in 17 crosses. This response of the F_1s also suggests an additive effect of the resistance alleles. Kaur et al. (2002) have reported such additive resistance in some wheats earlier. Further generations are being evaluated to examine the nature of the *Yr* genes in these cultivars.

Acknowledgment. The authors acknowledge financial assistance from the Indian Council of Agricultural Research, New Delhi, to carry out this work at Punjab Agricultural University, Ludhiana.

Table 1. Seedling and adult-plant reaction to stripe rust race 46S1198 for resistant parental lines and the F_1 with two susceptible cultivars for the 2002–04. Race 46S119 is avirulent on *Yr1*,*Yr5*, *Yr10*, *Yr15*, *Yr24*, *Yr26*, and *YrSP* and virulent on *Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr11*, *Yr12*, *Yr17*, *Yr18*, and *Yr27*. Infection type is according to Roelfs et al. (1992). F_1 infection type was scored at the adult-plant stage.

	Infection type and growth stage			
Cultivar/line	Seedling reaction	Adult plant	F_1s with Agra Local	F_1s with WL711
Ciano 79	S	0.2	2.50	1.5
CSP44	S	14.0	19.0	40.0
CIM5 (Roussalka/Azteca 67/Pavon 76)	S	25.0	40.0	50.0
CIM6 (Dove/Buck Buck)	S	0.0	12.5	20.0
CIM7 (Mirlo/Buck Buck)	S	0.0	7.5	7.5
CIM53 (pedigree unknown)	S	0.6	15.0	20.0
Diaz	S	2.0	11.0	30.0
Dove	S	0.1	0.1	0.25
VL404	R	0.6	20.0	20.0
Bajio 67	S	20.0	40.0	30.0
Cook	S	1.5	11.0	35.0
CIM33 (Patio/Alondra/PAT72300/3/Pavon 76)	S	30.0	40.0	60.0
HI977	S	25.0	35.0	45.0
Era	S	30.0	35.0	35.0
FKN	S	30.0	40.0	50.0
Lerma Rojo	S	25.0	30.0	35.0
Pitic 60	S	30.0	45.0	40.0
Son-Kl-Rend	S	45.0	50.0	50.0
Agra Local (susceptible parental line)	S	60.0		
WL711 (susceptible parental line)	S	75.0		

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Morphocytognetics of Triticum turgidum subsp. dicoccoides/Aegilops umbellulata hybrids.

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Aegilops umbellulata, a diploid species with the U genome, is a potential source for resistance to powdery mildew, Hessian fly, and greenbug. Leaf rust-resistance gene *Lr9* from *Ae. umbellulata* was transferred to cultivated wheat by Sears (1956). However, cytogenetic information of wheat/*Ae. umbellulata* hybrids is lacking and chiefly concerns hybrid production. No germ plasm is available globally for incorporating the genetic diversity for wheat improvement, thus, we are reporting on the production of *T. turgidum* subsp. *dicoccoides*/*Ae. umbellulata* hybrids.

Aegilops umbellulata accession 3732, received from H.S. Dhaliwal, Punjab Agricultural University, Ludhiana, India, was crossed as a male with *T. turgidum* subsp. *dicoccoides* accession 4637. No embryo rescue or culture techniques were used, and the hybrid embryos were allowed to develop on the female plants under field conditions. The average crossability rate was 2 %.

Morphologically, the F_1 hybrids were intermediate between the parents and were self-sterile. The hybrid status of the F_1 plants was confirmed cytologically. Somatic chromosome number of all hybrid plants was 2n = 3x = 21 (ABU genomes). Chromosome pairing in the F_1 hybrids averaged 21 univalents/meiocyte, which indicated a complete lack of homology between the parental AB and U genomes.

ITEMS FROM ITALY

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Capillary electrophoretic analysis of gliadins in wheat and related species.

A.R. Piergiovanni, N. Volpe, and G. Taranto.

The narrow genetic basis of modern wheat cultivars is the result of the genetic erosion that occurred in the last century. In recent years, many studies have focused on the utilization of wheat germ plasm and of some related *Triticum* species in wheat breeding. The main objective of this research is the broadening of the genetic bases of modern cultivars. The achievement of wheat-improvement programs is related strictly to the use of powerful techniques to analyze in detail the protein profile of germ plasm accessions of wheat and related *Triticum* species. This approach allows us to identify the subunits related to end-use quality traits that are present in each accession analyzed.

In the last decade, capillary electrophoretic analysis (CE) of monomeric gliadins and glutenins has assumed increasing importance. Capillary electrophoresis has proven to be a method alternative to PAGE and complementary to HPLC. Moreover, this technique allows rapid and high-resolution separation of proteins with full automation.

We are starting to analyze by CE some related *Triticum* species, such as the tetraploid the cultivated emmer *T. turgidum* subsp. *dicoccum*, hexaploid spelt, and *Ae. tauschii,* in order to evaluate the genetic variability for gliadins and glutenins of these species.

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Allelic variability at the waxy *loci in Italian wheat germ plasm.*

G. Boggini, M. Cattaneo, C. Basone, and P. Vaccino.

Waxy mutations in bread wheat are derived from the loss of functionality of the granule-bound starch synthase I (GBSSI), the key enzyme in amylose synthesis, whose coding loci, *Wx-A1*, *Wx-D1*, and *Wx-B1*, occur on the short arms of chromosome 7A, 7D, and the long arm of chromosome 4A, respectively. Wheat lines with one or two GBSS null alleles produces starch with reduced amylose content and are designated 'partial-*waxy*', whereas the loss of all three GBSS isoforms gives rise to amylose-free starch, termed *waxy*. *Waxy* wheats may find useful application in the production of modified food starch and for the improvement of the shelf-life of baked products; moreover, they strongly influence Asian noodle quality.

A breeding program was set up to develop *waxy* wheat lines adapted to Italian environments from partial-*waxy* cultivars previously identified from a screening of Italian germ plasm. Nine crosses were made and the F_1 and F_2 generations were grown in the greenhouse without any selection. F_3 generations were grown in the field and selection was performed on the basis of agronomic characters. Single F_3 plants were harvested, and a sample of seeds/plant was analyzed by means of colorimetric analyses with a solution of KI/I_2 followed by electrophoretic fractionation of the GBSS isoforms. A study involving PCR analysis is in progress in order to develop a relatively simple method, possibly automated, to screen rapidly each partial *waxy* wheat line. A couple of primers were able to detect the null allele at the *Wx-D* locus of Bai-Huo, but did not recognize the same locus in the Italian landrace Cologna Lunga, suggesting the presence of a new null allele is probable. The same primers seem to detect polymorphism for the *Wx-A1* locus among cultivars, whereas another set of primers tested seems to be specific for the *Wx-B1* locus.

Strampelli cultivars: biochemical, technological, and agronomic characterization.

G. Boggini, A. Brandolini, M. Perenzin, S. Empilli, P. Vaccino, and M. Cattaneo.

Nazareno Strampelli was one of the most important breeders in the world. His work preceded that of Norman Borlaug and the "Green revolution" by nearly 30 years. During his long career, he released more than 70 bread wheat cultivars, largely grown in Italy and other countries and that also appear in the pedigree of significant recent cultivars. The aim of this work combines the description of these cultivar, their comparison with modern wheats, and their rescue from loss.

According to the coefficient of parentage based on the pedigrees described by Strampelli, the cultivars were clustered in different groups that shared the local population Rieti as common parent. The narrow genetic background of the Strampelli germ plasm was confirmed by the limited variability observed in the gliadin and glutenin composition. An AFLP analysis also was used to assess the molecular genetic diversity. The high variability found appeared related to the incomplete homogeneity and stability of the material released by Strampelli, but also to the large use of heterogeneous local populations in the crosses.

Agronomic traits varied significantly among the cultivars, whereas rather low differences were shown for the most important quality traits. Exploitation of this germ plasm for breeding purposes is in progress.

Puroindoline and kernel hardness in Triticum aestivum and Triticum monococcum.

N.E. Pogna, L. Gazza, G. Boggini, M. Corbellini, and P. Vaccino.

Registered Italian cultivars were classified according to their hardness by means of Single Kernel Characterization System (SKCS) and puroindoline composition. Three groups were identified: very soft, with SKCS indices lower than

14; soft, with SKCS indices ranging from 20 to 43; and medium hard, with SKCS indices higher than 55. Only the cultivar Enesco was present in the range 44–55. A bulk sample of this genotype showing a bimodal distribution for SKCS index was grown as spaced plants, and the grain was characterized by SKCS, A–PAGE fractionation, and PCR amplification. According to previous results, very soft grain contained Pin A and Pin B glycine-type, whereas medium-hard grain texture was associated with either the absence of Pin A or the presence of a Pin B serine type. Studies are in progress on a plant heterozygous for the alleles Pin B serine and glicine type.

Breeding for resistance to powdery mildew.

A. Brandolini, M. Corbellini, and G. Reffo.

The breeding program for bread wheat cultivars based on backcrossing and MAS selection and aimed at the introgression of powdery mildew resistance gene *Pm13*, derived from *Ae. longissima*, is currently at the BC_5 stage. To fix the gene, a cycle of selfing was made, and top crosses to assess homozygosity of the lines are in progress. Line evaluation for similarity to the recurrent parents also is under way.

Genetic analysis of einkorn wheat quality traits.

A. Brandolini, P. Vaccino, P. Ramelli, M. Corbellini, and G. Boggini.

Gliadin and glutenin storage protein fingerprinting of 668 samples of domesticated einkorn was completed. Correlations with SDS-sedimentation test results from 2 years were performed. The total number of HMW-glutenin bands scored was 39; six belong to the *x* HMW-subunit group, eight to the *y* HMW-subunit group, and 25 to the LMW group. The total number of gliadin bands recorded were 44, 20 in the ω region, 10 in the γ region, and 14 in the α/β region. Eight glutenin bands and eight gliadin bands were correlated significantly with an increase in bread-making quality. Progenies of two-, three- and four-way crosses of lines with good agronomic and quality traits (earliness, free-threshing, short straw, gluten quality, and large kernel) are undergoing different stages of evaluation.

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Reaction to wheat soilborne mosaic virus of 85 cultivars of durum wheat during six seasons in northern and central Italy.

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Beginning in the 1995–96 season onward, about 30 of the durum wheat cultivars marketed in Italy are tested each season for resistance to WSBMV in a field near Bologna with WSBMV only and at a site near Rome with both WSBMV and WSSMV. Resistance is evaluated on the basis of symptom severity, virus concentration in leaves (with DAS–ELISA), and agronomic performance (i.e., grain yield, test weight, 1000-kernel weight, plant height, and heading date). A total of 85 cultivars were assayed in six seasons characterized by severe disease pressure (Bologna 1995–96, 1996–97, 2000–01, 2001–02, and 2002–03; Rome 1998–99). The cultivars tested are listed in Table 1. Each cultivar is classified for resistance to WSBMV on the basis of DAS-ELISA values recorded in one or more seasons. Only seven cultivars among all those tested showed ELISA values close to zero and very mild symptoms. Three of these cultivars were assayed in only one season, indicating that their seemingly high level of resistance needs confirmation.

Table 1. Reaction to wheat soilborne mosaic virus of 85 durum wheat cultivars based on DAS–ELISA readings in various seasons. Cultivars in italics were assayed only for one season. The cultivar Zenit showed conflicting results in the two seasons during which it was assayed.

Highly resistant cultivars.
Colorado, *Duprì*, *Dylan*, Ionio (= Ares), Neodur, Provenzal, and *Tiziana*.
Moderately resistant cultivars.
Avispa, *Campodoro*, Ceedur, *Ermocolle*, *Flaminio*, Giotto, Gianni, Iride, Lloyd, *Louxor*, Meridiano, *Mongibello*, Nefer, Pietrafitta, Rusticano, San Carlo, Solex, Svevo,and Vitromax.
Susceptible cultivars.
Agridur, Appio, *Arcobaleno*, Baio, Balsamo, *Brindur*, Bronte, Cannizzo, *Carioca*, Ciccio, Cirillo, Claudio, Colosseo, Cosmodur, Creso, *Derrick*, Duilio, *Elios*, Exeldur, Flavio, *Fortore*, Gardena, *Gargano*, Giemme, *Granizo*, Grazia, Italo, Ixos, Marco, *Nerone, Norba*, Ofanto, Orobel, Parsifal, *Peleo*, *Peres*, *Perseo*, Platani, *Plinio*, *Poggio*, *Portobello*, Portofino, Portorico, *Preco*, Quadrato, *Saadi*, Simeto, Torrebianca, Tresor, *Valbelice*, *Valnova*, *Valsalso*, *Varano*, Verdi, Vesuvio, Vetrodur, *Vettore*, Vitron, and Zenit.

Simple correlations between symptom severity scores and grain yields were highly significant in all these trials. The estimated yield loss attributable to SBWMV or to a mixed WSBMV and WSSMV infection (Rome 1998–99) are summarized in Table 2 (p. 71). Interestingly, even cultivars with relatively mild symptoms suffered severe losses; from a minimum of 17 to 39 %, depending on the season. Correlations between symptom severity scores and DAS–ELISA readings also were highly significant in all trials. Indeed, the results obtained for cultivars tested in various seasons indicate that breeders may achieve substantial progress towards WSBMV resis-

Table 2. Estimated grain yield losses (%) for durum wheat cultivars grown in a field with WSBMV only near Bologna, and in a field with WSBMV and WSSMV near Rome. Infection type is classified according to the symptom severity scores (0–4 scale) assigned each season. None of the cultivars marked with an * had symptom severity scores above 3.20 (1996), 3.60 (1997), 2.70 (2001), 3.20 (2002), 3.80 (2003), or 2.50 (1999).

Symptom severity score	Bologna 1995–96	Bologna 1996–97	Bologna 2000–01	Bologna 2001–02	Bologna 2002–03	***Bologna Mean loss***	Rome 1998–99
1.01–2.00	25	39	23	17	22	***25***	41
2.01–3.00	31	53	49	46	46	***45***	47
3.01–4.00	48	57	—*	37	50	***48***	—*

tance by selecting on the basis of visible symptoms alone. On the other hand, results also showed that highly resistant cultivars may be distinguished from moderately resistant ones only by the use of ELISA or other techniques which estimate virus concentration.

Reaction of 81 cultivars of common wheat in northern Italy to wheat soilborne mosaic virus during five seasons.

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Eighty-one common wheat cultivars currently marketed in Italy were assayed in a field near Bologna for resistance to WSBMV during five seasons characterized by severe disease pressure (1995–96, 1996–97, 2000–01, 2001–02, and 2002–03). Each cultivar was assayed for 1–5 seasons. Resistance was evaluated on the basis of symptom severity using ELISA values from extracts of leaves and agronomic performance. The cultivars tested are listed in Table 3 and classified for resistance to WSBMV on the basis of DAS–ELISA values only. Twenty-two cultivars among those tested showed ELISA values close to zero and very mild symptoms. None of the lines showed symptoms as severe as those displayed by the most susceptible durum wheats.

Simple correlations between symptom severity scores and grain yield were highly significant in all trials, except in the 2000–01 season, which was characterized by the presence of severe epidemics of other wheat diseases as well. The estimated yield losses attributable to WSBMV infection are summarized in Table 4 (p. 72). Like the durum wheats, even cultivars with relatively mild symptoms suffered severe losses, from a minimum of 13 % to a maximum of 29 %, depending on the season. Correlations between symptom severity scores and DAS–ELISA readings were highly significant in all trials. Few, if any, of the common wheats assayed suffered grain yield losses as severe as those recorded for the most susceptible durum wheats.

Table 3. Reaction to wheat soilborne mosaic virus of 81 common wheat cultivars based on DAS–ELISA readings in various seasons. Cultivars in italics were assayed one season only.

Highly resistant cultivars.
Arsenal[1], Artico, Belfiore, *Bisquit*, Centro, Colfiorito, Enesco, Etheco, Francia, Genio, Idice, Levis, Mol, Pandas, *Quality*, *Recital*, Santerno, Sirmione, Spada, *Taylor*, Tremie, and Victo.
Moderately resistant cultivars.
Alcione, *Blasco*, Brasilia, Eureka, and *Greina*.
Susceptible cultivars.
Agadir, *Amarok*, *Ariano*, Ariete, *Arnel*, *Arquà*, Barra, Bilancia, Bolero, *Bologna*, *Buon Pastor*, Centauro, *Cezanne*, Collerosso, Cranklin, Delfino, Dorico, Eridano, *Faro*, *Festa*, *Galibier*, Giava, Golia, Guadalupe, *Guarnì*, *Idra*, Isengrain, Lampo, Libero, Manital, *Marvao*, Mec, Mieti, *Nearco*, *Oderzo*, *Palesio*, Pascal, *Pompei*, Positano, Provinciale, Ravenna, Sagittario, Salgemma, Salvia, *Savio*, Serio, Sibilla, Soissons, Stroika, Tibet, Valoris, Villanova, *VTA7109*, and Zena.

Table 4. Estimated grain yield losses (%) for durum wheat cultivars grown in a field with WSBMV only near Bologna, and in a field with WSBMV and WSSMV near Rome. Infection type is classified according to the symptom severity scores (0–4 scale) assigned each season.

Symptom severity score	Bologna 1995–96	Bologna 1996–97	Bologna 2000–01 [1]	Bologna 2001–02	Bologna 2002–03	***Bologna Mean loss***
1.01–2.0	27	29	—	17	13	*22*
2.01–3.0 [2]	16 [3]	51 [3]	—	—	28	***31***

[1] The correlation between symptom severity scores and grain yield was not significant, owing to the effects of other diseases present in the field.
[2] None of the cultivars assayed had symtom severity scores above 3.3 (1996), 2.6 (1997), 1.3 (2002), or 2.8 (2003).
[3] Estimate based on the only cultivar in that category.

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Reaction of thirty cultivars of durum wheat to SBWMV during 2001–02.

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Wheat soilborne mosaic virus is widespread in Italy, especially in the northern and central regions, where it causes severe losses on both common and durum wheat crops. Yield losses of up to 50–70 % have been recorded on susceptible cultivars. Fields with WSBMV have been identified also in southern Italy and Sicily. During 2001–02, 30 durum wheat cultivars were assayed in a severely WSBMV-infested field situated near Minerbio (Bologna) to study their response to the virus. The cultivars were grown in 10-m^2 plots distributed in the field according to a randomized block design with three replicates. As in previous years, reactions to WSBMV were evaluated on the basis of DAS–ELISA readings, symptom severity, and agronomic performance. Samples for DAS–ELISA were collected 13 March and 3 April. Symptoms were scored 13 March, 3 April, and 22 April using a 0–4 scale. Disease pressure was severe and resulted in highly diverse reactions among cultivars (Table 1, p. 73). Mean symptom severity ranged from 0.1 to 3,2; mean ELISA values from 0 to 0.991, and grain yield from 1.08 to 5.91 t/ha. Most cultivars proved susceptible in terms of both symptom expression and ELISA values, and this was clearly reflected by their relatively low grain yields.

The cultivars Solex, Neodur, San Carlo, Gianni, Meridiano, and Verdi were highly resistant, even if none were symptomless throughout the season. The cultivars Cannizzo, Carioca, Claudio, Colosseo, Marco, Orobel, Vesuvio, and Vetrodur, with yields between 1.08 and 3.95 t/ha, proved particularly susceptible. Symptom severity scores were highly correlated with ELISA values (0.868**), grain yield (–0.668**), and plant height (–0.868**), but not with test weight, 1000-kernel weight, and heading date. Cultivars with symptom scores ranging from 2.1 to 3.2 had an estimated loss in grain yield of approximately 43 % and a plant height reduction of about 25 %. Cultivars showing only relatively mild symptoms (1.12.0) also were negatively affected in terms of grain yield (–17 %) and plant height (–7 %).

Table 1. Performance of 30 durum wheat cultivars in a field with WSBMV in northern Italy during 2001–02.

Cultivar	Mean symptom severity	Mean ELISA value	Grain yield (t/ha)	Test weight (kg/hl)	1,000-kernel weight (g)	Plant height (cm)
Campodoro	0.1	0.135	4.05	70.4	38.8	92
Cannizzo	3.1	0.991	1.55	64.1	31.3	62
Carioca	3.2	0.857	3.67	75.0	41.6	75
Claudio	2.9	0.971	1.08	74.6	41.2	65
Colorado	0.6	0.125	5.13	75.5	37.1	92
Colosseo	2.5	0.525	2.77	69.3	33.2	75
Creso	2.2	0.489	4.01	76.1	43.8	82
Duilio	0.5	0.111	5.49	75.4	41.2	94
Gianni	0.6	0.007	5.50	77.0	38.8	87
Giotto	1.8	0.002	4.05	71.0	37.3	85
Iride	1.0	0.628	4.57	73.3	34.1	83
Lloyd	1.1	0.397	3.81	70.1	35.6	91
Marco	3.0	0.865	3.44	70.5	39.7	80
Meridiano	0.3	0.012	5.91	73.5	39.9	95
Neodur	0.9	0.253	5.52	76.1	41.9	95
Orobel	3.2	0.918	3.90	73.4	37.5	74
Pietrafitta	0.3	0.103	4.45	74.2	40.8	101
Portofino	1.0	0.279	4.13	75.5	35.8	90
Portorico	1.9	0.823	4.29	71.7	39.2	92
Provenzal	1.7	0.130	4.31	74.2	33.4	84
Quadrato	1.9	0.252	4.66	75.6	45.2	97
San Carlo	0.9	0.000	5.05	75.9	39.4	83
Simeto	1.8	0.659	3.33	71.2	40.3	72
Solex	0.3	0.000	4.48	73.7	38.7	95
Torrebianca	1.9	0.285	4.91	74.7	44.8	97
Valsalso	1.6	0.983	3.93	68.0	35.8	91
Verdi	1.0	0.257	3.48	70.5	37.9	98
Vesuvio	2.9	0.837	2.38	66.1	33.2	72
Vetrodur	3.2	0.912	3.95	73.2	34.6	81
Vitromax	0.8	0.099	4.90	75.4	37.9	89
MEANS	1.6	0.430	4.09	72.8	38.3	86

Reaction of 33 cultivars of common wheat to wheat soilborne mosaic virus in 2001–02.

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During the 2001–02 season, 33 cultivars of common wheat were assayed in a severely WSBMV-infested field situated near Minerbio (Bologna) to study their response to the virus. Entries were grown in 10-m^2 plots distributed in the field according to a randomized block design with three replicates. Resistance to WSBMV was evaluated on the basis of DAS–ELISA readings, symptom severity, and agronomic performance. Samples for DAS–ELISA were collected 13 March and 3 April. Symptoms were scored on 26 February, 13 March, and 3 April using a 0–4 scale. As in all our previous trials, Italian common wheats showed much higher levels of resistance to WSBMV than durum wheat cultivars assayed in an adjacent field. Symptom severity scores among common wheats ranged from 0 to 1.3, ELISA values from 0 to 1.102, and grain yield from 4.77 to 7.33 t/ha (Table 2). The cultivars Belfiore, Enesco, Levis, Sirmione, Artico,

Table 2. Performance of 33 common wheat cultivars in a field with wheat soilborne mosaic virus in northern Italy during 2001–02.

Cultivar	Mean ELISA value	Mean symptom severity	Grain yield (t/ha)	Plant height (cm)
Alcione	0.3	0.255	6.05	86
Artico	0.2	0.002	6.89	87
Belfiore	0.3	0.000	5.04	78
Bilancia	0.1	0.349	6.38	85
Centauro	0.2	0.672	5.70	80
Centro	0.6	0.010	7.33	98
Colfiorito	0.2	0.003	5.98	85
Collerosso	1.3	1.035	4.77	88
Craklin	0.3	0.346	6.37	92
Delfino	0.8	1.102	5.68	89
Enesco	0.0	0.001	5.75	81
Etecho	0.0	0.064	6.83	97
Eureka	0.0	0.246	6.49	98
Genio	0.0	0.100	6.42	87
Giava	0.3	0.088	5.31	86
Golia	0.7	1.060	5.70	70
Guadalupe	0.7	0.401	6.10	93
Insegrain	1.1	0.595	5.47	87
Levis	0.1	0.001	5.24	95
Mieti	0.5	0.330	6.13	78
Pascal	0.4	0.482	5.37	89
Positano	0.9	0.918	5.04	88
Provinciale	0.7	0.440	6.51	96
Ravenna	1.1	0.735	4.94	75
Sagittario	0.6	0.572	5.47	81
Salgemma	0.6	0.267	4.86	72
Salvia	0.8	0.830	6.62	82
Serio	0.8	0.688	5.60	82
Sirmione	0.1	0.001	6.05	86
Soissons	1.2	0.600	5.66	89
Tibet	0.5	0.231	6.59	83
Tremie	0.0	0.010	6.75	87
Valoris	0.9	0.151	5.55	87
MEANS	0.5	0.381	5.90	86

Colfiorito, Tremie, and Centro showed slight symptoms and null or low ELISA values. The cultivar Centro produced the highest yields. Symptom severity scores highly correlated with ELISA values (0.716**) and grain yield (–0.447**) but not with test weight, 1000-kernel weight, plant height, or heading date. Cultivars with symptom scores ranging from 1.1 to 1.3 had an estimated mean grain yield loss of approximately 17 %.

Reaction of 114 cultivars of durum wheat to wheat soilborne mosaic virus in northern Italy.

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During the 2002–03 season, 114 cultivars of durum wheat of various origins were grown near Bologna in a field with natural inoculum sources of WSBMV and evaluated for resistance to this pathogen on the basis of symptom severity and virus concentration in leaves. Our main objectives were to provide breeders with information on the resistance of cultivars widely used as parents in their programs and to enable virologists around the world to investigate the existence of differential reactions to WSBMV. The latter aspect, in fact, has acquired renewed importance in that several authors, based on the results of nucleotide-sequence analyses, have recently suggested that the WSBMV found in Italy and other European countries is different from that present in North America. The experiment included cultivars obtained by national breeding programs in Australia, Austria, Canada, France, Italy, Spain, the U.S., ICARDA, and CIMMYT. The cultivars were grown in 122-cm, solid-seeded rows with two replications. Symptom severity was scored three times during the season (13 March, 2 April, and 16 April) using a 0 to 4 scale, where 0–1 = slight or no symptoms; 1.1–2 = mild mottling and stunting; 2.1–3 = mottling and stunting; and 3.1–4 = severe mottling and stunting, with virus-killed plants. Virus concentration was determined by DAS–ELISA on leaf extracts collected 13 March, 2 April, and 16 April. Extracts were from a bulk of the apical half of the second youngest leaf of 10 plants/plot. The results of the experiment are summarized in Table 3 (p. 75). About one-half of the cultivars assayed had very low ELISA values and mild symptoms (Table 3). A number of these cultivars had moderately high ELISA values and relatively more severe WSBMV in previous trials conducted at the same site, but none of those previously found resistant to WSBMV showed high ELISA values and/or severe symptoms. Evidently, disease pressure during the 2002–03 growing season was sufficient to uncover very susceptible cultivars but not to distinguish resistant types from moderately susceptible ones. The experiment will be repeated in 2003–04.

Table 3. Mean ELISA values and symptom scores for 114 durum wheat cultivars grown in a field with wheat soilborne misaic virus in Italy in 2002–03).

Cultivar	Mean ELISA value	Mean symptom score	Cultivar	Mean ELISA value	Mean symptom score	Cultivar	Mean ELISA value	Mean symptom score
Acalou	1.103	2.17	Excalibur	1.509	2.25	Neodur	0.067	0.58
Acavonlea	0.080	0.83	Exeldur	0.033	1.12	Ofanto	1.509	2.08
Acmelita	0.035	0.50	Extradur	1.397	1.25	Omrabi-3	0.308	0.92
Acmorse	0.051	0.53	Flavio	0.425	0.46	Orjaune	0.055	0.54
Acnavigator	0.248	1.17	Fortore	1.526	1.92	Platani	0.265	1.00
Acpathfinder	0.261	0.13	Frankodur	1.130	1.29	Plaza	0.035	1.08
Agridur	1.463	2.92	Galadur	0.056	0.17	Plenty	0.032	1.00
Altar 84	0.997	2.70	Gargano	1.195	1.25	Plinio	1.164	2.13
Anton	0.066	0.58	Goldur	0.055	0.25	Primadur	1.317	1.00
Appio	0.737	1.25	Grandur	0.374	0.67	Produra	1.474	3.08
Appulo	0.778	1.00	Grazia	1.343	2.72	Renville	0.046	0.17
Aramon	1.574	2.50	Heider	1.522	2.08	Reva	0.035	0.58
Arcalis	1.143	1.63	Helidur	0.233	0.25	Roqueno	1.323	3.17
Arcangelo	1.343	1.00	Hercules	0.049	0.71	Rugby	0.447	0.25
Arcobaleno	1.397	2.42	Ionio	0.102	0.45	Russello	0.952	1.13
Ardente	0.215	0.33	Iride	0.040	0.25	SanCarlo	0.059	1.00
Arstar	1.256	2.29	Italo	0.078	0.60	Saragolla	0.036	0.08
Auroch	0.091	0.83	Ixos	0.969	1.75	Sceptre	0.070	0.33
Belikh 2	0.136	0.46	Jabato	1.386	2.33	Semperdur	0.199	0.33
Belzer	0.928	2.42	Kabir	0.091	0.75	Simeto	1.230	2.17
Ben	0.035	0./83	Kamilaroi	0.124	0.75	Solex	0.071	0.00
Bravadur	0.063	0.92	Karel	1.563	2.03	Svevo	0.080	0.33
Brindur	0.245	0.50	Korifla	0.089	0.71	Tacna	1.486	1.92
Bronte	1.343	1.75	Kronos	1.074	2.83	Tetradur	0.312	0.54
Capeiti8	0.817	0.54	Kyle	0.044	0.67	Topdur	0.305	0.03
Cappelli	0.304	0.39	L35	0.083	0.64	Trinakria	1.053	1.20
Ciccio	1.487	1.67	Lakota	0.061	0.63	Valbelice	1.547	1.83
Colorado	0.067	0.29	Langdon	0.276	0.08	Valforte	1.450	2.75
Colosseo	0.256	1.83	Latino	0.350	1.00	Valnova	1.558	3.17
Cortez	1.229	1.58	Lira	0.139	0.25	Varano	1.360	2.33
Creso	0.498	1.25	Lloyd	0.037	0.67	Vic	0.078	1.29
Donpedro	0.066	0.25	Maier	0.089	1.03	Waha	1.571	3.00
Duilio	0.026	0.50	Messapia	1.651	2.29	Wallaroi	0.315	0.79
Duraking	0.084	0.25	Mexicali	0.323	0.46	WB881	0.716	0.54
Durex	0.691	0.71	Mindum	0.316	0.05	WBTurbo	0.074	0.83
Durfort	0.263	0.43	Mohawk	0.067	0.50	Yallaroi	0.153	0,67
Duriac	1.605	1.83	Munich	0.348	0.93	Yuma	0.071	0.00
Edmore	0.053	0.89	Nefer	0.079	0.71	Zenit	0.080	0.33
Means	0.580	1.11	Minimum	0.026	0.00	Maximum	1.651	3.17

ITEMS FROM JAPAN

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Near-isogenic lines for GA_3-sensitive and -insensitive semidwarfing genes in LD222 durum wheat.

Near-isogenic lines for GA_3-sensitive semidwarfing genes (*Rht12, Rht14, Rht16, Rht18*, and *Rht19*) in durum wheat cultivar LD222 were developed for research purposes. Near-isogenic lines for GA_3-insensitive semidwarfing genes in LD222 also were developed. The donors of the *Rht* genes were Cando (*Rht-B1b*), a NIL of Maringa for *Rht-B1c* (*Rht-B1c*), Saitama 27 (*Rht-B1d*), Krasnodari-1 (*Rht-B1e*), and W6824D (*Rht-B1f*).

JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES (JIRCAS)

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Specific glutenin allele frequencies of Japanese common wheat cultivars compared with the worldwide distribution of Glu-1 alleles.

Hiro Nakamura.

The quality of common wheat grain favored in bread and/or noodle-making quality is strongly affected by components of seed-storage protein, particularly the HMW-glutenin subunits. The HMW-glutenin 2.2 subunit controlled by the *Glu-D1f* allele is found frequently in Japanese common wheat cultivars and landraces. While investigating the factors affecting the distribution of this allele, the available data on HMW-glutenin alleles of common wheats from Japan were analyzed and compared with the data for intensity of winter habit and wheat flour hardness. The main factors affecting *Glu-D1f* allele frequency in Japanese wheats were the intensity of natural selection for winter habit and artificial selection for flour hardness. According to a study of the worldwide distribution of *Glu-1* alleles in common wheats, the *Glu-D1f* is rare. However, the *Glu-D1f* allele was the most common Japanese wheat seed-storage protein allele. We know that Chinese wheat contributed to Japanese landraces, and Japanese landraces contributed to modern cultivars from Japan. However, Japanese and Chinese common wheats differ in their frequencies of the *Glu-D1f* allele. These results may be explained either by the founder effect or by a selective bottleneck in Japanese common wheat genetic resources.

HMW-glutenin subunits represent a group of common wheat seed endosperm proteins characterized by molecular weights of between 80,000 and 145,000 and a complex biochemical structure involving disulfide bonds. HMW glutenin, the protein constituent of flour of wheat that gives elasticity to a dough, is built up of at least 20 different subunits. Studies investigating HMW-glutenin subunit composition and/or its relation to bread-making quality have been made in virtually all major wheat-producing countries. These studies involved both cultivars and landraces of common wheat. The results of these studies highlighted three important ideas: 1, the allelic variation for *Glu-1* loci that exists in *T. aestivum*; 2, the relationship between HMW-glutenin subunit composition and wheat quality parameters; and 3, the association between allelic distribution and ecogeographical parameters. Because the HMW-glutenin composition of common wheat cultivars from many countries now has been published, an analysis of these data and that for Japanese wheats will contribute to our knowledge of the worldwide distribution of *Glu-1* alleles. Our objective was to analyze this distribution in Japan, which is the most geographically remote region for common wheat production, concentrating mainly on HMW-glutenin allelic variation within common wheat and the factors which affect it in a worldwide context.

We know that common wheat cultivars from different countries differ in the frequency of *Glu-1* alleles. The 2.2 HMW–glutenin subunit controlled by the *Glu-D1f* allele was frequently found among improved cultivars and in Japanese landraces in this study. Investigating the factors affecting the distribution of the allele, the available data on the HMW-glutenin alleles of common wheats from Japan were analyzed and compared to published data (1,380 cultivars from 21 common wheat-producing countries) on the worldwide distribution of *Glu-1* alleles. The *Glu-D1f* has been reported to be a rare allele in the worldwide distribution of *Glu-1* alleles. However, the *Glu-D1f* allele has been characterized as the most common Japanese wheat seed storage protein in this study. This study showed a specific difference in the frequency of the *Glu-D1f* allele for Japanese common wheat cultivars and landraces. The allelic frequency of this subunit was shown to be in excess of 35 % among improved Japanese cultivars, 25.3 % among Japanese landraces, but was found in only 1.8 % of 274 Chinese wheats in this study. Genealogical examinations revealed that the *Glu-D1f* allele was not only present in the Nisikaze-komugi prevalent in the Kyushu district (southern Japan) but also frequently appeared in its pedigree. The *Glu-D1f* allele was absent in Horoshiri-komugi found in the Hokkaido district (northern Japan), but carried only in a few of its remote ancestors. A noticeable geographical cline has been reported in the frequency of the *Glu-D1f* allele. To elucidate the factors involved in the establishment of this cline, we investigated the association of the occurrence of the glutenin *Glu-D1f* gene with both winter habit and with flour hardness. In Japan, the environment for cultivating common wheats is made diverse by the distance of the islands from north to south, by improved Japanese cultivars, and by locally grown landraces differentiating into distinct types of winter habit. The intensity of the winter habit in Japan is the most important factor for common wheat production in the field. Generally, wheats with a weaker winter habit (I~III) are grown in southern Japan; stronger winter habit (V~VII) wheats are grown in the north. A strong correlation was observed between intensity of winter habit and occurrence of the *Glu-D1f* allele. Improved cultivars with a weaker winter habit tended to carry the *Glu-D1f* allele more frequently, but this allele was absent in the cultivars with the stronger winter habit. The *Glu-1* alleles have previously been reported not to be associated with ecogeographical parameters in a worldwide context. However, we have found that the *Glu-D1f* allele is associated with ecogeographical parameters in Japan, a finding of great interest to Japanese common wheat breeders and cereal chemists.

Flour hardness of common wheat grains is believed to be related closely to grain quality. Common wheat flour hardness is correlated with Japanese soft noodle-making quality and with hard common wheat cultivars having poor Japanese soft noodle-making quality. Thus, we investigated the relationship between flour hardness and the occurrence of the *Glu-D1f* allele in this study. We found that soft-flour cultivars tend to exhibit the *Glu-D1f* allele more frequently than hard-flour cultivars. Particular characters such as winter habit and wheat flour hardness also may be required as a breeding objective for common wheat in Japan. A current analysis of HMW-glutenin alleles shows a *post factum* status of these loci because, until recently, Japanese common wheat breeders did not manipulate the *Glu-1* alleles intentionally. So, this analysis reflects the results of indirect changes in the genetic constitution of common wheat because of selection for related or linked traits in Japanese wheat-breeding programs. The average *Glu-1* quality scores relating to good bread-making quality in Japan and China within the noodle-culture zones of the Far East have been shown to be less than those of known quality wheats from Europe, Australia, Canada, and the United States within the bread wheat-culture zones. Common parentage can influence the distribution of *Glu-1* alleles. Frequent involvement of the same successful parents in crosses will result in a large similarity in genetic structure.

Chinese wheat is well known to have contributed to Japanese landraces, and Japanese landraces contributed to modern cultivars from Japan. However, the common wheats of Japanese and Chinese differ greatly in *Glu-D1f* allele frequency in this study. Our findings suggest that the geographical clines in frequency of the *Glu-D1f* allele observed among Japanese improved cultivars and landraces may be caused by natural selection for winter habit and/or by artificial selection for wheat flour hardness. Japanese common wheat is characterized by the high frequency of alleles such as *Glu-B1g* and *Glu-D1f* at the *Glu-1* locus. Natural and artificial selection is thought to have narrowed the genetic base of Japanese common wheat. The frequent occurrence of the *Glu-D1f* allele would support this conclusion. This study has shown that the *Glu-1* allele frequencies differ between the noodle-culture zones of the Far East and the bread-culture zones. Probably, the factor most influencing *Glu-1* allele composition is a common wheat breeding strategy relating to bread-making quality in the bread-culture zone. The *Glu-1* alleles have been reported to directly affect wheat-gluten quality. Japanese specific differences in *Glu-1* patterns likely resulted from the intensity of selection pressure towards good Japanese soft-noodle making quality instead of selecting for good bread-making quality. As a consequence of its spread, adaptation, and phenotypic refinement, Japanese common wheat has developed a unique composition of *Glu-1* glutenin alleles and a narrow common wheat genetic base; an illustration of the result of artificial breeding and/or adaptation to the different winter climatic conditions spanning the length of the Japan. Cultivars with superior bread-making quality have higher *Glu-1* quality scores and tend to have limited genetic variation in their *Glu-1* loci, such as the

Glu-D1d gene demonstrating a narrowing of the genetic glutenin-protein variability when breeding common wheat for its bread-making quality.

The rich genetic diversity of common wheat landraces confers resistance to multiple diseases, environmental adaptation, and agronomic traits of economic significance. The *Glu-1* alleles could serve as markers for genes involved in adaptation. The range of *Glu-1* allelic variation in seed-storage proteins that is currently available to the wheat breeder is being extended by the introgression of glutenin alleles from primitive landraces and from alien common wheats. Linkage studies using SDS gel electrophoretic screening to determine the relationship between seed endosperm glutenin protein genes and genes for other agronomic characters might enable the incorporation of desired traits into new common wheat cultivars. Desirable traits may include improved cold tolerance, disease resistance, and improved quality for Japanese soft noodle-making. Investigating the contribution of the HMW-glutenin proteins that confer elasticity to dough by forming large aggregates to Japanese soft-noodle making will be of particular interest. Consequently, the *Glu-D1f* gene is being transferred into the many good soft-noodle making quality varieties at wheat-breeding programs in Japan.

The variability released by both environmental and genetic factors could easily lead to different subpopulations of the founders in turn, leading to the establishment of more than one reproductively isolated population from a single founder through population genetic mechanisms for common wheat. Each bottleneck was followed by a flush of rapid population growth, so, once again, there were optimal conditions for including genetic change. With this design from China, the common wheats were exposed to a selective bottleneck induced by the external environment, and a founder effect (because all populations went through a bottleneck of small size). Consequently, the selective bottleneck was extremely intense and, in fact, most ancestral populations may be become extinct in Japan. Although the selective bottlenecks discussed in this study were primarily induced by genetic environment, most of the predictions made in this study also would apply if the selective bottlenecks were induced by the external environment. The HMW-glutenin, subunit allele pattern of Japanese common wheat cannot be explained solely by the founder effect because, as already pointed out, the pattern also was affected by the artificial selection for bread-making or soft noodle-making quality in wheat-breeding programs. The ease with which genetic changes occur in Japan strongly implies a lack of genetic variability in natural populations of Japanese common wheats.

The theory presented here has increased the explanatory powers of wheat genetic revolution model of speciation and, more importantly, has generated testable predictions that can be examined in both the natural and artificial selection using current methodologies and systems.

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ITEMS FROM MEXICO

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Progress in exploiting Aegilops tauschii for wheat improvement.

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Introduction. In conventional improvement of bread wheat, breeders normally have made crosses between cultivars. Such crosses have few constraints and invariably all associations of parental traits and segregation are based on genetic recombination. The next step in bread wheat improvement is to tap the varied gene pools of other *Triticum* species. For swift output from such crosses, breeders utilize the numerous alien accessions of species whose genomes are similar to the A, B, or D genomes of bread wheat. These crosses allow for relatively easy alien gene transfers, are compatible with normal field research, and set the stage for the successful introgression of several genes simultaneously by homologous exchange. Elucidated here is the interspecific hybridization area where the focus is on the D-genome diploid *Ae. tauschii*.

An important component of CIMMYT's strategy for exploiting genetic diversity in order to improve wheat production constraints globally is on disease and stress tolerance research using durum-based synthetic hexaploids (*T. turgidum* subsp. *durum*/*Ae. tauschii*). This approach is aimed at protecting yield potential in farmers' fields, the environment, and farmers' incomes by reducing dependence on pesticides for disease and pest control. Screening work for biotic and abiotic stresses was conducted over the years in various locations in Mexico using primary synthetic hexaploids (SH) developed at CIMMYT. A wide diversity of resistance and tolerance in the various synthetics was observed when subjected to different biotic and abiotic stress pressures. Results indicated that such wheats were, in most instances, significantly superior for biotic/abiotic resistances/tolerances when compared to their durum progenitors. These results unequivocally showed that the synthetics possessed the genetic diversity for disease and stress tolerances that were contributed by the diploid donor species used in their synthesis. They are spring types, highly crossable to advanced bread wheats, and may be used easily in breeding. Hence, the transfer of this resistance/tolerance of the SH wheats to elite, bread wheat cultivars followed. Presented in this article is the data for SH wheats and their prebred wheat derivatives that show improved biotic and abiotic tolerances and are a conduit for global wheat improvement around novel germ plasm.

We also are adding brief additional information that elucidates the use of other species that have been used for development of different genetic stocks that could impact wheat improvement and assist molecular diagnostics.

Materials and methods. Germ plasm development. Elite, durum wheat cultivars were crossed with several hundred *Ae. tauschii* accessions. Embryos were rescued, plated in artificial media, differentiated, and yielded F_1 hybrids (2n = 3x = 21, ABD) that produced 2n = 6x = 42, AABBDD synthetic hexaploids upon colchicine treatment. Accession acquisition and procedures for SH production have been earlier described (Mujeeb-Kazi et al. 1996a). These SH wheats are maintained by increasing seed of each combination under controlled conditions by bagging at least 50 spikes/combination with glassine envelopes at each increase cycle. Based upon growth performance in two locations in Mexico (Ciudad Obregon and El Batan), an elite set of 95 SH entries has been assembled for global distribution. Distribution of this elite SH set is handled by CIMMYT's Genetic Resources Group. Further promising SHs for various stresses have been assembled into subsets.

Germ plasm screening. The SH germ plasm was screened for *H. sativum*, *F. graminearum*, *S. tritici*, and *T. indica* in Poza Rica, Toluca (Scab and Septoria), and Obregon, Mexico, respectively, over 3 to 5 years, which forms the basis of conclusions made in this paper. All evaluations were under field conditions. The synthetics were planted in hill plots. Evaluation protocols were similar to those earlier reported by Mujeeb-Kazi et al. (1996b) for *H. sativum*, Mujeeb-Kazi et al. (2000b) for *Fusarium*, Mujeeb-Kazi et al. (2000a) for *S. tritici*, and Mujeeb-Kazi et al. (2001) for *T. indica*.

Abiotic stress screening for salinity was conducted under greenhouse conditions at El Batan, Mexico, according to the hydroponic protocol of Gorham et al. (1987) and Shah et al. (1987) based upon K:Na discrimination after 21-day growth of the seedlings in 50 mM NaCl. Screening for drought and waterlogging was done in Obregon, Mexico.

Identification and utilization of resistant SH germ plasm. From the stress test data, resistant SHs were identified and hybridized with elite but stress-susceptible bread wheat cultivars according to a global priority. The hybrids were advanced by the pedigree method, with a focus on making selections for plant type, maturity, height, and specific plus multiple disease resistance . Protocols for evaluation and the test sites were similar to those described for the SH germ plasm above. The SH/BW or BW/SH entries from all biotic stress related germ plasm were field planted in 2- to 3-m double rows, tested, and led to desired selections that were stabilized routinely using the maize-based, DH protocol (Mujeeb-Kazi 2000) before international seed distribution.

Germ plasm distribution strategy. For each of the four biotic stresses, SH wheats and their advanced derivatives from crosses onto BW have been distributed to wheat breeding programs upon request and also registered as germ plasm stocks in *Crop Science* with samples of each entry reported deposited in the U.S. germ plasm bank and the Gene Bank of CIMMYT in Mexico. Small amounts (3 g) of the samples can be obtained from the author on a onetime basis only.

Table 1. Interspecific genetic stocks targeted for durum and bread wheat improvement.

Cross combination	Accessions involved	Amphiploids	Chromosomal status
Durum/*T. monococcum* subsp. *aegilopoides*	194	194	2n = 6x = 42;AABBAA
Durum/*T. monococcum* subsp. *monococcum*			2n = 6x = 42;AABBAA
Durum/*T. urartu*			2n = 6x = 42;AABBAA
Durum/*Ae. speltoides*	54	54	2n = 6x = 42;AABBBB
Durum/*Ae. tauschii*	815	1,200	2n = 6x = 42;AABBDD

Production of additional stocks. Similar to the production of D-genome hexaploids, the protocols and strategy for the development of new hexaploid stocks utilizing the A- and B-genome diploid accessions have been described (Mujeeb-Kazi 2003). In addition, to facilitate gene pyramiding, new tetraploids also have been produced involving A- and D-genome diploids. The current status of all these germ plasms are in Tables 1 and 2 (p. 81).

Development of mapping populations. The main biotic stress priority currently is *F. graminearum* head scab in bread wheat. Some superior advanced BW/SH derivatives have been identified that are being used by breeders at CIMMYT, the U.S., and some national breeding programs for wheat improvement. One such line (Mayoor//TKSN1081/*Ae. tauschii* 222) possesses FHB resistance across all four categories; type I (penetration), type II (spread), type III (toxin-DON), and type IV (test weight loss). This line also possesses multiple disease resistance to all three rusts, *H. sativum*, *S. tritici,* and *N. indica*. The bread wheat cultivar Flycatcher is susceptible to all scab types and the other six stresses. This line has formed the basis of developing a mapping population that involves crossing the resistant and the susceptible line. The $_{F1}$ derivatives were crossed with maize and 170 DHs were produced that form a mapping population for molecular study and phenotyping currently underway in Mexico. Listed in Table 10 (p. 87) are other populations produced for scab and drought tolerance.

Table 2. Status of D-genome synthetic hexaploids from an Elite I set of 95 entries for contributing beneficial diversity for wheat improvement.

Stress trait	# synthetics contributing	Resistant versus susceptible scores
Helminthosporium sativum	10	3-2 to 2-2 vs. 9-9
Neovossia indica	72	Immune vs. 45 %
Septoria tritici	15	2-2 to 2-1 vs. 9-9
Fusarium graminearum	35	7–12 % vs. 15 %
Salinity (K:Na)	95	>2.0 vs. 1.0 or <
Drought	23	(yield assessment)
Waterlogging	10	(chlorosis indicator)

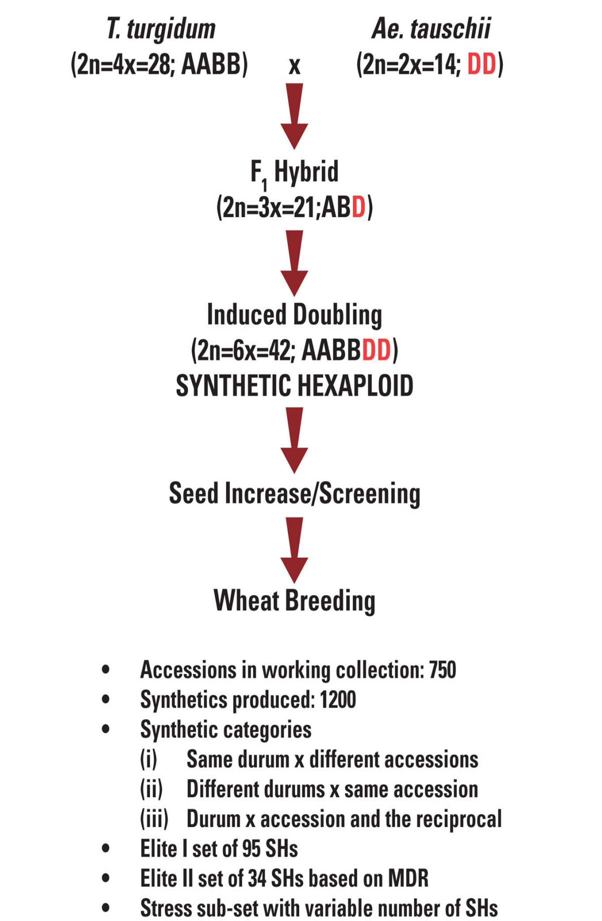

Fig. 1. Status of D-genome synthetic hexaploids.

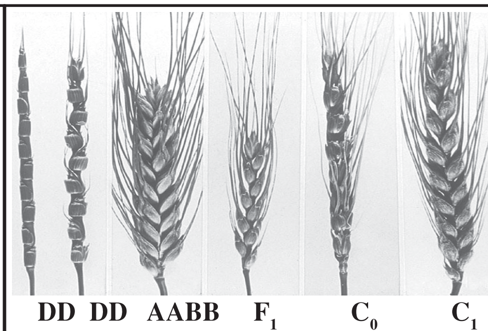

Fig. 2. Spike phenotypes from left to right as follows; DD = *Aegilops tauschii*; AABB = durum wheat; F_1 = *Ae. tauschii*/ durum (ABD); C_0 = F_1 amphiploid, ie., 2n = 6x = 42, AABBDD; and C_1 = selfed C_0.

Results and discussion. Interspecific combination stocks consist of amphiploids of the A-, B-, and D-genome diploid accession hybrids with durum wheat cultivars. These stocks are all hexaploid (2n = 6x = 42) and genomically AAAABB, AABBBB, and AABBDD. The A-genome sources are *T. monococcum* subsps. *aegilopoides* and *monococcum* and *T. urartu. Aegilops speltoides* accessions of the Sitopsis section were involved in the B-genome products, whereas *Ae. tauschii* accessions provided the D-genome accessional diversity as elucidated in Figs. 1 and 2. A- and B-genome stocks are targeted mainly for durum improvement, whereas the D-genome hexaploid contribution is principally for bread wheat. For a specific stress resistance, A- and D-genome accessions have led to new tetraploids (2n = 4x = 28, AADD) being produced, facilitating gene pyramiding for bread wheat improvement.

Focusing mainly by on the D genome, we report that practical outputs have emerged from interspecific combinations for numerous biotic/abiotic stresses. Currently, the most significant in practical usage are the D-genome SH stocks for FHB, *H. sativum*, Karnal bunt, *S. tritici,* drought, waterlogging, and salinity tolerance. Once these resistances/ tolerances are identified in the D-genome SH stocks, their combinations with elite but trait susceptible bread wheat cultivars have yielded derivatives that are free threshing, resistant/tolerant, and in good agronomic plant type. Data of some of these promising synthetics and their derivatives are presented in Tables 2 to 9.

Synthetics for each stress also have been grouped into subsets and are being utilized for DNA fingerprinting via collaborators who are applying the D-genome microsatellites for establishing polymorphisms, which are abundant in the germ plasm. Based on this molecular input, molecular mapping populations for some attributes have been produced by crossing susceptible BW/resistant SH F_1s with maize leading up to 100/170 DH/trait (Table 10, p. 87). Mapping populations produced are for drought and FHB. Precaution was taken to use parents for these populations that possess multiple disease resistances.

Table 3a. Synthetic hexaploids resistant to *Fusarium* head scab tested in Toluca, Mexico. Mean infection scores are for three crop cycles. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses.

	Type II % infection score		
Synthetic hexaploid pedigree	1	2	3
68.112/Ward//*Ae. tauschii* (369)	5.0	10.6	13.8
Dverd2/*Ae. tauschii* (1026)	7.5	2.0	13.8
Ceta/*Ae. tauschii* (1029)	7.6	10.0	13.8
Ceta/*Ae. tauschii* (1043)	4.0	1.7	16.5
Lck59.611//*Ae. tauschii* (313)	9.4	11.6	13.8
Gan/*Ae. tauschii* (437)	7.5	10.3	13.8
Flycatcher (BW S-check)	24.6	40.5	45.5
Sumai 3 (BW R-check)	12.4	11.3	17.4

Table 3b. Promising bread wheat/synthetic hexaploid derivatives with superior type-II scab resistance screened in Toluca, Mexico, for 5 consecutive years. A — indicates no data.

Entry No.	Pedigree	1999	2000	2001	2002	2003
4	Flycatcher (susceptible check)	49.1	28.5	31.3	20.7	32.0
5	Altar 84 (susceptible check)	45.8	45.7	36.2	34.4	33.7
6	Sumai #3 (resistant check)	15.2	13.0	8.6	8.9	8.3
7	Sumai #3 (resistant check)	22.7	11.1	9.2	7.6	12.2
8	Mayoor//TK SN1081/*Ae. tauschii* (222)	11.6	7.9	9.4	9.7	9.1
10	Mayoor//TK SN1081/*Ae. tauschii* (222)	11.9	5.2	9.5	10.9	8.1
19	Mayoor//TK SN1081/*Ae. tauschii* (222)	7.0	7.9	7.6	10.6	8.3
27	Mayoor//TK SN1081/*Ae. tauschii* (222)	9.3	7.4	10.1	7.8	11.7
29	Mayoor//TK SN1081/*Ae. tauschii* (222)	9.7	10.9	11.6	10.7	8.0
34	Mayoor//TK SN1081/*Ae. tauschii* (222)	11.1	9.1	11.0	—	7.3
36	Mayoor//TK SN1081/*Ae. tauschii* (222)	9.2	9.5	7.5	10.8	9.9
40	Mayoor//TK SN1081/*Ae. tauschii* (222)	7.0	9.7	10.9	9.8	6.1
41	Mayoor//TK SN1081/*Ae. tauschii* (222)	8.6	10.6	8.6	9.5	7.0
42	Mayoor//TK SN1081/*Ae. tauschii* (222)	11.7	11.1	10.8	9.8	5.5
43	Mayoor//TK SN1081/*Ae. tauschii* (222)	9.8	6.4	6.3	11.2	10.8
61	Mayoor//TK SN1081/*Ae. tauschii* (222)	6.9	10.5	11.1	9.8	6.7
65	BCN//DOY1/*Ae. tauschii* (447)	12.0	11.4	8.9	8.3	7.2
69	Altar 84/*Ae. tauschii* (224)//2*YACO	10.5	8.8	8.9	9.0	8.8
75	Opata/6/68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	8.7	12.0	8.2	11.7	7.1
78	SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)	10.7	7.4	11.5	8.6	12.5
86	Chirya.3	12.7	6.1	10.2	11.4	6.8
90	PJN/BOW//Opata*2/3/CETA/*Ae. tauschii* (1026)	—	—	11.6	7.8	11.1

Selection criteria for resistant/tolerant SHs and their derivatives. The criteria set for identifying resistance or tolerance to biotic/abiotic stress for traits of this study were set from data generated in our tests over several years of evaluation at sites in Mexico. The limits set were stringent for the germ plasms to be advanced for prebreeding objectives, not to exceed a 3-3 double digit score for *H. sativum* and 2-2 for *S. tritici*, 15.0 % or less type-11 infection score for *F. graminearum,* and less than 3.0 % infected kernels for *N. indica*. For salinity, tolerant germ plasms were to possess K:Na discrimination values of greater than 2.0 where values close to 1.0 were associated with non-tolerance to the stress. For drought tolerance the parameters comprised of grain yield, above ground biomass and 1,000-kernel weight, whereas chlorosis was the principal factor that discriminated entries tolerant to waterlogging conditions.

Synthetic related germ plasm for biotic stress resistances.

Fusarium graminearum. The SH wheats (*T. turgidum*/*Ae. tauschii*) most resistant (less than 15 % infection) to *F. graminearum* (type II) are presented in Table 3a (p. 82). The resistant BW check Sumai 3 scored around 15 % or slightly less, whereas the moderately susceptible BW check Flycatcher always had over 20 % infection and the durum wheat Altar 84 over 40 %. After several cycles of testing some advanced BW/SH scab-resistant entries were selected for type-II resistance (Table 3b, p. 82). These derivatives also generally possessed resistance to leaf rust, stripe rust, and *S. tritici*. Each scab-resistant entry selected had a disease score of less than 15 % across each test year. Sumai-3 averaged 12 % over the test years.

The most promising entries from the BW/SH combinations were further tested for the other three scab-resistance categories (types I, III, and IV). Three were found to possess combined resistance to all four types of scab. These are currently being used in bread wheat breeding at CIMMYT and in the collaborative activity with the U.S. Scab Initiative.

The combination 'Mayoor//TK SN 1081/*Ae. tauschii* (222)' and several of its sister lines exhibited superior scab resistance across the four categories and also have resistance to *S. tritici*, *N. indica,* and *H. sativum*. One line was crossed with Flycatcher (susceptible to all the above stresses), and the F_1 seed used to produce 170 DHs for molecular mapping/phenotyping. Various other lines also were utilized for additional mapping populations (Table 10, p. 87).

Septoria tritici. Septoria leaf blotch limits wheat production in high rainfall areas across 10.4 x 10^6 ha globally. *Septoria tritici*-resistant SHs crossed with the *S. tritici*-resistant wheat cultivars Seri M82, Yaco, Borlaug M95, Opata M85, Kauz, Papago M86, and the moderately resistant cultivar Bagula, gave advanced lines with good leaf blotch resistance.

Ratings of *S. tritici* resistance were based upon leaf damage recorded at water, milk, and dough growth stages using a double-digit modified

Table 4. Synthetic hexaploid (A) and advanced bread wheat/synthetic hexaploid (B) lines resistant to *Septoria tritici* blotch based upon evaluations in Toluca, Mexico. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses. Scoring scale is double digit (see Table 2 and text for explanation).

	Disease score	
A. Synthetic hexaploid	Year 1	Year 2
ACO89/*Ae. tauschii* (309)	2-1	2-1
Altar 84/*Ae. tauschii* (224)	3-1	3-1
DOY/*Ae. tauschii* (515)	1-1	2-1
D67.2/P66.270//*Ae. tauschii* (223)	3-1	3-1
GAN/*Ae. tauschii* (523)	2-1	2-1
MEXI/VIC//YAV/3/*Ae. tauschii* (659)	1-1	2-1
SCA/*Ae. tauschii* (523)	1-1	2-1
STN/*Ae. tauschii* (358)	1-1	3-1
YAR/*Ae. tauschii* (493)	1-1	2-1
YAV/DACK//RABI/3/Snipe/4/*Ae. tauschii* (460)	1-1	2-1
Esmeralda 86 (susceptible bread wheat check)	8-9	9-9
Opata 85 (susceptible bread wheat check)	9-9	9-9

	Disease score		
B. Advanced bread wheat/SH lines	2001	2002	2003
Altar 84/*Ae. tauschii* (B)//ESDA	2-1	1-1	1-1
Altar 84/*Ae. tauschii* (224)//2*YACO	2-2	1-1	1-1
CROC1/*Ae. tauschii* (205)//KAUZ	2-2	1-1	1-1
CROC1/*Ae. tauschii* (213)//PGO	2-2	1-1	1-1
Altar 84/*Ae. tauschii* (224)//2*YACO	2-1	1-1	1-1

scale. The disease ratings of each of the germ plasms indicated their superiority over the bread wheat check cultivars (scores of 2.1 or 1.1 versus 4.1 to 8.9). All germ plasms have a good agronomic plant type and were high yielding under optimum disease free environments. Pedigrees, disease scoring, and agronomic phenotype descriptor details of some of the most promising lines are in Tables 4a and 4b (p. 83).

Helminthosporium sativum. Spot blotch effects wheat crops across several environments from Latin America, Africa, Asia, and southeast Asia with Bangladesh being represented as a major disease location. Our Mexican screening site is the most severe. Several SH/BW germ plasms were evaluated at this location based upon damage recorded progressively (79 to 96 days) on leaves and grain. All lines possessed superior *C. sativus* resistance as compared with Mayoor a resistant check and Ciano 79 the susceptible check.

The SHs represent diverse accessional gene pyramiding and were developed by intercrossing several different *T. turgidum*/*Ae. tauschii* involving different *Ae. tauschii* accessions. From segregating F_2 populations, spot blotch-resistant plants were selected and hybridized with *Zea mays*. The resulting haploids (n = 3x = 21, ABD) were colchicine treated to yield homozygous doubled derivatives (2n = 6x = 42, AABBDD). Some of the best lines (SH and advanced lines) are listed in Tables 5a and 5b. The disease scores do not exceed 3-2 and grain finish is less than 2 versus susceptible scores of 9-9 and 4, respectively.

Table 5. Synthetic hexaploids (A) and bread wheat/synthetic hexaploid advanced (B) lines resistant to spot blotch in Poza Rica, Mexico. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses. Double digit scoring scale is 00 to 99, with data recorded at milk stage (a) and during soft dough stage (b). Grain infection scored for the severity of damage using a 1 to 5 scale.

	Disease score			Disease score		
	Leaves			Leaves		
A. Synthetic hexaploid	a	b	Seed	a	b	Seed
CPI/Gediz/3/GOO//Jo69/CRA/4/*Ae. tauschii* (409)	92	92	1	92	92	1
DOY1/*Ae. tauschii* (188)	93	94	2	92	93	1
DOY1/*Ae. tauschii* (333)	93	93	2	93	93	1
DOY1/*Ae. tauschii* (447)	92	93	2	92	93	1
DOY1/*Ae. tauschii* (458)	92	92	1	92	92	1
GAN/*Ae. tauschii* (408)	92	92	1	92	92	1
SCA/*Ae. tauschii* (518)	92	92	1	92	93	2
Scoop1/*Ae. tauschii* (358)	92	93	2	92	92	1
Snipe/YAV79//Dack/Teal/3/*Ae. tauschii* (877)	92	93	2	93	93	2
68.111/RGB-U//Ward/3/FGO/4/Rabi/5/*Ae. tauschii* (629)	92	92	1	92	92	1
68112/Ward//*Ae. tauschii* (369)	92	93	2	92	93	1
Ciano 79 (susceptible bread wheat check)	97	99	5	97	99	5
BH1146 (resistant bread wheat check)	95	97	3	95	97	3

	Disease scoring	
B. Bread wheat/synthetic hexaploid advanced lines	1999–99	2003–04
BCN/6/68.111/RGB-U//Ward/3/FGO/4/Rabi/5/*Ae. tauschii* (629)	1-1	1-1
Opata//CETA/*Ae. tauschii* (895)	3-3	1-1
Altar 84/*Ae. tauschii* (224)//YACO	3-3	1-1
BCN/4/68.111/RGB-U//Ward/3/*Ae. tauschii* (325)	3-3	1-1
Opata//Sora/*Ae. tauschii* (323)	3-3	1-1

Neovossia indica. Several of the *Ae. tauschii* accessions in our working collection were identified as sources of Karnal bunt resistance. These accessions were randomly hybridized with *T. turgidum* cultivars to yield SH wheats and resistant entries identified. The bread wheat germ plasm lines were derived from the Karnal bunt-resistant SHs crossed with Karnal bunt-susceptible bread wheat cultivars Flycatcher, Kauz, Yaco, Borlaug, and Papago M86. Segregating generations of the crosses were advanced by pedigree method. The mean agronomic performance of the germ plasm lines over 5 years of field tests demonstrates an acceptable phenotype; which is an asset for breeding use.

The disease score was based on the number of infected and healthy kernels at maturity in each plot. Synthetic hexaploid and bread wheat germ plasm line infections ranged from 0 % up to 1.97 % compared with a 30 % mean infection of WL711, the susceptible bread wheat check cultivar. The durum wheats in the pedigrees had infection levels from 0.3 to 1.6 %, whereas the SH wheats were immune. These germ plasms offer genetic diversity of the *Ae. tauschii* accessions as well as the A- and B-genome diversity of the durum cultivars in the SH pedigrees. Data of some resistant SH germ plasm lines is in Table 6.

Table 6. Synthetic hexaploids resistant to Karnal bunt in Obregon, Mexico. The mean % Karnal bunt (KB) score is for three crop cycles. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses.

Synthetic hexaploid	% KB Score
Altar 84/*Ae. tauschii* (188)	0.00
Altar 84/*Ae. tauschii* (198)	0.00
Altar 84/*Ae. tauschii* (221)	0.87
Altar 84/*Ae. tauschii* (223)	0.00
Croc1/*Ae. tauschii* (224)	0.00
DOY1/*Ae. tauschii* (188)	0.25
Duergand/*Ae. tauschii* (221)	0.00
YUK/*Ae. tauschii* (217)	0.00
68.111/RGB-U//Ward/3/FGO/4/Rabi/5/*Ae. tauschii* (890)	0.00
68112/Ward//*Ae. tauschii* (369)	0.45
WL711 (susceptible bread wheat check)	65.00

Drought tolerance. The results of this screening are presented in Table 7. The yield of the synthetics ranged from 638 kg/ha to 4,037 kg/ha with an overall mean yield of 2,098 kg/ha. The highest yielding synthetic was comparable to the highest yielding check cultivar, Nesser (4,065 kg/ha). Compared to the check cultivars, 1,000-kernel weight was significantly heavier on all the synthetic genotypes. Mean 1,000-grain weight ranged from 33.4 g to 51.2 g with an overall average of 42.2 g. Eighteen synthetic lines had biomass yield at maturity better than the highest biomass yielding check Nesser (10.8 t/ha).

Table 7. Mean agronomic trait values of 10 synthetic hexaploids (*Triticum turgidum*/*Aegilops tauschii*) and three bread wheat check cultivars under reduced moisture testing conditions in Obregon, Mexico. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses.

Synthetic hexaploid	Grain yield (kg/ha)	Above-ground biomass (t/ha)	1,000-kernel weight (g)	Flowering (days)	Physiological maturity (days)	Plant height (cm)
GAN/*Ae. tauschii* (897)*	4,037	11.9	38.7	82	120	99
D67.2/P66.270//*Ae. tauschii* (257)	3,277	12.4	46.2	99	136	109
DOY1/*Ae. tauschii* (458)	3,225	12.4	50.1	93	133	109
YAV3/SCO//Jo69/CRA/3/YAV79/4/*Ae. tauschii* (498)	3,181	12.4	46.5	94	133	91
Croc 1/*Ae. tauschii* (518)	3,153	9.4	46.1	85	126	90
DOY1/*Ae. tauschii* (428)	3,150	11.0	51.2	94	130	111
DOY1/ *Ae. tauschii* (188)	3,072	12.5	47.5	94	127	106
CPI/Gediz/3/GOO//Jo69/CRA/4/*Ae. tauschii* (208)	3,053	12.2	47.0	94	129	109
LCK59.61/*Ae. tauschii* (324)	3,025	11.9	40.0	106	137	101
GAN/*Ae. tauschii* (180)	3,022	13.8	43.6	94	130	100
Nesser (bread wheat check)	4,065	10.8	29.3	78	114	72
Dharwar Dry (bread wheat check)	3,276	9.2	29.1	80	114	94
Sitta (bread wheat check)	3,166	9.4	26.6	80	114	79
LSD (5 %)	209	0.5	1.2	1	1	3
CV (%)	9	10	6	2	2	5

Table 8. Percent leaf chlorosis and agronomic characteristics of synthetic hexaploids (*Triticum turgidum*/*Ae. tauschii*) tolerant to waterlogging. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses.

Synthetic hexaploid	Chlorophyll (%)	Yield/spike (g)	Days to flower	Physiological maturity (days)	Plant height (cm)	Spike length (cm)	1,000-kernel weight (g)	Grains/spike
Dverd2/*Ae. tauschii* (221)	7.3	1.59	102	136	77	11.1	49.9	32
Botno/*Ae. tauschii* (617)	7.6	1.57	106	140	95	11.5	46.1	34
68.111/RGB-U//Ward/3/*Ae. tauschii* (454)	8.2	1.54	96	129	85	9.5	36.1	43
Ceta/*Ae. tauschii* (895)	8.6	1.67	102	136	89	10.8	38.0	44
Sca/*Ae. tauschii* (409)	8.9	1.72	92	128	93	11.5	42.8	40
68.111/RGB-U//Ward/3/Pgo/4/Rabi/5/ *Ae. tauschii* (878)	12.0	0.88	99	131	93	8.4	34.2	26
Altar 84/*Ae. tauschii* (221)	12.3	2.10	106	139	83	12.6	40.8	51
SCA/*Ae. tauschii* (518)	12.7	1.47	106	139	84	12.4	46.2	32
68.111/RGB-U//Ward/3/Pgo/4/Rabi/5/ *Ae. tauschii* (878)	13.4	1.55	104	138	89	11.2	48.4	32
68112/Ward//*Ae. tauschii* (369)	13.7	1.82	100	134	81	12.8	50.5	36
GAN/*Ae. tauschii* (897)	14.5	1.98	97	132	87	10.5	45.8	43
DOY1/*Ae. tauschii* (458)	15.1	1.55	103	138	89	12.0	51.8	30
CPI/Gediz/3/GOO//Jo69/CRA/4/ *Ae. tauschii* (409)	16.1	1.75	101	136	88	11.9	52.9	33
68112/Ward//*Ae. tauschii* (369)	16.8	1.51	100	136	81	12.2	48.7	31
Ducula (tolerant check)	13.9	1.42	99	144	69	7.5	38.4	37
Pato Blanco (tolerant check)	16.9	1.17	102	139	68	8.4	31.9	37
Seri M82 (susceptible check)	74.8	1.62	101	141	66	8.8	37.9	43
LSD (0.05)	7.0	0.27	2	4	10	0.6	2.3	6
CV (%)	9	12	4	2	7	8	5	10

Table 9. Growth data (dry weight) and Na and K values at 50 mol/m^3 NaCl measured after 50 days of growth from some *Triticum turgidum* subsp. *durum* cultivars and their synthetic hexaploid derivatives. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses.

Cultivar or synthetic hexaploid	Dry weight (g)	Na (mol/m^3 plant sap)	K (mol/m^3 plant sap)	K:Na ratio
Chinese Spring wheat	4.42 ± 1.14	31 ± 3 (268 ± 21)	225 ± 5 (207 ± 4)	7.25
***T. turgidum* subsp. *durum* cultivars.**				
Rok/Kmli	1.07 ± 0.30	130 ± 4	150 ± 10	1.15
PBW 34	2.14 ± 0.35	139 ± 17	165 ± 22	1.18
Cpt/Gediz/3/Goo//Jo/Cr	1.80 ± 0.18	132 ± 1	141 ± 2	1.06
Mex/Vic//Yav	1.20 ± 0.36	123 ± 5	183 ± 3	1.48
Doy 1	2.29 ± 0.34	168 ± 13	111 ± 23	0.66
***T. turgidum* subsp. *durum*/*Ae. tauschii* synthetic hexaploids.**				
W-20 durum/*Ae. tauschii* (214)	1.98 ± 0.93	26 ± 12	200 ± 10	7.69
W-42 PBW 114/*Ae. tauschii*	2.28 ± 0.55	17 ± 7	226 ± 11	13.29
W-90 durum 3/*Ae. tauschii* (206)	3.13 ± 0.09	13 ± 4	213 ± 4	16.38
W-124 durum 4/*Ae. tauschii* (434)	1.13 ± 0.54	13 ± 8	230 ± 8	17.69
W-132 durum 5/*Ae. tauschii* (510)	6.87 ± 0.56	52 ± 28	183 ± 2	3.51

Waterlogging tolerance. Test were conducted under flooded basins 12 m wide by 11 m long. Twenty-four genotypes were planted in each basin. Waterlogging treatment commenced at 15 days after emergence for 7 weeks with continuous standing water maintained at 3–8 cm. Assessment of damage was based on degree of leaf yellowing (chlorosis) visually estimated on each plot at the end of the 49-days waterlogged treatment and mas made 1 day after the basins were drained.

Table 8 (p. 86) presents 14 synthetic lines tolerant or moderately tolerant to waterlogging as compared to the check cultivars. Adjusted mean percent chlorosis over 2 years ranged from 7 % to 75 % with an overall mean of 43 %. Five synthetic entries had leaf chlorosis scores of less than 10 % compared to 13.9 % of the most tolerant bread wheat check cultivar Ducula.

Salt tolerance. From the wide array of synthetic hexaploids produced in CIMMYT and after an initial field screening in Baja, CA (sea water dilution from 8 to 24 dS) we selected a few promising salt-tolerant types from the synthetic germ plasm that were subsequently evaluated in hydroculture (Table 9, p. 86). The hydroculture screening protocols for salinity levels maintained by NaCl over regimes between 0 and 250 mol/m^3 together with growth related parameters and Na and K estimations for establishing K^+/Na^+ discrimination values were identical to those adopted in the laboratory in Bangor, Wales (Gorham et al. 1987; Shah et al. 1987). K^+/Na^+ discrimination is a trait that enhances salinity tolerance in bread wheat compared to durum wheat and is present in the wheat ancestor *Ae. tauschii*. K^+/Na^+ ratios were lower in the durum parents (close to 1.0) than in the elite synthetics (over 1.0 and greater than 2.0 being selected for breeding use). This data confirmed that the K^+/Na^+ trait was present in the synthetics and demonstrated its poor expression in durum wheats.

Table 10. Mapping populations developed from promising synthetic-based germ plasm and susceptible bread wheats. *Ae. tauschii* accession number in the wheat wide crosses working collection are in parentheses.

Pedigree	No. of doubled haploids
Fusarium	
Mayoor//TK SN1081/*Ae. tauschii* (222)/3/FCT	171
Mayoor//TK SN1081/*Ae. tauschii* (222)/3/CNO	40
Mayoor//TK SN1081/*Ae. tauschii* (222)/3/Opata	171
Mayoor//TK SN1081/*Ae. tauschii* (222)/3/BCN	76
Sabuf/3/BCN//CETA/*Ae. tauschii* (895)/4/FCT	125
Sabuf/3/BCN//CETA/*Ae. tauschii* (895)/4/CNO	102
Sabuf/3/BCN//CETA/*Ae. tauschii* (895)/4/Opata	101
Sabuf/3/BCN//CETA/*Ae. tauschii* (895)/4/BCN	67
Turaco/5/CHIR3/4/Siren//Altar 84/*Ae. tauschii* (205)/3/3*BUC/6/FCT	128
Turaco/5/CHIR3/4/Siren//Altar 84/*Ae. tauschii* (205)/3/3*BUC/6/CNO	90
Turaco/5/CHIR3/4/Siren//Altar 84/*Ae. tauschii* (205)/3/3*BUC/6/Opata	126
Turaco/5/CHIR3/4/Siren//Altar 84/*Ae. tauschii* (205)/3/3*BUC/6/BCN	63
Drought	
CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (208)/5/Opata	188
YAV_3/SCO//JO69/CRA/3/YAV79/4/*Ae. tauschii* (498)/5/Opata	125
D67.2/P66.270//*Ae. tauschii* (257)/3/Opata	158
GAN/*Ae. tauschii* (897)//Opata	153
DOY1/*Ae. tauschii* (458)//Opata	113

Conclusions. Experts predict that today's worldwide population of just over 6.0 billion people will grow to 8.2 billion over the next two decades. By 2050, 12 billion people will crowd the planet with more than 90 % of the growth occurring in developing nations. Estimates are that the world would require one billion metric tons of wheat over the next 2 decades compared to the current production of slightly over 600 million metric tons. Hence one can extrapolate and conclude that the mean global yield of wheat would have to shift from 2.5 t/ha to over 4 t/ha. These ominous circumstances are placing a formidable task before agricultural scientists and the food management sector. This productivity only can happen around an invigorated research program with super integration of multidisciplinary activities in which germ plasm and genetic resources would remain paramount. Plant breeders involved in crop improvement efforts in order to meet the ever-increasing demand for food are finding less and less appropriate germ plasm with desired traits among cultivated crops themselves with which to make the needed improvements. Fortunately, new and useful genetic resources are being found in wild, uncultivated plants. The challenge is to incorporate this germ plasm into existing food crops, which forms the crux of this article.

The main focus addressed here has been on utilizing novel genetic diversity that resides in the wild wheat progenitor species, with major emphasis on one diploid progenitor only; *Ae. tauschii* (2n = 2x = 14; DD). Many options are available to utilize this species source and in each case the end product will yield diversity that is beneficial for wheat improvement. The outputs reported here address only a few stresses and, from such a resource, cultivars have already been released in China showing superior rust resistance and in Spain with good quality coupled in both cases with high yield. Hence, the future provides an optimistic avenue for wheat improvement that will be made more efficient due to the allelic diversity of the alien sources that support molecular applications. All germ plasms are freely available for wheat researchers globally by contacting the senior author at the m.kazi@cgiar.org.

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AGRONOMIC RESEARCH STATION
Bahawalpur, Pakistan.

Prospects for resistance to loose smut of wheat in southern Punjab.

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Summary. One hundred forty-four advance strains and 18 commercial cultivarss of wheat were screened for resistance to loose smut of wheat by artificial inoculation in southern Punjab during three consecutive years (2001–03). Of the 144 advanced wheat genotypes, 55 were highly resistant, 56 resistant, 11 moderately resistant, 9 moderately susceptible, 19 susceptible, and 12 highly susceptible. The commercial cultivars Inqlab-91, CRS-1, Punjab-96, Faisal-85, Bwp-95, Derawar-97, and MH-97 had a susceptible reaction, whereas Iqbal-2000, Uqab-2000, and Bwp-2000 were resistant. The resistant genotypes could be used in future breeding programs for the development of disease-resistant cultivars.

Introduction. Wheat is attacked by large number of pathogens and pests. However, rusts and smut fungi are highly destructive and cause enormous damage. Looking at the long list of diseases and pests (Bajaj and Gosal 1986) to which wheat is prone, the tremendous job of breeding for disease resistnce is of high priority to escape crop losses. Loose smut of wheat occurs commonly throughout the country and is characterized by the appearance of black, sooty ears containing fungal spores in place of normal grain. On average, loose smut causes 1 % damage, but in humid parts of the country and the foot-hill districts, damage can be as high as 10–20 % depending upon the wheat cultivar under cultivation. Epidemiological studies have indicated that if loose smut is not controlled, the disease will increase every year in some localities but remain constant in others (Hafiz 1986). The peculiar behavior of these fluctuations is becuse of the variation in humidity at the time of flowering in various localities. Based on surveys conducted in northwestern India, a 2–4 % yield reduction of wheat from loose smut is estimated every year (Joshi et al. 1985; Srivastava et al. 1992).

Artificial inoculation of anthers to test genotypes with *U. segetum* causes a wide range of embryonic infection (up to 84 %) in seed, depending upon the resistance against the disease. When these test seeds are sown, a direct correlation is observed between the level of embryo infection and the field expression of the pathogen. Evaluating germ plasm for resistance to loose smut of wheat through a screening process is the best and effective control measure. The present studies were conducted under stress conditions to identify the sources of resistance among different wheat cultivars and advanced lines by artificial inoculation.

Material and Methods. Studies were conducted at Regional Agricultural Research Institute, Bahawalpur, for 3 years (2001–03). One hundred forty-four advanced wheat strains and 18 commercial cultivars were screened for resistance to loose smut. Two lines of each entry were sown in 2-m rows with a 4-cm plant-to-plant distance in the field on 20 November of each year. Entries were inoculated with the fresh inoculum collected from the naturally occurring loose smut affected heads in the field (Mishra et al. 1990) by preparing a spore suspension. Undehisced anthers were selected for artificial inoculation of loose smut. The experiment was repeated for 2 years to test the stable response of the strains or cultivars. Observations were recorded on the following scale:

Grade	Disease intensity	Reaction
1	No dymptoms on any plant or < 1 % infection	Highly resistant (HR)
2	1–5 % of the plants with smutted heads	Resistant (R)
3	6–10 % of the plants with smutted heads	Moderately resistant (MR)
4	11–20 % of the plants with smutted heads	Moderately susceptible (MS)
5	21–50 % of the plants with smutted heads	Susceptible (S)
6	> 51 % of the plants with smutted heads	Highly susceptible (HS)

Data recording and observations on infection percent began in 2001 at the appearance of black sooty ears containing spores of the fungus instead of normal grains.

Results and Discussion. Out of 144 advanced wheat cultivars and 18 commercial cultivars tested for resistance to loose smut, 55 were immune or had less than 1 % infection, an HR reaction, 56 were R , 11 MR, 9 MS, 19 S, and 12 HS (Table 1). These results show that the resistance in the 144 advanced wheat lines are indicative of the entire 3-year consecutive study could be compared with the yearly resistance response (Table 3, p. 91). The comparative data reflects the gradual trend towards a stable resistance pattern with a distinctive increase in response between the first and second years for preinoculated advanced wheat cultivars, followed by the minor edges during third year due to maintenance of resistance. Beniwal et al. (1998) reported similar findings regarding stable source of resistance during evaluation of some 2,190 wheat cultivars in India from 1981–82 to 1996–97. The results obtained in the third year (Table 3) showed a gradual increase in reaction (resistant to susceptible) that remained consistently higher than that of the preceding years, which represents the potential of the test cultivars.

Table 1. Response of different advanced cultivars/lines to loose smut of wheat (*Ustilago segetum* var. *tritici*) in artificially inoculated conditions in 3 years of testing (2001–03) at the Regional Agricultural Research Institute, Bahawalpur, Pakistan.

No.	Reaction	Strain or cultivar
1	HR	96B-2014, 96B-2030, 96B-2034, 96B-2035, 97B 2221, 97B-2336, 97B-2342, 98B-2025, 98B-2030, 98B-2031, 98B-2043, 98B-2049, 98B-2441, 99B-2236, 99B-2237, 99B-2252, 99B-2276, 99B-2277, 99B-2278, A1V-2460, A1V4344, A1V-5011, A1V-5054, AV-5061, A2V-5441, A2V-5584, A3V-6138, A3V-6259, A3V-6350, A3V-6369, A3V-6479, A3V-7148, A3V-7151, V-2500, V-2503, V-2505, MB-2295, MB-2299, MB-2344, 2-Ist012512, 2-Ist012514, 2-Ist012515, 2-Ist 6364-99-00, 2-Ist5592-99-00, M-A-W-I, V01B-2523, V01B-2533, VO1B-2538, VO1B-2543, VO1B-2549, VO1B-2555, VO1B-2568, VO1B-2583, and VO1B-2591
2	R	95B4027, 95B-4033, 95B-4039, 95B-4074, 96B-2009, 96B-2069, 96B-2070, 96B-2071, 96B-2098, 96B-2099, 97B-2236, 97B-2206, 97B-2213, 97B-2223, 97B-2243, 97B-2317, 97B-2333, 97B-2329, 97B-2560, 97B-2562, 98B-2003, 98B-2012, 98B-2017, 98B-2018, 98B-2021, 98B-2039, 98B-2040, 98B-2045, 98B-2051, 98B-2060, 98B-2449, 98B-2452, 98B-2460, 98B-2556, 99B-2223, 99B-2254, A1V-2445, A1V-4423, A2V-5282, A2V-5306, A2V-5390, A2V-5395, A2V-5404, A2V-5541,WSN-21, MB-2319, V01B-2540, V01B-2544, V01B-2556, V01B-2571,V01B-2524,V01B-2525, and V10B-2530
3	MR	95B-4056, 95B-4073, 96B-2107, 97B-2209, 97B-2558, 98B-2007, 98B-2083, 99B-2222, WSN-3, MB-2305, and MB-2353
4	MS	95B-4055, 96B-2074, 96-2088, 98B-2062, and 98B-2071
5	S	95B-4068, 95B4071, 95B-4072, 97B-2207, 97B-2217, 97B-2250, 98B-2056, 98B-2063, 98B-2078, and 98B-2079
6	HS	96B-2043, 96B-2044, 96B-2046, 96B-2047, 96B-2106, 97B-2212, 97B-2248, 98B-2008, 98B2084, and 96B-2048

Our experiment also tested 18 commercial cultivars that have been sown in the Bahawalpur region for many years (Table 2, p. 91). The data showed that two cultivars, Bwp-97 and Iqbal-2000, were free of infection in 2001 and over the next 2 years exhibited responses ranging from HR to R. Two other cultivars, Uqab-2000 and Bwp-2000, also maintained their resistance to loose smut during the 3 years (Table 3, p. 91).

Nine cultivars, Blue Silver, Pak-81, Faisal-85, Faisal-83, Derawar-97, Bwp-97, Pasban-90, Rohtas, and Kohinoor-83, did not resist the inoculum pressure and were susceptible to loose smut of wheat with 11–20 % infection.

Table 2. Yearly response of commercial cultivar to loose smut of wheat by artificially inoculated conditions in 3 years of testing (2001–03) at the Regional Agricultural Research Institute, Bahawalpur, Pakistan. 0 = highly resistant, R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

Cultivar	2001	2002	2003
Blue Silver	MS	S	S
Pak-81	MS	MS	S
Faisal-83	MR	S	S
Punjab-96	MR	MS	MS
Faisal-85	MS	MS	S
Inqlab-91	R	MR	MS
Derawar-97	MS	S	S
Bwp-95	MS	MS	S
Pasban-90	MS	S	S
Sutluj-86	MS	S	HS
Rohtas	S	S	S
Bwp-97	0	R	R
Kohinoor-83	MS	S	S
MH-97	MS	MS	MS
Iqbal-2000	0	HR	HR
CRS-1	MS	MS	MS
Uqab-2000	HR	R	R
Bwp-2000	HR	HR	R

Table 3. Overall grading of test entries for resistance to loose smut of wheat after artificially inoculation in 3 years of testing (2001–03) at the Regional Agricultural Research Institute, Bahawalpur, Pakistan. 0 = highly resistant, R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

Grade	Reaction	2001	2002	2003
1	HR	69	55	54
2	R	63	53	53
3	MR	10	15	11
4	MS	2	5	5
5	S	0	9	10
6	HS	0	7	11

Sutluj-86 had the highest susceptibility (76.32 %). This cultivar, however, could be used in further screening investigation as a source of inoculum. Inqlab-91, the most popular cultivar of the Punjab province, was rated R, MR, and MS in the years 2001, 2002, and 2003, respectively, which reflects its meagre potential against the disease. Due to susceptibility of this cultivar, smutted heads from Inqlab-91 were easily available for preparation of inoculum suspensions.

Beniwal et al. (1999) evaluated resistance in 19 wheat cultivars commercially grown in the North-Western Plain zone of India during the 1995–96 and 1996–97 crop seasons. Popular cultivars such as WH-147 and HD-2329 were highly susceptible to loose smut of wheat. Sharma et al. (1998) screened 17 bread wheat and three durum wheat genotypes plus 19 Canadian loose smut differential lines for resistance to *U. segetum* in 1994–95. Few genotypes were resistant to disease.

Different methods af artificial inoculation were used for studying the degree of resistance in the test cultivars. Mishra et al. (1990) screened 92 cultivars against *U. segetum* by needle inoculation in 1980–82. Fifteen lines were R and three were rated MR. Sherif et al. (1991) graded Giza 155, Giza 160, and Giza 162 as R, Sakha 61 and Sakha 92 as S out of 10 Egyptian cultivars. The resistant source found during these studies will be the best for future breeding programs wanting to minimize the effect of loose smut in the new wheat cultivars.

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Effect of high moisture stress on wheat genotypes under late-sowing conditions.

Manzoor Hussain, Altaf Hussain Tariq, Ghulam Hussain, Lal Hussain Akhtar, Muhammad Zubair Khan, and Abdul Majeed Iqbal.

Abstract. Four approved wheat cultivars and six newly developed wheat strains were compared for yield and yield components under acute drought conditions during 1999–2000 and 2000–01 at the Regional Agricultural Research Institute, Bahawalpur. Significant differences were observed in grain yield, plant height, number of kernels/spike, and 1,000-kernel weight. The maximum grain yield was produced by 962098; the minimum by 972317. Maximum plant height was in Bahawalpur 2000 and the minimum in 972317. Higher kernel numbers were in Inqlab-91 and 962098 and the minimum in 972317. Bahawalpur-2000 and 962098 produced the maximum 1,000-kernel weight, whereas 972317 and 962552 were very low.

Introduction. Wheat is often sown in month of December in the cotton-growing districts of Pakistan. The wheat crop faces moisture stress due to shortage of water in rivers and the cleaning of canals. Millions of acres of wheat in southern Punjab produce low grain yields because of moisture stress resulting in a loss of billions of rupees. The Bahawalpur Region is hot and dry. During 1999, the lowest rainfall (155 mm) in Punjab was received in Bahawalpur (Agriculture Statistics of Pakistan 2000). The crop season often passes with very low rainfall. Drought is a problem in only Pakistan but is worldwide, which is why many countries are breeding for drought tolerance in wheat. ICARDA (Syria) is one very important institute in world that is working on drought tolerance. The wheat Cham 6 was released by ICARDA in 1991 as commercial cultivar for areas of Syria with less than 350 mm rainfall (Anonymous 1992). Low rainfall areas are those that receive an annual rainfall of 250–350 mm; moderate rainfall areas have 350–600 mm annually (Anonymous 1999). Siakia et al. (1999) studied the different responses of wheat cultivars related to yield under rainfed conditions. Singh and Uttam (1995) observed a considerable effect of rainfed conditions on grain yield, straw yield, number of spikes/m^2, number of seeds/spike, water use efficiency, and maximum root development when they were studying the behavior of wheat cultivars under rainfed conditions. Tanveer et al. (2002) observed significant differences among wheat cultivars in plant height, spike length, and harvest index. The objective of our study was to compare wheat genotypes for yield and yield components under acute drought conditions following late planting.

Materials and Methods. The experiment was conducted at Regional Agricultural Research Institute, Bahawalpur, during 1999–2000 and 2000–01. Ten wheat cultivars and lines, 962098, 972236, Bahawalpur-2000, 962552, Chakwal-86, 972563, 972561, Kohistan-97, Inqlab-91, and 972517, were planted in a randomized complete block design with three replications. Plot size was 5 x 1.8 m^2. The experiment was late sown, i.e., sowing was on 10 December after harvest of a cotton crop. N and P_2O_5 fertilizers were applied at 90 and 60 kg/ha, respectively, at the time of soil preparation. For germination, a soaking dose (Rowni) was applied. No supplemental irrigation was applied. The size of the harvested plot size was 5 x 1.2 m^2. Data for some quantitative characteristics like plant height (cm), average number of kernels/spike, 1,000-kernel weight (g), and grain yield (kg/ha) and some qualitative characters like plant color, waxiness, and spike sterility were recorded. Rainfall and temperature (maximum and minimum) also were recorded at the Cotton Research Station, Bahawalpur. Analysis of variance was done by the method as described by Steel and Torrie (1980) and observations were compared by using the Duncan's Multiple Range Test (Duncan 1955).

Results and Discussion.

Environment—rainfall. During 1999-2000, only 12 mm of rainfall was received during January of the growing season, only a trace in 2000–01, and 21 mm was received in April after crop maturity (Table 4). Total Precipitation (soaking rains and other rainfall) during 1999–2000 was 112 mm. The 100 mm received in 2000–01 was only as a soaking dose, showing acute drought conditions.

Table 4. Rainfall during the two wheat growing seasons at the Regional Agricultural Research Institute, Bahawalpur, Pakistan.

Year	December	January	February	March	April	Total
1999–2000	0	12	0	0	0	12
2000–2001	0	0	0	0	21	21

Environment—maximum temperature. During the 1999–2000 season, the maximum temperature was 22°C to 39.8°C; in 2000–01 it was 22.1°C to 39.5°C. During both years, high temperature were observed in April and low temperatures in January (Table 5).

Table 5. Maximum temperature (°C) recorded at the Cotton Research Station, Bahawalpur, Pakistan, during the years 1999 to 2001.

	1999	2000	2001
December	26.1	25.4	—
January	—	20.7	22.1
February	—	22.4	24.9
March	—	27.4	30.6
April	—	39.8	39.5

Environment—minimum temperature. During the 1999–2000 crop season, minimum temperatures ranged from 6°C to 21.4°C. The highest minimum temperature was recorded in April 2000 and the lowest minimum temperature in January 2000 (Table 6).

Table 6. Minimum temperature (°C) recorded at the Cotton Research Station, Bahawalpur, Pakistan, during the years 1999 to 2001.

	1999	2000	2001
December	7.3	5.5	—
January	—	6.0	6.2
February	—	7.6	8.1
March	—	12.9	15.1
April	—	21.4	21.8

During 1999—2000, 12 mm of rainfall was received in January, which increased the tillering capacity by delaying a moisture shortage and resulted in better yields. During 2000–01, only a soaking dose was received, which was one of the causes of low yields. Temperatures in February and March play an important role in yield. Maximum and minimum temperatures in February and March 2000–01 were less than those in 1999–2000. Lower maximum and minimum temperatures help to prolong the growing period, which results in higher yields.

Grain yield and yield components—grain yield. Differences in grain yield among the strains and cultivars were significant during both years; the values for individual cultivars and lines are given in Table 7. During 1999–2000, strain 962098 (3,750 kg/ha) out yielded all the wheat genotypes. Strain 972236 was similar to Bahawalpur 2000 and 962552 but was different from all other wheat genotypes. Bahawalpur 2000 was significantly different from 962098, 972561, Koh-97, Inqlab-91, and 972517. The strain 962552, with a yield of 2,833 kg/ha was different from 962098, 972561, Koh-97, Inqlab-91, and 972517 but not different from the remaining genotypes. Ch-86, with a grain yield of 2,792 kg/ha, was different from all genotype except Bahawalpur-2000, 962552, 972563, and 972561. Line 972563 (2,708 kg/ha) was different from all except Bahawalpur 2000, 962552, Ch-86, and 972561. Inqlab-91, Koh-97, and 972517 had similar low yields in 2000–01. In 2000–01, 962098 again was the best performer at 2,677 kg/ha). 972236 was different from all genotypes except 962098, and Ch-86 (2,300 kg/ha) was different from 962098 and 972563. Inqlab-91 was significantly different from 972517, 962552, Ch-86, 972236, and 962098. The strain 972317 (1,111 kg/ha) was lowest significantly. Seven wheat genotypes

Table 7. Wheat yield factors from trials under moisture stress during the two wheat growing seasons at the Regional Agricultural Research Institute, Bahawalpur, Pakistan. Letters indicate significant differences between values for each cultivar.

No.	Cultivar	Grain yield (kg/ha)	Plant height (cm)	Kernels/spike (average)	1,000-kernel weight (g)
1999–2000 crop year.					
1	962098	3,750 a	83 ab	33 ab	28 abc
2	972236	3,208 b	81 ab	32 ab	30 ab
3	BWP2000	3,083 bc	84 ab	27 bcd	32 a
4	962552	2,833 bc	72 cd	24 d	22 de
5	CH-86	2,792 cd	78 abc	32 ab	25 bcde
6	972563	2,708 cd	80 ab	30 abc	28 abc
7	972561	3,625 de	71 de	25 cd	27 acd
8	INQ-91	2,250 e	68 de	35 a	29 ab
9	972517	2,250 e	65 e	24 d	21 e
10	KOH-97 (Check)	2,417 e	67 de	28 bcd	25 bcde
2000–2001 crop year.					
1	962098	2,677 a	80 ab	34 a	28 ab
2	972236	2,533 ab	78 abc	30 ab	27 abc
3	Ch-86	2,300 bc	77 abc	33 a	26 abcd
4	962552	2,244 cd	80 ab	26 bd	22 de
5	BWP-2000	2,150 cde	82 a	29 ac	30 a
6	972563	2,011 def	71 cd	26 bd	25 bcd
7	Inq-91	2,011 def	65 de	33 a	28 ab
8	972561	1,806 f	68 de	23 c	24 bcde
9	972317	1,111 g	62 e	22 d	20 e
10	KOH-97 (Check)	1,844 f	64 de	26 b	23 cde

performed better than check during moisture stress, KOH-97 during both the years. Similar studies were conducted by S.K.Tanveer and coworkers in 1999–2000 and 2000–01 at the NARC, Islamabad, Pakistan. They found that Inqlab-91 gave 3,836 kg/ha when 242 mm precipitation was received during the 1999–2000 growing season, whereas in 2000–01, Inqlab-91 produced 3,817 kg/ha with 96 mm precipitation during the wheat cropping season.

Grain yield and yield components—height. Differences in plant height were significant in 1999–2000; similar to those of S.K. Tanveer and coworkers. Bahawalpur 2000 achieved maximum height in both years under moisture stress. In 1999–2000, BWP-2000 did not differ from 992236, Chachwal-86, or 972563 but was different from 962552, KOH-97, Inqlab-91, 972561, and 972517. In 2000–01, Bahawalpur 2000 was significantly different from 972317, 972561, KOH-97, Inqlab-91, and 972563 but did not differ from 972236, Ch-86, or 962552.

Grain yield and yield components—average number of kernels/spike. Response within the cultivars and strains to high moisture stress was significant during both the years of the study. In 1999–2000, Inq-91 had the greatest average number of grains/spike; significantly different from 972517, KOH-97, 972561, 962552, and BWP-2000. No significant differences were found among 962098, 972236, Ch-86, 962552, BWP-2000, Inqlab-91, and 972563. The strain 962098 and Inq-91 were significantly different from 972317, 972561, and KOH-97.

Grain yield and yield components—1,000-kernel weight. Under high moisture stress, the wheat strains and cultivars also showed significant differences. BHP-2000 had a high 1,000-kernel weight during both the years. BHP-2000 was different from 972517, 962552, KOH-97, and CH-86. In 1999–2000, 972517 and 962552 were badly affected by moisture stress. In 2000–01, BHP-2000 was different from 972317, 972561, Koh-97, 972563, and 962552 but did not differ from 962098, 972236, CH-86, Inqlab-91, 972317, and 962552, which were affected greatly by the moisture stress.

Qualitative characteristics. The following characteristics were recorded in all the genotypes under an acute moisture stress conditions:

plant color changed to dark green in all entries,
waxiness increased in all the genotypes,
leaf curling was observed in all genotypes, and
genotypes with long spikes like Inqlab-91 showed tip sterility.

Conclusion. High moisture stress affects grain yield and yield components. Wheat genotypic response to high moisture stress was found to be significant. The strains 962098 and 972236 gave the maximum grain yield during both cropping years, whereas 972317 was affected badly. Bahawalpur 2000 and Chakwal-86 were found to be better than Inq-91 and KOH-97 under conditions of high moisture stress. Inqlab-91 should not be cultivated under high moisture stress. Moisture levels in the soil of the cotton zone is sufficient to produce yields of 2,000 kg/ha or more.

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Comparative genotypic resistance to Russian wheat aphid in the wheat crop in the southern Punjab, Pakistan.

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Summary. To identify resistance to RWA in different wheat genotypes, 10 wheat cultivars or strains were sown in a randomized complete block design with three replications at the at Regional Agricultural Research Institute Bahawalpur. The wheat cultivar Uqab-2000 was found to be the most resistant, giving a maximum grain yield (3,062 kg/ha) with 50 aphids/tiller. The strain V-2333 was second best with 43 aphids/tiller and a grain yield of 2,964 kg/ha. V-2278 was found to be less attractive to the aphids (34 aphids/tiller). Wheat strains V-2237 and V-4012, with 46 and 44 aphids/tiller, respectively, had better grain yield (2,816 kg/ha[I] for V-2237 and 2,865 kg/ha for V-4012). Two commercial wheats, Inqlab-91 and Iqbal-2000, had low grain yields (2,371 kg/ha) with a comparatively low number of aphids/tiller (35 each). This situation is alarming because Inqlab-91 covers maximum area in the province and Pakistan. A new wheat cultivar, Manthar-3, was resistant to aphids when compared to Inqlab-91. The wheat strain V-2460 was affected badly.

Introduction. Wheat is an important food crop in Pakistan, being sown on an area of 8.057 x 10^6 ha (Agriculture Statistics of Pakistan 2001–2002). The wheat crop passes through a series of stresses from sowing to harvesting, including heat, moisture shortage, disease, and insects. In Pakistan, attacks by aphids are increasing on the wheat crop, especially in cotton zones of Multan, D.G. Khan, and Bahawalpur. Aphids hinder photosynthesis but infestations during the last few years on leaves, stems, and spikes have been severe, causing necrosis and blackening of these parts. Necrosis and blackening affect grain yield. During 2002–03, aphid attacks on wheat fields in southern Punjab was at the maximum and the aphid population increased to a dangerous level. A good wheat crop had been expected in Pakistan in 2003, similar to that of 1999–2000, which was a record 21.078 x 10^6 tons (Agricultural Statistics of Pakistan 1999–2000). In 2002–03, the average yield per unit area also was less than the expectations due to aphid attack on wheat. In the present study, the behavior of wheat genotypes against aphid attack was investigated.

Bahawalpur is characterized by low humidity with drought stress. Russian wheat aphid is most often found in low humidity areas with moderate drought stress (Anonymous 1992). The RWA injects a toxin into the plant tissue that destroys the chloroplast membrane, causing longitudinal chlorotic streaks to develop (Anonymous 1999). At the ICARDA research field, 10 RWA nymphs/plant were found at tillering stage (Anonymous 1999). The RWA is a harmful pest damaging grain yield worldwide. The importance of the RWA to the U.S. wheat industry is substantiated by the reported economic damage of over \$130 x 10^6 USD in 1987–88 (Peairs et al. 1989).

Materials and Methods. The experiment was sown at the research area of the Regional Agricultural Research Institute, Bahawalpur, in 2002–03. The trial was consisted of five approved cultivars (Manthar-3, Uqab-2000, Punjnad-1, Inqlab-91, and Iqbal-2000) and five advanced wheat lines (V-2237, V-2460, V-2278, V-4012, and V-2333). The experiment was conducted by using an randomized complete block design with three replications. Plot size was 6 m^2. N and P_2O_5 fertilizers were applied at the rate of 160 and 110 kg/ha, respectively. The experiment was sown on two dates, S_1 (30 November, 2002) and S_2 (20 December, 2002) to ensure maximum chance of RWA infestation. Four irrigations were applied to each sowing. Weeds were controlled chemically with Bromoxynil. Yield (kg/plot) and RWA population were recorded from 10 tillers selected at random from each plot. Harvesting was complete by 25–26 April, 2003. Analysis of variance was performed following the method described by Steel and Torrie (1980), and the treatments were compared using a Duncan's Multiple Range test (1955).

Table 8. Russian wheat aphid populations on different wheat cultivars and lines recorded in field plots at the Regional Research Institute, Bahawalpur, Pakistan, in 2002–03. The average number of aphids/tiller was recorded for two different sowing times, S_1 (30 November) and S_2 (20 December). Items with different letters are significant at $P = 0.05$.

	Aphids/tiller	
Cultivar/line	S_1	S_2
V-2460	49 bcd	61 a
V-2278	38 d	31 cde
V-4012	49 bcd	39 bc
V-2333	47 bcd	39 bc
V-2237	55 bc	37 bd
Iqbal-2000	41 cd	29 cde
Panjnad-1	78 a	19 e
Inqalab-91	43 cd	27 cde
Uqab-2000	65 a	34 bd
Manthar-3	61 b	46 b

Results and Discussion.

Aphid infestation. Aphid attack always is found at the reproductive stage of the crop in the reported area. Aphids were found on each tiller, present on heads, leaves, and stems (Table 8). At the early sowing date

(S_1), a significant difference in RWA populations was observed. Maximum aphid populations were found on Punjnad-I (78 ahpids/tiller) and Uqab-2000 (65 aphids/tiller), which is significantly different from all other cultivars or strains but there was no difference between these two wheat cultivars. The wheat Manthar-3 was significantly different from Inqlab- 91, V-2460, V-2278, Iqbal-2000, Punjnad-I, and Uqab-2000, but was not significantly different from V-2237, V-2233, and V-4012. The line V-2237 with 55 aphids/tiller was similar to Inqlab-91, V-2460, V-4012, Iqbal-2000, and V-2333, but different from Punjnad-I, Uqab-2000, Manthar-3, and V-2278. The lines V-2460 and V-4012, both with 49 aphids/tiller, were significantly different from cultivars Punjnad-I and Uqab-2000 but was similar to all the other cultivars and lines.

At the second planting date, S_2, significant differences in aphid population were observed. Line V-2460, with 61 aphids/tiller, was more attractive than all other wheat cultivars or lines, whereas Punjnad-I at this sowing date was less attractive to the RWA. Manthar-3 (46 aphids/tiller) was similar to Uqab-2000, V-2237, V-2333, and V-4012, but different from V-2460, Inqlab-91, V-2278, Uqab-2000, and Punjnad-I. Lines V-4012 and V-2333 were found to be statistically different from V-2460 and Punjnad-I but similar to the other six lines. The wheat Punjnad-I was statistically different from V-2460, Manthar-3, V-2333, and V-4012.

Table 9. Grain yield data for different wheat cultivars and lines recorded in field plots infested with Russian wheat aphids at the Regional Research Institute, Bahawalpur, Pakistan, in 2002–03. The yield in kg/ha was recorded for two different sowing times, S_1 (30 November) and S_2 (20 December). Items with different letters are significant at $P > 0.05$; other data with no significant differences.

Cultivar/line	S_1 yield	S_2 yield
V-2460	2,371 g	2,470
V-2278	3,359 bc	2,470
V-4012	3,260 bcd	2,470
V-2333	3,754 a	2,174
V-2237	2,964 def	2,668
Manthar-3	3,458 a	1,581
Uqab-2000	3,754 a	2,371
Inqalab-91	2,470 g	2,272
Panjnad-1	2,470 g	2,075
Iqbal-2000	3,063 cde	1,679

Grain yield. At the early sowing date, significant differences in grain were observed (Table 9). Uqab-2000 and V-2333 produced higher yield than all the other cultivars or strains except Manthar-3. Uqab-2000, V-2333, and Manthar-3 had better resistance than all other genotypes. Strain V-2278 showed comparatively better resistance than V-2237, Punjnad-1, Iqbal-2000, Inqlab-91, and V-2460, but was similar in resistance to V-4012 and Uqab-2000. Strain V-4012 had a similar level of resistance with that of V-2278, Uqab-200,0 and V-2237 but had better resistance than Inqlab-91, V-2460, and Punjnad-1. Three wheats, Inqlab-91, V-2460, and Punjnad-1, were less resistant to RWA.

At the second sowing date, no significant differences in the wheats were found. Wheat strains V-2237 produced the highest grain yield (2,668 kg/ha); Manthar-3 the lowest (1,581 kg/ha).

Conclusions. Average data for the differenct cultivars and strains is given in Table 10. The wheat cultivar Uqab-2000 was found to be the most resistant to RWA, producing the highest grain yield (3,062 kg/ha) with 50 aphids/tiller. The wheat strain V-2333 with 43 aphids/tiller had the second highest yield at 2,964 kg/ha. Line V-2278 was less attractive to the RWA (34 aphids/tiller). Wheat strains V- 2237 and V- 4012 with 46 and 44 aphids/tiller yielded 2,816 kg/ha and 2,865 kg/ha respectively. Two commercial wheat cultivars, Inqlab-91 and Iqbal 2000, had low grain yields (2,371 kg/ha) with a comparatively low number of aphids/tiller (35). Because Inqlab-91 covers maximum area under wheat in the province and the country, this situation is alarming. The new wheat cultivar Manthar-3 exhibited better resistant to RWA compared to Inqlab-91. Wheat strain V-2460 was infected badly. Study on RWA occurrence in the area and identification of resistant cultivars should be encouraged. Area sown to cultivars with low levels of resistance should be decreased.

Table 10. Average data on aphid attack and grain yield for different wheat cultivars and lines recorded in field plots infested with Russian wheat aphids at the Regional Research Institute, Bahawalpur, Pakistan, in 2002–03.

Cultivar/strain	Aphids/tiller	Yield (kg/ha)
V-2460	55 a	2,421 c
V-2278	34 c	2,915 a
V-4012	44 ac	2,865 a
V-2237	46 abc	2,816 ab
V-2333	43 ab	2,964 a
Manthar-3	53 a	2,520 bc
Uqab-2000	50 ab	3,062 a
Punjnad-I	49 abc	2,273 c
Inqlab-91	35 bc	2,371 c
Iqbal-2000	35 bc	2,371 c

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The role of exotic sources in the evolution of wheat cultivars in Pakistan.

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Introduction. After the introduction of semidwarf wheat, wheat yields in the world increased. CIMMYT is working in many different aspects of wheat research. Every year, new wheat lines are tested and selected for different climatic zones in the world. Selected wheat entries are included in different wheat nurseries and trials and are distributed worldwide and relevant data collected. This new, circulated material is tested at local wheat research stations in the world and also is selected for local planting. The best performing entries are put into national testing programs and are released as cultivars in different countries. For example, the Veery line, which is cross between spring and winter wheat lines has the pedigree 'KavKaz/Buho's//Kal/BB (CM-33027)'. From this cross, 53 cultivars were released in different countries of the world. In Pakistan, Veey #5 was approved as the cultivar Pak-81, and it performed very well in the wheat fields of Pakistan. Different research stations and institutes in Pakistan also receive exotic material for testing under local conditions for a few years. The best performing lines are approved as cultivars.

Some researchers feel that wheat lines crossed locally and studied under local conditions can give better performance. For example, Inqlab-91, pedigree 'WL-711/CROW S' is a local cross made at Faisalabad. Generation studies were completed at Faisalabad (Proposal of a wheat cultivar 85060-1 (Approved) 1991). Inqlab-91 is the first wheat cultivar to be grown on 60–70 % of the country for many years. The cultivar still is present in the farmers' fields and will probably be around for about 5 more years. The success of Inqlab-91 supports the opinion of those experts who favor local hybridization. This study will help decide the dependency of agriculture research of wheat on exotic sources in Pakistan. At different research stations in Pakistan, valuable material resulting from local crosses is available and the best results can be achieved by interchanging material in Pakistan. Genetic variability in Pakistan can be achieved by crossing present material with the old species.

Materials and Methods. The National Uniform Wheat Yield Trial is comprised of 20 wheat entires from all research stations and institutes in Pakistan and is controlled by the Coordinator for Wheat, NARC, Islamabad. The nurseries were planted in a randomized complete block design with four replications. Plot size was '5 x 1.2 m' or 6 m^2. Results are complied and published by the Coordinator for Wheat, NARC, Islamabad. In this study, 10 years of data have been collected from the results of National Uniform Wheat Yield Trials. Entries are divided in two groups, local crosses and selection from exotic sources. The number of wheat cultivars and strains have been compared by a percentage.

Results and Discussion. During 10 years of study, 167 entries were tested. The results are discussed here on province basis (see also Table 11, p. 98).

The Punjab. The Punjab province consisted of six research stations/institutes and contributes a large number of entries. The Wheat Research Institute, Faisalabad, is the major wheat research institute of Pakistan. From Punjab, 97 entries were tested in national wheat program. Seventy-four entries were result of local crosses and 23 were selections from exotic nurseries and trials.

The Sindh and Baluchistan. Five research stations are in the Sindh and Baluchistan provinces of Pakistan. During the 10 years under study, 23 entries were tested in the National Uniform Wheat Yield Trials. Ninteen entries were selections from exotic crosses and four were local crosses.

The North-West Frontier Province. Five research stations/institutes are working on wheat in this province. During the 10 years under study, 37 entries were contributed by the province; 36 strains were selections from exotic sources and one was a local cross.

National Agricultural Research Centre, Islamabad. During the 10-year study, 10 entries were tested at this Institute. One strain was a selection from a local cross and nine were from exotic sources.

Total for Pakistan. The percentage of the entries from Pakistan tested in the National Uniform Wheat Yield Trials for 10 years is given in Table 11.

Wheat cultivars approved. During the 10-years period, 32 of 167 entires in the National Uniform Wheat Yield Trials were approved as cultivars. The percentages from local crosses or selected from exotic sources are given in Table 11.

Table 11. Source of entries in the National Uniform Wheat Yield Trial in Pakistan over the last 10 years grouped by province.

Crosses	No. of entries	%
Punjab.		
Local	74	76
Exotic	23	24
Total	97	—
The Sindh and Baluchistan.		
Local	04	17
Exotic	19	83
Total	23	—
The North-West Frontier Province.		
Local	1	3
Exotic	36	97
Total	37	—
NARC, Islamabad.		
Local	1	10
Exotic	9	90
Total	10	—
Pakistan.		
Local	80	48
Exotic	87	52
Total	167	—
Approved cultivars.		
Local	11	34
Exotic	21	66
Total	32	—

During the 10-year period, 32 wheats were released for general cultivation. Of these lines, 34 % were selections from local crosses and 66 % were selections from exotic sources. The greatest number of cultivars were developed from exotic sources during the 10 years (1990–91 to 2000–01). However, cultivars grown over the greatest area in Pakistan were from local crosses. These wheats were approved for different purposes, such as for irrigated areas, rainfed areas, hilly areas, or late-sowing. Some important cultivars from this source are Inqlab-91, Punjab-96, Uqab-2000, Iqbal-2000, MH-97, Kirran, Anmol-91, Soughat, Marvi-2000, Bahawalpur-2000, Punjnad-1, Bakkar-2002, Noshera, Suleman, Daman-98, Sariab-92, and Zarlashta-99. The research institutes and stations in Punjab have produced 16 cultivars of which nine (56 %) were selected from local crosses and seven (44 %) were selected from exotic sources. During the 10 years, the main wheat cultivars planted to the greatest area in Pakistan were Inqlab-91, TJ-83, Parwaz-94, Punjab-96, and MH-97. Inqlab-91, Parwaz-94, and Punjab-96 resulted from local crosses and covered 60 to 70 % of wheat-growing area of Pakistan. TJ-83 and MH-97 are selections from exotic sources, but cover a smaller area of the country.

Conclusion. During the 10 year study from 1990–91 to 2000–01, 167 entries were tested in the National Uniform Wheat Yield Trials in Pakistan. Out of 167 entries, 48 % were selected from local crosses and 52 % were selections from exotic sources. For the Punjab province, 76 % were from local crosses and 24 % were from exotic sources. During this period, 32 varieties were released for general cultivation out of which 34 % were selections from local crosses and 66 % were selections from exotic sources. Wheat cultivars developed from local crosses covered the greatest area of the wheat fields in Pakistan during these 10 years. Local hybridization programs are very important and should be strengthened in future with increased facilities. Farmers in Pakistan have accepted these wheat cultivars.

Causes of low wheat yield in southern Punjab, Pakistan, during 2002–03.

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Introduction. During 2002–03, the wheat crop in the Punjab province of Pakistan looked very good. With the expectation of a 15.36 x 10^6 ton grain yield (Anonymous 2003), the average yield in the province of Punjab was only 2.52 t/ha.

What happened to the grain yield? The main problems for low grain yield in the southern Punjab are late planting, shortage of irrigation water, weeds, and disease and insect pests. In 2002–03, the aphid population was at its maximum limit in the southern districts of Punjab; up to 78 aphids/tiller, which can cause high damage. In many countries, aphids damage the wheat crop at leafy stage but in southern parts of Punjab it attacks in the latter stages during the month of March. In the U.S. in 1987–88, an economic loss of 130 x 10^6 USD was reported (Peairs et al. 1988). Aphids may become a serious problem on wheat in the future. Heliothis also may attack the wheat crop in the southern Punjab, which is a special cotton growing area of Pakistan. Heliothis attacks leaves, awns, and especially the grain. Heliothis on wheat crop also has been reported in India. In the southern Punjab, the wheat crop is sown mostly in December and matures in mid April. Seasonal changes in this area also affect the average grain yield. The average number of days to maturity here ranges from 110–125, whereas under normal sowing it takes about 130–145 days. The technically called forced maturity occurs when wheat genotypes can not take proper time to mature. In this study, we have tried to elucidate situations preventing high grain yield in the southern district of Punjab during 2003. Temperatures during grain filling in this area play an important role in grain yield. We will discuss the possible causes of low grain yield and the expectations.

Materials and Methods. The experiment was conducted at Regional Agriculture Research Institute, Bahawalpur. Ten wheat genotypes were sown using RCBD design. Each wheat variety in the experiment was sown in three replications with plot size of 6 m^2 (5 m x 1.2 m). The N and P_2O_5 were applied at the rate of 160 and 110 kg ha^{-1}. Weeds were controlled chemically. No. of aphids per tiller and number of predators per plot were recorded. Climatic data was recorded at CRS, Bahawalpur.

Results and Discussion.

Insect pests—aphids and predators. This year, aphids occurred on a large scale and three predators, Chrysopa, lady bird beetles, and syrphid flies, were found on the wheat crop in the farmers' fields and at the experimental area of the Regional Agricultural Research Institute, Bahawalpur (Table 12).

Table 12. Aphid and predator populations observed in farmers' fields and at the Regional Agriculture Research Institute, Bahawalpur, Pakistan, for two different dates in 2003 and the growing-season average.

	Average number of	
Cultivar	aphids/tiller	predators
18 March, 2003.		
Inqalab-91	43	23
V-2460	49	24
V-2278	38	19
V-4012	49	28
Iqbal-2000	41	17
V-2333	47	26
V-2210	61	19
Uqab-2000	65	23
Panjnad-1	78	30
V-2237	55	27
Average	53	24
26 March, 2003.		
Inqalab-91	27	9
V-2460	61	5
V-2278	31	9
V-4012	39	11
Iqbal-2000	29	16
V-2333	39	10
V-2210	46	7
Uqab-2000	34	14
Panjnad-1	19	9
V-2237	37	11
Average	36	10
2003 season average.		
Inqalab-91	35	16
V-2460	55	15
V-2278	34	14
V-4012	44	20
Iqbal-2000	35	17
V-2333	43	18
V-2210	53	13
Uqab-2000	50	19
Panjnad-1	49	20
V-2237	46	19
Average	44	17

The average aphid population recorded on 18 March was high, 53 aphids/tiller, and decreased by 26 March to 36 aphids/tiller. On 18 March, wheat crop was lush green; by 26 March, the leaves were rather hard. Tender leaves attracted aphids and drying leaves were less preferred. The highest aphid populations were observed on 18 March on Punjnad-1 (78 aphids/tiller). The lowest populations were observed on V-2278 (38 aphids/tiller). V-2278 is light green, whereas Punjnad-1 has a dark green leaf.

Crysopa, ladybird beetles, and syphrid flies were found in farmers' wheat fields and at the experiment fields of the Regional Agricultural Research Institute, Bahawalpur. Crysopa was the dominant aphid predator averaging 24/plot, the highest number recorded, on 18 March and decreased to 10/plot by 26 March (Table 12). The predator population/plot was the highest (30/plot) on Punjnad-1 and V-2278 on 18 March; the highest number on 26 March was 16/plot on Iqbal-2000.

For the growing season 2003, the highest average number of aphids/tiller was 44 on V-2460; the lowest average was on V-2278 (34–55). The greatest number of predators were on V-4012 and Punjnad-1, whereas the minimum aphid population/tiller was found on V-2210 (13/

plot, mean population range 13–20). The average predator population for the entire season was 17/plot.

Insect pests—Heliothis (Helicoverpa armigera). Heliothis has damaged the wheat crop for many years in Punjab. During 2003, no Heliothis was observed in wheat crop, possibly because of the high population of Crysopha.

Wheat cultivar response to aphids. Aphid infestations were reported on all wheat cultivars. Inqulab-91 covered the greatest area, followed by Punjab-96, Uqab-2000, MH-97, and Punjnad-1 (Table 12).

Climatic factors—maximum and minimum temperatures, rainfall, and humidity. Data on climatic factors for a few years is in Table 13. Data for 2002 show that the warmest temperature was low (24°C) compared to that of 2001. No difference in the maximum temperature during last 2 weeks of March from 2001 to 2003 was observed. Temperatures during the first and second weeks were favorable to the wheat crop. The warmest temperature during last 15 days was 32°C, which was similar to 2001 but less than that of 2002.

Table 13. Maximum temperatures recorded in 2001–03 at the Regional Agriculture Research Institute, Bahawalpur, Pakistan.

	March				April
Year	Week 1	Week 2	Week 3	Week 4	Week 1
2000	28	30	32	34	37
2001	29	32	34	34	35
2002	27	28	29	35	35
2003	24	27	31	33	34

Maximum temperature during last 15 days of March (grain-formation period).

Day	2001	2002	2003
17	33	30	31
18	33	33	31
19	32	35	30
20	35	37	32
21	34	37	34
22	36	38	37
23	34	36	28
24	35	36	32
25	35	37	31
26	36	37	34
27	35	37	35
28	32	37	33
29	32	38	32
30	33	38	32
31	33	40	33
Average	33	36	32

The weekly data in Table 14 (p. 101) show that in 2003, the first and second weeks of March were cooler than in the other years. The thrid week of March was hotter than 2000, which was a record year for grain yield. In the last week of March 2003, temperatures were higher than for 2001 or 2002. The first week of April 2003 was hotter than the similar period in 2000–01. Night temperatures during the last 15 days of March was higher than in 2002. From 25 March to 28 March, the minimum temperature was double that of 2002.

No rain fell during the month of March in 2000–03 (Table 15, p. 101). No significant difference in rainfall was noted during the 2000 and 2002 crop seasos. No considerable diference in humidity for 2000–03 was noted (Table 15).

Conclusions. Maximum temperature and minimum temperature during growing season (2002–03) favored the wheat crop. However, higher minimum temperature during last 15 days of March 2003 disturbed the wheat crop. Hot nights in the last 15 days of March 2003 during grain filling decreased grain weight of wheat crop in the cotton region. No considerable changes in rainfall and relative humidity were noted. Aphids were at their maximum population during March 2003 in the southern Punjab. Increases in aphid populations caused an increase in the predators present, Crysopa, lady bird beetles, and syrphid flies. Crysopa was able to attack aphids better than the other predators. Heliothis was not present during the year, which may be because of Crysopa. We estimate that damage due to aphid and temperature may range from 57 % in the southern Punjab.

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Table 14. Minimum temperatures recorded in 2001–03 at the Regional Agriculture Research Institute, Bahawalpur, Pakistan.

	March				April
Year	Week 1	Week 2	Week 3	Week 4	Week 1
2000	10	8	9	12	12
2001	7	14	13	14	13
2002	12	12	16	16	18
2003	7	7	13	17	15

Minimum temperature during last 15 days of March (grain-formation period).

Day	2001	2002	2003
17	14	12	10
18	12	11	13
19	13	13	12
20	13	12	14
21	12	12	19
22	12	10	19
23	14	11	14
24	15	9	12
25	15	8	15
26	14	7	14
27	15	9	18
28	16	10	20
29	13	14	16
30	12	14	17
31	12	16	17
Average	13	11	15

Table 15. Rainfall (mm) and humidity (%) during the 1999 and 2003 growing seasons at the Regional Agriculture Research Institute, Bahawalpur, Pakistan.

Month	1999	2000	2001	2002	2003
Rainfall					
November	0	—	20	15	—
December	0	0	10	15	—
January	11	12	0	10	0
February	—	0	0	0	22
March	—	0	0	0	0
April	—	0	21	0	0
Humidity.					
November	71	71	73	72	—
December	69	69	72	73	—
January	—	75	74	73	72
February	—	73	71	70	76
March	63	65	65	67	69
April	70	63	65	57	59