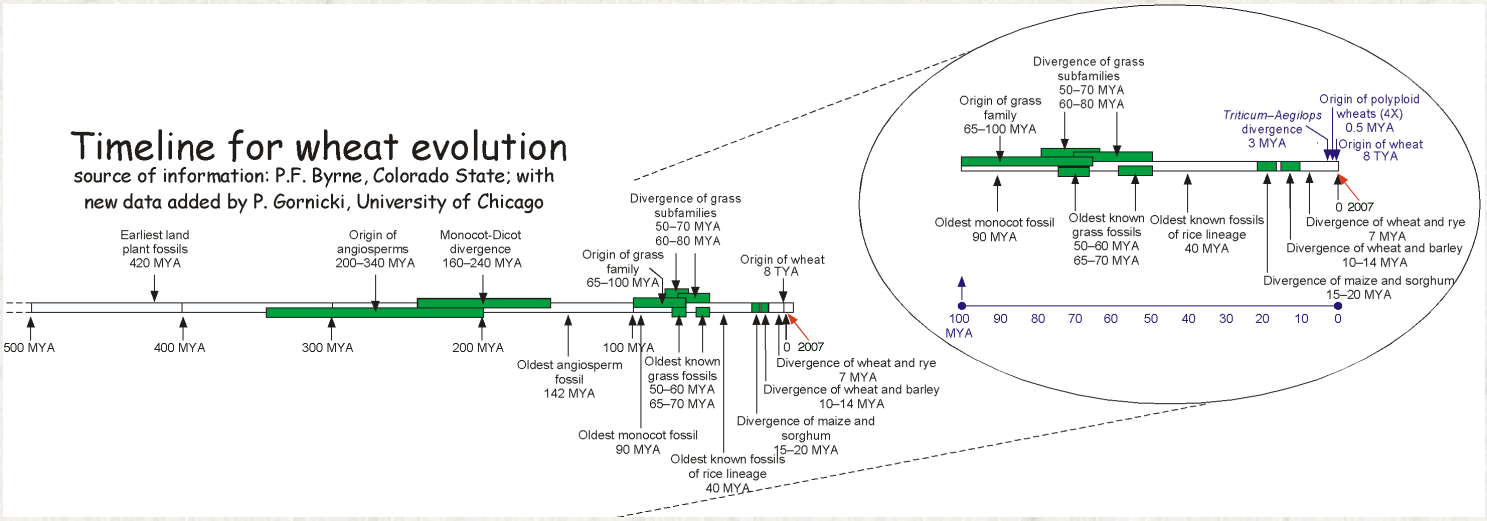
ANNUAL WHEAT NEWSLETTER

Volume 57



Contribution no. 12-045-D from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

ANNUAL WHEAT NEWSLETTER

Volume 57

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1 August, 2011.

Contribution no. 12-045-D from the Kansas Agricultural Experiment Station, Kansas State University, Manhattan.

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IN DEDICATION TO DR. DONALD MCVEY

Dr. Donald V. McVey, retired USDA–ARS Research Plant Pathologist, Cereal Disease Laboratory, St. Paul, passed away at home, surrounded by family on December 16, 2010. He was 88 years old. Don retired from the Agricultural Research Service on 3 Septembe, 2001, after more than 40 years of service.

Don's research played a pivotal role in the protection of cereal crops from leaf and stem rust, especially in spring and winter wheat cultivars in the Central and Northern Great Plains. Don began his career with ARS in 1960 working in Puerto Rico testing wheat accessions for resistance to race 15B of stem rust, which had caused serious losses in wheat in1953 and 1954. In 1965, Don was transferred to the Cooperative Rust Laboratory.

Don was best known for his work in testing wheat breeding lines for resistance to stem and leaf rust resistance. Don excelled in evaluating rust resistance in field nurseries, using carefully selected rust races and methods that enabled selection for resistant genotypes to be made each season. Don was a leader in postulating the identity of leaf and stem rust resistance genes that were present in advanced breeding lines from wheat programs throughout the country. Working with Dr. Bob Busch, Don was involved with the release of 'Era' wheat in 1970. Era was the first semidwarf spring wheat cultivar in the upper Midwest that was released by a public institution. Era offered a significant yield advantage over previous spring wheat cultivars and was resistant to stem and leaf rust. Era has been used as a parent in wheat breeding programs and is in the pedigree of many of the present day spring wheat cultivars. Don was also contributed greatly in the development of the cultivar 'Marshall' that was released by Minnesota in 1982. Marshall had high yield potential and was the yield standard for the hard red spring wheat. Another notable cultivar that Don helped to develop was the winter wheat 'Siouxland' released by Nebraska. This cultivar was the first wheat to have two leaf and stem rust resistance genes derived from wild relatives of wheat. Siouxland was widely adapted to the Great Plains region and was grown from Texas to South Dakota.

In his latter years at the Cereal Disease Laboratory, Don worked particularly closely with the wheat breeding programs at the University of Minnesota, South Dakota State University, and the University of Nebraska. Don was listed as an author on many wheat cultivars that were released by these institutions. A recent cultivar from Minnesota that Don helped to develop is 'McVey', which was one of the first modern spring wheat cultivars with some resistance to Fusarium head blight. The fact that stem rust was virtually eliminated as a pathogen of wheat in the U.S. can be attributed to the thorough screening for stem rust resistance that Don performed for wheat breeding programs throughout the U.S. In his last years at the Cereal Disease Laboratory, Don also assumed responsibility for conducting the annual race survey of wheat stem rust in the U.S. that has been very important in the development of breeding lines for stem rust resistance. Through his publications and participation in workshops and conferences, Don's contributions were widely recognized and appreciated by both cereal rust pathologists and wheat breeders.

WHEAT WORKER'S CODE OF ETHICS

This seed is being distributed in accordance with the 'Wheat Workers' Code of Ethics for Distribution of Germ Plasm', developed and adopted by the National Wheat Improvement Committee on 5 November, 1994. Acceptance of this seed constitutes agreement.

1. The originating breeder, institution, or company has certain rights to the material. These rights are not waived with the distribution of seeds or plant material but remain with the originator.

2. The recipient of unreleased seeds or plant material shall make no secondary distributions of the germ plasm without the permission of the owner/breeder.

3. The owner/breeder in distributing seeds or other propagating material grants permission for its use in tests under the recipient's control or as a parent for making crosses from which selections will be made. Uses for which written approval of the owner/breeder is required include:

   (a) Testing in regional or international nurseries;
   (b) Increase and release as a cultivar;
   (c) Reselection from within the stock;
   (d) Use as a parent of a commercial F_1 hybrid, synthetic, or multiline cultivar;
   (e) Use as a recurrent parent in backcrossing;
   (f) Mutation breeding;
   (g) Selection of somaclonal variants; or
   (h) Use as a recipient parent for asexual gene transfer, including gene transfer using molecular genetic techniques.

4. Plant materials of this nature entered in crop cultivar trials shall not be used for seed increase. Reasonable precautions to ensure retention or recovery of plant materials at harvest shall be taken.

ITEMS FROM ARGENTINA

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

Genetic progress after 10 cycles of recurrent selection in bread wheat.

Ariel Demarchi and Ricardo Héctor Maich

Seed samples of 11 segregating and recombinant populations corresponding to 10 cycles of a recurrent selection program (C_0 to C_{10}) performed under rainfed condition were sown in 2009 at the Experimental Farm of the College of Agriculture (Córdoba National University). Fifty seed/population were seeded directly with 0.20 cm between populations. Those plants with a minimum number of fertile tillers were threshed to obtain enough seed for the next S-derived family evaluation (four/population) in one-row plots with replications and using a seeding rate of 150 seed/m^2. In 2010, the material were directly seeded using a completely randomized design replicated twice. From a random sample of 15 plants/plot, we measured or estimated plant height (cm), harvest index/plant (%), 1,000-kernel weight (g), seed/spike, seed/spikelet, and grain yield/spike (g). Table 1 gives the statistical analysis of the C_0, C_2, C_4, C_6, C_8, and C_{10} data.

Table 1. Statistical analysis of populations corresponding to 10 cycles of recurrent selection. The means in each column followed by similar letter(s) are not significantly different at a 5% probability level using the DGC Test.

Cycle	Plant height (cm)	Harvest index/plant (%)	1,000-kernel weight (g)	Seed/spike (g)	Seed/spikelet (g)	Grain yield/ spike (g)
C_0	104.3 b	28.3 a	38.8 b	22.4 a	1.20 a	0.87 a
C_2	99.0 b	25.5 a	32.3 a	26.8 b	1.29 a	0.84 a
C_4	93.6 a	31.1 b	36.5 b	28.8 b	1.43 b	1.02 b
C_6	91.8 a	31.2 b	37.1 b	28.3 b	1.40 b	1.04 b
C_8	98.0 b	31.6 b	38.6 b	27.8 b	1.25 a	1.08 b
C_{10}	98.0 b	33.0 b	38.3 b	31.0 b	1.50 b	1.14 b

These preliminary results give us a clue about the changes in the original genetic pool. Contrary to the results obtained by Maich et al. (2007), after six cycles of recurrent selection where none of the variables analyzed in the present study varied significantly, we observed some of the physiological and physical yield components were moving in the desired direction. A significant, positive, and linear (R^2= 0.47) association between grain yield/spike and the cycle of recurrent selection performed was detected (b = 0.03).

Reference.

Maich R, Ortega D, Masgrau A, and Manera G. 2007. Genetic achievements under rainfed conditions. *In:* Wheat Production in Stressed Environments (Buck HT, Nisi JE, and Salomón N, Eds), Proc 7th Internat Wheat Conf. Springer, New York, NY. Pp. 321-329.

ITEMS FROM BRAZIL

BRAZILIAN AGRICULTURAL RESEARCH CORPORATION — EMBRAPA
Rodovia BR 285, km 294, Caixa Postal 451, Passo Fundo, RS, Brazil.

The triticale crop in Brazil.

Alfredo do Nascimento, Junior.

In Brazil, between 2000 and 2004, the area on which triticale was grown stabilized between 109 and 126 x 10^3 ha; a maximum area (134,868 ha) was harvested in 2005. This area has declined since 2007. In 2009, 69,350 ha of triticale were recorded, the smallest area in nine years. The national average yield of triticale grain in 2009 was 2,157 kg/ha, less than that of the previous year (2,441 kg/ha), and significantly below the global average of 3,927 kg/ha in 2009 (FAO 2010, IBGE 2010). When comparing grain yields, however, the plant type should be considered. In Brazil, triticale cultivars are spring type, the same as in Australia with similar yields in both countries. In countries such as Germany, France, Poland, and Sweden, triticale is a winter crop requiring longer cycles and vernalization, with average grain yields higher than 5,000 kg/ha.

Currently, triticale is sown in the states of Rio Grande do Sul, Santa Catarina, Paraná, Mato Grosso do Sul, São Paulo, and Minas Gerais in Brazil. The IBGE data do not include Mato Grosso do Sul and Minas Gerais. The largest areas of triticale were harvested in Paraná and São Paulo, and the average grain yield was highest in São Paulo in 2009. Together, Paraná and São Paulo account for 86% of the national triticale production. In the states of Paraná, São Paulo, Mato Grosso do Sul, and Minas Gerais, blast (*Pyricularia grisea*) is the main problem effecting triticale and wheat. Other cereals, such as barley, oat, and rice, and species of weedy grasses, also are hosts for blast. In green house experiments, we observed that all Brazilian triticale cultivars were susceptible. In 2009, the disesase reduced triticale production up to 100% in some areas.

In southern Brazil, Fusarium head blight is one of the most yield-limiting factors for triticale and other winter cereals. The search for less susceptible genotypes to the disease is a constant in our breeding programs.

References.

Food and Agricultural Organization of the United Nations. 2011. FAOSTAT – http://faostat.fao.org/site/567/default.aspx?PageID=567#ancor.

Instituto Brasileiro de Geografia e Estatística. Levantamento Sistemático da Produção Agrícola. http://www.ibge.gov.br/home/estatistica/indicadores/agropecuaria/lspa/default.shtm.

BRS Saturno – the newest triticale cultivar developed in Brazil.

Alfredo do Nascimento, Junior, Márcio Sóe Silva, Eduardo Caierão, and Pedro Luiz Scheeren.

Pedigree and breeding method. The cultivar BRS Saturno resulted from the cross 'PFT 512/CEP 28–Guará' made by Embrapa Trigo in 1995. The line PFT 512 was derived from the cross 'ANOAS/CEP 23–Tatu' at the International Centre for Maize and Wheat Improvement Center (CIMMYT) in El Batan, Mexico, in 1986. This line was introduced by Embrapa into the 26th International Triticale Yield Nursery (ITYN) in Passo Fundo (RS) in 1993. The ITYN, composed of inbred triticale lines, was sent to several countries for evaluation and selection. Entry number 11 (of the 26th ITYN) with the selection sequence CTM86.123-17MI-2MI-13BI-2Y-0PAP-1Y-0B was selected. Number 11 was subjected to modified mass selection in Passo Fundo, where atypical and agriculturally inadequate plants were eliminated and superior and homogeneous plants selected, resulting in the following selection sequence: CTM86.123-17MI-2MI-13BI-2Y-0PAP-1Y-0B-0F (0F = selection in Passo Fundo-RS) resulting in the line PFT 512. Segregating populations were developed and selected in Passo Fundo, by the pedigree method, from 1997 on, leading to the selection of 100 spikes from plot 710108. In 1998, all 100 spikes were sown in rows, one spike/row, and spikes were selected, one/plant, from 12 plants of row 7 in plot 820485, which were separately sown in rows (one spike/row) in 1999. In the same year, spikes

of two sister lines were harvested from the plots 920356 and 920357. Twelve spikes/row were phenotypically selected increase homogeneity. In 2000, the genotype was included in the internal collection of Embrapa–Wheat for agronomic and biological evaluation and was simultaneously grown in a spike-multiplication plot for seed production. In 2001, the genotype was labeled PFT 112, for the preliminary triticale trial (EPRTCL) in Passo Fundo. Between 2002 and 2004, seed of the line was multiplied and purified and again selected in rows (one spike/row) with subsequent mass multiplication. From 2003 to 2010, PFT 112 was tested in the Value for Cultivation and Use of Triticale Trial (VCUTCL) at various locations in southern Brazil, where it stood out for its grain yield, hectoliter weight, and less susceptibility to Fusairum head blight. PFT 112 was assessed in the Distinctness, Uniformity and Stability (DUS) Trials in 2003, 2004, and 2005 by Embrapa–Wheat, in Passo Fundo.

Performance. The triticale cultivar BRS Saturno is resistant to powdery mildew and leaf rust; tolerant to blight; moderately resistant to leaf spots (*B. sorokiniana*, *Drechslera* spp., and *St. nodorum*) and to soilborne wheat mosaic virus (SBWMV); moderately susceptible to preharvest sprouting, barley yellow dwarf virus (BYDV), and bacterial leaf streak (*Xanthomonas translucens* and *Pseudomonas* spp.); and susceptible to blast (*Pyricularia grisea*) and Fusarium head blight, with a lower susceptibility level to Fusarium than other triticale cultivars in Brazil.

BRS Saturno is hexaploid, has a medium cycle (70–85 days from emergence to heading and 135–150 days to maturity), and a tall plant height (117 cm in Passo Fundo). Anthocyanin pigmentation in the coleoptile is strong to very strong, and low to mean in the auricle. Waxiness of the flag leaf sheath is strong. The spikes are long, completely awned, and light in color at maturity. The hair density of the stem is high.

This is the second Brazilian triticale cultivar developed by crosses made in Brazil. The lower susceptibility to FHB than that of other triticale cultivars (types I, II, III, and V), excellent grain quality, higher hectoliter weight than of the recommended varieties, and considerable yield adaptability indicate that this cultivar is valuable in production systems.

In the VCU studies conducted in Rio Grande do Sul, Santa Catarina, Parana, Mato Grosso do Sul, and São Paulo between 2003 and 2005, the grain yield of BRS Saturno was 3,946 kg/ha, exceeding by 12.3% the mean yield of the two best triticale cultivars at each site (BRS 148, BRS 203, Embrapa 53, or Iapar 23–Arapoti) used as standards.

The mean performance of BRS Saturno for each state between 2003 and 2010 is in Table 1. Grain yield (1,121 kg/ha) was lowest in Mato Grosso do Sul and highest (8,347 kg/ha) in Sao Paulo (both in 2006). The mean value was 4,310 kg/ha. According to field observations, and despite the spring growth habit, low temperatures during the vegetative growth favor the performance of BRS Saturno. Thus, environments with drought and high temperatures do not allow for the maximum yield expression of the cultivar. However, environments with adequate water availability and lower temperatures during plant development show the yield potential of BRS Saturno, which exceeds those of the main varieties in Brazil, especially in years of excessive rainfall with the occurrence of FHB during flowering, due to the lower susceptibility of BRS Saturno. Table 1 shows that 17 of the 29 entries that exceeded 4,000 kg/ha were grown in the southern states (RS, SC, and PR), with exception of the maximum yield in São Paulo in 2006.

Due to the performance of BRS Saturno and the similarity of climate and cultivation between Santa Catarina and Rio Grande do Sul (southern region) and Paraná, Mato Grosso do Sul, and São Paulo (central south region) and the currently available cultivation technologies, this triticale cultivar was included in the National Registry of Plant Varieties

Table 1. Grain yield average (kg/ha) of BRS Saturno, from 2003 to 2010, in experiments in the Value for Cultivation and Use Trials in the southern states of Brazil (— indicates no yield trials were conducted at these locations in the respective year).

State	Year								
	2003	**2004**	**2005**	**2006**	**2007**	**2008**	**2009**	**2010**	**Mean**
Rio Grande do Sol	4,203	3,765	4,198	4,221	3,897	4,455	4,420	5,021	4,273
Santa Catarina	5,517	4,246	2,874	4,871	4,166	5,093	—	—	4,461
Paraná	3,527	4,784	4,525	7,677	5,654	6,229	—	3,991	5,198
São Paulo	3,231	3,833	3,607	8,347	—	—	—	—	4,755
Mato Grosso do Sul	—	2,988	1,207	1,121	—	—	—	3,317	2,158
								General mean	4,310

(no. 26744, on 21 May, 2010), for grain production and trade in all wheat-growing regions in south and south-central Brazil (RS, SC, PR, MS, and SP), under rainfed cultivation in the cold season.

The grains of BRS Saturno can be used in human and animal nutrition and the flour for the production of cookies and pasta food.

Seed maintainence and distribution. BRS Saturno is a protected cultivar; Embrapa is in charge of basic seed multiplication, by the Serviço de Negócios para Transferência de Tecnologia da Embrapa (SNT), and the multiplication of certified seed in partnership with the Fundação Pró-Sementes de Apoio à Pesquisa.

Wheat in Brazil – the 2010 crop year.

Eduardo Caierão, Pedro L. Scheeren, Márcio Só e Silva, Ricardo Lima de Castro, Adeliano Cargnin, and Alfredo do Nascimento Junior.

In the 2010 crop year, Brazilian wheat production was nearly 6 x 10^6 tons (Conab 2011), which is enough to supply 50% of the domestic demand (Table 2). The deficit in production makes Brazil the largest wheat importer. The southern region, comprised of the states of Rio Grande do Sul, Santa Catarina, and Paraná, accounts for 94% of the national production. Nonetheless, due to the characteristics of the cultivation system utilized, the average grain yield is not the highest in the country.

Table 2. Cultivated area, total production, and grain yield of wheat in Brazil in 2010 (Source: CONAB 2011).

Region	Area (ha x 1,000)	Production (t x 1,000)	Grain yield (kg/ha)
North	—	—	—
Northeast	—	—	—
West–central	55.4	153.2	7,765.0
Southeast	66.8	196.6	2,943.0
South	2,027.6	5,531.0	2,728.0
Brazil	**2,149.8**	**5,881.6**	**2,736.0**

In 2010, the wheat area planted was lower than 2009 (2,149.8 to 2,428.0). Total production and average grain yield/ha in 2010 were about 15.0% smaller than those of 2009. The average grain yield in the southern region of Brazil in the 2010 crop season was the highest in the history. Low temperatures during the vegetative and grain-filling stages associated with sunny days contributed to high productivity. The grain quality was good as well.

Reference.

CONAB, 2011. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Disponível em: http://www.conab.gov.br/conabweb/index.php?PAG=131.

Wheat genetic progress from 2007 to 2010 in the state of Rio Grande do Sul, Brazil.

Ricardo Lima de Castro, Eduardo Caierão, Adeliano Cargnin, Pedro Luiz Scheeren, Márcio Só e Silva, and Alfredo do Nascimento Junior.

Rio Grande do Sul State is one of the main wheat-growing areas in Brazil (around 35% of the Brazilian production). Important wheat breeding research is based in the State. The genetic progress and benefit resulting from these programs were compared through estimates for the period of 2007 to 2010. The analysis was performed on grain yield data (kg/ha) collected in the annual state yield trials network using the minimum squares method by the Brazilian Wheat Research Commission. The inclusion, exclusion, permanence, and renewal rates of the genotypes in the trials and in the recommended wheat lists also were studied on the same set of data. The genetic progress made in wheat yield estimated for Rio Grande do Sul was 7.8% for 2007–10. The genotype inclusion rate was 0.0%, 25.6% and 17.1% for the years 2008, 2009, and 2010, respectively. The genotype exclusion rate was 0.0%, 20.9% and 26.8% in the years 2008, 2009, and 2010, respectively. The maximum rate of genotype renewal was in 2009, reaching 32.4%. The Rio Grande do Sul wheat breeding programs were highly effective fpr the period studied with annual mean genetic gain of 1,9% (62.7 kg/ha/year).

Active Wheat Germplasm Bank of Embrapa: current situation and future perspectives.

Adeliano Cargnin, Eduardo Caierão, Ricardo Lima Castro, Marcio Só e Silva, Pedro Luiz Scheeren, Luciano Consoli, Sandra Brammer, and Flavio Santana.

The Active Wheat Germplasm Bank (AGB–Wheat) located at Embrapa Trigo, Passo Fundo, RS, Brazil, was funded in 1978, and since that time is concerned with enhancement as well as biodiversity conservation of wheat and related species. Today there around 15,000 wheat accessessions, including related species, registered and stored at AGB-Wheat. At this moment, AGB-Wheat is under restructuring in order to resize the bank and eliminate of the redundance, which means the actual number of accession will be reduced in the future. Under conservation are species from the genera *Triticum*, *Aegilops*, *Agropyron*, *Elymus*, *Elytrigia*, and *Leymus*. The accession data are managed by an appropriate software system. As a routine, AGB-Wheat activities include diversity enhancement, conservation, characterization, and evaluation. In the last two years, 1,742 new accessions from Brazil and other countries were introduced into the AGB, and 1,130 access were distributed in exchange to different institutions including other Embrapa stations. During this time, we multiplied/regenerated and morphologically characterized 2,512 accessions in the field and in the greenhouse. The organization and validation of a core collection of 240 accessions will be increased in the near future to better represent the whole AGB collection. Characterization and evaluation related to the main concerns for wheat growing in Brazil, such as biotic stress (Fusarium head blight and wheat blast), abiotic stress (sprouting), and technological flour quality will be made on the core collection. In addition, molecular and cytological analyses will be done.

ITEMS FROM CROATIA

BC INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS
Rugvica, Dugoselska 7, 10370 Dugo Selo, Croatia.
Department of Cereal and Forage Crops, Botinec, Zagreb, Croatia.
www.bc-institut.hr

Slobodan Tomasović, Rade Mlinar, Ivica Ikić, Branko Palaveršić, Katarina Jukić, Tomislav Ivanušić, and Marko Maricević.

A new generation of winter wheat cultivars developed at the Bc Institute Zagreb.

Work on breeding winter wheat at the Zagreb Bc Institute have been in progress continuously for more than 60 years. The results of this work are many cultivars registered in the Republic of Croatia and abroad. A new generation of winter wheat cultivars have been developed taking into account the needs and demands of the producers, including Bc Mira, Bc Renata, Dora, Marina, Bc Lidija, Bc Lira, Bc Irena, and Bc Anica.

Bc Irena dnd Bc Anica are the newest registered winter wheat cultivars from the Bc Institute in 2010 (Table 1 and Table 2, p. 8). The main characteristics of these cultivars is a broad genetic base that provides a high yield potential, stability, and very good grain and flour quality. These cultivars represent progress in wheat breeding. The results of the Committee for Variety Registration, small- and large-scale trials, and seed production confirm a high agronomic value of the newly released Bc winter wheats (Table 3, p. 8, and Figs. 1 and 2, p. 8). They have

Table 1. Yield results of the new winter wheat cultivar Bc Irena compared with the standard cultivars (The Committee for Variety Registration of the Republic of Croatia, 2007–10).

Cultivar	Yield results (t/ha)				Sana = 100	Žitarka = 100	Divana = 100
	2007–08	2008–09	2009–10	Average			
Bc Irena	9.069	7.690	5.234	7.331	101.0	104.7	121.7
Sana	9.201	7.124	5.456	7.260	100.0		
Žitarka	8.221	7.328	5.463	7.004		100.0	
Divana	6.962	6.416	4.688	6.022			100.0

surpassed the check for the most important yield components in these tests. Because of thier morphology and biology, these new cultivars are resistance to lodging and the most important wheat diseases. Bc Renata and Bc Lira also are suitable for ecological production and under rationalized technology achieve very good results. Dora, Marina, Bc Lidija, Bc Irena, and Bc Anica meet the requirements of the milling and baking industry, and Bc Mira, Bc Renata, and Bc Lira can be grouped into a class of high-quality cultivars (Table 4, p. 9). This new generation of Bc cultivars provides an opportunity for our farmers to sow and produce better material with increased quality, which is a step forward in wheat production, certainly the goal of breeding.

Table 2. Yield results of the new winter wheat cultivar Bc Anica compared with the standard cultivars (The Committee for Variety Registration of the Republic of Croatia, 2008–10).

Cultivar	Yield results (t/ha)			Srpanjka = 100	Žitarka = 100	Divana = 100
	2008–09	2009–10	Average			
Bc Anica	8.539	6.576	7.558	112.4	115.4	132.9
Srpanjka	7.956	5.492	6.724	100.0		
Žitarka	7.666	5.435	6.551		100.0	
Divana	6.590	4.788	5.689			100.0

Table 3. Yield results (t/ha) of 14 winter wheat cultivars in the large-scale trials of the Zagreb Bc Institute at the Ţupanja, Lovas, and Agromeđimurje locations in 2010.

Cultivar	Županja	Lovas	Agromeđimurje	Average
Marija	7.17	8.09	6.81	**7.36**
Sana	6.84	8.80	7.58	**7.74**
Zdenka	6.27	7.92	6.85	**7.01**
Prima	7.25	8.43	8.71	**8.13**
Bc Antea	6.87	7.88	7.04	**7.26**
Tina	7.23	8.54	7.71	**7.83**
Adriana	7.22	7.56	7.57	**7.45**
Bc Renata	6.47	8.10	7.45	**7.34**
Bc Mira	6.41	7.95	7.95	**7.44**
Dora	6.93	7.69	7.46	**7.36**
Marina	6.93	7.98	7.11	**7.24**
Bc Lidija	7.01	7.54	7.09	**7.21**
Mihelca	6.92	7.17	7.14	**7.08**
Bc Lira	6.14	6.54	7.06	**6.58**
Average of trial locations	**6.81**	**7.87**	**7.40**	

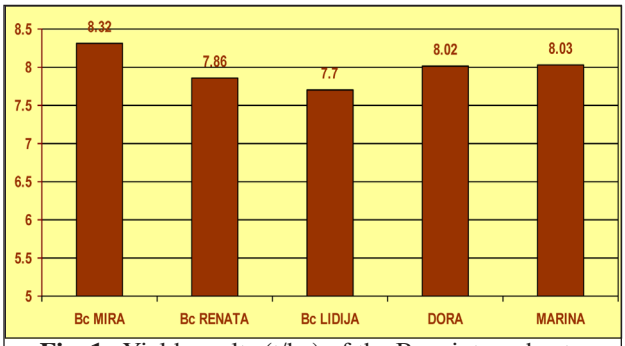

Fig. 1. Yield results (t/ha) of the Bc winter wheat cultivars in large-scale trials, 2009 and 2010.

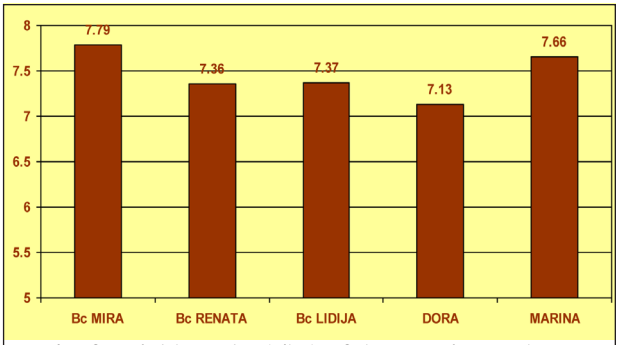

Fig. 2. Yield results (t/ha) of the Bc winter wheat cultivars in small-scale trials, 2009 and 2010.

Table 4. Test results of the milling and baking quality in large-scale trial at the Agromeđimurje location, 2009–10.

Cultivar	Sedimentation (mL)	Protein (%)	Wet gluten (%)	Falling number (sec)
Bc Lira	54	14.5	33.9	228
Bc Renata	49	13.7	31.14	218
Dora	42	13.3	28.3	242

Farinogram							Extensogram			
Water absorption (%)	Dough development time (min)	Stability (min)	Resistance (min)	Degree of softening (FJ)	Quality number	Quality group	Energy (cm^2)	Extensibility (mm)	Resistance (EJ)	R/E
65.4	4.0	2.8	6.8	50	72.5	A2	121.0	217	225	1.04
61.2	2.4	2.9	5.3	50	71.9	A2	101.3	211	225	1.07
65.5	2.1	0.6	2.7	60	63.5	B1	50.5	159	155	0.97

The effect of Fusarium head blight on grain yield reduction in wheat.

Fusarium head blight is the most important wheat disease in the world. Apart from reducing yields, FHB also affects grain quality by producing the mycotoxins deoxynivalenon and zearalenone. Because chemical protection is ineffective, breeding for resistance is the best means of control. We examined the influence of FHB on grain yield, 1,000-kernel weight, and test weight in winter wheat lines. Two identical experiments with 25 wheat lines were planted; one was artificially inoculated by spraying with a spore suspension of *F. graminearum*, and the other was under natural conditions. The trials were planted at Botinec in 2007 and 2008. Under natural conditions, infection with *F. graminearum* was mild, and average yields of 5,325.3 kg/ha in 2007 and 9,453.5 kg/ha in 2008 were achieved. Under artificial infection, average yields were lower by 24.0% in 2007 and 29.3% in 2008 (Table 5; Fig. 3, and Figs. 4 and 5, p. 10). Significant correlation coefficients were obtained between the infection severity and grain yield reduction (r = 0.48 and r = 0.76). Correlations also were found between infection severity and 1,000-kernel weight reduction (r = 0.58 and r = 0.42) and between infection severity and the reduction in test weight (r = 0.70 and r = 0.68) in 2007 and 2008, respectively. Fusarium head blight greatly influenced yield reduction, 1,000-kernel weight, and test weight in more susceptible wheat lines. Some wheat lines, on the contrary, did not show any substantial yield reduction even under severe infection. In the years of testing, high levels of resistance to FHB compared with the source of resistance in conditions of artificial infection were found in 11 winter wheat lines (Bc 8, Bc 9, Bc 4, Bc 20, Bc 18, and Bc 5 in 2007 and Bc 12, Bc 1,

Table 5. The effect of *Fusarium graminearum* on average grain yield (kg/ha), 1,000-kernel weight (g), and test weight (kg) of 25 winter wheat genotypes under conditions of artificial and natural spike infection at Botinec, Croatia, in 2007 and 2008.

Year	Grain yield		% reduction	1,000-kernel weight		% reduction	Test weight		% reduction
	Natural infection	Artificial infection		Natural infection	Artificial infection		Natural infection	Artificial infection	
2007	5,325.3	4,049.3	24.0	37.7	32.2	14.6	73.6	63.3	14.0
2008	9,453.5	6,680.2	29.3	42.8	35.6	16.9	71.6	63.1	11.9
Average	7,389.4	5,364.8	26.7	40.2	33.9	15.7	72.6	63.2	13.0

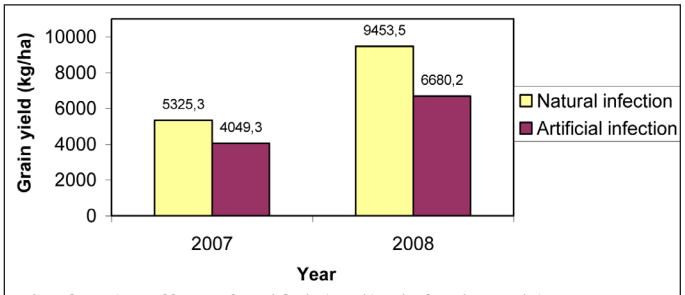

Fig. 3. The effect of artificial spike infection with *Fusarium graminearum* on average grain yeild in 25 winter wheat genotypes at Botinec, Croatia in 2007 and 2008.

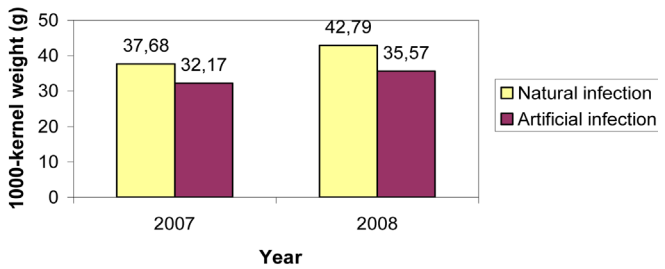

Fig. 4. The effect of artificial spike infection with *Fusarium graminearum* on average 1,000-kernel weight in 25 winter wheat genotypes at Botinec, Croatia in 2007 and 2008.

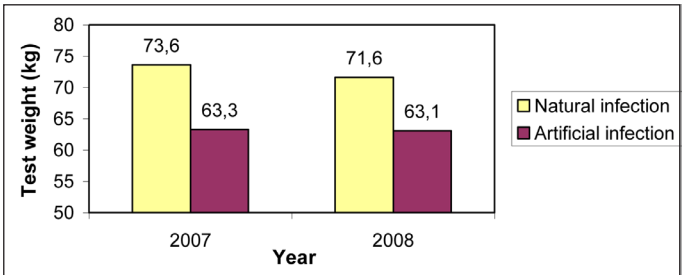

Fig. 5. The effect of artificial spike infection with *Fusarium graminearum* on average test weight in 25 winter wheat genotypes at Botinec, Croatia in 2007 and 2008.

Bc 9, Bc 17, and Bc 18 in 2008) and five winter wheat cultivars (Bc Mira, Bc Renata, Bc Lira, Dora, and Marina) (Table 6).

Acknowledgement. The above data were obtained as a result of the scientific project (Breeding wheat for yield, quality, and resistance to Fusarium head blight, 106-1780691-2155) partialy supported by the Croatian Ministry of Science, Education and Sports and represents a complementary part of program No. 1780691 (Research and improvement of genetic traits of field crops).

Table 6. A survey of winter wheat genotypes in cultivar trials with the highest level of resistance to Fusarium head blight (FHB) compared with the source of resistance under artificial infection conditions at Botinec, Croatia, in 2007 and 2008 (+ = moderately resistant; ++ = resistant).

Cultivar	FHB VRI (%)
2007	
Bc Renata	3.96 ++
Bc 8	5.96 ++
Bc 9	6.36 ++
Bc 4	6.91 ++
Bc 5	14.99 +
Bc Mira	15.01 +
Average	10.46
Source of resistance	
Roazon	14.62 +
(D48x42x6)2	20.67
Poncheau	7.22 ++
Average	14.17
Total average	12.31
2008	
Bc 12	10.77 ++
Bc Lira	11.28 ++
Bc 1	16.03 +
Bc 9	21.64 +
Bc 17	21.68 +
Bc 18	21.69 +
Average	17.18
Source of resistance	
Roazon	22.34 +
(D48x42x6)2	13.78 ++
Poncheau	4.08 +
Average	13.4
Total Average	15.29

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ITEMS FROM ETHIOPIA

CIMMYT–ETHIOPIA AND THE ETHIOPIAN INSTITUTE FOR AGRICULTURAL RESEARCH
Debre Zeit, Ethiopia

Bekele Abeyo (CIMMYT) and Firdissa Iticha, Kebede Tadesse, Ayele Badebo, and Asefa Yilma.

A number of international nurseries were planted at various sites in Ethiopia during the 2009–10 cropping season. Off-season the nurseries were planted only at Debre Zeit because of the availability of irrigation. A total of 7,214 wheat lines were evaluated for stem rust resistance, including 806 durum wheat lines from CIMMYT, 2,107 bread wheat lines, 3,295 durum wheat lines, 974 synthetics from ICARDA, and 32 bread wheat lines from the Russian Federation. The nurseries were planted on time, were well managed, and infector rows well distributed. Because the temperature was warmer than normal, the disease pressure was higher. Only CIMMYT nursery data are presented in Table 1. Most of the lines tested during this season were durum wheat. Of the 622 total lines tested, 297 (or 48%) were found to have 20% or less infection rates. The data were submitted to the respective coördinating breeders at CIMMYT–Mexico.

Table 1. International nurseries tested at Debre Zeit, Ethiopia, during the off-season in 2009–10.

	Number tested	≤ 20^% sten rust	Comment
Durum wheat			
CD10 MCDZ	208	146 (70%)	Many resistant lines
F6 SR	175	131 (75%)	Many resistant lines
CD10_BHADERDZZ	35	2 (6%)	
CD10_DDPDZ	204	18 (9%)	
TOTAL	622	18 (9%)	
Bread wheat			
4th SRRNSN BW	184	79 (43%)	Many resistant lines
TOTAL	806	376 (47%)	

The main 2010 season was characterized by wide spread yellow rust epidemics on the major cultivars Kubsa and Galama. These two cultivars have served for over 15 years and can not be blamed. Efforts were made to spray fungicides to minimize damage. In addition, the new CIMMYT cultiars Picaflor and Danphe, with good resistance/tolerance to yellow rust, were released to replace the susceptible, older cultivars this year. Different nurseries were obtained from in 2010, including 1,190 bread wheats, 1,297 durum wheats, and 202 triticales from CIMMYT; 4,185 bread wheats and 318 durum wheats from ICARDA; 243 bread wheats from Egypt; and 2,100 durum wheats from the USDA. These nurseries were planted at different sites. Kulumsa is an area for wheat where many lines can express their yield potential by tolerating the high rust development. Holetta, a hot-spot for Septoria, is an ideal site for screening for Septoria resistant lines. Many CIMMYT international nurseries were tested at Holetta for quarantine purposes and most of them were found susceptible to the existing strain of Septoria. In the future, Septoria screening only will be evaluated at Holetta. Melkasa is the quarantine site for the semi-arid environments of the country. Last year, plentful rainfall during the growing season lead to a high incidence of stem and yellow rust at Melkasa. Debre Zeit is the screening site for durum wheat to the three rusts. Only data on CIMMYT materials are reported here. About 77% of the total bread wheat nurseries tested at Kulumsa, Melkasa, and Debre Zeit were found to have 20% or less infection rates of either stem rust or yellow rust. This is good news for the national program, where yellow rust epidemics have wiped out the popular cultivars from production. Durum wheat and triticale nurseries were planted at Debre Zeit and Holetta. The disease pressure at Debre Zeit was relatively high. As a result, only 341 durum wheat lines (26%) of the total 1,297 lines evaluated were found to have lower than or equal to 20% severity or infection rate for the two rusts. Triticale was found to better tolerate Septo-

ria at Holetta. The lower number of materials maintained at Holetta is mainly due to Septoria. Most leaves were killed by the time the plants flowered causing shriveled grain with poor germination.

ITEMS FROM GERMANY

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Association mapping in hexaploid wheat – The project GABI-Wheat.

GABI-Wheat is designed as an association mapping study in hexaploid wheat. The aim of the project is the identification of associations of molecular marker data with traits that are important for breeding new cultivars. Populations employed in association studies consist of (mostly) unrelated individuals from a broad population. In this project, the population comprises 358 elite, Western-European hexaploid winter wheat cultivars and 14 spring wheat cultivars. The wheats were cultivated on one location in 2009 and three locations in 2010 in France, and on two locations in 2009 and 2010 in Germany, utilizing an alpha-design. Field trials and phenotyping for yield, yield components, and baking quality traits were performed by industrial project partners. Genotyping was performed for a total of 800 microsatellite markers. Inoculation trials for *Fusarium culmorum*/*Fusarium graminearum*, *Septoria tritici*, and *Drechslera tritici-repentis* were performed by the Julius-Kühn-Institut (B. Rodemann) in 2009 and 2010 for each disease at two locations in Germany.

After correction for rare alleles (less than 3% frequency in the population), data from 781 loci, corresponding to 732 microsatellite marker and from 17 candidate genes chosen from the literature, are available for the 372 cultivars. From those microsatellites, 650 are mapped in the ITMI mapping population with an average distance of 7.6 cM. No apparent population structure was detected employing the STRUCTURE program and principal component analysis. Hence, a marker-based kinship matrix was used to reduce the number of false positive associations caused by spurious relationships between the cultivars. Linkage disequilibrium analysis showed small values for R^2 between unlinked markers as well as physically linked markers. The correlation between R^2 and physical marker distance also is weak. Mixed linear models are employed for the analysis of marker–trait associations. The Genstat and Tassel programs are currently used to evaluate the data. Preliminary results revealed significant associations for the first traits investigated so far.

Sustainable grain yield loci in bread wheat detected via an association mapping approach.

A core collection of 96 winter wheat genotypes from 21 different countries and five continents was considered for a genome-wide association mapping analysis. These genotypes were selected from a larger collection created at the Institute of Field and Vegetable Crops, Novi Sad, Serbia. The collection was phenotyped for grain yield in field plots in Novi Sad during six growing seasons between 1994 and 1999. Genotyping using DArT markers was performed by Triticarte Pty. Ltd. (Canberra, Australia). The calculation of testing for an association between markers and traits was done with the software programs TASSEL 2.01. and TASSEL 2.1 exploiting the general linear model and mixed linear model, respectively.

Only stable marker–trait associations (MTAs) significant in both models in three out of five years were considered. In total, 10 MTAs were identified on chromosomes 1AL, 3AL (two), 3BL, 4AL, 4BL, 5BL, 6BS, 7AS, and 7BL. Interestingly, there was coincidence with MTAs described in a study performed by CIMMYT using different sets

of germ plasm. Identical MTAs were detected on chromosomes 1AL, 3AL, and 7BL. In addition, we found grain yield MTAs in highly comparable regions on chromosomes 3BL and 7AS.

Mapping of QTL for resistance to stem rust (Ug99) in durum wheat.

Ninety-seven recombinant inbred lines (RILs) that were developed from the cross 'Kristall / Sebatel', both durum wheat cultivars, has been characterized for stem rust response in Ethiopia. Seven consecutive field trials at two locations were carried out in main- and off-season under natural and artificial inoculation with stem rust race Ug99 and a mixture of highly virulent races of Ethiopia. Based on the means of the seven environments, the phenotypic distribution showed that resistance to Ug99 in this population is controlled by major gene/QTL, accounting for most of the phenotypic variation. The parents were screened for polymorphism with 502 SSR markers. We have found 258 polymorphic and, accordingly, we used these markers to genotype the whole population. Using composite interval mapping, eight consistent and major QTL for stem rust (Ug99) were identified on chromosomes 1AS, 2AL, 2BS, 3AS, 4BS, 6AL, 7AS, and 7AL. An additional, minor consistent QTL also was identified on the long arm of chromosome 5B. From these QTL regions, 1AS, 2AL, 3AS, 4BS, and 7AS are not harboring any of the characterized stem rust resistance genes of durum wheat. These results suggest that durum wheat resistance to the Ethiopian races of stem rust (Ug99) is likely oligogenic and that there is potential to identify previously uncharacterized resistance genes of minor effect. If successfully validated, the markers associated with these QTL will be useful for breeding new durum wheat cultivars that are resistant to Ug99 and related races.

The relationship among seed characters based on QTL analysis in bread wheat.

QTL mapping was applied on a new mapping population (HTRI 11712/HTRI 105), which was developed at IPK, Gatersleben, and contained 133 $F_{2:3}$ families (see Annual Wheat Newsletter Vol. 55:56). Mapping analysis revealed four QTL for 1,000-kernel weight on chromosomes 7A, 4B (two QTLs), and 1B of which three were detected repeatedly in two experiments. The explained phenotypic variation (R^2) by a single QTL ranged from 8.7 to 26.5% and both parents contributed increasing alleles. For seed length, 13 QTL were detected of which three were identified repeatedly in at least two experiments. The R^2 for a single QTL ranged from 8.3 to 26.9%, and the increasing alleles originated from both parents. QTL analysis for seed width showed five QTL of which two were identified repeatedly in at least two experiments. The R^2 of a single QTL ranged from 7.9 to 15.7%.

Thousand-kernel weight showed a higher correlation with seed width compared to seed length. With regard to the co-localization of the QTL for seed-related traits, and considering only the repeated QTL in the present study, there was only one QTL on chromosome 4BL common among all the traits. However, seed width showed another QTL on chromosomes 4BS in common with 1,000-kernel weight. This is in agreement with the coefficient of correlation observed in the present study between these traits, which show higher correlation of 1,000-kernel weight with seed width compared to seed length. This might suggest that 1,000-kernel weight is determined more by seed width than seed length. Therefore, in order to increase 1,000-kernel weight, seed width should be enhanced, in accordance with practical wheat breeding.

Studies on seed longevity in bread wheat.

An association mapping approach was utilized to visualize the genomic regions responsible for the maintenance of viability of bread wheat seeds. Seeds of 96 accessions selected from a large panel based on contrasting agronomic and phenotypic traits were available from the regeneration cycle of 2009. The genetic map for these lines consisted of 525 mapped and 315 unmapped DArT (Diversity Arrays Technology) markers.

The lines showed high initial germinations after standard germination tests, which ranged from 68% to 98.5% with the mean germination of 93.72±5.05%. Accelerated ageing tests were performed to assess the seed longevity. Germination percentages after artificial ageing (AA) and controlled deterioration tests (CD) ranged from 0% to 60.5% and 5.5% to 95% with the mean of 10.97±12.80% and 61.05±25.33%, respectively. In total, association mapping revealed 73 significant marker trait associations (MTAs) for seed longevity, 38 of which were with mapped markers, 20 with unmapped markers with known chromosomal location only, and 25 with completely unknown location. The MTAs were

located on 14 out of 20 marked chromosomes. When the two methods were compared, AA gave 40 and CD gave 33 significant MTAs. Based on bin information, 15 markers with significant MTAs were genetically characterized.

The bins carrying these markers contain many genes important in various aspects of seed vigor and viability such as encoders of seed maturation protein, cold- and heat-shock proteins, plasma membrane proteins, biostress-related proteins, senescence-related proteins, and membrane proteins along with various enzymes associate with seed longevity. When compared with the similar studies performed in barley, we found that the chromosomal segments of 7B MTAs in wheat matches with the location of a 7H QTL for longevity in barley giving the indication of shared mechanisms of seed viability in both cereals.

Variability of Rc (red coleoptile) alleles in wheat and wheat–alien genetic stock collections.

Anthocyanin accumulation in vegetative organs has a relationship to stress resistance in plants. In wheat, the ability to accumulate anthocyanins in the coleoptile is inherited and controlled by the *Rc* (red coleoptile) genes. Our goal was to find potential sources of 'strong' *Rc* alleles conferring very high levels of anthocyanin production and to study the effect of genetic background on *Rc* expression. We measured the relative anthocyanin content (OD530) in the coleoptile of different wheat and wheat–alien genetic stocks and accessions to find potential sources of strong *Rc* alleles conferring very high levels of anthocyanin production. The OD530 values varied from 0.514 to 3.311 in genotypes having red coleoptiles. The highest anthocyanin content was detected in coleoptiles of four *T. turgidum* subsp. *dicoccoides* accessions originating from Israel and the Russian *T. aestivum* cultivar Novosibirskaya 67, suggesting that their *Rc* alleles can be used to increase anthocyanin content in the coleoptile of wheat cultivars. Rye *Rc* alleles, such as that of Russian cultivar Selenga, can possibly be used to increase anthocyanin content in triticale seedlings.

Embryo lethality in wheat x rye hybrids: mode of inheritance and identification of a complementary gene in wheat.

Crosses between hexaploid wheat and rye can only succeed when pre- and post-zygotic barriers are overcome. A rye gene determining embryo lethality (*Eml-R1*), which is involved in post-zygotic isolation, has been mapped to chromosome 6R. The mode of inheritance of *Eml-R1* was studied using a wheat-rye chromosome 6R addition line. *Eml-R1* exists in at least two alternative forms, with the mutant allele *Eml-R1b* dominant with respect to wild-type allele *Eml-R1a*. The attempt to test whether the Dobzhansky-Müller model can explain the embryo lethality seen in wheat–rye hybrids was performed by examining hybrid caryopses formed by a cross between the set of nullisomic-tetrasomic (NT) lines of Chinese Spring and rye lines carrying *Eml-R1b*, since differentiated embryos should only be formed in hybrids lacking the wheat chromosome carrying a complementary wheat gene. In parallel the NTs were crossed with rye inbred lines carrying *Eml-R1a* to prove the capacity of each of the lines to produce differentiated viable hybrid seeds. The crosses of NT lines with rye lines carrying *Eml-R1b* detect a complementary wheat gene present on chromosome 6A. This gene has been designated *Eml-A1*. Crosses of NT lines with rye lines carrying wild-type allele *Eml-R1a* revealed that wheat chromosomes 1B, 1D, and 6B carry genes indispensable for normal development of wheat-rye caryopses.

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ITEMS FROM HUNGARY

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The wheat season. A rainy spring and summer characterized the 2009–10 wheat season. Precipitation exceeded 1,000 mm compared to the average of 550 mm. Due to the wet conditions, heavy *Septoria*, *Helminthosporium*, head blight, and leaf rust epidemics occurred. The national wheat average reached only 3.72 t/ha, slightly lower than the 3.85 t/ha harvested in the dry year 2009. Quality of wheat harvested was average.

Breeding.

Z. Bedö, L. Láng, O. Veisz, G. Vida, M. Rakszegi, I. Karsai, K. Mészáros, S. Bencze, and G. Gulyás.

Breeding. Four Martonvásár winter wheat cultivars were registered in Hungary in 2010.

Mv Tallér (Mv 10-07) is an early maturing cultivar with outstanding yield potential and medium breadmaking quality, selected from the cross 'Andy-2/F15//Gore/3/Mambo'. The cultivar has very good winter hardiness, good lodging resistance. Mv Tallér is a medium quality milling wheat with a wet gluten content of 30–32%, Farinograph quality B1, and Alveograph W value of 180–190. Mv Tallér has good field resistance to powdery mildew and leaf rust, and moderate resistant to stem rust.

Mv Apród (Mv 17-07) is a medium, early maturing semi dwarf hard red winter wheat. The advantage of Mv Apród compared to the previous cultivars is the combination of the semidwarf plant height with the high gluten (protein) content and high yield. The average wet gluten content of Mv Apród is 34–37% and the gluten quality is medium (B1 Farinograph quality and 160 Alveograph W). With reliable winter hardiness, Mv Apród is resistant to powdery mildew and leaf rust, and moderately resistant to stem rust.

Mv Kikelet (Mv 07-07) is a facultative wheat with medium winter hardiness. Mv Kikelet was tested together with real winter types and outyielded the standards. In spring sowings, the yield potential is competitive with spring cultivars. The quality of Mv Kikelet is good in autumn sowings and has higher gluten content and even better gluten quality in spring sowings. Mv Kikelet is moderately resistant to the major leaf diseases.

Mv Melodia (Mv09-07) is a hard red winter wheat with good breadmaking quality. Mv Melodia was selected from the cross 'Lone/OD162//Ukrainka'. Wet gluten content is typically between 30–34% and the Farinograph quality is A2-B1. Mv Melodia has good field resistance against leaf diseases and moderate susceptibility to head blight.

Breeding for quality traits.

Breeding of wheat with high arabinoxylan and protein content. Analyses carried out in the framework of the HEALTHGRAIN FP6 EU project headed by Peter Shewry demonstrated that the Yumai-34, an exotic Chinese wheat cultivar, contains large quantities of water-extractable arabinoxylan (WE-AX). A crossing program was aimed at breeding wheat genotypes with good agronomic adaptation and high dietary fiber content. The protein content also was analyzed in this population in order to select for genotypes with several advantageous traits. Lines with WE-AX contents similar to that of Yumai-34 and improved protein content were identified in the F_5 generation. These will be further analysed in the next generation.

Selection of durum wheat with high tocol content. Tocol content was determined in 36 durum wheat cultivars and breeding lines and was found to vary widely. Extreme values were 29.1 and 52.7 g/g in the first year and 28.5 and 56.9

g/g in the second. The fact that the maximum values were almost double the minimum values justified the initiation of a breeding program aimed at improving the tocol content. Total tocol contents in excess of 50 g/g were recorded for seven of the 36 durum cultivars and lines investigated. Three of these were chosen as crossing partners on the basis of their agronomic and chemical quality traits. One line, MvTD37-08, is now in its second year of state variety trials, whereas the other two lines are still being tested in field and laboratory trials. The compound with the most beneficial physiological effect, tocopherol, made up 11.3–22.8% of the total tocol content, with values of over 8 g/g in the best lines. In Mv Makaróni, 22.77% of the over 50 g/g total tocol content consisted of tocopherol (11.69 g/g). The second highest tocopherol content (9.33 g/g) was observed for the advanced line MvTD07-09. The results achieved in the second year confirmed observations made in the first year; the same two genotypes had extraordinarily high tocopherol content compared to the other lines.

Disease resistance studies.

The weather in Hungary in 2010 was favorable for the pathogens responsible for Fusarium head blight. In order to determine the species composition, damaged spikes were collected from several regions of the country and pure cultures were developed from a total of 114 infected grains. Morphological species determination was carried out in Tulln (Austria). The results showed that *Fusarium graminearum* was the dominant pathogen (present on 110 of the 114 samples), two isolates were identified as *F. sambucinum*, and one each as *F. culmorum* and *F. verticillioides*.

The QTL mapping of the 'Bánkúti 1201-9086/Mv Magvas' population developed to analyze the FHB resistance of old Hungarian wheat cultivars was continued by testing the parental liness with a total of 140 microsatellite markers. Eighty of the primers examined gave products, 55 of which were polymorphic. The entire population was tested with 33 SSR markers and with 24 different AFLP combinations. Data analysis resulted in the identification of 286 polymorphic markers suitable for mapping. The 319 polymorphic markers now available are sufficient to initiate the analysis of linkage groups.

An artificial inoculation and evaluation method was elaborated under greenhouse conditions to investigate resistance to *Mycosphaerella graminicola*, the fungal species responsible for the Septoria leaf spot disease. Mv Kolo, Mv Regiment, and three breeding lines proved to have outstanding resistance.

Genotypes with designated leaf rust resistance genes were tested for infection in an artificially inoculated nursery. Genes *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr28*, *Lr29*, and *Lr35* provided effective protection against leaf rust in Martonvásár in 2010.

Studies on the composition of the wheat powdery mildew population showed that race 76 was present in the highest ratio (42.6%) in 2010, followed by race 77 (29.6%). Race 51, which infected all the cutlivars used for differentiation, appeared with lower frequency than in previous years (16.0%). The virulence complexity of the pathogen population was 5.79, which represented a decline compared with previous years, mainly due to the reduced frequency of race 51.

In the framework of international and Hungarian projects (Bioexploit-EU FP6 and DTR_2007), resistance genes *Lr9*, *Lr24*, *Lr25*, *Lr29*, *Lr35*, *Lr37*, *Pm21*, and *Stb2* were introduced into wheat cultivars adapted to Hungarian conditions. By the joint incorporation of several resistance genes (pyramiding), winter wheat genotypes carrying new *Lr* gene combinations were developed.

Abiotic stress resistance studies.

To investigate the genetic regulation of heat tolerance, the responses of lines from a two-parental, doubled-haploid population to heat stress during the early stages of embryo development were analyzed on the basis of yield components and phenological parameters. Averaged over the population, high temperature was found to cause the greatest reduction in the grain number, which ranged from 3–75% compared with the control. In order to compile a molecular marker map of the population, the application of two molecular marker systems was begun: 16 AFLP reactions were carried out using AFLP primers exhibiting great polymorphism, and mapping was performed using 29 SSR markers with known chromosome localization.

The genetic diversity of active wheat breeding programs in southeastern Europe was analyzed using AFLP and SSR markers on a collection of 114 winter wheat cultivars . Considerable differences were found between cultivars originating from different countries, with the greatest similarity between those from Hungary and Romania and Serbia and Macedonia. When the phenotypic traits of the same cultivars were investigated, the powdery mildew and leaf rust resistance was found to be closely correlated with genetic diversity, whereas heading date, plant height, and a number of yield components were completely independent of genetic diversity. The parallel determination of genotypic and phenotypic diversity made it possible to distinguish groups of wheat cultivars with a similar genotype but a different phenotype, and with a different genotype but a similar phenotype. This information can be put to direct use in breeding during the selection of crossing partners.

Fourteen wheat genotypes (Ukrainka, two lines of Mv Hombár, M3, Glenlea, Mv Verbunkos, Mv Toborzó, Mv 4, Mv Mezőföld, Mv Magvas, the 9086 line of Bánkúti 1201, Plainsman, Mv Magma, and Tommi) and two durum genotypes (PWD1216 and MvTD10-98) were tested using 84 SSR markers. These genotypes are the parental pairs of mapping populations. After evaluating the polymorphism identified, work will begin on the detailed testing of the various populations.

Experiments proved that, among the yield components of wheat, grain mass decreased to the greatest extent in response to water withholding at first node appearance. The yield-increasing effect of enhanced atmospheric CO_2 concentration was greatest when applied at first node appearance. The grain mass and grain number only decreased as the result of drought during the ripening period at the higher carbon dioxide level, but the values recorded were still higher than at normal concentration.

When examining the joint effect of drought and enhanced atmospheric CO_2 concentration, a relative increase in the protein content of wheat grains was found when water deficit occurred at first node appearance, and this increase was greater at normal atmospheric CO_2 concentration. Drought during heading caused a similar increase in grain protein content at both carbon dioxide levels. Higher atmospheric CO_2 concentration caused a reduction in the grain protein content. This reduction was greatest when the treatment was applied at heading. An increase in the duration of drought stress had the most significant effect on the protein content when the stress occurred at first node appearance.

Photosynthesis was stimulated by higher atmospheric CO_2 concentration, so that in response to water withholding, the decrease in the carbon fixation of the wheat plants proceeded at a slower rate and only reached a significant level at lower values of soil moisture. The assimilation of the plants also remained at a more intensive level when an enhanced atmospheric CO_2 concentration was applied during heading or ripening, which could be attributed to the slower plant development at a higher atmospheric CO_2 concentration. The photosynthetic activity declined to a lesser extent during ripening than in the earlier developmental phases.

Considerable genotypic differences were found in the responses of the wheat varieties to water withholding and enhanced atmospheric CO_2 concentration. Mv Mambó proved to be a drought-tolerant cultivar, with smaller changes in yield parameters in response to stress, whereas the yield and physiological parameters of Mv Regiment decreased substantially when subjected to drought. However, Mv Regiment made better use of surplus CO_2, so it produced outstanding yields in a CO_2-enhanced environment.

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Development of a wheat genotype combining the recessive crossability alleles *kr1kr1kr2kr2* and the T1BL·1RS translocation for the rapid enrichment of 1RS with new allelic variation. The main objective of this work was to develop a wheat genotype containing both the recessive crossability alleles (*kr1kr1kr2kr2*), allowing high crossability between 6x wheat and diploid rye, and the T1BL·1RS wheat–rye translocation chromosome. This wheat genotype could be used as a recipient partner in wheat–rye crosses for the effcient introduction of new allelic variation into 1RS in translocation wheats. After crossing the wheat cultivars Mv Magdaléna and Mv Béres, which have the T1BL·1RS translocation involving chromosome arm 1RS from Petkus rye, with the line Mv9 *kr1*, 117 F_2 plants were analyzed for crossability, 10 of which had higher than 50% seed set with rye and, thus, presumably carried the *kr1kr1kr2kr2* alleles. Four of the 10 plants contained the T1BL·1RS translocation in the disomic condition as detected by GISH. The wheat–rye F_1 hybrids produced between these lines and the rye cultivar Kriszta were analyzed in meiosis using GISH. T1BL·1RS/1R chromosome pairing was detected in 62.4% of the pollen mother cells . The use of FISH with the repetitive DNA probes pSc119.2, Afa family, and pTa71, allowed the 1R and T1BL·1RS chromosomes to be identified. The presence of the 1RS arm from Kriszta, besides that of Petkus, was demonstrated in the F_1 hybrids using the rye SSR markers RMS13 and SCM9. In four of the 22 BC_1 progenies analyzed, only Kriszta-specific bands were observed with these markers, although the presence of the T1BL·1RS translocation was detected using GISH. We concluded that recombination occurred between the Petkus and Kriszta 1RS chromosome arms in the translocated chromosome in these plants.

GISH reveals different levels of meiotic pairing with wheat for individual *Ae. biuncialis* chromosomes. The *T. aestivum–Ae. biuncialis* (2n=4x=28; $U^bU^bM^bM^b$) disomic addition lines $2M^b$, $3M^b$, $7M^b$, and $3U^b$ were crossed with the wheat cultivar Chinese Spring *ph1b* mutant genotype in order to induce homoeologous pairing, with the final goal of introgressing *Ae. biuncialis* chromatin into cultivated wheat. Wheat–*Aegilops* homoeologous chromosome pairing was studied in metaphase I of meiosis in the F_1 hybrid lines. Using U and M genomic probes, GISH demonstrated the occurrence of wheat–*Aegilops* homoeologous pairing for chromosomes $2M^b$, $3M^b$, and $3U^b$, but not for $7M^b$. The wheat-*Aegilops* pairing frequency decreased in the following order: $2M^b > 3M^b > 3U^b > 7M^b$, which may reflect differences in

the wheat-*Aegilops* homoeologous relationships between the examined *Aegilops* chromosomes. The selection of wheat–*Aegilops* homoeologous recombinations could be successful in later generations.

Molecular cytogenetic evaluation of chromosome instability in *T. aestivum–S. cereale* disomic addition lines. The genetic stability of wheat–rye (Chinese Spring–Imperial) disomic addition lines was checked using the Feulgen method and FISH. Feulgen staining detected varying proportions of disomic, monosomic, and telosomic plants among the progenies of the disomic addition lines. The greatest stability was observed for the 7R addition line, whereas the most unstable lines were those with 2R and 4R additions. Chromosome rearrangements also were detected using FISH. Based on the specific hybridization patterns of repetitive DNA probes pSc119.2 and (AAC)5, as well as ribosomal DNA probes (5S and 45S), isochromosomes were identified in the progenies of 1R and 4R addition lines. These results draw attention to the importance of continuous cytological checks on basic genetic materials by using FISH, because this method reveals chromosome rearrangements that could not be detected either with the conventional Feulgen staining technique or with molecular markers.

Selection of U and M genome-specific wheat SSR markers using wheat–*Ae. biuncialis* and wheat–*Ae. geniculata* addition lines. Wheat SSR markers specific to the U and M genomes of *Aegilops* species were selected. A total of 108 wheat SSR markers were successfully tested on *Ae. biuncialis* (2n = 4x = 28, $U^bU^bM^bM^b$), on five wheat–*Ae. biuncialis* addition lines ($2M^b$, $3M^b$, $7M^b$, $3U^b$, and $5U^b$) and on a wheat–*Ae. geniculata* ($1U^g$, $2U^g$, $3U^g$, $4U^g$, $5U^g$, $7U^g$, $1M^g$, $2M^g$, $4M^g$, $5M^g$, $6M^g$, and $7M^g$) addition series. Among the markers, 86 (79.6%) were amplified in the *Ae. biuncialis* genome. Compared with wheat, polymorphic bands of various lengths were detected in *Ae. biuncialis* for 35 (32.4%) of the wheat microsatellite markers. Three of these (8.6%) exhibited specific PCR products in wheat–*Ae. biuncialis* or wheat–*Ae. geniculata* addition lines. The primers GWM44 and GDM61 gave specific PCR products in the $2M^b$ and $3M^b$ wheat–Ae. biuncialis addition lines, but not on the $2M^g$ addition line of *Ae. geniculata*. A specific band was observed on the $7U^g$ wheat–*Ae. geniculata* addition line using the BARC184 primer. T hese three markers specific to the U and M genomes are helpful for the identification of $2M^b$, $3M^b$, and $7U^g$ chromosome introgressions into wheat.

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ITEMS FROM INDIA

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Application of Real-Time PCR in marker-assisted selection for stem rust resistance gene Sr24.

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Introduction. Real-Time PCR (RT–PCR) is a technique mainly used to amplify and simultaneously quantify a targeted DNA molecule (Gibson et al. 1996). Currently, four different chemistries, TaqMan® (Applied Biosystems, Foster City, CA, USA); Molecular Beacons (Newark, New Jersey, USA); Scorpions® (Sigma-Aldrich, St. Louis, MO, USA); and SYBR® Green (Life Technologies, Carlsbad, CA, USA), are available for RT-PCR. All of these chemistries allow

detection of PCR products via the generation of a fluorescent signal. Among the SYBR Green is a fluorogenic dye that exhibits little fluorescence when in solution, but emits a strong fluorescent signal upon binding to double-stranded DNA (Arya et al. 2005).

Real-time PCR can be applied to traditional PCR applications as well as new applications that would have been less effective with traditional PCR. With the ability to collect data in the exponential growth phase, the power of PCR has been expanded into applications such as viral quantitation, quantitation of gene expression, array verification, drug therapy efficacy, DNA damage measurement, quality control and assay validation, pathogen detection, and genotyping. Recently, this technique has been used to develop molecular markers and to evaluate critical aspects for olive oil authentication (Giménez et al. 2010).

This study used RT-PCR as a tool in the marker-assisted selection (MAS) in crop plants in general, and wheat in particular. Screening for stem rust resistance gene *Sr24* by RT-PCR was carried out using primers specific to a SCAR marker.

Materials and methods.

Plant material. The wheat genotypes and segregating lines used in this study are listed in Table 1.

DNA extraction and quantification. DNA was extracted from the leaves of 1 month old wheat seedlings according to Nalini et al. (2004). The DNA was quantified by using fluorimeter (Hoefer DyNA Quant 200).

Polymerase chain reaction. PCR screening used a Realplex4 (Eppondorf, Germany). A SCAR marker (SCS1302609) for the *Sr24*/*Lr24* gene (Gupta et al. 2006) using specific primers (5' CGCAGGTTCCAAATACTTTTC 3' and 5' CGCAGGTTCTACTAATGCAA) were used in a total volume of 25 µl reaction mixture containing 1X PCR buffer (10 mM Tris-HCl (pH-9.0), 1.5 mM $MgCl_2$, 50 mM KCl, and 0.01% gelatin), 100 µM of each dNTP (Sigma, St. Louis, MO, USA), 0.75 U Taq DNA Polymerase (Bangalore Genei Pvt. Ltd, Bangalore, India), 4.0 picomoles of each primer, 0.4X SYBR green dye (Sigma, St. Louis, MO, USA), and 100 ng of genomic DNA. Amplifications were performed using the following thermal cycling profile: 1 cycle of 94°C for 2 min, 35 cycles of 94°C for 1 min, 60°C for 1 min, 72°C for 1 min, and a final extension of 72°C for 7 min.

Table 1. Screening of genotypes for presence of stem rust resistance gene Sr24 using RT-PCR. Cultviars with an * are the F_2 of the cross 'Kalyan Sona/Vaishali' (phenotyping of the individuals by rust inoculations were by Das et al. (2006). *Sr24* gene status: RR = homozygous, Rr = heterozygous). Melting curve samples were scored positive if the melting temperature was 83.9°C. +/– assay samples were scored as positive if the peak was above the threshold line.

Cultivar	*Sr24* gene status	Scoring for band based on:		
		Ethidium bromide staining followed by PCR	Melting curve	+/– assay
Unnath Kalyan Sona	+	+	+	+
KS-1	+	+	+	+
KS-3	+	+	+	+
Unnath Sonalika	+	+	+	+
FLW-2	+	+	+	+
Kalyan Sona	–	–	–	–
PBW343	–	–	–	–
MACS 2496	–	–	–	–
B-6 (154A)	+	+	+	+
Vaishali	+	+	+	+
Vidisha	+	+	+	+
Agra Local	–	–	–	–
163B*	+ (RR)	+	+	+
163C*	+ (Rr)	+	+	+
164A*	+ (RR)	+	+	+
164B*	+ (Rr)	+	+	+

Analysis of results. The presence or absence of a band in MAS were analyzed in three ways, using a quantification curve, by a melting analysis, and using a +/– assay of the RT–PCR technique. To compare RT–PCR results, PCR products were resolved on 2% agarose gels, stained with ethidium bromide solution (0.5%), and visualized under a UV transilluminator where the presence or absence of bands were scored.

Results and discussion. The protocol parameters were optimized. We observed that samples with DNA concentration of 100 ng and a primer concentration of 4.0 picomoles (each) gave well resolved peaks. Thermal cycling conditions were similar to that used in the Master Cycle Gradient 5300.

Analysis using a quantification curve. Progress of DNA amplification during PCR could be monitored in real time by measuring the intensity of fluorescent dyes during amplification using quantification curve. A quantification curve is the curve obtained by plotting the increase in fluorescence (Y axis) as the amplification of the target DNA is started (X axis). Carriers increase in fluorescence as the amplification of target DNA started, and noncarriers of *Sr24* gene showed no increase in fluorescence because it lacks the target DNA (Fig. 1). However, using a quantification curve for the analysis needs to be further standardized.

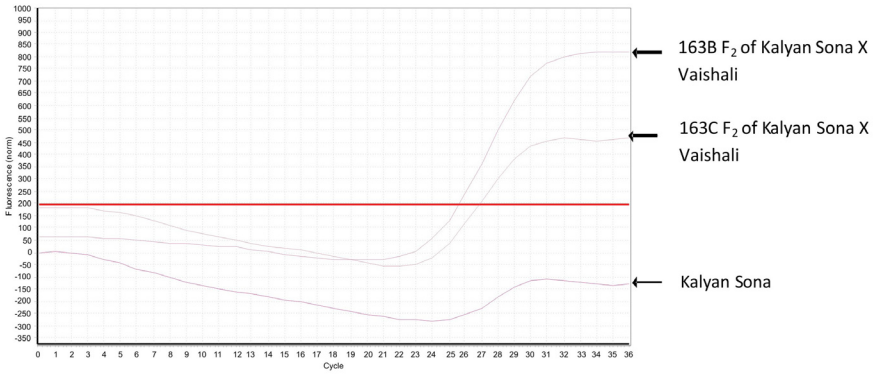

Fig. 1. Analysis of results based on a quantification curve. Carriers of the *Sr24* gene, such as 163B and 163C, show sharp peaks above the threshold level of 200 fluorescence units, whereas the noncarrier Kalyan Sona does not show any peak.

Analysis using a melting curve. Melting curves were performed at the end of SYBR green quantitative RT–PCR to check for primer-dimer or nonspecific product formation. Using plots of dI/dT against temperature after amplification, the results were analyzed using peaks indicating the Tm (melting temperature) of the amplified products. From the melting curve analysis, we could differentiate between individuals carrying *Sr24* gene and noncarriers (Table 1, p. 21). We also could distinguish homozygous *Sr24* (RR) individuals from heterozygous individuals (Rr) (F_2 of 'Kalyan sona / Vaishali) and also the susceptible parent (rr). The peak height of a heterozygous plant was approximately half that of a homozygous plant (Fig. 2).

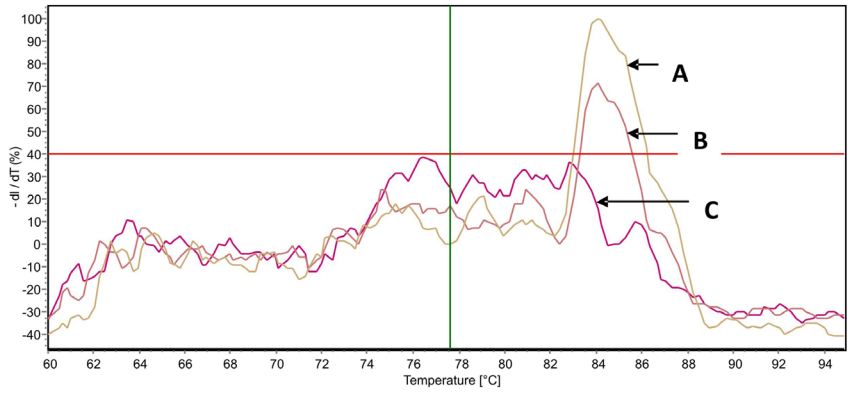

Fig. 2. Analysis of results based on a melting curve. The melting temperature was approximately 83.9°C. A – relative fluorescence units was 120% for carriers of the *Sr24* gene with homozygous allele 163B*; B – 163C* with heterozygous allele for *Sr24*, the relative fluorescence unit was 70%, approximately half that of homozygous 163B; and C – Kalyan Sona with no peak. * F_2 'Kalyan Sona (susceptible parent, rr) / Vaishali (*Sr24*).

Analysis by +/– assay. In RT–PCR, the +/– assay can be used to score the presence or absence of a marker/gene based on the quantification curve, where an increase in the fluorescence unit above a threshold level will be considered positive and below the threshold level will be considered negative. The threshold level also can be manually adjusted and examined for positives and negatives of the *Sr24* gene (Table 1, p. 21).

Conclusions. In MAS, a large number of populations have to be screened using conventional PCR techniques, and requires post-PCR processing, such as resolving in agarose gels, which is time consuming and sometimes may lead to false results due to cross contamination. To overcome these delays and errors, and also to screen a large number of populations, the RT–PCR technique has been used to screen a large number of samples for the presence or absence of a gene of using specific primers. Application of RT–PCR in MAS has not been reported in literature, but the use of this technique for the development of molecular markers has been reported in olive plants by Giménez et al. (2010). We used a specific primer for a SCAR marker reported for stem rust resistance gene *Sr24* (Gupta et al. 2006). The results of phenotypic

and genotypic data of conventional PCR and RT–PCR (melting curve) were compared, and they were found to match exactly, indicating the advantage of using RT–PCR in MAS. This method could avoid post-PCR processing with agarose gel electrophoresis and, thereby, save time. However, the use of a quantification curve for the analysis needs further standardization.

Acknowledgements. The authors would like to thank Dr. S.F.D'Souza, Head, NABTD and Dr. S.K. Apte, Head, MBD, for their constant encouragement and support. A part of the work was carried out by Ms. Kiruba Shankari (Project Trainee) at BARC.

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Threshability in recombinant inbred lines of wheat.

S.G. Bhagwat.

Recombinant inbred lines of bread wheat arising from two cultivars. Kalyan Sona and Sonalika. were raised in the field at Trombay in 2010–11 season. The lines were sown at two sowing dates corresponding to normal and late sowing. At harvest, one spike each from each RIL was collected at random. Spikelet number and rachis length were recorded. The spikes were threshed by hand and a rating was given, beginning with 1.0 for the softest threshing up to 5.0 for very hard threshing.

Results and discussion. As in earlier years, Kalyan Sona was softer threshing than Sonalika. The RILs showed differences in threshability. Lines softer and harder than the parents were observed. The distribution for threshability of the late sown lines is shown in Table 2. Correlation coefficients were calculated between some of the traits using Microsoft Excel (Table 3).

A significant correlation was found between the threshability ratings for 2009–10 and 2010–11. Although the ratings are based on single spikes and are recorded using a subjective assessment, the correlation showed that the procedure gave repeatable results. Lower ratings were less consistent and the reliability was better for lines with higher ratings. When the ratings were for soft (1.0 to 2.5), intermediate (3.0 and 3.5), and hard (4.0 to 5.0), the frequencies were 52, 62, and 24 (2009–10) and 68, 46, and 24 (2010–11), respectively. Significant correlations for rachis length and spikelets/cm of rachis indicated that the RILs were stabilized for these traits. These RILs could be used to identify loci governing threshability and spike morphology.

Table 2. Scores for threshability in field grown recombinant inbred lines between Kalyan Sona (soft threshing) and Sonalika (hard threshing). Spikes were rated from 1.0 for the softest threshing up to 5.0 for very hard threshing.

Description	Rating	Frequency
Very soft	1.0	17
Intermediate	1.5	00
Kalyan Sona type	2.0	45
Intermediate	2.5	06
Sonalika type	3.0	25
Intermediate	3.5	21
Hard threshing	4.0	15
Intermediate	4.5	02
Very hard threshing	5.0	07

Table 3. Correlation coefficients between selected traits for "Kalyan Sona/ Sonalike' recombinant inbred lines (RIL). ** indicates significance at the 1% level.

Trait	Number of RILs	Correlation coefficient
Threshability rating; 2009–10 and 2010–11	138	r = 0.56**
Rachis length; 2009–10 and 2010–11	130	r = 0.54**
Spikelets/cm of rachis; 2009–10 and 2010–11	137	r = 0.58**

During the domestication of bread wheat, selection for the free threshing habit enhanced its suitability for cultivation. Two mutations, *q* to *Q* on chromosome 5A and *Tg* to *tg* on chromosome 2D, mainly are responsible for the free threshing habit of bread wheat. Because threshability is an important trait, many studies have sought to map the loci involved. Jantasuriyarat et al. (2004) analyzed the ITMI mapping population and observed that two QTL that affected threshability were located on chromosomes 2D and 5A. The QTL on 2D probably represented the effect of *Tg*, the gene for tenacious glumes. The QTL on 5A are believed to represent the effect of *Q*. Free threshing-related characteristics were more affected by *Tg* and to a lesser extent by *Q*. Other QTL that were significantly associated with threshability in at least one environment were located on chromosomes 2A, 2B, 6A, 6D, and 7B.

Nalam et al. (2007) analyzed RILs developed by ITMI and a 'Chinese Spring/Chinese Spring 2D' F_2 population and observed that in the ITMI population, two QTL affected threshability and their location coincided with the two QTL affecting glume tenacity. In the 'Chinese Spring/Chinese Spring 2D' F_2 population, the location of QTL that affected glume tenacity coincided with *Tg1*. These results suggest that the effect of *Tg1* and threshability is through the level of attachment of the glumes to the rachilla. In our experiments, we observed that RILs obtained from two free-threshing cultivars showed variation for threshability. The variation was studied using hand threshing. More observations were made during the winter season of 2010–11, which are reported here.

Acknowledgement. To Shri Vikas and Shri Sudhakar Mali for help with the field work.

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Current activities.

Suman Bakshi, S.G. Bhagwat, Chun Mei Chang, and A.S. Shitre.

Bread wheat cultivars were grown in a replicated experiment and measurements were made on the canopy temperature depression. Another study monitored translocation of reserves from stem to the grain. Analysis of the data is in progress. An RIL population from the intervarietal cross 'Sonalika/Kalyan Sona', a bread wheat RIL population for grain protein content, and early flowering mutant lines in the background of cultivar C306, genotype MP3054, and Hindi62 were carried forward. Grain size and shape mutants of the long grain durum genotype PBND 1625 and morphological mutants in a bread wheat genotype carrying multiple phenotypic markers were carried forward. The backcross populations carrying sphaerococcum locus in Kalyan Sona background were carried forward. Other genetic stocks, such as an ADH variant (tall and dwarf) and a lax mutant of sphaerococcum type in Kalyan Sona background were carried forward.

Wheat seeds are exposed to soil conditions after sowing, which may include salinity and could affect germination. Seeds of *T. turgidum* subsp. *dicoccum* and *T. aestivum* subsp. *aestivum* were soaked in increasing concentrations (100–500 mM) of NaCl and the germination percent and seedling height were measured. We observed that the germination percent decreased beyond 300 mM; seedling growth was reduced by 40–45% at 100 mM. The aleurone layers of *T. turdigum* subsp. *dicoccum* and *T. aestivum* subsp. *aestivum* were incubated in liquid medium in the presence of different concentrations of NaCl and assayed for amylase stimulation, protein secreted in medium, mitochondrial activity, and weight loss. There was no effect on secreted protein, however, amylase stimulation, respiration, and weight loss were affected by NaCl.

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Performance of timely and late-sown cultivars under different sowing times.

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Summary. A field experiment was conducted during winter seasons of 2005–06 to 2006–07 at the Directorate of Wheat Research, Karnal, to evaluate the timely sown and late sown recommended cultivars under normal, late, and very late sowing conditions. A clear picture will be provided as to whether or not timely sown cultivars perform equally good under late and very late sowing conditions. A pooled analysis of two years data revealed a reduction grain yield of 14.4% as sowing was delayed from normal to late sown conditions. Cultivar differences were observed for anthesis, maturity, spike length, grain-filling period, grain production rate, and yield and yield attributing parameters. The interaction between sowing time and cultivars was significant for grain yield. Three timely sown cultivars (PBW 343, HD 2687, and PBW 502) performed better under normal sowing condition whereas the late-sown cultivar UP 2425 produced a maximum grain yield (42.24 q/ha) under late sowing conditions and Raj 3765 produced a maximum grain yield (42.79 q/ha) under very late sowing conditions, which was significantly higher than other cultivars. The resultsshowed that timely sown cultivars did not perform better across the sowing time and that there is a need to develop different cultivars for various sowing conditions.

Introduction. Wheat is the second most important crop after rice in India and in 2008–09 occupied approximately 28×10^6 ha with a production of 78.4×10^6 metric tons. India ranks second in wheat production after China. The area, productivity, and production of wheat have increased 119, 236, and 634%, respectively, since 2005 compared with 1965–66 (base year). Weather is cool and dry in the early part of wheat-growing season (November to February) whereas temperature rises during the grain-filling period (March–April), which is more pronounced in eastern part of Indo-Gangetic plain, resulting in a reduced wheat-growing period. Wheat is grown under different agroclimatic conditions each having variable productivity levels. In India, wheat is generally grown under three sowing conditions, i.e., normal (November sown), late (December sown), and very late sown (January sown) conditions. The normal sown wheat crop is generally preceded by crops such as upland rice, soybean, sorghum, bajra, or even grown after fallow. The late sown wheat crop is generally preceded by crops such as basmati rice, low land rice, cotton, and pigeon pea and very late-sown wheat is grown after toria, pea, potato, and sugarcane ratoon. Delayed wheat sowing (normal to late, mid-November to the first two weeks of December) resulted in a decrease in yield by 15.5, 32.0, 27.6, 32.9, and 26.8 kg/ha/day under NHZ, NWPZ, NEPZ, CZ, and PZ, respectively, for the timely sown cultivars. For the late-sown cultivars, a delay in sowing (late to very late, first two weeks of December to the first two weeks of January) decreased the grain yield by 42.7, 44.8,

51.6, and 44.2 kg/ha/day under NWPZ, NEPZ, CZ, and PZ, respectively (Tripathi et al. 2005).

Some of the scientists think that timely sown recommended varieties do equally well under late and very late sown conditions even under Indian subcontinent where hot and dry wind prevails during the grain-filling period. If this holds true, then the separate breeding programs for late sown conditions are not neede. To test this hypothesis, we selected a set of timely sown and late sown recommended cultivars and grew them under normal, late, and very late sown conditions.

Materials and methods. A field experiment was conducted during the 2005–06 and 2006–07 winter seasons at the Directorate of Wheat Research, Karnal (Latitude 290 43' N, longitude 760 58' E and altitude 245 m). Six culivars, three timely (PBW 343, HD 2687, and PBW 502) and three late sown (PBW 373, UP 2425, and Raj 3765), were evaluated under normal, late, and very late sown conditions. The experiment was conducted in split-plot design and replicated three times. Three sowing times in main plot, i.e., normal (11 and 12th November in 2005 and 2006), late sown (9th and 12 th December in 2005 and 2006), and very late sown (5th and 6th January in 2006 and 2007). After harvesting rice as a fore crop, the field was prepared with a cultivator and disk and in each subplot 250 viable seeds were planted. Fertilizer (150 N, 60 P_2O_5, 40 K_2O) was applied to the crop. A one-third dose of nitrogen in the form of urea, full phosphorous in the form of diammonium phosphate, and potash in the from of muriate of potash was applied as basal, i.e., before sowing and the remaining nitrogen was top dressed in two splits at the first node stage (DC 31) (Zadoks et al. 1974) and at boot stage (DC 41). Irrigation was applied as needed. Weeds were controlled with an application of sulfosulfuron 25 g/ha in 400 liters of water 30 days after sowing. Observations were recorded on biomass, anthesis, maturity, grain-filling period, and grain-production rate, yield and its component characters. Standard statistical methods of analysis were followed for the parameters under study (Gomez and Gomez 1984).

Results and discussion. Delayed sowing from normal to late and very late increased the canopy temperature depression significantly, whereas other parameters such as anthesis, maturity, spike length, and grain-filling period were reduced as sowing was delayed. The difference between the time taken for anthesis under normal and very late sown situations was about 25 days, whereas for grain-filling period, the difference was only 5 days. Canopy temperature depression under very late sown conditions was almost double that of the timely sown plants, whereas spike length was reduced about 1.5 cm when very late sown. Yield and yield-attributing parameters also were significantly different due to sowing time in both the years. From mean of two years, grain yield was reduced to 14.4 % as sowing was delayed from normal to late sown conditions. This observation is in agreement with findings of Tripathi et al. (2005). Protein content increased in delayed sowing.

Cultivar differences were observed for anthesis, maturity, spike length, grain-filling period, grain production rate, and yield and yield-attributing parameters (Table 1 and Table 2, p. 27). PBW 343 took 90 days for anthesis,

Table 1. Effect of sowing time and cultivar on anthesis, maturity, canopy temperature depression (CTD), spike length, grain-filling period, and grain production rate.

Treatment	Canopy temperature depression		Anthesis (days)		Maturity (days)		Spike length (cm)		Grain-filling period (days)		Grain production rate (kg/ha/day)	
Sowing time	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**
Normal	1.98	1.93	101	100	134	134	8.7	8.5	33	34	130	141
Late	2.13	2.07	88	90	119	119	7.6	7.5	31	30	136	122
Very late	4.29	3.86	76	78	106	106	7.2	7.0	30	28	130	140
C D at 5 %	0.38	0.42	0.1	0.6	0.9	0.9	0.2	0.3	0.8	0.3	8.5	11.6
Cultivar												
PBW 343	2.80	2.62	91	90	122	121	7.3	7.0	31	31	136	134
HD 2687	2.86	2.64	89	90	121	119	7.9	7.7	31	29	130	142
PBW 502	2.96	2.63	90	90	121	121	7.4	7.2	30	31	143	132
PBW 373	2.79	2.76	89	89	121	121	7.0	6.8	32	32	134	131
UP 2425	2.71	2.52	86	89	116	119	8.9	8.9	30	30	136	129
Raj 3765	2.70	2.56	84	87	118	119	8.5	8.3	34	31	115	138
CD at 5 %	NS	NS	0.1	0.6	0.3	1.0	0.5	0.4	0.3	1.0	5.5	10.7

Table 2. Effect of sowing time and cultivar on yield, yield-attributing parameters, and protein content.

Treatment	Spikes/m²		1,000-kernel weight (g)		Grains/spike		Yield (q/ha)		Biomass (q/ha)		Protein (%)	
Sowing time	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**
Normal	339	337	41.22	45.15	32.2	32.7	43.32	48.29	109.12	111.72	9.55	11.00
Late	393	389	40.89	32.07	26.5	30.0	42.15	36.25	108.79	88.81	9.01	11.58
Very late	335	330	35.89	39.79	33.3	31.2	39.17	39.54	100.59	80.81	11.03	11.53
C D at 5 %	48	39	0.91	2.39	5.11	4.8	1.87	3.76	7.99	7.16	1.13	0.54
Cultivar												
PBW 343	352	349	38.67	36.95	31.6	33.9	42.12	42.22	100.86	95.21	9.83	11.32
HD 2687	342	339	37.00	35.26	33.1	34.8	40.56	41.61	107.67	101.39	8.95	11.07
PBW 502	368	362	40.89	40.72	29.2	28.9	42.87	40.59	105.09	99.38	10.08	11.41
PBW 373	374	376	39.22	43.77	29.7	26.3	43.21	42.09	106.61	101.54	10.16	11.51
UP 2425	335	331	39.00	39.43	32.3	30.9	40.72	39.12	110.32	91.97	10.15	11.58
Raj 3765	361	355	41.22	37.89	28.1	32.6	39.79	42.51	106.48	89.19	9.97	11.53
CD at 5 %	32	32	1.23	5.50	3.1	5.5	1.84	3.05	4.69	8.11	1.27	0.45

whereas the late sown cultivar Raj 3765 was 86 days. All cutivars matured in 119 to 121 days. Late sown cultivar UP 2425 possessed longest spike length, which was significantly higher than others. The greatest number of spikes/m² was observed in PBW 373 and the lowest in UP 2425. Thousand-kernel weight was greatest in PBW 502 and the lowest in HD 2687. PBW 373 produced the maximum grain yield (42.65 q/ha) followed by PBW 343 (42.17 q/ha); the minimum was in UP 2425 (39.92 q/ha).

A significant interaction between sowing time and cultivar was observed for grain yield. All the three timely sown cultivars (PBW 343, HD 2687, and PBW 502) performed better under timely sown conditions, whereas late sown cultivar UP 2425 produced the maximum grain yield (42.24 q/ha) under late sown conditions, which was significantly higher than yield obtained by timely sown cultivars HD 2687 and PBW 502 under late sown conditions. Under very late sown conditions, Raj 3765 produced the maximum grain yield (42.79 q/ha), which was significantly higher than other cultivars (Table 3). Thus, the hypothesis that timely sown cultivars will perform better under late and very late sown conditions was not true. The few late sown cultivars that exceeded the yield level over timely sown cultivars under late and very late sown situations provides a sound reason for developing cultivars separately for timely sown and for late sown conditions.

Table 3. Interaction between sowing time and cultivar on grain yield (q/ha, pooled basis). TS = timely sown recommended cultivar and LS = late sown recommended cultivar.

	Sowing time			
Cultivar	**Normal**	**Late**	**Very late**	**Mean**
PBW 343 (TS)	47.97	40.66	37.88	42.17
HD 2687 (TS)	47.68	36.73	38.86	41.09
PBW 502 (TS)	47.85	38.89	38.46	41.74
PBW 373 (LS)	47.09	42.24	38.63	42.65
UP 2425 (LS)	43.48	36.78	39.50	39.92
Raj 3765 (LS)	40.76	39.91	42.79	41.15
Mean	45.80	39.20	39.35	
CD at 5 % (sowing time)			2.00	
CD at 5 % (cultivar)			1.58	
CD at 5 % (sowing time x cultivar)			3.18	

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Pathogenic evolution of wheat rust pathogens in relation to resistance genes in Indian wheat cultivars – some suggestions for strengthening wheat rust resistance in India.

Wheat (*T. aestivum*, *T. turgidum* subsps. *durum* and *dicoccum*) is one of the prime cereal crops of India and is attacked by the three rusts, stem or black, leaf or brown rust, and stripe or yellow rust. Stem rust survives throughout the year only in the Nilgiri Hills of southern India. The Himalayas in northern India are too cold for the pathogen to survive during winter. Therefore, after the wheat harvest in the Nilgiris Hills of southern India, stem rust drastically disappears from India because of low inoculum build up in absence of the host. A *P. striiformis* that needs low temperature survives for the whole year in the Himalayas is of epidemic consequences to the wheat crop in Himachal Pradesh, Uttranchal, Punjab, Haryana, West Uttar Pradesh, and north Rajasthan. Leaf rust needs an intermediate temperature, and, thus, survives and spreads from both southern and northern foci and is important throughout India (Nagarajan and Joshi 1985). Systematic work on wheat rusts in India began in 1931 by Dr. K.C. Mehta. We haver made an effort to update the list of rust races that have prevailed in different parts of India since 1975 by consulting ICAR monographs (Mehta 1940, 1952) and Annual Wheat Workshop Reports regularly released by the All India Coordinated Wheat and Barley Project, previously from the IARI, New Delhi, but now from the Directorate of Wheat Research (ICAR), Karnal (Table 1).

Table 1. New pathotypes in Indian rust flora over the years. New race names are based upon the binomial system of nomenclature of Nayar et al. (1997, 2003).

Period	Stem/black rust	Leaf/brown rust	Stripe/yellow rust
Up to 1975	11, 11A, 14, 15, 17, 21, 24, 24A, 34, 34-1, 40, 42	10, 11, 12, 12a, 17, 20, 63, 77, 106, 107, 108, 162	13, 14, 19, 20, 31, 38
1975–80	21-1, 40A, 21A-2	77A, 104	14A, 20A, 38A, I
1980–85	117A-1	114A, 104B, 12-2	K
1985–90	40-1,117-1	77-1, 77-2, 77-3, 12-1, 12-3, 12-4, 107-1, 108-1	L, N, P
1990–95	117-2, 117-3, 117-4, 117-5, 117-6	77-4, 77-5, 104-2, 104-3	T, U, CI, CII, CIII
1995–2011	40-2	77-6, 77-7, 77-8, 77-9, 77-10	*Yr9* virulence (46S119 and 78S84)

Changes in the distribution patterns of wheat rust pathotypes in India – an historical account.

Vast areas under high-yielding wheat cultivars resulted in changes in the frequency and spectrum of stem, leaf, and stripe rust pathogens. Race 12 (5R5) of *P. triticina* was the most predominant between 1972 and 1977 in the north and east zones with an overall frequency of 46%. During this period in the Nilgiris Hills in southern India, race 77 (45R31) was predominant with a frequency as high as 56%. Race 12 (5R5), although it virulence for very few genes, remained most predominant in the country during these five years, except in the Nilgiris Hills. Race 104 (17R23), which was first detected in samples from Nepal in 1972, was the second most prevalent race and predominated between 1972–77. However, the frequency of these races declined during 1982–87 and were replaced by 104B (29R23). Although the frequency of race 77 (45R31) declined in the Nilgiris Hills to 5% in 1982–87, it became most predominant race in the Northern Hills, Northern Plains, and Eastern and Far Eastern zones replacing the virulent race 12 (5R5). The increase in the frequency of race 77 (45R31) in rest of India appears primarily due to the increase in area of cultivars specifically susceptible to race 77. A second reason may be the presence of a greater number of virulence genes. In the Nilgiri Hills, other biotypes of race 77, possessing additional pathogenicity for *Lr10* and *Lr10+Lr26*, replaced race 77 (45R31). This group of biotypes is well distributed all over India and was found in over 46% of the samples analyzed. The shift in virulence pattern from races 12 (5R5), 104 (17R23), and 77 (45R31) in 1972–77 to 77A (109R31), 77A-1 (109R23), 77-1 (109R63), and 104B (29R23) in 1982–87 is the result of a shift in varietal pattern over different parts of India (Table 2, p. 29). *Puccinia striiformis* races 14(66S0), 20 (70S0) and 38 (66S0-1) prevailed in India before the cultivation of dwarf wheats. After widespread cultivation of Mexican wheats, three variants 14A (66S64), 20A (70S64), and 38A (66S64-1) predominated during 1975–80 in northwest India. Race I (38S102), which matches Sonalika, predominates in

the Nilgiri Hills. Since 1982, race K (47S102) had the highest frequency in northwest India until the emergence of new races N (46S102), P (47S103), and *Yr9* (46S119 and 78S84) (Table 3).

Table 2. Population shift in *Puccinia triticina* over the years and consequential breakdown of erstwhile cultivars/ genes.

Period	Prevalent population (>60% frequency)	Important new races emerged/ built up	Susceptible genes/genotypes
1961–65	20, 77, 162	107A, 162A, 17, 131	NP770 and NP824, NP710 and NP809, *T. turgidum* subsp. *dicoccum*
1966–70	12, 77, 162, 162A	104, 104A, 77A	*Lr3*: Democrat, Bowie, Texas *Lr10*: Federation, Gabo, Ridley
1971–75	12, 77, 104A, 162	104B	Sujata, C306, Sonora 64 *Lr13*: Sonalika, Kalayansona, Lerma Rojo
1976–80	12, 77, 104B	77A-1	*Lr13*: HD2009, WL711
1981–90	104B, 77A-1	12-3, 77-3, 77-4, 107-1, 108-1	*Lr23*: HD2285, HI977, DL153-2, GW173, HD2278, K8804 *Lr10+Lr13*: HD2329
1991–97	77-3, 77A-1	77-5, 104-2, 104-3	*Lr26*: WH3004, UP2338, CPAN3004, DWR162, HP42, HS277
1997–2011	77-5	77-7, 77-8, 77-10	*Lr9* by 77-7, *Lr19* by 77-8 and *Lr28* by 77-10

Table 3. Population shift in *Puccinia striiformis tritici* over the years and consequential breakdown of erstwhile cultivars/genes.

Period	Prevalent population (>60% frequency)	Important new races emerged/ built up	Susceptible genes/genotypes
1961–65	14, 19, 20, 31, A	38	NP770, 792, 809, 824, 710, NP200, 201, 202, K65, C591
1966–75	14, 19, 20, 38, A	14A, 20A, 38A	*Yr2*: Kalyansona, Sonalika, Lerma Rojo, Sonora 64
1976–85	20, 38, 14A	I, K	*Yr2* (KS): WL711, Kalyansona, HD2009
1986–90	12, 77, 104B	77A-1	*Lr13*: HD2009, WL711
1991–96	N, K	P, race *Yr9*	*Yr9*: WH542, CPAN3004, UP2338
1997–2011	*Yr9* virulences	—	*Yr9*: PBW 343, DBW 17

New variability in rust pathogens renders genes ineffective from time to time.

The wide-spread cultivation of high-yielding cultivars over a large area with a high level of disease resistance since 1970 exerted directional selection pressure on the rust pathogen population. In response, new rust pathogens evolved to match the resistance genes incorporated into the new wheat cultivars. In *P. triticia*, 17 new races emerged after 1970 from different regions of the country. The additional virulence was observed in race 12 (5R5) for *Lr20+Lr23*, *Lr23*, *Lr26*, *Lr15+Lr26*, *Lr9*, *Lr19*, and *Lr28*. The race 104 (17R23), isolated from Nepalese samples in 1972, has now arisen with biotypes having virulence for *Lr20*, *Lr23*, and race 77 (45R31) has acquired virulence to *Lr10*, *Lr10+Lr23*, and *Lr10+Lr26*.

For *P. striiformis*, eight new races or biotypes were encountered over the last 20 years; 14A (66S64), 20A (70S64), and 38A(66S64-1), all virulent on Kalyansona; I (38S102), which matched Sonalika and Strubes Dickopf; and *Yr1*, L (70S69), N (46S102), L (70S69), and P (47S103) had additional virulence for hybrid 46 (*Yr3b*, *Yr4b*), Chinese 166 (*Yr1*) and *Yr3a+Yr4a*. *Yr9* races have now emerged and spread into the northwest plains, where a major portion of the area is under cultivation with wheats having the *Yr9* gene.

For *P. graminis tritici*, the evolution of new races has been comparatively less, because wheat cultivation is not that intensive in the Nilgiri Hills of southern India (inoculum source for stem rust target areas). The most remarkable emergence of a new race has been that of 40-1, which is virulent on gene *Sr24* and present in very few cultivars released for cultivation in southern, central, and peninsular India.

Rust-resistant stocks used in Indian wheat breeding programs for protection from leaf and stripe rusts.

The 'boom and bust' cycle, which occured particularly after the introduction of Mexican semidwarf wheats in the Indian subcontinent, was eliminated by incorporating effective rust resistance genes (*Lr* and *Yr*) using specific resistant donor lines in Indian wheat breeding programs (Tables 4 and 5).

Table 4. *Lr* genes used to date in Indian wheat breeding programs for leaf or brown rust resistance.

Gene	Source	# of cultivars/lines	Cultivar/line name
Lr1	Malakoff, Sharbati, Sonora	4	Khushal 69, Moti, UP301, MP846
Lr3	Democrat (CI 3384)	1	CPAN1235
Lr10	Lee, Timstein	6	BW11, NI747-19, I5439, HD2009, HD2329, HS86
Lr11	Hussar (CI 4843)	1	HS86
Lr13 APR	Thatcher, Frontana	7	UP115, WL2265, PBW65, HS86, IWP72, Sonalika
Lr14	Hope, H44	2	Sonalika, WL711
Lr17	RL6041, 6008	1	NP846
Lr23	Gaza durum	13	HI977, HYB65, HD2135, HD2270, HD2278, HD2204, HD2258, HD2281, HD2285, HUW213, UP262, DL153-2, Girija
Lr26	*Secale cereale*	22	HUW206, AKW1071, CPAN1874, DL802-3, DL803-2, CPAN1922, CPAN3004, DWR162, DWR195, GW190, HD2610, HPW42, HS207, HS240, HS277, HUW318, K8804, MACS2496, PBW299, 343, UP2338, WH542
Lr34	Chinese Spring	23	C306, DWR39, GW173, HD2189, HD2329, HD2501, 2610, HI977, 1077, HP1209, HPW42, HS207, 240, 295, K9006, Kalyansona, NI5439, PBW175, PBW299, UP262, UP2338, WH147, WH54

Table 5. *Yr* genes used to date in Indian wheat breeding programs for resistance to stripe or yellow rust.

Gene	Source	Documented line
Yr2	Heines VII type	HD2009, 2189, 2278, 2285, 2329, 2380, HI977, 1077, HP1209, 1633, HS86, HUW234, HW741, HW971, IWP72, J405, K8020, NI5439, PBW175, PBW222, RAJ2184, RAJ3077, Sonalika, Swati, UP262, VL421, VL616, WH283
Yr2 (KS)	Heines VII type B	W11, GW173, HD2402, HD2428, HDR77, HI1123, HP1102, HUW234, K7410, K8027, LOK-1, PBW65, WL711
Yr3	Vilmorin type	HS295
Yr9	*Secale cereale*	CPAN1922, 3004, DL803-3. WR162, 95, GW190, HD2610, PW42, HS207, 240, 277, HUW206, 318, K8804, MACS2496, PBW299, 343, UP2338, WH533, 542
Yr18	*Lr34* sources	C306, DWR39, GW173, HD21892, HD2329, HD2610, HI1077, HP1209, HPW42, HS207, 295, K8962, K9006, NI5439, PBW175, 299, UP2338, WH147, 542

In search of additional/new genes.

Unfortunately, the genetic base of rust resistance in India wheat cultivars languishes in front of the array of new pathotypes that have emerged or built up during the last 2 to 3 decades. To sustain wheat yields in India, the search for new genetic sources of resistance becomes imperative. A number of genes are available and need to be exploited to alleviate resistance base of Indian wheat germ plasm (Tables 6 and 7).

Table 6. Unutilized genes for resistance to leaf or brown rust useful for Indian wheat breeding programs.

Gene	Source	Remarks
Lr2a	Webster (CI 3780)	Useful component of multiple gene resistance.
Lr4–Lr8	Waban (CI 12992)	Difficult to characterize, not of much use.
Lr9	*Ae. umbellulata*	Present in very limited Indian cultivars, widespread effectiveness.
Lr11	Hussar (CI 4843)	Temperature insensitive, slow ruster.
Lr12	Spring	Adult-plant resistance.
Lr15	Kenya W1483	Temperature sensitive, effective at 15–18°C.
Lr16	Selkirk	Frequency of virulence remains low.
Lr17	Timson	Useful in multiple gene resistance.
Lr18	*T. timopheevii*	Temperature adability.
Lr20	Thew, Chinese Spring	Durable resistance
Lr21	*Ae. tauschii* var. *meyeri*	Adult-plant resistance.
Lr22	*Ae. tauschii*	No known virulence.
Lr24	*Thinopyrum ponticum*	Undesirable red grains.
Lr25	*Secale cereale* cv. Rosen	No known virulence.
Lr27+Lr31	CS*6/Hope 3B	Complementary genes.
Lr28	*Ae. speltoides*	No virulence in India.
Lr29	*Th. ponticum*	Virulence in Pakistan and Turkey.
Lr30	Terenzio	Slow ruster.
Lr32	*Ae. tauschii* (RL 5497-1)	Wider stability.
Lr33	Thatcher*6/PI 58548	Effective in combination.
Lr35	*Ae. speltoides*	Adult-plant resistance.
Lr36	*Ae. speltoides*	Not studied much.
Lr37	*Ae. ventricosa*	Effective field resistance.
Lr38	*Th. intermedium*	Virulence unknown.
Lr39–Lr44	*Ae. tauschii*	Not studied much.

Table 7. Unutilized genes for resistance to stripe or yellow rust useful for Indian wheat breeding programs.

Gene	Source	Remarks
Yr1	Chinese 166	Becomes susceptible to barley races, world wide.
Yr4	Hybrid 46	Low level of virulence in India.
Yr5	*T. aestivum* subsp. *spelta album*	Rare virulence.
Yr6	Heines Kolben	Higher resistance at low temperature.
Yr7	Iumillo durum	High frequency of virulence worldwide.
Yr8	Ae. comosa	Resistance is not durable.
Yr10	Moro (PI 178383)	No known virulence in India.
Yr11	Joss cambier	Adult-plant resistance (presumed).
Yr12	Mega	Adult-plant resistance (presumed).
Yr13	Maris Huntsman	Adult-plant resistance (presumed).
Yr14	Hobbit	Adult-plant resistance (presumed).
Yr15	*T. turgidum* subsp. *dicoccoides*	Virulence unknown.
Yr16	Cappelle Desprez	Adult-plant resistance and durable resistance.
Yr17	*Ae. ventricosa*	More susceptible at low temperature.
Yr18	Terenzio	Adult-plant resistance.

Durable resistance – global experience and lessons to Indian wheat breeders.

Durable disease resistance remains effective in a cultivar even though it may be widely grown over a long period of time in an environment that favors disease epidemics. This descriptive term does not provide an explanation for the basis of inheritance of this trait. Durable resistance has the following dimensions: 1. covers a large area, 2. grown for many years, and 3. high inoculum load and favorable weather. On the basis of multilocational data on triticale, cultivar Coorong was selected from a CIMMYT trial for widespread cultivation in Australia, because the alien gene *Sr27* gave total resistance to stem rust. Almost immediately after the commercial release of Coorong, stem rust was observed because the pathogen developed matching virulence in Australia. The durability of genotype, therefore, cannot be assessed by means of small field trials or multilocation evaluation for a few seasons. The *Sr26* gene, derived from *Thinopyrum elongatum*, has been used in Australia since 1970, is present in a number of wheats, and is designated as durable. Multilocation tests do not guarantee resistance nor are the alien genes are always durable. Vanderplank rationalized that non-specific or horizontal resistance will neither lead a cultivar into boom-and-bust cycle nor exert any directional selection pressure on the pathogen and, therefore, will be durable. Although Vanderplank considered durable resistance to be a polygenic trait, he cited a number of examples such as the maize–*P. polysora* system in Africa, where a single resistance gene contained the disease for a number of years.

The oat cultivar Red Rustproof is still durable to crown rust even after one-hundred years. The wheat cultivars Thatcher and Lee have withstood stem rust for 55 and 30 years, respectively. Cappelle Desprez has expressed a moderate resistance to stripe rust at the adult-plant stage for the last 20 years. Cappelle Desprez carries both seedling and adult-plant resistance with genes *Yr3a* and *Yr4a*. No detectable race-specific component has been detected in the adult-plant stage in Cappelle Desprez; but all cultivars with *Yr3a* and *Yr4a* have not been durable. Genetic analysis of Cappelle Desprez shows that chromosomes 5BS and 7BS contribute substantially to durable resistance. Further analysis showed that the long arms of homologous chromosomes 5A, 5B, and 5D increase susceptibility, whereas the short arms of these chromosome had the opposite effect. Cappelle Desprez appears to possess an optimal balance between the effects of genetic loci in increasing resistance and those favoring susceptibility.

Several lines derived from H44 and Hope also exhibit durable stem rust resistance. Cultivars such as Thatcher, Lee, Hope, Kenya Page, Africa Mayo, and Selkirk, which have been used globally, possess the *Sr2* adult-plant resistance gene. This gene is tightly linked with the pseudo-black chaff gene and when present in combination with other genes, as in Selkirk, produces a durable resistance. In Australia, wheats with five to six different resistance genes are cultivated. Gene *Sr36* derived from *T. timophevii* (*SrTt-1*) is present in cultivars Mengavi, Mendos, Timson, Cook, Timgalen, and Shortim and in various blends,with *Sr5*, *Sr6*, *Sr7a*, *Sr8*, *Sr9c*, *Sr11*, and *Sr17*. In race surveys, the occurrence of matching virulences was detected for most of the genes either alone or in combination. However, combined virulence for *Sr36* was very low in frequency in Australian wheat despite the fact that *Sr36* was released in varietal background as early as 1967. Therefore, like *Sr2*, combining *Sr36* with other resistance genes can render wheat cultivars durable.

Many host resistance genes that are matched by the pathogen survive in breeding populations for a long time, because these gene are not totally overcome by the pathogen and they still carry some amount of residual resistance. In the barley–*Erysiphe graminis hordei* system, they are referred to as defeated genes. In the wheat–*P. striiformis* system, segregation for resistance to stripe rust can be obtained through minor gene effects, temperature-sensitive genes, adult-plant genes, and various forms of disease resistance. The breeding strategy and selection methodology needs to be viewed accordingly.

Pyramiding resistance genes – one of the effective approaches to curtail fast emergence of new, virulent mutants of rust pathogens.

The idea of pyramiding genes was conceived as an alternative to breeding for polygeneic traits. When only a single resistance gene is present in a host, it soon becomes susceptible. Subsequently, adding one or more resistance genea in that cultivar will increase resistance. Conversely, if four or five cultivars with single resistance genes are grown, all of them are exposed to the same pathogen population and this does not reduce vulnerability to epidemic. However, if these genes are brought into one background, because of additive gene action, the wheat will have resistance to a wide spectrum of pathotypes and the resistance will be durable. Virulence is gained at the cost of fitness, so a pathotype able to infect all the resistance genes in such a cultivar is likely to be less fit in nature and may not induce an epidemic. The approach of pyramiding resistance genes also might prolong their usefulness.

Pyramiding resistance gene provides greater durability if the pathogen is solely dependent on an asexual life cycle and mutation and recombination are less pronounced (Marshall 1977). Combinations of resistance genes have provided good field resistance to wheat stem rust in Australia for several years (McIntosh 1992). Because the alternate host of *P. graminis tritici* is nonfunctional, in Australia pyramiding resistance genes has paid rich dividends. In North America, resistance gene combinations involving *Sr2* have provided durable resistance to stem rust, and *Lr13* and *Lr34* when combined with other leaf rust resistance genes also have provided durable resistance (Kolmer et al. 1991). Pyramiding resistance genes has provided durable resistance in some cases. For instance, the French cultivar Cappelle Desprez has durable resistance to eyespot; the other source is VPM, derived from a cross involving the wild grass *Ae. ventricosa*. Molecular markers linked to these genes have been identified (Worland et al. 1988; Koebner and Martin 1990). Seedlings with both these genes with better eyespot resistance (Doussinault and Douaire 1978) can be selected using molecular markers facilitating selection for better resistance. In view of the rust-management philosophy described above, several unexploited gene(s) may be useful for pyramiding in popular Indian wheat cultivars (Table 8).

Table 8. Suggested sources of adult-plant resistance for strengthening leaf and stripe rust resistance in Indian wheats.

Gene	Source	Remarks
LEAF RUST		
Lr2a	Webster (CI 3780)	Useful component of multiple gene resistance.
Lr11	Hussar (CI 4843)	Temperature insensitive, slow ruster.
Lr12	Spring	Adult-plant resistance.
Lr17	Timson	Useful in multiple gene resistance.
Lr20	Thew, Chinese spring	Durable resistance.
Lr21	*Ae. tauschii* var. *meyeri*	Adult-plant resistance.
Lr22	*Ae. tauschii*	No known virulence.
Lr28	*Ae. speltoides*	No virulence in India.
Lr30	Terenzio	Slow ruster.
Lr32	*Ae. tauschii* (RL 5497-1)	Wider stability.
Lr35	*Ae. speltoides*	Adult-plant resistance.
Lr37	*Ae. ventricosa*	Effective field resistance.
Lr38	*Th. intermedium*	Virulence unknown.
Slow rusters (adult-plant genotypes possessing useful seelding resistance genes in India (Kumar et al. 1999).		
Lr34 alone	HP 1731, C 306	
Lr34+Lr10+Lr13	NIAW 34, HD 2329	
Lr34+Lr23	GW 232, HI 977, HI 1077, GW 173, PBW175	
Lr34+Lr26	PBW 343, PBW 373, HS 240, UP 2363, WH 594, WH 596	
Lr34+Lr23+Lr26	DL 802-3, HS 317, Gabo, Frontana	
STRIPE RUST		
Yr4	Hybrid 46	Low level of virulence in India.
Yr5	*T. aestivum* subsp. *spelta album*	Rare virulence (in snowy conditions only).
Yr10	Moro PI 178383	No known virulence in India.
Yr11	Joss Cambier	Adult-plant resistance.
Yr12	Mega	Adult-plant resistance.
Yr13	Maris Himtsman	Adult-plant resistance.
Yr14	Hobbit	Adult-plant resistance.
Yr15	*T. turgidum* subsp. *dicoccoides*	Virulence unknown.
Yr16	Cappelle Desprez	Adult-plant resistance and proven durable resistance
Yr17	*Ae. ventricosa*	More susceptible at low temperature
Yr18	Terenzio	Adult-plant resistance.

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Genetics of leaf rust and leaf blight resistance in different crosses of common wheat.

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Abstract. Leaf blight caused by *Alternaria triticina* (HLB) and leaf rust caused by *Puccinia triticina* are two of the important diseases of wheat that are widespread in India. Postulating the genes in most of the released cultivars, a chi-square test applied for HLB and leaf rust separately. The HLB reaction in the F_2 generation was a 3:1 (susceptible:resistant) ratio was observed in two crosses, and we conclude that the susceptible reaction is governed by a dominant gene(s) in both the crosses. A 15:1 ratio fitted in three crosses showed that susceptible reaction is governed by duplicate gene(s). Tests also were used for leaf rust reactions to check the validity of expected ratio in the F_2 generation. The 3:1 ratio (susceptible:resistant) fit three crosses and this resistant type reaction is governed by a dominant gene(s). Two crosses fit a 15:1 ratio indicating a resistant type infection governed by duplicate gene(s).

Introduction. Among cereals, wheat is ranked second after rice and is the staple food, especially in northern India, where most people are vegetarian. The crop is grown successfully between an altitude of 30°0–60°0 N and 27°0–40°0 S. Wheat is extensively cultivated under diverse agroclimatic conditions in India covering most of the states except Kerala. All wheat cultivated in India is spring type but grown during the winter. Wheat, the main food crop of India, contributes significantly to the central pool. The cultivation of wheat in India started very early, during prehistoric times and, thus, the origin of wheat is still a matter of speculation. Wheat research to develop high-yielding cultivar and improve management techniques started about a century ago in India. A large number of valuable cultivars were bred and released for commercial cultivation. These cultivars were tall and mainly suited to low-input management with low yield potential. However, a turning point came in the history of wheat breeding during mid-1960s with the introduction of semidwarf, photo-insensitive, high-yielding Mexican wheat breeding material developed at CIMMYT under the guidance of Nobel Laureate Dr. Norman E. Borlaug. These cultivars were tested under the All India Coordinated Wheat Improvement Project and, as a result, three genotypes, Lerma Rojo, S 308, and Sonora 64, which out yielded the old tall wheat cultivars, were released for general cultivation in major wheat-growing areas of India.

Wheat is cultivated on over 217.53 x 10^6 ha in world with 610.87 x 10^6 metric tons produced during 2007–08. The wheat-growing area in India is about 28.00 x 10^6 ha with highest production of 78.4 x 10^6 tons (Anonymous 2008). Globally, the maximum area under wheat is in China followed by U.S.A. and India. In terms of production per unit area, the U.S.A. stands first followed by the Russian Federation. In India, wheat is the main cereal crop and is second only to rice. Uttar Pradesh, Madhya Pradesh, Punjab, Rajasthan, Bihar, Haryana, Maharashtra, and Gujarat are the major wheat-growing states in the country.

Three species of genus *Triticum*, *T. aestivum* subsp. *aestivum* (bread wheat or common wheat), *T. turgidum* subsp. *durum* (macaroni wheat), and *T. turgidum* subsp. *dicoccum* (emmer or khapli wheat) are grown in India. Common wheat, with 2n = 6x = 42 chromosomes, is the most important and mainly grown for chapatti making on a wide area. *Triticum turgidum* subsp. *durum* is grown in some states primarly for pasta products. Stem, leaf, and stripe rust have been major concerns for quite some time, because rust epidemics before or during flowering are most detrimental. The symptoms for stripe rust (also called yellow rust and glume rust) caused by *P. striiformis* usually appear earlier in the spring than symptoms for leaf or stem rust. Leaf rust (also called brown rust) is one of the most common wheat diseases in the world. Rough estimates of up to 40 percent yield losses due to leaf rust at various flag leaf severities and different growth stages have been reported (RL Bowden, personal communication). Leaf rust can inflict serious yield losses in epidemic years (Joshi 1976; Kolomer 1996). Although the disease has more or less been contained in India because of research efforts over the last 50 years, efforts to identify novel genes conferring resistance to this disease need to be continued because of fast evolution of the leaf rust pathogen (Nayer et al. 1996, 2000). So far, nearly 60 genes conferring resistance to leaf rust have been identified and designated *Lr1* through *Lr60* (Mclntosh et al. 2007). Germ plasm collections have been evaluated India for resistance to leaf rust and many accessions the resistance cannot be ascribed to any of the known genes (Shiwani and Saini 1993; Saini et al. 1999). Resistance breeding is the most important control strategy, and its success depends on the identification of resistance genes in genotypes.

Foliar blight is an important disease of wheat occurring all over India, perticularly in major wheat-growing regions and ranks close to rust in destructiveness (Directorate of Wheat Research 1999). The disease occurs as a complex in which causal organisms are *Alternaria triticina* and *Bipolaris sorokiniana*. the disease has been observed from initial stage up to growth stage 47 on Zadoks Scale (Zadok et.al. 1974). The dominant pathogen is *A. triticina* and after growth stage 57, *B. sorokiniana* appears and causes significant damage (Chaurasia et al. 2000). A field heavily infected with *Alternaria* blight diseases presents a burnt look and crop loss may be more than 90 percent (Raut et al. 1983).

Materials and methods. Seven bread wheat cultivars were obtained from Directorate of Wheat Research, Karnal (DBW 14, HUW 468, HUW 533,GW 273, PBW 502, DL 788-2, and PBW 443). The material was grown in a randomized block design with three replications at the Research Farm of Janta Vedic College (JVC), Baraut, Baghpat, during rabi season 2005–06. Each genotype was sown in a 3.0-m three-row plot, keeping the plant-to-plant and row-to-row distance of 10 cm and 23 cm, respectively. All recommended agronomic and cultural practices were adopted to ensure a good crop. A total of five straight cross combinations, I (DBW14/HUW468), II (DL788-2/PBW502), III (DBW14/HUW533), IV (GW273/HUW468), and V (PBW443/HUW533) were attempted and sufficient seed was ensured for each cross. The F_1 generations of all five combinations were advanced at Lahaul and Spiti (HP) during summer 2006. In addition, the BC_1 and BC_2 populations of each combination also were obtained in summer nursery. This way, a complete set of breeding material comprising the seven parents, five each of the F_1, F_2, BC_1, and BC_2 generations was obtained and planted along with an infecter row during the rabi season 2006–07 at JVC. The plot size for the parental lines, F_1s, BC_1, and BC_2 was two 2.5-m rows; each F_2 population was grown in 10 2.5-m rows plot. The entire plot was surrounded by one row with an infector cultivar to create epidemic conditions in the plots.

Result and discussion. ***Leaf blight.*** The inheritance of Helminthosporium leaf blight resistance in bread wheat was studied in five crosses that were screened under artificial epidemic conditions by spraying with a spore suspension of a mixture of virulent races. Plants with less than 46 percent of the leaf area infected were considered resistant and those with a greater leaf area infected were considered susceptible. The F_1s of most all the crosses had a susceptible reaction, indicating dominance of susceptibility over resistance. The chi-square analysis test fit a ratio of 3:1 (3 susceptible:1 resistant) plants in the F_2 generations of crosses I and III, suggesting that the susceptible reaction is governed by dominant gene(s). Plants in the F_2 generation of crosses II, IV, and V segregated 15:1 (15 susceptible:1 resistant), suggesting that susceptibility is governed by duplicate gene in the progenies of these crosses (Table 1, p. 36). These findings are similar to those of Narula et al. (1971) and Kulshrestha et al. (1976) who reported that a susceptible reaction was inherited as a dominant gene in bread wheat. Kaur et al. (2003) reported the susceptible reaction is governed by two dominant genes with complementary effect.

Table 1. Segregation in the F_2 generation of five crosses of bread wheat to foliar leaf blight in the field after artificial inoculation. * Significant at 0.05 % level (X^2 value 3.841 at 1 degree of freedom).

Cross combination	Total plants	F2 reaction						
		Observed		Expected		Expected ration	X^2	Gene action
		S	R	S	R			
DBW14/HUW468	60	49	11	45.00	15.00	3:1	1.422*	Dominant
DL788-2/PBW502	60	56	4	56.25	3.75	15:1	0.017*	Duplicate
DBW14/HUW533	60	48	12	45.00	15.00	3:1	0.800*	Dominant
GW273/HUW468	60	56	4	56.25	3.75	15:1	0.017*	Duplicate
PBW443/HUW533	60	57	5	56.25	3.75	15:1	0.445*	Duplicate

Leaf rust. The inheritance of leaf rust resistance in wheat was studied in five crosses that were screened under artificial epidemic conditions by spraying with an aqueous suspension of urediospores of pathotype 77-5. The parents, F_1s, and F_2 generations also were evaluated for disease severity against pathotype 77-5 at adult-plant stage under field conditions. The leaf rust response and severity was recorded in the F_2. The F_1 plants of all the crosses showed a resistant type reaction, indicating dominance of resistance over susceptibility. The chi-square analysis gave a good fit for a 3:1 (3 resistant:1 susceptible) ratio in the F_2 of crosses II, IV, and V, suggesting that resistance is monogenic dominant (Table 2). A 15:1 (15 resistant:1 susceptible) ratio was found in crosses I and III, indicating that resistance in these crosses is governed by duplicate gene(s). Leaf rust is widespread in India. Most of the released cultivars and advanced varietal trial entries are susceptible to the highly virulent pathotype121R63 (Nayar et al. 2001). These findings agree with those of Nayar et al. (1993, 1997), Datta et al. (2004), Basandrai et al. (2004), Haghparast et al. (2004), and Honrao et al. (2004).

Table 2. Segregation in the F_2 generation of five crosses of bread wheat to leaf rust in the field after artificial inoculation with pathotype 77-5. All F_1 plants had a resistant reaction. * Significant at 0.05 % level (X^2 value 3.841 at 1 degree of freedom).

Cross combination	Total plants	F2 reaction						
		Observed		Expected		Expected ration	X^2	Gene action
		S	R	S	R			
DBW14/HUW468	60	56	04	56.25	3.75	15:1	0.018*	Duplicate
DL788-2/PBW502	60	42	18	45.00	15.00	3:1	0.800*	Dominant
DBW14/HUW533	60	46	14	45.00	15.00	3:1	0.087*	Dominant
GW273/HUW468	60	56	06	56.25	3.75	15.:1	1.440*	Duplicate
PBW443/HUW533	60	51	09	45.00	15.00	3:1	3.200*	Dominant

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ITEMS FROM ITALY

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

Behavior of wheat cultivars in organic farming tested at the seedling stage with Stagonospora nodorum.

Angela Iori, A. L'Aurora, and A. Niglio.

The Septoria disease complex is caused by two pathogens, *Phaeosphaeria nodorum* (anamorph *Stagonospora nodorum*) and *Mycosphaerella graminicola* (anamorph *Septoria tritici*) that frequently occur together on the same plant in Italy. Both the fungi attack the epigeous parts of the plant with similar symptoms and can cause quantitative and qualitative damage. *Septoria nodorum* also infects the kernels with damage to the grain. Because *S. nodorum* is a seedbome fungus, infected seed is an important source of primary inoculum and can be a more dangerous vehicle of infection for organic farming than in conventional agriculture.

The agronomic, qualitative, and phytopathological aspects concerning National Organic Network of many cultivars of durum and bread wheat have been studied in Italy for some years (Perenzin et al. 2010; Quaranta et al. 2010, Iori et al. 2010). In 2009–10, data collected from field surveys again showed the prevalence of Septoria disease complex on both durum and bread wheats, confirming an increase in the economic importance of this plant disease already observed in recent years. Data related to naturally acquired diseases were reported by Iori et al. (2010).

Our aim was to analyze the behavior of same wheat cultivars at the seedling stage artificially inoculated with *S. nodorum* in greenhouse that were previously observed in field for Septoria disease complex. Seventeen bread wheat and

20 durum wheat cultivars were tested. Seedlings were grown in greenhouse at 20°C with a 12-hour photoperiod. Artificial inoculations were made using four isolates of *S. nodorum* (Sn 16268, Sn 16271, Sn 16357, and Sn 16165). These isolates were collected from naturally infected durum and bread wheat plants collected in different regions of Italy. The method of isolation and preparation of isolates followed that of Iori and L'Aurora (2010). The fungal suspension was prepared immediately before inoculation at a concentration of 1 x 10^6 conidia/mL plus the addition of Tween 20. For each cultivar, 20 seedlings at the second-leaf stage were inoculated and 20 seedlings were used as noninoculated controls. After inoculation, the seedlings were put in a humidity chamber for 72 hours and then returned to the greenhouse. Disease severity was evaluated at 5, 7, and 10 days on the first leaves using the scale of Liu et al. (2004).

The results of the durum wheat cultivar screening are given in Table 1. All cultivars were resistant to isolate Sn 16268. All cultivars were susceptible to Sn 16271, except Anco Marzio. Claudio, Normanno, and San Carlo were resistant to both bread wheat isolates and one isolate from durum wheat.

The bread wheat cultivars showed a different behavior with the isolates (Table 2). Cultivars Adelaide, Antille, Aubusson, Azzoffe, Bramante, Egizio, PR22R58, Saigemma, and Sirtaki were resistant or moderately resistant to all wheat isolates tested. Only Blasco and Genesi were susceptible or moderately susceptible to the four isolates used. Other bread wheat culitvars showed a behavior ranging from resistant to susceptible with the different isolates.

The *S. nodorum* resistance in bread and durum wheats at the seedling stage is interesting, because some authors reported a high relationship between seedling and field tests (Karyalainen 1986; Wicki et al. 1999; El-Bana and Galal 2007). Consequently, our seedling results inform us about cultivar resistance to *S. nodorum*, which is especially important in organic farming.

Acknowledgements. Cultivars were provided by Dr. M. Perenzin and F. Quaranta from material used in National Organic Networks.

Table 1. Durum wheat cultivars artificially inoculated at the seedling stage with *Stagonospora nodorum* isolates collected from durum (^{D}) and bread (^{W}) wheat leaves. Symptom severity was evaluated using a 0–5 scale (Liu et al. 2004), where 0 = highly resistant; 1 = resistant, 2 = moderately resistant, 3 = moderately susceptible, 4 = susceptible, 5 = highly susceptible, and — = missing data. Average values based on repeated trials are reported.

Cultivar	Sn 16268^D	Sn 16271^D	Sn 16357^W	Sn 16165^W
Anco Marzio	1.0	2.5	3.5	2.2
Ciecio	2.0	3.5	1.5	3.0
Claudio	1.0	4.5	2.5	2.5
Colosseo	2.0	4.0	4.0	4.0
Creso	1.5	4.0	4.0	3.0
Duilio	1.0	3.0	1.5	3.6
Dylan	2.0	3.2	3.0	3.0
Iride	2.0	3.7	4.0	2.5
Karalis	—	3.5	—	2.5
Latinur	1.0	3.0	2.5	3.0
Meridiano	1.5	2.7	0.5	3.0
Neolatino	1.5	3.2	3.0	2.7
Norrnanno	1.0	3.7	1.5	2.5
San Carlo	2.0	3.7	2.5	2.5
Saragolla	1.5	3.7	2.0	3.5
Severo	1.5	3.5	1.5	2.9
Simeto	1.5	4.5	2.5	3.7
Svevo	—	3.7	2.5	3.0
Tirex	2.0	4.0	3.5	3.2
Vinci	1.5	4.5	3.0	3.2

Table 2. Bread wheat cultivars artificially inoculated at the seedling stage with *Stagonospora nodorum* isolates collected from durum (^{D}) and bread (^{W}) wheat leaves. Symptom severity was evaluated using a 0–5 scale (Liu et al. 2004), where 0 = highly resistant; 1 = resistant, 2 = moderately resistant, 3 = moderately susceptible, 4 = susceptible, 5 = highly susceptible, and — = missing data. Average values based on repeated trials are reported.

Cultivar	Sn 16268^D	Sn 16271^D	Sn 16357^W	Sn 16165^W
Adelaide	1.5	2.0	2.0	2.5
Albachiara	3.5	2.0	4.0	3.0
Antille	2.5	2.0	1.5	2.5
Aquilante	1.5	2.5	1.5	4.0
Aubusson	2.0	1.5	1.0	1.0
Azzoffe	2.0	2.5	2.0	2.5
Blasco	3.5	3.0	3.5	4.0
Bolero	3.0	3.5	3.0	2.0
Bramante	0.5	1.0	0.5	2.5
Egizio	0.5	1.5	0.5	2.5
Enesco	2.5	3.0	2.5	2.0
Epidoc	2.5	3.5	3.5	3.0
Genesi	3.0	4.0	4.0	3.5
Lilliput	3.0	3.0	2.0	3.5
PR22R58	2.5	1.0	1.0	2.5
Salgemma	1.5	1.5	1.5	1.0
Sirtaki	1.5	2.0	2.5	2.0

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Effects of Stagonospora nodorum on durum wheat cultivars artificially inoculated in the field.

A. Iori, F. Quaranta, P. Cacciatori, C. Cecchini, C. Cristofori, Mi. Chierico, Ma. Chierico, A. L'Aurora, and M. Foschia.

Phaeosphaeria (syn. *Leptosphaeria*) *nodorum* (E. Müll.) Hedjar (anamorph *Stagonospora* (syn. *Septoria*) *nodorum* (Berck.) Castell. & Germano) is a necrotrophic fungal pathogen that is the causal agent of *Stagonospora nodorum* blotch (SNB) on durum and bread wheat. A widespread disease in various parts of the world, SNB is generally observed every year on wheats in Italy. The first symptoms of fungal attack are chlorotic spots. As the disease develops, oval leaf lesions with a yellow border surrounding the necrotic area appear. Finally, large leaf portions die, damaging the photosynthetic capacity of the plant.

This preliminary study was to assess some characteristics related to the behavior of eight durum wheat cultivars in the field and evaluate the effects of the disease on some quantitative and qualitative traits. Eight durum wheat cultivars were artificially inoculated in field with *S. nodorum* during the 2009–10 crop season using an isolate obtained from a naturally infected plant. The spore suspension (1 x 10^6 conidia/mL) was prepared immediately before use from 7-day-old cultures followed by the addition of Tween 20. The trials were carried out in an experimental field located in Montelibretti (Rome). The cultivars were sown in the field in '1 x 1.5-m' plots replicated twice. The plots were artificially inoculated and a control plot was treated with fungicides. Inoculation was at spike emergence. Inoculated plants were covered for 48 h with a transparent plastic film to retain moisture; a bucket with water also was placed under the plastic. The control plots were sprayed with commercial fungicides (once with Horizon and twice with Folicur). Plots were harvested at maturity. Disease assessments were made considering the percentage of flag leaf and spike area affected by *S. nodorum*. The following qualitative and quantitative traits were analyzed: grain yield, kernel weight, hectoliter weight, protein content, and SDS sedimentation test.

During the first months of 2010, high humidity favored the development of *S. nodorum* and inoculated plants showed significant attacks on both the flag leaf and spike. The highest disease were observed in cultivars Ciccio and Svevo (Table 3). Inoculated samples had lower grain yield, hectoliter weight, and 1,000-kernel weight than the control, but this was not observed in grain yield for cultivars Ciccio and Normanno. The hectoliter weight of Simeto was similar in both inoculated and treated samples. All the inoculated cultivars, with the exception of Dylan, showed 1,000-kernel weight lower than that obtained from the control plots. Grain protein content and SDS sedimentation test, which is related to the gluten strength in durum wheat samples, were higher in inoculated samples compared with the controls. In particular, the protein content of the inoculated samples had an average value of 14.7%, whereas it was 12.7% in the treated controls. The highest protein content was in Creso, and Saragolla had similar values for bothe the inoculated and treated samples. For the SDS sedimentation test, the inoculated samples and treated controls were equal only the cultivar Simeto. The data is summarized in Table 3, p. 40.

Table 3. Effects of *Staganospora nodorum* infection on yield, heading date, plant height, hectoliter weight, 1,000-kernel weight, protein content, and SDS sedimentation test on eight durum wheat cultivars artificially inoculated in field. I = inoculated cultivar, means of duplicate plots; T = treated cultivar; — = missing data.

Cultiar	*S. nodorum* on flag leaf (%)	*S. nodorum* on spike (%)	Grain yield (kg/plot)	Heading date (days after 1 April)	Plant height (cm)	Hecto-liter (kg/hl)	1,000-kernel weight (g)	Protein content (%)	SDS sedimen-tation (mL)
Ciccio I	60	50	0.345	20	72	60.1	38.7	15.8	41
Ciccio T	0	0	0.322	22	65	66.2	41.8	12.5	40
Creso I	60	5	0.299	31	72	69.6	41.7	17.1	42
Creso T	0	0	0.575	31	70	73.8	43.5	12.4	40
Dylan I	50	5	0.479	28	72	71.1	42.3	13.7	48
Dylan T	0	0	0.707	28	75	73.8	40.1	12.6	40
Iride I	60	20	0.636	20	70	70.0	41.6	13.4	47
Iride T	0	0	0.707	21	75	77.5	43.6	12.3	43
Nonnanno I	60	20	0.672	26	75	73.5	40.9	14.7	47
Normanno T	0	0	0.360	27	70	74.6	43.1	10.6	44
Saragolla I	—	—	0.400	19	70	66.8	46.9	13.6	44
Saragolla T	0	0	0.700	20	75	76.5	48.4	13.5	42
Simeto I	50	20	0.338	22	70	67.1	43.2	15.0	41
Simeto T	0	0	0.380	24	70	66.8	49.5	14.1	41
Svevo I	90	90	0.478	19	75	72.0	42.4	14.3	40
Svevo T	0	0	0.649	20	75	77.7	46.4	13.7	32

The results of this study highlight the susceptibility of these cultivars after artificial inoculation with *S. nodorum* at the adult-plant stage. Grain yield, 1,000-kernel weight, and hectoliter weight of the inoculated samples were lower than those of the treated controls, and this is consistent with the expectations (Karialainen and Salovaara 1988; Gilbert and Tekauz 1992; Bhathal et al. 2003). The protein content and SDS sedimentation tests of the inoculated samples weregenerally higher than those of the controls. The highest protein content in the inoculated samples agrees with previous reports that severe infection increases the protein content (Karyalainen and Salovaara 1988). This preliminary study examined some effects of *S. nodorum* infection on durum wheat cultivars grown in an experimental field in Italy. Currently, we are in the second year of field tests, which will allow us to optimize the experimental conditions with a better assessment of the effect of the same pathogen on durum wheat quality.

Acknowledegment. The authors thank Dr. M.G. D'Egidio for his helpful suggestions.

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ITEMS FROM KAZAKHSTAN

KOKSHETAU STATE UNIVERSITY AFTER SH. UALIKHANOV
Abay, 76. Kokshetau 020000, Kazakhstan.

Effect of arsenic on leaf area and content of photosynthetic pigments in plants of the cultivar Omsk–17.

A.S. Kurmanbaeva and N.M. Safronova.

Photosynthetic organisms are highly adaptable to changing environmental conditions because of regulation of the rate of photosynthesis at the genetic, metabolic, anatomic, morphologic, and physiologic levels. All levels of regulation have been intensively studied, however, some aspects of photosynthetic regulation in conditions of heavy metal substrate contamination are poorly understood. We studied the effect of different doses of arsenic on the content of photosynthetic pigments and leaf area unit.

Wheat seeds were sterilized a 16% solution of hydrogen peroxide and germinated in Petri dishes on filter paper moistened with a solution of sodium arsenite at concentrations 12.5 and 25 mg/L. In the control, the filter paper was wetted with distilled water. Leaf area of the wheat seedlings was determined by the linear dimensions of the first leaf (Shcherbina et al. 1985). The content of photosynthetic pigments was determined in the alcoholic extract (Gusev 1982).

Arsenic has a strong effect on leaf surface area. With increasing concentrations of arsenic, the leaf area of 14-day-old seedlings decreased. At 12.5 mg/L, the area of the first leaf was 15% less than that of the control. Increased arsenic concentrations up to 25 mg/L even more significantly effected the formation of the leaf area; decreasing 31% compared to the control.

Chlorophyll determination in the shoots of 14-day wheat seedlings of Omsk-17 shows that an arsenic concentration of 12.5 mg/L insignificantly decreases the amount of chlorophyll (6%) (Fig. 1). At a concentration of 25 mg/L, significant changes are observed. The chlorophyll content decreased by 54% compared with that of the control. The amount of chlorophyll a in the test samples varied depending on the metal concentration. When the concentration of arsenic is 12.5 mg/L there was a slight decrease of 15%. A concentration of 25 mg/L caused a sharp increase in the chlorophyll content of the wheat seedlings, almost seven-fold increase compared with that of the control. Similar results were obtained under the action of elevated concentrations of chromium in algae (Ermazarova 2006).

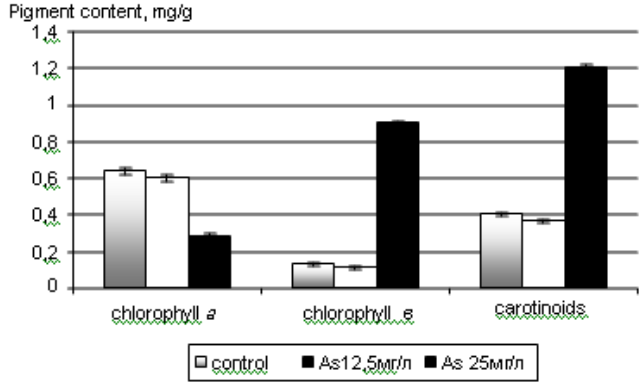

Fig. 1. Pigment content (mg/g) of chlorophyll and carotinoids in leaves of wheat seedlings exposed to arsenic levels of 12.5 and 25 mg/L The control plants were grown in distilled water.

Carotenoid content varied similar to those of chlorophyll. When the concentration of arsenic was 12.5 mg/L, pigments decreased by 7.5%; a concentration of 25 mg/L increased by 3 times. The high concentration of arsenic in the environment, in general, increased the chlorophyll content in leaves of wheat seedlings. Obviously, we can conclude that this is one of the ways plants adapt to extreme environmental factors. As the stress begins to increase, the carotenoids, which also serve as collectors of energy, transfer it to chlorophyll a. Carotenoids protect cells from singlet formation of active oxygen, which has a devastating effect on the organic compounds directly related to cells and chlorophyll.

Perhaps, the long phytotoxic action of arsenic in the plant cell causes a chemical transformation, leading to the formation of oxygen radicals, and an increase in the number of carotenoids is a adaptive response of plants. Changes in

the ratio of photosynthetic pigments in arsenic may be considered an adaptive response of the assimilation apparatus of the wheat seedlings to excess of it in the solution. Thus, arsenic leads to changes in the photosynthetic pigment content resulting in a reduction of chlorophyll a and increased levels of auxiliary chlorophyll and carotenoid pigments.

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ITEMS FROM KENYA

CIMMYT
Nairobi, Kenya

Stem rust resistance screening facilities in Kenya.

Sridhar Bhavani.

National Performance Trials of high-yielding elite lines carrying stem rust resistance and new cultivars in the pipeline. Three lines, selected from the CIMMYT–Kenya shuttle breeding program, were promoted to the National Performance Trials and tested at seven diverse agroecological sites (Njoro, Eldoret, Naivasha, Narok, Rongai, Kitale, and Lanet) distributed over the predominant wheat-growing areas of Kenya. The trials were conducted under the guidelines of the Kenya Plant Health Inspectorate Service, who is the authorized body for national variety testing and release. The 2008–09 data showed that of the three lines, two CIMMYT lines outperformed the check cultivars at a majority of the sites in terms of yield and resistance (Table 1). These lines carry a combination of seedling and APR genes. In addition, these lines were found to be early maturing and produced high-quality grain. The two cultivars, Kenya Robin and Kenya Eagle10, are currently under large-scale multiplication.

Table 1. CIMMYT lines outperforming the check cultivars in the National Performance Trials in Kenya, 2008–09.

Cultivar	Parentage	Level of resistance	Amount of seed for multiplication
Kenya Robin	BABAX/LR42//BABAX*2/3/TUKURU	10MR	20 tons
Kenya Eagle 10	EMB 16/CBRD//CBRD	10MR	20 tons

Evaluation of wheat materials received from different countries against stem rust (Ug99) in Kenya during 2010.

The 2010 off-season screening nurseries accommodated more than 18,000 entries from 16 countries/institutes (Argentina, Australia, Bangladesh, Egypt, France, India, Kazakhstan, Kenya, Pakistan, PR China, South Africa, Tajikistan, Uruguay, the USA, CIMMYT, and ICARDA). Disease development was very good, but a disturbed the soil profile, probably because of land leveling, caused problems in germination and plant development in some areas.

The 2010 main season nursery accommodated over 27,000 entries of which 5,000 entries were winter materials and 3,000 were barley accessions. Samples were sent from 19 countries and institutions (Afghanistan, Australia, Bangladesh, Canada, Ethiopia, India, Iran, Iraq, Israel, Kazakhstan, Kenya, Nepal, Pakistan, PR China, South Africa, Turkey,

the USA, and segregating populations from CIMMYT and ICARDA). The 2010 main season was the best in terms of crop growth, management practices, and disease pressure for screening.

For both seasons, communications/logistics were established with relevant scientists/originators for scoring their material and assistance was provided to collaborating countries for collecting data. Data was recorded, documented, and exchanged timely with the respective collaborators.

Field management strategies and developments at the Kenyan Agricultural Research Institute, Njoro.

Land management. Screening international nurseries was carried out over the last two years had some serious setbacks on leveling and soil fertility. For the nurseries, 14 ha of land, with varying topography and soil profile/maintenance, is used with a land rotation practice of 3 ha each season. The land was split into 10 leveled terraces at a 1.5% slope after developing contour topographical maps to maximize the full potential of the facilities by improving irrigation, germination, and plant growth. The field layout was designed to avoid border effects with deficiencies, and the field was divided in to smaller subplots to accommodate the nurseries

Improving soil fertility. Plot leveling, even though a good practice, damaged by disturbing the top fertile layers (the soil was not deep enough) and led to copper deficiency that resulted in sterility and stunted growth in some areas of the offseason nurseries in 2009. A comprehensive soil analysis was performed to identify and rectify soil deficiencies. An application of lime at 5t/ha and copper-oxychloride at 3 ppm, and cover crop of peas and beans, was advocated in the main season 2010.

Irrigation facilities. Over the years, one persistent problem for screening was irrigation, especially during the offseason, and the irrigation system of the KARI could not meet the demand for the field activities. The entire area now is equipped with a dual-drip and sprinkler irrigation system. A borehole submersible pump dedicated only to this facility was established. A reservoir tank of 1,000 cubes is under construction to store water pumped from underground for periodic drip irrigation during both seasons. After construction and implementation of the reservoir, KARI will have a well-developed irrigation system adequate for 12 ha.

Outcome. These changes had a tremendous impact on the 2010 main season crop growth and establishment. Drips served the purpose in the first week of crop establishment, however plenty of rain ensured good growth and the build up of disease for screening. Several improved practices, such as leveling, drips, soil amendments, and crop rotation, definitely showed a significant impact on main season nursery in 2010

Green house operations. At this stage, the greenhouse is functional. An investment was made to renovate, however additional funds would be needed to keep it operational to meet the demand of several collaborators expressing interest in screening their materials for major genes in the greenhouse. Protocols for in-house screening against Ug99 have been optimized. Close to 1,500 lines have been screened so far, including mapping populations developed at CIMMYT and the Plant Breeding Institute, Sydney, Australia.

Pathogen surveys and race identification. ***Stem rust.*** Apart from the known virulence within the Ug99 lineage (*Sr31*, *Sr24,* and *Sr36* virulent races) no new race(s) have been detected. The predominant race is Ug99+*Sr24* virulence, which is used for screening activities. Isolates collected during surveys are collected and sent to Minnesota for further characterization.

Strip rust. The main season of 2010 experienced a fair amount of natural stripe rust infestation. Samples were sent to Denmark. Mogens report from Denmark suggests that the Kenyan race is unique with virulence to *Yr27*. This aggressive strain has evolved and has acquired virulence for *Yr1*, which needs further confirmation by DNA fingerprinting.

ITEMS FROM MEXICO

CIMMYT — INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER
Molecular Wheat Breeding, El Batan, Mexico.

Susanne Dreisigacker.

Marker-assisted selection in the CIMMYT wheat breeding programs.

Marker-assisted selection (MAS) summary 2010. The number of data points produced to assist phenotypic selection with molecular markers in the CIMMYT wheat breeding programs remained constant in 2010 compared to previous years. During the selection cycles in Cd. Obregon and Toluca, about 28,000 and 18,000 DNA extractions, along with 49,700 and 39,000 marker data points, respectively, were provided. Thus, a total of about 46,000 DNA extractions and 88,700 marker data points were performed in the laboratories in El Batan and Cd. Obregon in 2010. Molecular markers were applied across all breeding programs. In the programs targeted to rain-fed and irrigated environments and the durum wheat and wide crosses program, parental lines to be used for crosses were initially characterized. Markers were subsequently used for allele enrichment in the top cross and F_2 generations in the program targeted to rain-fed environments and durum wheat program during selection. Marker or gene presence was confirmed in the F_3 to F_7 and advanced backcross generations. In the winter wheat program, the 18th FAWWON and various selected sets of germ plasm, e.g., a historical set of winter wheat cultivars, were screened with a subset of markers.

The markers applied in the wheat programs during 2010 are listed in Table 1. Markers linked to rust resistance genes were most frequently used in bread and durum wheat. The amplification of the markers commonly revealed the

Table 1. Markers applied for marker-assisted selection in the bread and durum wheat programs in 2010 at CIMMYT–Mexico.

Gene	Reference	Data points	Gene	Reference	Data points
Bread wheat			**Durum wheat**		
T1A·1R/T1B·1R	Weng et al. 2007	12,050	*Lr19/Sr25*	Zhang et al. 2008	9,059
Lr19/Sr25	William, personal communication	8,318	*Lr14a*	Herrera-Foessil et al. 2008	7,009
Sr26	Liu et al. 2010	3,964	*Lr47*	Dubcovsky et al. 1998	5,249
Rht1, *Rht2*	Ellis et al. 2002	3,720	*Sr22*	Khan et al. 2005	2,905
Cre1	Ogbonnaya et al. 2001	3,547	*Cre1*	Ogbonnaya et al. 2001	1,239
Sr2	Anderson et al. 2001, Spielmayr et al. 2010	3,179	*GPC-B1*	Distelfeld et al. 2006	974
Vrn-A1	Yan et al. 2004	1,772	*Vrn-A1*, *Vrn-B1*	Fu et al. 2005, Yan et al. 2004	704
Ppd-D1	Beales et al. 2007	1,472	*VPM*	Helguera et al 2003	700
Vrn-B1, *Vrn-D1*	Fu et al. 2005, Yan et al. 2004	1,472	*Fhb1*	Liu et al. 2008	500
Lr34	Lagudah et al. 2009	1,472	*Ppd-A1*	Bentley et al. 2010	176
Sr24	Mago et al. 2005	1,297	*Bo1*	Schnurbusch et al. 2007	171
VPM	Helguera et al. 2003	1,297	*Lr53*	Wellings, personal communication	172
Cre3	Martin et al. 2004	1,032	*Rln1*	Mather, personal communication	81
Sr36	Tsilo et al. 2007	1,032			
Sr22	Khan et al. 2005	1,032			
Ppd-A1	Bentley et al. 2010	265			
SrCad	Hiebert et al. 2010	89			

expected results, with some exceptions. Similar to previous years, the marker for *Cre1* showed segregation distortion in various populations. Less individuals than expected were observed containing the tolerance allele for *Cre1*. The comparison of marker data for *Cre1* and phenotypic screening in Turkey furthermore indicated that *Cre1* might not be effective in some Middle East and South Asian countries, which has to be confirmed in subsequent screenings in 2011. When characterizing parental materials, we noticed that the marker for VPM amplified in various synthetic derivatives, which are not expected to have the *Ae. ventricosa* fragment.

New markers – optimization and validation. New markers tested were linked to the genes *Ppd-A1*, *SrCad*, *Sr26*, *Sr2*, *Lr47* (co-dominant marker), and *H25*. For the first time, the marker diagnostic for *Ppd-A1* in durum wheat was tested in germ plasm targeted to rain-fed environments. The *Ppd-A1* allele G105 from durum wheat was confirmed to be present in the CIMMYT germ plasm, introduced via a synthetic hexaploid wheat and its derivatives. The stem rust resistance gene *SrCad* was confirmed in the Canadian sources AC Cadillac, AC Taber, and AC Vista. The gene was not present in a set of CIMMYT germ plasm tested to date. The new CAPS marker for *Sr2* (Spielmayr et al. 2010) was evaluated in the 1st Stem Rust Screening Nursery and germ plasm targeted to irrigated environments. The marker confirmed the presence of the gene in CIMMYT lines, however with exceptions. Examples are the cultivar Siete Cerros, released in 1966, and the Pastor, which were expected to carry *Sr2* but lacked the characteristic SNP detected in Hope. The cultivar Thatcher is not known to carry *Sr2* but amplified the corresponding allele with the CAPS marker. Thus, the marker does coincide with the presumed *Sr2* genotype in various, but not all, cases.

The marker linked to *H25* was used to validate the source of the gene and a set of parents that will be used for crosses in durum wheat. The only marker that could not be successfully optimized is the co-dominant marker for *Lr47*. Amplification was not able to clearly distinguish between lines carrying the genes and heterozygotes. Markers successfully tested will be further validated and subsequently used in the wheat breeding programs.

SNP development.

Gene polymorphisms based on SNP or indels (insertion/delitions) have been converted to 'KASPar' SNP assays, a platform provided by the company KBioscience (http://www.kbioscience.co.uk) in order to move the marker technology at the Batan laboratories from slab gels to a higher throughput platform. SNP assays designed and validated on a larger set of CIMMYT germ plasm are given (Table 2). Primers required for the SNP assay were designed on the basis of available sequence information of the respective genes. Validation was performed with a set of lines known to carry or not carry the genes. SNP assays are to be used for MAS via outsourcing up to 5,000 samples to KBioscience. Outsourcing is expected to increase in 2011.

Table 2. Validated SNP markers with a set of lines known to carry or not carry the gene of interest.

Gene	SNP ID
Lr34	Lr34_TCCIND
Glu-D1	Glu-D1d_SNP
GPC-B1	GPC-B1_DUP
Cre8	Cre8_SNP
Rht-B1	Susan_RhtB1_SNP
Rht-D1	Susan_RhtD1_SNP
Rln1 (DW)	Rlnn1_SNP/1

During the validation of the SNP assays in Batan, a number of advantages of the SNP assays in comparison of the previously used markers were observed. The SNP assays provided marker data three times faster and, based on initial cost analyses, at least two times more cost efficient and under the current conditions of the Batan laboratories. The amplification of the SNPs was simpler and more robust. A unique PCR program was used across all assays, and amplification was more stable with less missing data or weak amplifications. The assays required similar to SSR or STS markers, only standard DNA quality and reactions permitted varying DNA quantity across samples so that no DNA adjustments were required. The design of SNP assays for an additional set of genes was initiated during 2010 (Table 3) and will be validated in 2011.

Table 3. SNP markers under development and validation at CIMMYT-Mexico.

Gene	SNP ID
Fhb1	Fhb1_UMN10_IND
VPM	VPM_SNP
Rln1	Rlnn1_SNP2
Rln1	Rlnn1_SNP3
Glu-A1	Glu-Ax1/x2*_SNP
Glu-A1	Glu-Ax2*_IND
Glu-B1	Glu-Bx17_IND
Glu-B1	Glu-By8_SNP
Glu-B1	Glu-By9_IND
Glu-A3a to *Glu-A3g*	Glu-A3a to GluA3g_SNP
Glu-B3a to *Glu-B3i*	Glu-B3a to GluB3i_SNP
Sr36	STM773-2_IND
Lr19/*Sr25*	WMC221_IND

The design of some SNP assays failed (VPM, PinA, PinB), mainly due to the amplification of primers in one of the nontargeted homologous genomes. The assay development will be repeated for those genes.

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Greenhouse evaluation of germ plasm for reaction to tan spot and Stagonospora nodorum blotch.

Wide-crosses material. Successful evaluation of 86 entries (including four checks) for tan spot was possible and 38 entries were resistant and 48 were susceptible. For *Stagonospora nodorum* blotch, 84 entries (including four checks) were evaluated of which 25 were resistant and 59 were observed to be susceptible. There were nine entries giving resistant reactions to both diseases (Table 4, continued on p. 47).

Table 4. Disease reaction of the most promising breeding lines of the Wide-Crosses and Durum Programs to tan spot (TS) and *Stagonospora nodorum* blotch (SNB) under greenhouse tests.

GID	Cross/name	TS	SNB
Resistant Wide-Crosses Lines			
6002836	GAN/*Ae. tauschii* (408)//2*BERKUT	1.83	1.83
6123554	GAN/*Ae. tauschii* (897)//OPATA/3/BERKUT	1.92	1.69
6123557	GAN/*Ae. tauschii* (897)//OPATA/3/BERKUT	1.92	1.96
6123505	YAV_3/SCO//JO69/CRA/3/YAV79/4/*Ae. tauschii* (498)/5/OPATA/6/PASTOR	1.71	1.99
6123562	GAN/*Ae. tauschii* (897)//Opata/3/BERKUT	1.25	1.50
6123563	GAN/*Ae. tauschii* (897)//Opata/3/BERKUT	1.38	1.50
6123569	YAV_3/SCO//JO69/CRA/3/YAV79/4/*Ae. tauschii* (498)/5/2*OPATA	1.75	1.37
5929330	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/2*INQALAB 91	1.25	1.50
5929356	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/2*INQALAB 91	1.50	1.34
Resistant Durum Lines			
3829630	Svevo	1.85	1.53
5081890	Meridiano	1.72	1.33
5532383	SOOTY_9/RASCON_37//LLARETA INIA	1.72	1.57
5081011	1A.1D 5+10-6/3*MOJO//RCOL/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	1.68	1.40
5545239	GUAYACAN INIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN	1.77	1.71
5546969	CMH83.2578/4/D88059//WARD/YAV79/3/ACO89/5/2*SOOTY_9/ RASCON_37/6/1A.1D 5+10-6/3*MOJO/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)// PLATA_13	1.97	1.90
5541716	SILK_3/DIPPER_6/3/ACO89/DUKEM_4//5*ACO89/4/PLATA_7/ILBOR_1//SOMAT_3	1.88	1.79
5828212	BCRIS/BICUM//LLARETA INIA/3/DUKEM_12/2*RASCON_21/4/1A.1D 5+10-6/2*WB881//1A.1D 5+10-6/3*MOJO/3/BISU_1/PATKA_3	1.83	1.94
5828385	NUS/SULA//5*NUS/4/SULA/RBCE_2/3/HUI//CIT71/CII*2/5/ARMENT//SRN_3/NI-GRIS_4/3/CANELO_9.1	1.88	1.83
5828419	PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBAD/5/AVO/HUI/7/PLATA_13/8/ RAFI97/9/MALMUK_1/SERRATOR_1/10/ARMENT//SRN_3/NIGRIS_4/3/CANE-LO_9.1/11/SHAG_21/DIPPER_2//PATA_2/6/ARAM_7//CREX/ALLA/5/ENTE/ MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69	1.75	1.50
5827254	LLARETA INIA/4/SKEST//HUI/TUB/3/SILVER/5/LHNKE/RASCON//CONA-D/6/ GREEN_32/CHEN_7//SILVER_14/3/DIPPER_2/BUSHEN_3/4/SNITAN	1.42	1.67
5828254	STOT//ALTAR84/ALD/3/THB/CEP7780//2*MUSK_4/6/ECO/CMH76A.722//BIT/3/ ALTAR84/4/AJAIA_2/5/KJOVE_1/7/RASCON_37/2*TARRO_2/4/ROK/FGO//STIL/3/ BISU_1/5/MALMUK_1/SERRATOR_1	1.93	1.63
5828341	ALBIA_1/ALTAR84//YAZI_1/4/CREX//BOY/YAV_1/3/PLATA_6/5/SOMAT_4/IN-TER_8/6/LIRO_2/CANELO_9	1.52	1.53
5828439	ALTAR84/BINTEPE85/3/STOT//ALTAR84/ALD/4/POD_11/YAZI_1/5/ VANRRIKSE_12/SNITAN/6/SOOTY_9/RASCON_37//WODUCK/CHAM_3	1.83	1.92

Table 4. Disease reaction of the most promising breeding lines of the Wide-Crosses and Durum Programs to tan spot (TS) and *Stagonospora nodorum* blotch (SNB) under greenhouse tests.

GID	Cross/name	TS	SNB
6004713	SOMAT_4/INTER_8/4/GODRIN/GUTROS//DUKEM/3/THKNEE_11/5/1A.1D5+10-6/2*WB881//1A.1D 5+10-6/3*MOJO/3/BISU_1/PATKA_3/4/GODRIN/GUTROS//DUKEM/3/THKNEE_11	1.75	1.72
6004721	ODIN_15/WITNEK_1//ISLOM_1/5/TARRO_1/TISOMA_2//TARRO_1/3/COMB-DUCK_2/ALAS//4*COMB DUCK_2/4/SHAG_9/BUTO_17/6/VANRRIKSE_6.2//1A-1D 2+12-5/3*WB881/5/TARRO_1/TISOMA_2//TARRO_1/3/COMBDUCK_2/ALAS//4*COMBDUCK_2/4/SHAG_9/BUTO_17	1.44	1.64
6005034	SWAHEN_2/KIRKI_8//PROZANA_1/4/ADAMAR_15//ALBIA_1/ALTAR 84/3/SNITAN/11/GUAYACANINIA/GUANAY/10/LD357E/2*TC60//JO69/3/FGO/4/GTA/5/SRN_1/6/TOTUS/7/ENTE/MEXI_2//HUI/4/YAV1/3/LD357E/2*TC60//JO69/8/SOM-BRA20/9/JUPAREC 2001	1.62	1.73
6004804	MOHAWK/5/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOMAT_3/4/SOOTY_9/RASCON_37	1.90	1.50
5549135	SNITAN/5/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOMAT_3/4/SOOTY_9/RASCON_37/6/SNITAN	1.42	1.99
5550695	TOPDY_18/FOCHA_1//ALTAR84/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/4/SOMAT_3/GREEN_22/5/VRKS_3/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13	1.76	1.90
6004507	USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV1/6/ARDENTE/7/HUI/YAV79/8/POD9/9/ADAMAR_15//ALBIA_1/ALTAR84/3/SNITAN/10/MINIMUS_6/PLATA_16//IMMER/3/SOOTY_9/RASCON_37	1.92	1.94
6004540	ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/4/TOSKA_26/RASCON_37//SNITAN/5/PLAYERO	1.42	1.85

Durum material. A total of 104 entries (including four checks) were screened for tan spot and 31 entries were resistant and 73 were susceptible. For *Stagonospora nodorum* blotch, a higher proportion of resistance was observed with 63 entries showing resistant reaction and 41 entries susceptible. A total of 22 entries had resistant reactions to both diseases (Table 4, continued on p. 46). Some of the parents of the mapping populations gave differential reaction, so genetic analysis of tan spot and *Stagonospora nodorum* blotch resistance in these populations will be attempted.

Evaluation of germ plasm for reaction to spot blotch.

A total of 1,380 genotypes from the Bread Wheat Irrigated (EPCBWIR09-10, entries = 540), Bread Wheat Rainfed (C29SAWSN, entries = 382), Durum (D10PR-SETHLB, entries = 100), Nepal Program (HLB Resistance Stocks, entries = 100), and 1st CSISA Spot Blotch Trial (entries = 258) were evaluated for reaction to spot blotch under field conditions at Agua Fria. Additionally, inoculum was provided to the Wide Crosses Program to facilitate their efforts in developing spot blotch resistant germ plasm.

Bread Wheat Irrigated Trial. Spot blotch development in the nursery was good and consistent throughout the nursery. Twenty lines were early of which 19 entries were the checks Sonalika (18) and CIANO T 79 (1) and the breeding line 'Fret2*2 / Kukuna*2 / SNLG' (GID: 5993859) that had heading less than 63 days. Normal heading was found in 278 entries and 242 lines had late maturity. The AUDPC scores of this nursery ranged from 302.47 to 1,408.64 with a mean score of 632.38. Based on the selection criteria's from the EPCBWIR nursery, 190 breeding lines have been selected to be evaluated in 2011 in replicated trials. The ten most promising lines are given in the Table 5 (p. 48-49).

Bread Wheat Rainfed Trial. The check Sonalika (seven entries) was only early maturing and had heading less than 63 days. Normal heading was found in 280 entries and 95 lines had late maturity. The AUDPC scores of this nursery ranged from 388.89 to 1,330.86 with a mean score of 623.13. Based on the selection criteria's from the C29SAWSN nursery, 105 breeding lines have been selected to be evaluated in 2011 in replicated trials. The ten most promising lines from this nursery are given in the Table 5 (pp. 48-49).

Table 5. Disease reaction of the ten most promising breeding lines of different nurseries evaluated for spot blotch resistance at Agua Frias, Mexico, in 2010.

GID	Cross/name	AUPDC score
Resistant Bread Wheat Irrigated (EPCBWIR09-10) lines.		
5996123	SHA7/VEE#5//ARIV92/3/PBW343*2/KUKUNA	302.47
5996302	YUNMAI 48/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ	362.96
5849285	TILHI/SOKOLL	371.60
5996303	YUNMAI 48/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ	388.89
5994383	PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR	388.89
5996554	PBW343/PASTOR/4/YAR/*Ae. tauschii* (783)//MILAN/3/BAV92/5/PBW343*2/KUKUNA	406.17
5995752	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/CROC1/*Ae. tauschii* (205)//KAUZ/3/2*KAUZ*2/YACO//KAUZ	406.17
5996837	FRET2/KUKUNA//FRET2/3/YANAC/4/FRET2/KIRITATI	406.17
5996681	NSM*4/14-2/5/2*FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	414.81
5996430	ALTAR84/AE.SQ//OPATA/3/2*WH542/7/VEE#8//JUP/BJY/3/F3.71/TRM/4/BCN/5/KAUZ/6/MILAN/KAUZ/8/ATTILA*2/PBW65	414.81
Resistant Bread Wheat Rainfed (C29SAWSN) lines.		
6000943	SW89-5124*2/FASAN//2*UP262	388.89
6001233	BAV92/SERI	388.89
6001232	BAV92/SERI	401.85
5999827	VORB/4/CROC_1/*Ae. tauschii* (205)//BORL95/3/KENNEDY	406.17
5999832	VORB/4/CROC_1/*Ae. tauschii* (205)//BORL95/3/KENNEDY	406.17
6000906	SOKOLL*2/TROST	406.17
6000909	SOKOLL*2/TROST	406.17
6001064	SOKOLL/TRCH	406.17
6001175	SOKOLL//FRTL/2*PIFED	406.17
5999831	VORB/4/CROC_1/*Ae. tauschii* (205)//BORL95/3/KENNEDY	414.81
Resistant durum (D10PR-SETHLB) lines.		
5828254	STOT//ALTAR84/ALD/3/THB/CEP7780//2*MUSK_4/6/ECO/CMH76A.722//BIT/3/ALTAR84/4/AJAIA_2/5/KJOVE_1/7/RASCON_37/2*TARRO_2/4/ROK/FGO//STIL/3/BISU_1/5/MALMUK1/SERRATOR1	388.89
6005064	ALTAR84/CMH82A.1062//ALTAR84/3/DIPPER/RISSA//ALTAR84/AOS/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/5/MINIMUS/COMBDUCK_2//CHAM_3/3/RCOL/4/YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN	425.62
5081011	1A.1D 5+10-6/3*MOJO//RCOL/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	427.78
6004809	MOHAWK/4/DUKEM_1//PATKA_7/YAZI_1/3/PATKA_7/YAZI_1	427.78
5548129	CAMAYO/GUANAY/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	432.10
5828350	LD357E/2*TC60//JO69/3/FGO/4/GTA/5/SRN_1/6/TOTUS/7/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/8/SOMBRA_20/9/JUPAREC2001/10/SOMAT_3/PHAX_1//TILO_1/LOTUS_4/11/SOOTY_9/RASCON_37//WODUCK/CHAM_3	432.10
6004804	MOHAWK/5/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOMAT_3/4/SOOTY_9/RASCON_37	432.10
6004488	RASCON_37/GREEN_2/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9	434.26
5512003	AG 1-23/2*ACONCHI//2*UC1113	434.26
5543994	TADIZ/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9	436.42
Resistant 1st CSISA Spot Blotch Trial (CSISA) lines.		
911521	CHIRYA.3	303.91
5793174	TILHI/4/CROC_1/*Ae. tauschii* (213)//PGO/3/CMH81.38/2*KAUZ	309.67
5793393	CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/4/TROST	337.04

Table 5. Disease reaction of the ten most promising breeding lines of different nurseries evaluated for spot blotch resistance at Agua Frias, Mexico, in 2010.

GID	Cross/name	AUPDC score
5792804	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/4/KRONSTAD F2004	341.36
5793392	CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/4/TROST	345.68
5792823	PBW343*2/KUKUNA//KRONSTAD F2004/3/PBW343*2/KUKUNA	348.56
5792874	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/5/CNO79//PF70354/MUS/3/PASTOR/4/BAV92	350.00
5793111	TILHI/PALMERIN F2004	352.88
5793110	TILHI/PALMERIN F2004	355.76
5793395	CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/4/TROST	360.08

1st CSISA Spot Blotch Trial. This nursery consisted of 258 entries replicated four times of which three were inoculated with pathogen and the fourth replicate was protected by multiple application of fungicide Opus (epoxiconazole). Spot blotch development in the nursery was good and consistent throughout the nursery. The check Sonalika (three entries) was only early maturing and had heading less than 63 days. Normal heading was noted in 86 entries and 169 lines had late maturity. The AUDPC scores of this nursery ranged from 204.53 to 1,271.81 with a mean score of 520.46. In this nursery, the resistant check Chirya had a mean score of 278.34 and the susceptible check Sonalika had the score of 1,231.00. There was negative correlation (–0.56) between spot blotch AUPDC scores and days-to-heading. Based on the rigorous selection criteria from the CSISA nursery. 50 breeding lines have been selected to be send across different location worldwide and evaluated in 2012. Presently, the selected lines are being increased at Mexicali to be forming the 2nd CSISA Spot Blotch Nursery. The most promising ten lines from this nursery are given in Table 5 (pp. 48-49).

Septoria tritici blotch research.

Field screening of germ plasm for resistance to *Septoria tritici* blotch. A total of 243 genotypes from the Bread Wheat-Irrigated (BWIR: 115 entries) and the Bread Wheat Rainfed (BWR: 128 entries) Program were evaluated for reaction to *Septoria tritici* blotch at two locations, Toluca and Boximo. At each location there was a randomized block design with two replicates. The disease assessment utilized a double-digit scale and multiple evaluations were conducted, which were later used to develop AUPDC score.

The development of *Septoria tritici* blotch at both the locations was similar. For the BWIR nursery, the range of *Septoria tritici* blotch AUDPC scores (mean of all reps/location) was between 201.81 and 993.43 with a mean score of 397.97. From this nursery, 50 lines were selected based on AUDPC scores and pedigree information, which may be part of the ISEPTON nursery. The most promising genotypes identified from this nursery are listed in Table 6 (p. 50). For the BWR nursery, the range of *Septoria tritici* blotch AUDPC scores (mean of all reps/location) was between 168.52 and 358.64 with a mean score of 291.13. From this nursery, 40 lines were selected that may be part of the ISEPTON nursery. The most promising genotypes identified from this nursery are listed in Table 6 (p. 50).

20th International Septoria Observation Nursery. The 20th International Septoria Observation Nursery (20th ISEPTON) comprised of 53 entries of genetically diverse genotypes was distributed to Ethiopia, Iran, Mexico, Morrocco, Syria, Tunisia, and Uruguay (20 sets). The genotypes were selected based on low *Septoria tritici* blotch scores and availability of seed.

Greenhouse screening protocol for *Septoria tritici* blotch. Two experiments were conducted to develop protocols for induction of *Septoria tritici* blotch under greenhouse conditions. Each experiment was conducted as a randomized block design with two replicates. Each replicate consisted of five genotypes with known reaction to *Septoria tritici* blotch (Table 7, p. 50). The experimental unit consisted of five plants/entry that were planted in big pots. The planting was done on 24 August.

Inoculation for the first experiment was on 8 October. Inoculum was made from isolate P8. Spore inoculum from isolate P8 was made by culturing the fungus on medium of agar, malt, and levadura (4 g extract of levadura, 4 g extract of malt, 4 g sacarosa, 15 g agar, and 1,000 mL distilled water). The prepared medium with isolate P8 was left for

Table 6. Disease reaction of the ten most promising breeding lines from Bread Wheat-Irrigated (BWIR) and the Bread Wheat Rainfed (BWR) Programs to Septoria tritici blotch under field tests at Boximo and Toluca, Mexico.

GID	Genotype	AUPDC score
Resistant BWIR lines.		
5849246	CHEN/*Ae. tauschii* (TAUS)//BCN/3/BAV92/4/INQALAB 91*2/KUKUNA	201.81
5995732	WBLL1*2/VIVITSI/4/D67.2/P66.270//*Ae. tauschii* (320)/3/CUNNINGHAM	217.17
5996488	BABAX/LR43//BABAX/6/MOR/VEE#5//DUCULA/3/DUCULA/4/MILAN/5/BAU/MILAN/7/SKAUZ/BAV92	217.81
5995748	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/CROC_1/*Ae. tauschii* (205)//KAUZ/3/2*KAUZ*2/YACO//KAUZ	218.45
5996074	MILAN/PASTOR/3/C80.1/3*BATAVIA//2*WBLL1	224.93
5996189	THB/KEA//PF85487/3/DUCULA/4/WBLL1*2/TUKURU	244.88
5995992	CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/WEAVER/5/2*KAUZ/6/TIMBA	245.46
5996796	UP2338/3/HE1/3*CNO79//2*SERI/4/RABE/2*MO88	257.58
5994285	PBW343*2/KUKUNA*2//YANAC	264.26
5996195	THB/KEA//PF85487/3/DUCULA/4/WBLL1*2/TUKURU	266.22
Resistant BWR lines.		
5999769	BABAX/LR42//BABAX/3/VORB	168.52
5999771	BABAX/LR42//BABAX/3/VORB	172.84
5999774	BABAX/LR42//BABAX/3/VORB	183.64
5999775	BABAX/LR42//BABAX/3/VORB	183.64
5999807	VORB/4/D67.2/P66.270//*Ae. tauschii* (320)/3/CUNNINGHAM	199.85
5999926	PROINTA SUPERIOR/4/RL6043/4*NAC//PASTOR/3/BAV92/5/KLEIN SAGITARIO	207.41
5999956	POTCH 92/2*ROLF07	209.57
5999957	POTCH 92/2*ROLF07	225.77
5999970	POTCH 93/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92	231.17
5999972	ACHTAR*3//KANZ/KS85-8-5/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92	235.49

3 days for incubation at room temperature (18–22ºC). The spores were harvested and a spore suspension prepared at a concentration of 10^7 conidia/mL. The plants were spray inoculated until run-off. Inoculated plants were left in a mist-chamber for 48 hours with continuous misting. Subsequently, the humidifiers were turned off, plants were left to dry, and then the plants were put in GH8 at a temperature of 18ºC min and 28ºC max. In the second experiment inoculation was on 29 October with isolate ST2. The rest of the protocol was similar to that in the first experiment. Disease evaluation was based on percentage of *Septoria tritici* blotch infection.

Murga, a known source of resistance gave no disease symptoms in both the experiments, whereas the other lines with moderate to high susceptibility to *Septoria tritici* blotch gave disease symptoms as expected (Table 7). More disease was observed in first experiment then the second experiment, indicating that plant age may play role in disease development. Additionally, differences in the development of disease in the two experiments can be attributed to the two isolates used and the greenhouse temperature; temperatures were a bit lower in the second experiment. However, we were able to induce *Septoria tritici* blotch under greenhouse conditions for the first time at the Main Station. The challenge now lies in optimizing and further reducing the time taken in evaluating the disease in greenhouse conditions.

Table 7. Percent infection of *Septoria tritici* blotch on the five lines evaluated under greenhouse conditions at El Batan, Mexico, in 2010.

Line	First experiment		Second experiment	
	1 November	8 November	16 November	22 November
HPO/TAN/VEE/3/2*PGO/4/Milan/5/5Seri 1	20	50	10	40
SAAR//PBW343*2/Kukuna/3/PBW343*2/Kukuna	50	70	10	50
Kauz//Altar 84/Aus/3/Milan/Kauz/4/Avites	20	50	20	50
Catbird	40	50	10	40

Fusarium head blight research.

High-throughput field screening operations at El Batan, Mexico. A total of 1.8 ha was planted at El Batan, Mexico, in mid-May 2010 to screen wheat and barley material under artificial field inoculation for FHB. Plots were inoculated with the help of precision CO_2 backpack sprayers equipped with a flat fan nozzle for liquid inoculum (50,000 conidia/mL) at a pressure of 40 psi and a rate of 39 mL of inoculum/m. The inoculum was of a mixture of five different *F. graminearum* isolates collected during the preceding year in naturally infected fields. Ten spikes/plot were tagged and spray inoculated at anthesis. The inoculation is repeated 2 days later. A programmable misting system maintains a humid microclimate, which is favorable for the disease development.

For preliminary material screened for the first time, only the absolute number of infected spikelets/spike was evaluated, and the average number of infected spikelets for all ten spikes calculated. For advanced material in replicated trials in the second and third year of screening, the percent of infected spikelets/spike was evaluated by counting the number of infected spikelets and the total number of spikelets for each spike. Subsequently, the FHB index was calculated using the following formula:

$$\text{FHB index (\%)} = \frac{\text{Severity}}{\text{Incidence}}$$

where severity = the average severity of all spikes that show infection (totally healthy spikes are not considered for calculation of severity) and incidence = the percent of spikes that show infection.

The difference in evaluation methods between the preliminary and advanced material is due to the fact that the number of preliminary materials is much higher than the number of advanced materials. Assessing FHB resistance for the preliminary materials would be too labor- and time-intensive. On the other hand, a difference only between 'resistant' and 'susceptible' for first year material proved not to be valuable, because it does not take into account that resistance to FHB is a quantitative trait. The evaluation of the absolute number of infected spikelets/spike (regardless the total number of spikelets) was found to be the middle ground between these two approaches.

In addition to the candidates and entries of the international nurseries and mapping populations, F_3- and F_4-derived head rows also were planted, which had been spaced planted in Obregón to select for agronomic type. This research is a significant contribution of the Fusarium program in resistance breeding efforts for FHB and how the information generated in former years aids the development of new promising lines.

Bread wheat lines for irrigated areas: Results of PCFusarium White and Red Grain Nursery. A total of 290 entries from the PCFusarium White Grain (1,076 entries) and PCFusarium Red Grain (246 entries) nurseries planted in 2009 were selected, assembled in the PCFusarium White and Red Grain Nursery (PCFusWGyRG), and tested again in the summer of 2010 at El Batan in replicated trials. Entries with FHB indices below 11 % are shown in Table 8 (pp. 51-54).

Interestingly, despite the normally lower levels of resistance for white-grained material, relatively high levels of resistance in terms of disease symptoms (FHB index) and mycotoxin contamination were observed for these types in this trial. This demonstrates that white-grained bread wheats with levels of resistance similar to that of red-grained materials are available, which is a breakthrough in bread wheat breeding.

Table 8. White- (W) and red-grained (R) bread wheat genotypes for irrigated areas in the PC Fusarium White and Red Grain Nursery tested for the 2nd year in the summer of 2010 and results of FHB index and DON contamination.

CID	GID	Cross	Grain color	FHB index (%)	DON (ppm)
4965	10004	Sumai #3 (resistant check)		1.7	0.5
520956	6123270	FN/2*mazar 99//GONDO/TNMU/3/FRANCOLIN #1	W	3.0	0.9
516901	6123192	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	3.6	2.3
516852	6122669	PFAU/WEAVER*2//BRAMBLING/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/PFAU/WEAVER//BRAMBLING	R	3.9	1.9
516093	6121931	HPO/TAN//VEE/3/2*PGO/4/MILAN/5/SSERI1/6/GONDO	W	4.1	1.3

Table 8. White- (W) and red-grained (R) bread wheat genotypes for irrigated areas in the PC Fusarium White and Red Grain Nursery tested for the 2nd year in the summer of 2010 and results of FHB index and DON contamination.

CID	GID	Cross	Grain color	FHB index (%)	DON (ppm)
520950	6123240	SHA3/CBRD//TNMU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	4.1	4.4
516901	6123199	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	4.4	2.0
516068	6123620	CBRD/FILIN	R	4.9	1.8
520950	6123246	SHA3/CBRD//TNMU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	R	5.0	1.4
516900	6123179	PBW343/mazar 99*2/6/TURACO/5/CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC	W	5.0	2.3
120634	2589783	Heilo (moderate resistant check)		5.4	1.7
516775	6122143	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/mazar99/7/CHUM18/BORL95//CBRD/8/CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/mazar 99	W	5.5	6.0
516068	6123635	CBRD/FILIN	R	5.7	0.8
516068	6123623	CBRD/FILIN	R	6.3	1.3
516772	6122128	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES/5/CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	6.4	7.0
516852	6122665	PFAU/WEAVER*2//BRAMBLING/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/PFAU/WEAVER//BRAMBLING	R	6.7	1.5
516852	6122662	PFAU/WEAVER*2//BRAMBLING/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/PFAU/WEAVER//BRAMBLING	R	6.8	2.3
516852	6122658	PFAU/WEAVER*2//BRAMBLING/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/PFAU/WEAVER//BRAMBLING	W	6.8	1.8
516104	6122002	WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/5/GONDO	W	6.8	3.4
516901	6123187	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	6.9	1.3
516874	6122758	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES/5/SHA3/SERI//SHA4/LIRA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	R	7.0	0.8
516844	6122610	WBLL1/FRET2//mazar 99/3/SHA3/SERI//SHA4/LIRA/4/WBLL1/TACUPETO F2001//mazar 99	R	7.0	2.8
520950	6123245	SHA3/CBRD//TNMU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	R	7.1	2.8
520964	6123343	HEILO/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)/8/VORB/FISCAL	R	7.2	1.7
516772	6122127	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES/5/CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	7.3	5.9
516901	6123188	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	7.3	1.9
516901	6123191	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	7.4	3.1
516068	6123629	CBRD/FILIN	R	7.7	1.0
516068	6123617	CBRD/FILIN	R	7.8	0.7
520950	6123242	SHA3/CBRD//TNMU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	R	7.9	2.7
516775	6122145	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/mazar99/7/CHUM18/BORL95//CBRD/8/CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/mazar 99	W	8.0	3.8

Table 8. White- (W) and red-grained (R) bread wheat genotypes for irrigated areas in the PC Fusarium White and Red Grain Nursery tested for the 2nd year in the summer of 2010 and results of FHB index and DON contamination.

CID	GID	Cross	Grain color	FHB index (%)	DON (ppm)
520949	6123236	NG8675/CBRD/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/WBLL1*2/CHAPIO	R	8.1	1.0
516068	6123625	CBRD/FILIN	R	8.1	1.6
516772	6122129	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES/5/CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	8.1	2.5
516901	6123186	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	8.3	1.5
516871	6122748	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES*2/5/CHIL/CHUM18	W	8.3	9.8
516068	6123628	CBRD/FILIN	R	8.3	1.4
516843	6122590	WBLL1/FRET2//mazar 99*2/3/GONDO	W	8.4	1.7
516070	6123660	CHIL/CHUM18//GONDO	R	8.6	1.5
516871	6122741	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES*2/5/CHIL/CHUM18	W	8.6	9.5
516901	6123193	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	8.7	1.0
516901	6123195	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	8.7	1.7
516901	6123189	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	8.7	0.7
516901	6123196	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	8.9	0.8
520950	6123247	SHA3/CBRD//TNMU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	R	8.9	2.0
516772	6122123	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES/5/CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	8.9	2.0
520949	6123231	NG8675/CBRD/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/WBLL1*2/CHAPIO	R	9.0	2.3
516900	6123185	PBW343/mazar 99*2/6/TURACO/5/CHIR3/4/SIREN//ALTAR 84/*Ae. tauschii* (205)/3/3*BUC	R	9.0	1.4
516776	6122173	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/mazar99*2/7/CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/WEAVER/5/2*mazar 99	W	9.1	4.3
516852	6122654	PFAU/WEAVER*2//BRAMBLING/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/PFAU/WEAVER//BRAMBLING	W	9.2	3.6
516070	6123661	CHIL/CHUM18//GONDO	R	9.2	2.7
520949	6123235	NG8675/CBRD/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/WBLL1*2/CHAPIO	R	9.3	0.9
516107	6122040	WBLL1*2/KURUKU//HEILO	W	9.4	2.5
516772	6122104	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES/5/CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	9.5	7.9
516901	6123200	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	R	9.6	0.9
516068	6123630	CBRD/FILIN	R	9.6	1.6
516901	6123198	PBW343/mazar 99*2/3/WUH1/VEE#5//CBRD	W	9.6	1.4
516789	6122272	WAXWING/KIRITATI*2/3/SHA3/SERI//SHA4/LIRA	R	9.6	4.0
516068	6123634	CBRD/FILIN	R	9.9	1.4
520948	6123221	CHIL/CHUM18//GONDO/3/WBLL1*2/KURUKU	R	10.0	2.1
520956	6123283	FN/2*mazar 99//GONDO/TNMU/3/FRANCOLIN #1	R	10.0	2.3
520947	6123209	CHIL/CHUM18//FN/2*mazar 99/3/PRL/2*mazar 99	R	10.1	2.5

Table 8. White- (W) and red-grained (R) bread wheat genotypes for irrigated areas in the PC Fusarium White and Red Grain Nursery tested for the 2nd year in the summer of 2010 and results of FHB index and DON contamination.

CID	GID	Cross	Grain color	FHB index (%)	DON (ppm)
516852	6122657	PFAU/WEAVER*2//BRAMBLING/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)/8/PFAU/WEAVER//BRAMBLING	W	10.1	3.3
516107	6122042	WBLL1*2/KURUKU//HEILO	W	10.1	2.7
516068	6123616	CBRD/FILIN	R	10.2	1.1
516883	6123013	PRINIA/PASTOR//CHIL/CHUM18/3/PRINIA/PASTOR	R	10.4	1.2
516772	6122097	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES/5/CROC_1/*Ae. tauschii* (205)//KAUZ/3/SASIA/6/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	W	10.4	3.8
520974	6123365	KAUZ/mazar 99//PBW343*2/3/HEILO	W	10.4	1.8
520950	6123243	SHA3/CBRD//TNMU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	R	10.5	2.9
516871	6122746	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES*2/5/CHIL/CHUM18	W	10.7	4.8
520949	6123229	NG8675/CBRD/7/IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)/8/WBLL1*2/CHAPIO	W	10.7	3.3
516883	6123007	PRINIA/PASTOR//CHIL/CHUM18/3/PRINIA/PASTOR	W	10.7	2.5
516098	6121958	KAUZ/mazar 99//PBW343/3/HEILO	W	10.7	2.9
516093	6121935	HPO/TAN//VEE/3/2*PGO/4/MILAN/5/SSERI1/6/GONDO	W	10.8	2.4
516070	6121915	CHIL/CHUM18//GONDO	W	10.9	2.5
516068	6123631	CBRD/FILIN	R	10.9	2.9
1860	5536	GAMENYA (susceptible check)		92.5	8.1

Bread wheat for marginal areas: Results of the 27th Semi-Arid Wheat Screening Nursery (SAWSN) and 20th High Rainfall Wheat Screening Nursery (HRWSN). The 27th SAWSN and the 20th HRWSN were tested again in the 2010 summer cycle in El Batan. Entries with an FHB index less than 20% (27th SAWSN) and 18% (20th HRWSN) also were tested for DON contamination (Table 9, continued on p. 55, and Table 10, pp. 55-56).

Table 9. Bread wheat genotypes for marginal areas from the 27th Semi-Arid Wheat Screening Nursery tested for the 2nd year in the summer of 2010 and results of Fusarium head blight (FHB) index and DON contamination.

CID	GID	Cross	FHB index (%)	DON (ppm)
4965	10004	SUMAI #3	0.5	2.8
120634	2589783	HEILO	5.3	2.7
450346	5427852	SW94.2690/SUNCO	11.5	2.2
279807	3855011	VOROBEY	12.9	4.2
450346	5427842	SW94.2690/SUNCO	13.1	3.7
450352	5427939	VEE/MJI//2*TUI/3/mazar 99/4/BERKUT	13.2	3.1
473247	5435908	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	13.3	2.1
450346	5427849	SW94.2690/SUNCO	13.5	2.8
437257	5423751	OASIS//TC14/2*SPER/3/ATTILA/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA	13.5	3.7
452364	5428200	PASTOR/4/WEAVER/TSC//WEAVER/3/WEAVER/5/URES/PRL//BAV92	13.9	3.6
454534	5428538	*T. dicoccon* PI94625/*Ae. tauschii* (372)//3*PASTOR	14.3	3.1
450346	5427856	SW94.2690/SUNCO	14.6	3.9
450352	5427940	VEE/MJI//2*TUI/3/mazar 99/4/BERKUT	14.7	2.0

Table 9. Bread wheat genotypes for marginal areas from the 27th Semi-Arid Wheat Screening Nursery tested for the 2nd year in the summer of 2010 and results of Fusarium head blight (FHB) index and DON contamination.

CID	GID	Cross	FHB index (%)	DON (ppm)
427650	5422808	OASIS//TC14/2*SPER/3/ATTILA/4/WBLL4	15.0	2.7
437245	5423717	A93324S.7197.29/4/KAUZ//ALTAR 84/AOS/3/KAUZ/5/PASTOR	16.2	4.3
450356	5427957	FILIN/3/CROC_1/*Ae. tauschii* (205)//KAUZ/4/FILIN/5/VEE/MJI//2*TUI/3/ mazar 99	16.5	3.7
450355	5427955	BERKUT/3/ATTILA*2//CHIL/BUC	16.7	3.2
437240	5423682	TAN//TEMPORALERA M 87/AGR/3/FRET2/4/URES/PRL//BAV92	17.1	4.9
435275	5423325	BABAX/LR42//BABAX/3/ER2000	17.3	4.8
473281	5436044	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN	17.9	5.8
472868	5435731	SOKOLL/3/PASTOR//HXL7573/2*BAU	18.2	4.5
452470	5428491	PASTOR//HXL7573/2*BAU/3/CMH82.575/CMH82.801	18.3	3.5
437257	5423741	OASIS//TC14/2*SPER/3/ATTILA/10/ATTILA*2/9/KT/BAGE//FN/U/3/ BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA	18.4	2.2
454534	5428531	*T. dicoccon* PI94625/*Ae. tauschii* (372)//3*PASTOR	18.4	3.2
460356	5429403	PASTOR//HXL7573/2*BAU/3/WBLL1	19.1	5.8
435388	5423482	MILAN/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/ SERI/7/VEE#10/8/OPATA	19.5	1.4
1860	5536	GAMENYA	60.3	0.2

Table 10. Bread wheat genotypes for marginal areas from the 20th High Rainfall Wheat Screening Nursery tested for the 2nd year in the summer of 2010 and results of Fusarium head blight (FHB) index and DON contamination.

CID	GID	Cross	FHB index (%)	DON (ppm)
4965	10004	Sumai #3 (resistant check)	0.5	0.3
4749	9774	Shanghai #8	4.1	0.9
451641	5685994	NING MAI 96035/FINSI//HEILO	5.3	2.8
120634	2589783	Heilo (moderate resistant check)	6.2	1.6
442354	5686022	ATTILA/HEILO	6.9	1.1
451641	5685999	NING MAI 96035/FINSI//HEILO	7.3	2.5
442354	5686027	ATTILA/HEILO	9.0	0.9
475170	5685928	CPI8/GEDIZ/3/GOO//ALB/CRA/4/*Ae. tauschii* (208)/5/ HAHN/2*WEAVER/6/SKAUZ/BAV92	9.7	2.6
444320	5686059	BURI/JARU//METSO	9.8	2.4
442354	5686023	ATTILA/HEILO	10.4	2.3
480883	5551988	WAXWING//PFAU/WEAVER	12.6	3.0
451641	5685998	NING MAI 96035/FINSI//HEILO	12.6	3.3
279807	3855011	VOROBEY	13.2	3.1
442354	5686025	ATTILA/HEILO	13.3	2.1
451641	5686001	NING MAI 96035/FINSI//HEILO	13.6	2.1
475170	5685929	CPI8/GEDIZ/3/GOO//ALB/CRA/4/*Ae. tauschii* (208)/5/ HAHN/2*WEAVER/6/SKAUZ/BAV92	16.1	2.6
476919	5535312	ND643//2*PRL/2*mazar 99	16.4	3.0
448397	5398611	BABAX/LR42//BABAX*2/3/KURUKU	17.3	3.5
444913	3826276	FUNDACEP 30	17.4	1.2

Table 10. Bread wheat genotypes for marginal areas from the 20th High Rainfall Wheat Screening Nursery tested for the 2nd year in the summer of 2010 and results of Fusarium head blight (FHB) index and DON contamination.

CID	GID	Cross	FHB index (%)	DON (ppm)
451809	5685991	IAS58/4/KAL/BB//CJ71/3/ALD/5/CNR/6/THB/CEP7780/7/TNMU/8/ METSO	17.5	3.0
475170	5685927	CPI8/GEDIZ/3/GOO//ALB/CRA/4/*Ae. tauschii* (208)/5/ HAHN/2*WEAVER/6/SKAUZ/BAV92	17.9	2.4
451641	5685996	NING MAI 96035/FINSI//HEILO	17.9	2.9
1860	5536	GAMENYA (susceptible check)	64.2	4.9

Wheat blast caused by Magnaporthe grisea.

Defining disease prone climatic conditions and wheat blast risk assessment. Wheat blast or 'brusone', induced by *Magnaporthe grisea*, infects the spikes of wheat grown in subtropical climates. The disease has been recorded in the wheat cropping areas of Brazil since the mid 1980s and occurs in similar climatic conditions in Paraguay and Bolivia. No reports exist on the occurrence of wheat blast outside South America. Damage potential is high and can account for 10 to 100% crop losses. Control of the disease is limited by lack of effective fungicide spray schemes and resistant cultivars. This study estimated the potential risk of wheat blast to occur in other wheat-growing areas in the world based on a climate similarity approach. The assessment was based on categorizing blast sites in South America for moderate and high disease severity levels and their corresponding climate profiles. Climate similarity with wheat production areas in nontraditional, warmer areas on other continents was derived from the Worldclim database considering the coolest quarter in which wheat is grown and similarity comparisons with the areas of cultivation in the northern hemisphere were drawn from the warmest quarter of the year.

Our preliminary analysis revealed areas of wheat blast risk in significant parts of central India, Bangladesh, and parts of Ethiopia. The wheat-growing regions in South Africa or Australia did not match with the blast climate profile. Similarity also was identified with large areas of wheat production in the northern hemisphere, Eurasia, and North America. However, determining the similarity of sites using the Homologue software showed that northern Eurasia and North America did not match a year-round climate comparison with areas in South America where brusone is known to occur. Areas generally at the border of wheat-growing areas in the Indian subcontinent and in parts of Africa show a 40–60% to 60–80% similarity with affected areas in South America underlining that risk of wheat blast pathogen survival exists. From the limited knowledge available from the wheat blast pathogen, its survival in the cool or cold season is unlikely, diminishing the current risk of wheat blast in production zones of the northern hemisphere.

The first international workshop on wheat blast held in Passo Fundo, Brazil.

To address wheat blast or 'brusone', which is responsible for 5–100% of wheat yield losses in regions of South America and has the potential to spread to other countries, the 'Wheat blast: A potential threat to global wheat production" workshop was held in Passo Fundo, Brazil, 3-5 May, 2010, followed by a field visit to the Brasilia region. The workshop was organized by Embrapa Wheat, Embrapa Cerrados, and CIMMYT with the support of the project to ensure a participation of scientists from national programs besides Brazil. The workshop was attended by representatives from 11 countries. Wheat blast was identified for the first time in 1985 in the State of Paraná in southern Brazil, from where it quickly spread to neighboring countries. Four years later, blast caused serious damage (40–100%) in the wheat fields of Paraguay. In the lowlands of Bolivia, it was responsible for a loss of 90,000 ha of wheat between 1997 and 2000. In 2007, the disease was seen in summer-sown experimental wheat trials in Chaco, Argentina, and although researchers in Uruguay have not observed the disease in wheat, they have found the fungus on barley. The 2009 outbreak cut Brazilian wheat production by up to 30%.

Of great concern is that chemical control of wheat blast may not be working. Some farmers are using four fungicide applications with no results, which suggests the current chemicals are not effective against the fungus or are not properly applied. To date, resistant cultivars are unavailable and only limited tolerance can be found. Climate

change is adding to the problem. 'A more hot and humid climate favors fungal diseases such as wheat blast, which needs high temperatures of about 24–28°C and long periods of rain to occur,' explained researcher Gisele Torres of Embrapa Wheat. Changes in rainfall may create environmental conditions favorable to wheat blast in other parts of the world such as South Asia or Africa and was the main reason for inviting researchers from different wheat-producing countries on several continents to discuss wheat blast in Brazil.

The most important diseases that affect wheat production worldwide are leaf rust (5 x 10^6 ha), tan spot (4.5 x 10^6 ha), and Fusarium (4 x 10^6 ha). 'So far, new diseases like wheat blast in South America have been limited to a few countries,' said Man Mohan Kohli, ex-CIMMYT researcher once posted in South America. 'Similarly, the distribution of the stem rust Ug99 in Africa has been limited, but has been the object of studies by several research institutes around the world.' Efforts to improve wheat resistance to Ug99 and to reduce the risk of its spread to other countries show how international collaborative research and investment facilitates scientific response to new virulent pathotypes, or races of pathogens, that could become potentially devastating. Researchers from the following institutions participated in the workshop, which was supported by EMBRAPA and BMZ (Germany): Göttingen University (Germany), Kansas State University (United States), CIRAD (France), CIAT (Bolivia), INTA (Argentina), INIA (Uruguay), CIMMYT (Mexico), USDA/ARS (United States), MAG/ DIA (Paraguay), and Wageningen University (Netherlands), as well as Brazil Embrapa Cerrados, Embrapa Wheat, Embrapa Labex Europa, BIOTRIGO, COODETEC, FUNDACEP, UPF, UNESP, and Fapa/Agrária.

Safe movement of germ plasm.

The project 'Safe movement of germ plasm' was concluded in March 2010. Recommendations for 15 crops under the CGIAR mandate were published on line as part of the SGRP GPG2 Knowledge Portal. We corresponded with all CGIAR centers scientists working on seed crops to obtain the technical information on import/export permits, technical guidelines, and best practices in seed health for all CGIAR mandate seed crops. We revised and edited the materials receive from other centers. Please consult http://cropgenebank.sgrp.cgiar.org.

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NATIONAL INSTITUTE FOR FORESTRY, AGRICULTURE, AND LIVESTOCK RESEARCH (INIFAP–CIRNO)

Campo Experimental Valle del Yaqui, Apdo. Postal 155, km 12 Norman E. Borlaug, entre 800 y 900, Valle del Yaqui, Cd. Obregón, Sonora, México CP 85000.

Identification of genes of agricultural importance in bread wheats for the state of Sonora, Mexico.

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Introduction. Southern Sonora is characterized by having a large area sown with irrigated wheat every year. Farmers, through their economic contributions to agricultural research, demand wheats with high yield potential, quality, and

resistance to diseases; however, leaf rust caused by *Puccinia triticina* Eriks. is an endemic and highly destructive disease in this region. The pathogen has the capacity to mutate (Rajaram and Campos 1974), and multiply rapidly (Singh et al. 2001). A severe infection reduces the photosynthetic area, there is water loss which debilitates the radical system, plant growth stops, kernels are shriveled, and the plant may die (Roelfs 1978). This disease is the main cause of cultivar replacement and the increase in the use of fungicides making the wheat crop less profitable. A more recent threat to the wheat crop is the TTKS or Ug99, a variant of stem rust. Although there is no records of its presence in the American continent, research has been intensified looking for resistance genes for this and other diseases.

Materials and methods. Experimental plots were established at the Norman E. Borlaug Experimental Station, which belongs to the Northwest Regional Research Center of the National Institute for Forestry, Agriculture and Livestock Research (CENEB-CIRNO-INIFAP), during the crop season autuman–winter 2009–10. The station is located in block 910 of the Yaqui Valley at 27°22' latitude north and 109°55' longitude west, 37 masl. Seven commercial cultivars released by INIFAP were evaluated (Onavas F2009, Tepahui F2009, Villa Juarez F2009, Navojoa M2007, Roelfs F2007, Kronstad F2004, and Tacupeto F2001), as well as 29 advanced lines from the CIMMYT bread wheat breeding program, for the presence of genes *Lr34*, *Sr22*, *Sr24*, *Sr26*, and *Sr36* (Table 1, continued on p. 60). DNA was extracted from plant material following the method described by Saghai-Maroof et al. (1984). PCR reactions were carried out in the Biotechnology Laboratory of CIMMYT in El Batan, state of Mexico. For gene *Lr34*, a final volume of 9.5 μl were used for the reaction (6.5 μl of RED Sigma TAQ, 1.5 μl of primer CSLV34, and 1.5 μl of L34PLUS), and 5 μl of DNA for genes *Sr22* (CFA2123), *Sr24* (Sr24#12), *Sr26* (Sr26#43), and *Sr36* (STM773-2). PCR products obtained were separated by horizontal electrophoresis in 2.5 and 3.0% agarose gels, depending on the gene; separation was in TBE1X buffer, then stained with ethidium bromide, visualized under UV light, and documented with digital photography.

Table 1. Bread wheat advanced lines and commercial cultivars evaluated during the 2009–10 crop season in the Yaqui Valley, Sonora, Mexico.

#	Cultivar/line	Selection history
1	Chewink	CGSS03B00074T-099Y-099M-099Y-099M-6WGY-0B-3B
2	Navojoa M2007	CMSS97Y04045S-040Y-050M-040SY-030M-14SY-010M-0Y
3	Villa Juarez F2009	CGSS01B00062T-099Y-099M-099M-099Y-099M-12Y-0B
4	KEA/TAN/4/TSH/3/KAL/BB//TQFN/5/ Pavon/6/SW89.3064/7/Sokoll	CMSS04Y00153S-099Y-099ZTM-099Y-099M-5WGY-0B
5	Becard	CGSS01B00063T-099Y-099M-099M-099Y-099M-33WGY-0B
6	Onavas F2009	CGSS01B00069T-099Y-099M-099M-099Y-099M-20Y-0B
7	PBW343//CAR422/ANA/3/ELVIRA	CMSS02M00409S-030M-1Y-0M-040Y-10ZTB-0Y-02B-0Y
8	Babax/LR42//Babax*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ	CGSS01B00045T-099Y-099M-099M-099Y-099M-26Y-0B
9	Roelfs F2007	CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B
10	Whear/Kronstad F2004	CGSS04Y00106S-099Y-099M-099Y-099M-9WGY-0B
11	Whear/Kronstad F2004	CGSS04Y00106S-099Y-099M-099Y-099M-3WGY-0B
12	Tepahui F2009	CMSW00WM00150S-040M-040Y-030M-030ZLM-3ZTY-0M
13	Babax/LR42//Babax/3/ER2000	CMSA01Y00176S-040P0Y-040M-030ZTM-040SY-24M-0Y-0SY
14	TOBA97/Pastor	CMSS97M05756S-040M-020Y-030M-015Y-3M-1Y-3M-0Y
15	PFAU/Milan/3/Babax/LR42//Babax	CMSS02M00056S-030M-28Y-0M-040Y-25ZTB-0Y-01B-0Y
16	Babax/LR42//Babax/3/ER2000	CMSA01Y00176S-040P0Y-040M-030ZTM-040SY-30M-0Y-0SY
17	Whear/Sokoll	CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B
18	Thelin/2*WBLL1	CGSS02Y00079T-099B-099B-099Y-099M-6Y-0B
19	TC870344/GUI//Temporalera M 87/ AGR/3/2*WBLL1	CMSA01Y00725T-040M-040P0Y-040M-030ZTM-040SY-10M-0Y-0SY
20	Waxwing*2/Kronstad F2004	CGSS04Y00020T-099M-099Y-099ZTM-099Y-099M-3WGY-0B
21	ROLF07/YANAC//Tacupeto F2001/Brambling	CGSS05B00121T-099TOPY-099M-099NJ-4WGY-0B
22	Kronstad F2004	CMSS92Y01425T-16Y-010M-010Y-010Y-1M-0Y-50EY-0Y
23	PFAU/MILAN//TROST/3/ PBW65/2*SERI.1B	CMSS04M01426S-0TOPY-099ZTM-099Y-099M-3RGY-0B

Table 1. Bread wheat advanced lines and commercial cultivars evaluated during the 2009–10 crop season in the Yaqui Valley, Sonora, Mexico.

#	Cultivar/line	Selection history
24	Tacupeto F2001	CGSS95B00016F-099Y-099B-099Y-099B-15Y-0B
25	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/WH576/7/WH 542/8/Waxwing	CMSS04Y00364S-099Y-099ZTM-099Y-099M-2WGY-0B
26	CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/*Ae. tauschii* (213)//PGO	CMSA02Y00509T-040M-040P0Y-040ZTM-040SY-040M-6ZTY-03M-0Y
27	Reolfs F2007	CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B
28	CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/*Ae. tauschii* (213)//PGO	CMSA02Y00509T-040M-040P0Y-040ZTM-040SY-040M-15ZTY-03M-0Y
29	OR 9437534/Sokoll//Sokoll	CMSA04Y01203T-040ZTM-040ZTY-040ZTM-040SY-5ZTM-04Y-0B
30	Sokoll/Excalibur	CMSA03Y00010S-3P0Y-0ZTY-010M-010SY-010M-9ZTY-03B-0Y
31	Babax/LR42//Babax/3/ER2000	CMSA01Y00176S-040P0Y-040M-030ZTM-040SY-28M-0Y-0SY
32	CHEN/*Ae. tauschii* (TAUS)//BCN/3/BAV92/4/Berkut	CMSA02Y00104S-040P0Y-040ZTM-040SY-040M-8ZTY-02M-0Y
33	Sokol//Sunco/2*Pastor	CMSA04Y00294S-040ZTY-040ZTM-040SY-8ZTM-01Y-0B
34	CROC_1/*Ae. tauschii* (213)//PGO/3/CMH81.38/2*KAUZ/4/Berkut	CMSA02Y00059S-040P0Y-040ZTM-040SY-040M-5ZTY-01M-0Y
35	VEE/MJI//2*TUI/3/Pastor/4/Berkut	CMSA01M00075S-040P0M-030ZTM-040SY-040M-13Y-0M-0SY
36	MTRWA92.161/Prinia/5/SERI*3//RL6010/4*YR/3/Pastor/4/BAV92	CMSA02M00279S-040ZTM-040ZTY-040ZTM-040SY-2ZTM-03Y-0B
37	KRONSTAD F2004	CMSS92Y01425T-16Y-010M-010Y-010Y-1M-0Y-50EY-0Y
38	CROC_1/*Ae. tauschii* (213)//PGO/3/CMH81.38/2*KAUZ/4/Berkut	CMSA02Y00059S-040P0Y-040ZTM-040SY-040M-7ZTY-03M-0Y
39	Tacupeto F2001	CGSS95B00016F-099Y-099B-099Y-099B-15Y-0B
40	Navojoa M2007	CMSS97Y04045S-040Y-050M-040SY-030M-14SY-010M-0Y

Results. Amplification by PCR indicated that out of the 40 genotypes analyzed (taking into consideration the replication of three cultivars), only three were positive for gen *Lr34* (Fig. 1), which were 'KEA/TAN/4/TSH/3/KAL/BB//TQFN/5/Pavon/6/SW89.3064/7/Sokoll', 'Sokoll / Excalibur', and cultivar Tepahui F2009. Genes such as *Lr34* for nonspecific races called durable resistance or slow-rusting, are expressed in adult plants, and are related to grain yield decrease (Singh and Huerta 1997); on the other hand, other studies indicate that *Lr34* contributes to a significant increment in protein content (Labuschagne et al. 2002). However, the statistical analysis did not show a correlation with yield and protein due to the low number of positives in the amplification of *Lr34*. Gen SR22 was originally identified in the diploid wheat *T. monococcum* subsp. *monococcum* (Gerechter-Amitai 1971) and transferred to tetraploid and hexaploid wheat through interspecific hybridizations. Gene *Sr22* is effective against Ug99, however, its presence has a negative effect on

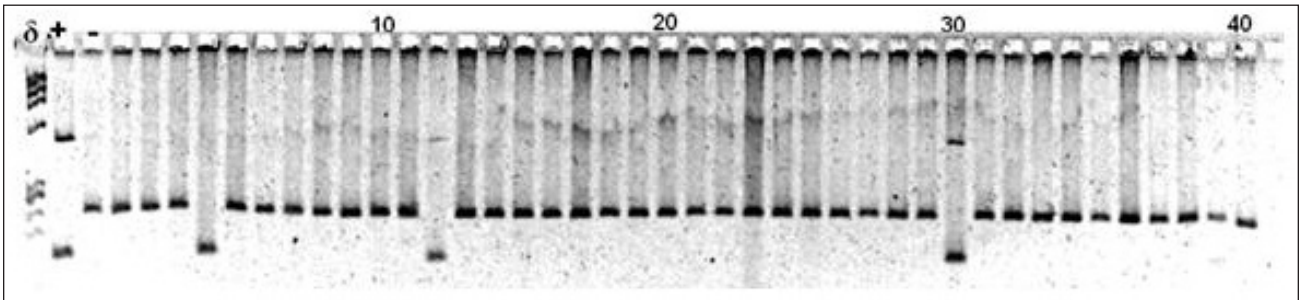

Fig. 1. PCR amplification for gene *Lr34* in bread wheat lines and commercial cultivars evaluated furing the 2009–10 crop season in the Yaqi Valley, Sonora, Mexico. See Table 1 (pp. 59-60) for line identification.

grain yield. Based on results from PCR, the presence of *Sr22* was detected in Chewink, Becard, 'Thelin / 2*WBLL1', 'ROLF07/Yanac//TACUPETOF2001/Brambling', and in the cultivars Tacupeto F2001, Roelfs F2007, and Onavas F2009 (Fig. 2). Gene *Sr24* confers resistance to most races of stem rust, including virulent race Ug99 (TTKSK) established in Eastern Africa and Ethiopia. Resistance of this gene during devastating epidemics of stem rust have been reported in South Africa and India (Mago et al. 2005), however, *Sr24* is not effective against a more recent variant of Ug99, designated as TTKST. Materials that possess *Sr24* are 'Babax/LR42//Babax/3/ER2000', 'TOBA97/Pastor', 'PFAU/Milan/3/Babax/LR42//Babax', 'Sokoll/Excalibur', and 'Sokoll//Sunco/2*Pastor' (Fig. 3). *Sr26* was not found in the materials evaluated; this gene is one of the few with major resistance effective against race TTKSK and its derivatives TTKST, making it ideal for pyramiding resistance. Gene *Sr36* was not found during analysis of the materials evaluated. Previous studies indicate that *Sr36* confers resistance to Ug99, however, other variants of Ug99 affect this gene, so, it is recommended to use it to pyramid with other genes. Genetic resistance is considered the most important strategy for disease management in wheat. This resistance implies an aggregated value to materials when they are released as cultivars; therefore, different breeding programs invest a great deal of their resources to disease management, as a response to a possible event that might occur.

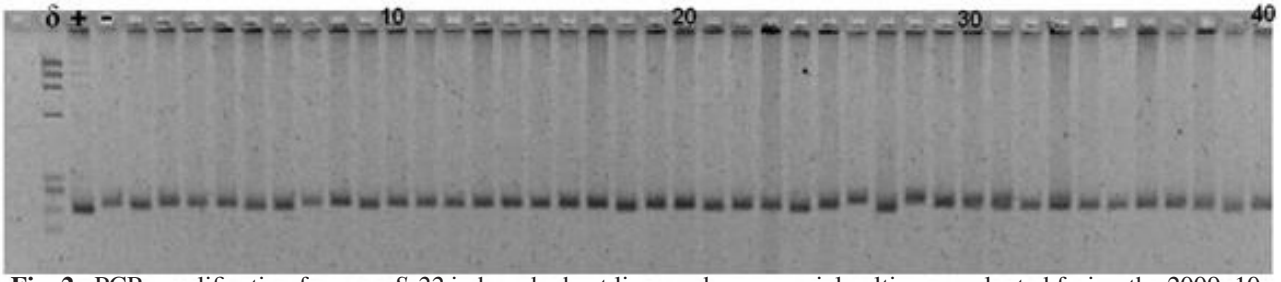

Fig. 2. PCR amplification for gene *Sr22* in bread wheat lines and commercial cultivars evaluated furing the 2009–10 crop season in the Yaqi Valley, Sonora, Mexico. See Table 1 (pp. 59-60) for line identification.

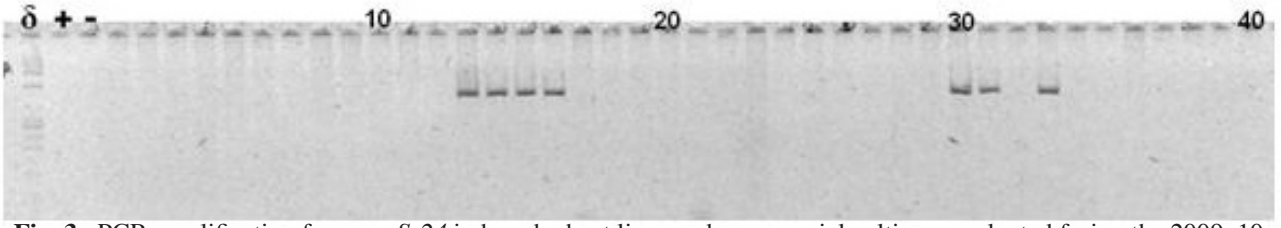

Fig. 3. PCR amplification for gene *Sr24* in bread wheat lines and commercial cultivars evaluated furing the 2009–10 crop season in the Yaqi Valley, Sonora, Mexico. See Table 1 (pp. 59-60) for line identification.

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Effect of tillage methods on wheat grain yield and fuel consumption in the Yaqui, Valley Sonora, Mexico.

Juan Manuel Cortés-Jiménez, Alma Angélica Ortiz-Ávalos, and Guillermo Fuentes-Dávila.

Introduction. In The Yaqui Valley, Sonora, Mexico, about 100,000 ha are managed with equipment for conventional tillage, such as the plough or chisel. The cost of ploughing is $56.50 (11.5 exchange rate), chiseling $47.80, and disk harrowing $30.40. In terms of economic impact, more importance now is focused on the energy cost of agriculture, and agricultural diesel is the primary source of energy for tillage practices. The cost increase derived from tillage and the commitments of the Kyoto Protocol are factors that make more important the use of efficient practices, taking into consideration their influence on competitiveness in agricultural activities. Moreover, greenhouse gases produced by the use of fossil fuels, such as diesel, are one of the most significant environmental problems to be addressed; therefore, agricultural tractors ought to be used more efficiently (Pérez de Ciriza 2004). Deep tillage is considered essential for yield improvement but, with the exception of deep-rooted plants, many crops yield well with 12–15 cm of tillage (Prasad 1996). Reduced tillage in wheat requires less equipment and energy in comparison to conventional tillage, where the plow is used and yields are very similar; an economic advantage to the farmer (Gemtos et al. 1999). However, occasionally plowing is recommended for weed control (Turley et al. 2003). Our objective was to determine the effect of conventional tillage on wheat grain production and diesel consumption in a clay soil in the Yaqui Valley, Sonora, Mexico.

Materials and methods. The study was conducted at the Norman E. Borlaug Experimental Station, which belongs to the Mexican National Institute for Forestry, Agriculture and Livestock Research (INIFAP), during the period 2006–07 to 2009–10. The station is located at 27°22' north latitude and 109°55' west longitude. The plot size was 5,760 m^2. The soil was prepared with secondary tillage based on the use of disk harrowing during five years (2002 to 2006), and from the sixth year on, the plot was divided into three subplots of 1,920 m^2. In each crop season, one of the subplots was prepared just with disk harrowing, another with disk harrowing followed by plowing, and the third with disk harrowing followed by chiseling. Plowing and chiseling were done to a depth of 40 cm and harrowing to 30 cm. In all cases, there was no summer rotation. Sowing date and agronomic management followed the recommendations of INIFAP for the region. During 2009 and 2010, diesel consumption was measured from the time the tractor started with a full tank in each treatment. Tractor brand and models for this study were New Holland 7610, John Deere 6403, and 4455.

Results. Plowing or chiseling did not produce a higher wheat grain yield as compared to disk harrowing in any of the years of evaluation (Table 2), which indicates that primary tillage based on plowing and chiseling only contributed to unnecessary increase in production costs. Only after four years of plowing, there was a slight increase in wheat grain yield; however, this increase was not sufficient to pay for the cost of this tillage method.

Table 2. Wheat grain yield (t/ha) obtained in conventional and secondary tillage in the Yaqui Valley, Sonora, Mexico, during four crop seasons.

	Crop season			
Tillage method	**2007**	**2008**	**2009**	**2010**
Plowing	6.450	7.643	6.460	8.220
Chiseling	6.710	7.660	6.888	7.663
Disk harrowing	6.724	8.085	7.758	8.013

Diesel consumption for each tillage method evaluated and tractors used are reported in Table 3. The levels of consumption were consistent with those reported by manufacturers; however, some variations are expected depending on the type of tractor, equipment size, and operating conditions such as depth, speed, size, and shape of the field. In this study, diesel consumption for the disk harrowing method was half the amount used with chiseling, and from 26 to 32% with plowing, depending on the type of tractor.

Table 3. Fuel consumption in conventional and secondary tillage methods in wheat in the Yaqui Valley, Sonora, Mexico (NH = New Holland; JD = John Deere tractors).

	2009 season		2010 season	
Tillage method	**L/ha**	**Tractor**	**L/ha**	**Tractor**
Plowing	24.3	NH 7610	32.2	JD 6403
Chiseling	16.3	JD 4455	16.4	JD 6403
Disk harrowing	7.9	NH 7610	8.5	NH 7610

Conclusions. The use of secondary tillage based on disk harrowing showed greater grain yield and profitability as compared with conventional tillage based on plowing or chiseling, under conditions of the Yaqui Valley, Sonora. The elimination of conventional tillage practices in wheat management, reduced diesel consumption and therefore the emission of greenhouse gases like carbon dioxide, without affecting grain yield.

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Evapotranspiration as a tool to predict quantity of water for wheat irrigation in the Yaqui Valley, Sonora, Mexico.

Alma Angélica Ortiz-Avalos, Juan Manuel Cortés-Jiménez, Guillermo Fuentes-Dávila, and Xóchitl Marisela Bravo-Peña (Colegio de Estudios Científicos y Tecnológicos del Estado de Sonora, Periférico S/N, Esquina con Tamaulipas, Bacobampo, Sonora, México CP 85287).

Abstract. The evapotranspiration data used in this study was taken from the weather station network in the Yaqui Valley from 1 December, 2008, to 15 April, 2009, which corresponded to the wheat crop season. A database created in an Excel spreadsheet was imported into the Idrisi Kilimanjaro program, in order to convert it into a digital file, and through interpolation by the nearest neighboring method, the value of evapotranspiration was projected for the entire Yaqui Valley. The total value for the period of evaluation was 507 mm, however, evapotranspiration values were different throughout the whole region. Therefore, we concluded that it cannot be generalized the application of the same quantity of irrigation water to wheat across the Valley.

Introduction. Evapotranspiration is a key parameter for establishing the frequency and amount of water to be applied in an irrigated crop (Gurovich 1985). Evaporation is affected by climate, crop characteristics, and management (FAO 1998). In the Yaqui Valley, where wheat has occupied the largest area during the autumn-winter for many years, evapotranspiration is higher than precipitation, therefore, irrigation is necessary in order to make agriculture a profitable business (Cortés et al. 2009). The FAO (1998) recommends to study evapotranspiration in this type of regions to monitor crop water demand. The objective of this evaluation was to identify the evapotranspiration reference values in the Yaqui Valley through data recorded by the weather station network,and to determine whether these values could be used as a general criterion for irrigated wheat scheduling.

Materials and methods. Evapotranspiration data was taken from the weather station network in the Yaqui Valley, Sonora (PIEAES 2009) reported from 1 December, 2008, to 15 April, 2009. An Excel spreadsheet data base was created for each of the stations with their respective coordinates. The data base was saved as text (tab delimited) and imported into the Idrisi Kilimanjaro program, which created a map of points (known as vector) (Eastman 2003). The map was taken to a process of interpolation (nearest neighboring method), and it also was added the minimum and maximum limit in X, Y, of the Yaqui Valley, in order to get the map with the spatial distribution of evapotranspiration. The accumulated monthly evapotranspiration was used to make graphs.

Results and discussion. The evapotranspiration value is a very important tool for agricultural irrigation programming. However, it should be considered that even within the same region, values are not equal (Fig. 4, p. 64). The region where the highest evapotranspiration was recorded is located in block 2920 near the coast known as Siari Island. Evaporation is higher in coastal areas, because there is more area with bare soil and the evaporation from a soil under this condition is greater than a soil with a vegetative cover, because solar radiation is mitigated by the plant cover (Miliarum.com 2009).

During the wheat season of evaluation, the highest value of evapotranspiration (143 mm) occurred in March (Fig. 5). However, the evaluation covered just 15 days in April, so if sowing was carried out after the first day of December, the physiological crop cycle would be shifted so that more days would be considered in April for the purpose of this study. Therefore, the value of evapotranspiration would increase as this month reported a total value of 162 mm.

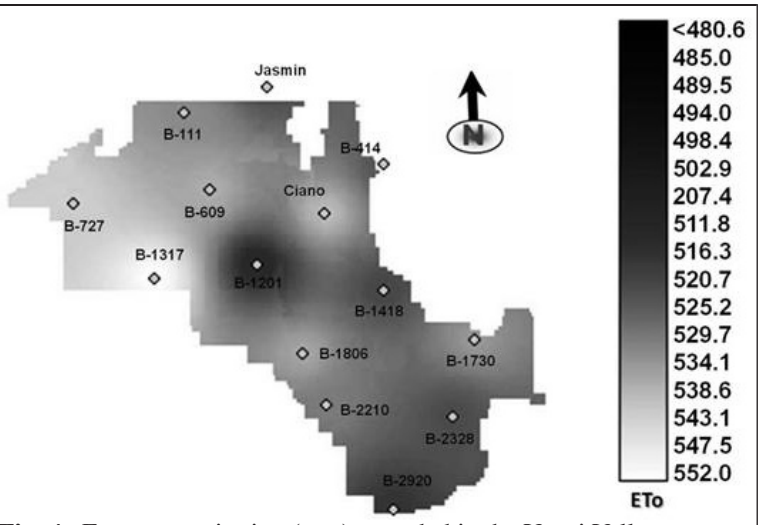

Fig. 4. Evapotranspiration (mm) recorded in the Yaqui Valley, Mexico, from Novermber 2008 to April 2009.

In irrigated agriculture, optimizing water management is necessary to increase the efficiency of using water resources through technical procedures, which provide the necessary information to irrigate a crop with an optimal frequency and timing (Singh and Chauman 1996). Although evapotranspiration is a useful tool for irrigation scheduling, it can not predict its application, therefore, it is necessary to incorporate other values such as rainfall, crop type and phenological stage, type and quality of soil, soil moisture, and water quality (FAO 1998).

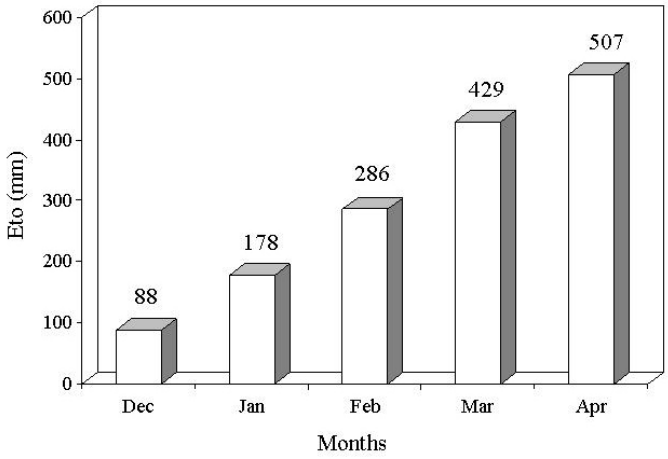

Fig. 5. Evapotranspiration (mm) accumulated from 1 December, 2008, to 15 April, 2009, in the Yaqui Valley, Mexico.

Conclusions. Results of the average spatial distribution of evapotranspiration for the Yaqui Valley are not the same across the region, so that the value of evapotranspiration can not be taken as a single criterion for irrigation scheduling.

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Effect of two biofertilizers on wheat grain yield in the Yaqui Valley, Sonora, Mexico.

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Abstract. The use of biofertilizers is a practice that has generated great interest in recent years. In this process, the seed is inoculated with beneficial microorganisms that exist naturally in soil, thus increasing its concentration in the rhizosphere. In general, their effects reside in promoting plant growth, developing tolerance to moderate stress, and increasing the efficiency of nutrient absorption. In this study, the simple effects and interactions between nitrogen, phosphorus, *Glomus arbuscular*, and *Azospirillum brasilense* as fertilizers on wheat yield were evaluated. Results from simple interactions indicated that plots with a nitrogen application produced greater grain yield than untreated ones, a phosporus application did not increase yield, and the highest yield was obtained with *Azospirillum* in plots treated with just biofertilizers. The highest grain yield from chemical fertilizer + biofertilizer interactions was obtained with the treatment nitrogen + the mixture *Glomus* + *Azospirillum*.

Introduction. Research and technology contributed to increase crop yields during the 1960s and 1970s, but the ecological price has been high (FAO 1995). The conventional agricultural model adopted by the middle of last century was based on a production system that was highly efficient, but dependent on elevated synthetic inputs (FIDA-RUTA-CATIE-FAO 2003), as well as the use of methods that caused soil erosion, salinization, pollution, desertification, and loss of biodiversity (FAO 1995). Twenty-first century agriculture in Mexico and the world will have to use science as an alternative to generate a revolution in agricultural production systems that overcome all areas (economy, productivity, and ecology) of the production systems used during the last century. Agriculture in Mexico is promoting the use of *Rhizobium etli* and *Azospirillum brasilense*, bacteria that fix atmospheric nitrogen in conjunction with the mycorrhizal fungus (*Glomus arbuscular*) are the basis for the production of the so-called biofertilizers (Morales 2007). Biofertilizer is a product that contains one or more soil microorganisms and can be applied to the seed or soil in order to increase their population; it can be associated directly or indirectly to the plant root system, encourage its interaction, and increase growth and reproduction of the host plant (Aguirre et al. 2010). These microorganism-biofertilizers are normally distributed in the soil, but its concentration is insufficient (between 103–104 cells/g of soil) to cause the desired beneficial effect on plants, hence, the importance of increasing their population size (between 106–108 cells/g of soil) (Dibut 2009). In addition, these biofertilizers are environmentally friendly and low cost.

In the Yaqui Valley, Sonora, fertilization represents the main cost of wheat production, which affects the profitability of this crop. In this study, the simple effects and interactions between nitrogen, phosphorus, *Glomus*, and *Azospirillum*, as fertilizers on wheat yield were evaluated.

Materials and methods. The study was carried out at the Norman E. Borlaug Experimental Station (INIFAP) during the 2008–09 crop season. A factorial experimental design was used with the following factors: A) nitrogen rates 0 and 200 kg/ha as urea; B) phosphorus rates 0 and 52 kg P_2O_5/ha in the form of monoammonium phosphate; and C) biofertilizers control, *Glomus*, *Azospirillum*, and *Glomus* + *Azospirillum*. Experimental plots were 4.8 m^2 and treatments had three replications. Mean comparisons used Tukey's test (0.05). Planting date and agronomic management of durum wheat cultivar Samayoa C2004 followed recommendations of INIFAP for the region.

Results and discussion. The single addition of 200 kg/ha of nitrogen produced on average 756 kg of grain/ha more than the control (Table 4); a greater yield was obtained in plots without phosphorus application than in treated plots. In the case of biofertilizers, the highest grain yield was obtained with the application of *Azospirillum*, which was 699 kg/ha more than the con-

Table 4. Effect of biofertilizers, phosphorus, and nitrogen on grain yield of the durum wheat cultivar Samayoa C2004 during the 2008–09 crop season at the Norman E. Borlaug Experimental Station. Grain yield was evaluated at 12% humidity content. Tukey (p = 0.05) = 0.172.

	Grain yield (t/ha)				
	Rate of fertilizer N–P (kg/ha)				
Treatment	0–0	0–52	200–0	200–52	Average
Control	6.560	6.385	7.773	7.594	7.078 a
Glomus	6.895	6.573	7.600	7.452	7.130 a
Azospirillum	7.259	6.918	7.287	7.738	7.301 a
Glomus + *Azospirillum*	6.760	6.381	7.839	7.273	7.063 a
Average	6.869 b	6.564 b	7.625 a	7.514 a	

trol. The interaction that produced the highest yield was the mixture of *Glomus* + *Azospirillum* with a N–P rate of 200–0, respectively; however, the difference with respect to the control was only 66 kg/ha.

A greater response to biofertilizers was observed in treatments without chemical application (Fig. 6), plots treated with *Azospirillum* showed a yield increase of 9.6%, *Glomus* 4.9%, and 3.0% with the mixture *Glomus* + *Azospirillum*. Plots treated with nitrogen and the mixture *Glomus* + *Azospirillum* showed a yield increase of 0.8%, whereas those treated with nitrogen, phosphorus, and *Azospirillum* 1.9%. This type of response can be attributed the lack of fixation of atmospheric nitrogen by the biofertilizers, because nitrogen availability in the soil is high and therefore the symbiotic process is not established (Aguirre et al. 2010).

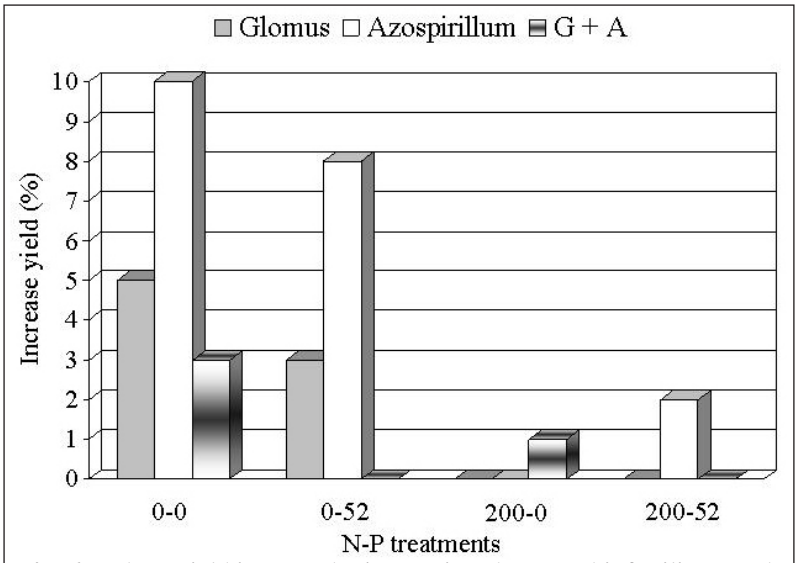

Fig. 6. Wheat yield increase by interactions between biofertilizers and urea (N) and monoammonium phosphate (P).

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Characteristics and descriptions of phenotypic components of Huatabampo Oro C2009, a new durum wheat cultivar for southern Sonora, Mexico.

Guillermo Fuentes-Dávila, Víctor Valenzuela-Herrera, Gabriela Chávez-Villalba, José Luis Félix-Fuentes, Pedro Figueroa-López, and José Alberto Mendoza-Lugo.

Introduction. Before the 1990s, bread wheat was the dominant class in northwest Mexico. In the state of Sonora, bread wheat occupied more than 50% of the area dedicated to wheat from the agricultural season of 1983–84 to 1993–94. However, many wheat producers have turned to durum wheat since the implementation of the domestic quarantine No. 16 (SARH, 1987), which limited the cultivation of bread wheat in fields where Karnal bunt had been detected at levels greater than 2% infected grains. Other important factors were that durum wheat showed greater grain yield than bread wheat and that, during that period of time, this crop did not have problems with leaf rust. In addition, there were opportunities for export of durum wheat.

Durum wheat was consolidated as the dominant class grown in Sonora beginning with the agricultural season 1994–95. Altar C84 was the most cultivated cultivar up to 2002–03, despite the fact that its resistance to leaf rust had already been overcome by a wheat race, which caused production losses during 2000–01 and 2001–02. Seed production of cultivar Júpare C2001 (Camacho-Casas et al. 2004) (resistant to leaf rust) through the collaborative project between

the Mexican National Institute For Forestry, Agriculture, and Livestock Research (INIFAP) and the International Maize and Wheat Improvement Center (CIMMYT) with support by the farmer's union (PIEAES) of the Yaqui Valley, made it the most widely grown cultivar in southern Sonora from 2003–04 to 2008–09 (Table 5, Fuentes-Dávila et al. 2010a). Átil C2000, a high-yielding cultivar released in 2001 that became susceptible to leaf rust in 2001–02 (Figueroa-López et al. 2002), occupied 53,106.07 ha.

Table 5. Area (ha) grown with wheat during the 2008–09 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	% of total area
Durum wheat		
Júpare C2001	119,327.38	42.34
Átil C2000	53,106.07	18.84
Samayoa C2004	29,062.75	10.31
Banámichi C2004	13,652.76	4.84
Platinum	7,741.92	2.75
Aconchi C89	1,067.14	0.38
Altar C84	491.66	0.17
Rafi C97	478.20	0.17
Nácori C97	10.00	0.004
TOTAL	224,937.90	
Bread wheat		
Kronstad F2004	29,818.81	10.58
Tacupeto F2001	23,733.23	8.42
Tarachi F2000	1,615.60	0.57
Rayón F89	1,045.33	0.37
Abelino F2004	638.18	0.23
Navojoa M2007	9.60	0.003
Roelfs F2007	9.60	0.003
TOTAL	56,870.34	

Table 6. Area (ha) grown with wheat during the 2009–10 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	% of total area
Durum wheat		
Átil C2000	81,777	33.07
Júpare C2001	53,164	21.50
Samayoa C2004	23,318	9.43
Sáwali Oro C2008	4,761	1.93
CIRNO C2008	3,256	1.32
CEVY Oro C2008	3,233	1.31
Platinum	2,655	1.07
Patronato Oro C2008	2,325	0.94
Aconchi C89	1,019	0.41
RSM Imperial C2008	980	0.40
Banámichi C2004	826	0.33
RSM Chapultepec C2008	499	0.20
Rafi C97	351	0.14
Río Colorado	296	0.12
Nácori C97	241	0.10
Altar C84	105	0.04
TOTAL	178,806	
Bread wheat		
Tacupeto F2001	40,552	16.40
Kronstad F2004	25,021	10.12
Abelino F2004	736	0.30
RSM-Norman F2008	659	0.27
Rayón F89	636	0.26
Tarachi F2000	384	0.16
Roelfs F2007	248	0.10
Navojoa M2007	235	0.10
Monarca F2007	4	0.00
TOTAL	68,475	

Júpare C2001 did not comply with the expected protein content in the grain and color, which are very important parameters of quality. In addition, new races of leaf rust present during 2008–09 overcame its resistance, and the area occupied with this cultivar decreased significantly in 2009–10, while that for Átil C2000 increased (Table 6, Fuentes-Dávila et al. 2011). Therefore, options for cultivars resistant to leaf rust for this region must be increased so that they contribute to help the long-lasting use by wheat producers in Sonora and in northwest Mexico and at the same meet current minimum quality requirements for export.

Pedigree, history selection and description of Huatabampo Oro C2009. After evaluation of grain yield since the 2007–08 agricultural season at the Yaqui Valley Experimental Station (renamed as Norman E. Borlaug Experimental Station, CENEB, since March 2010), we proposed the release the experimental durum wheat line 'GUAYACAN INIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN' as cultivar Huatabampo Oro C2009 (Fuentes-Dávila et al. 2010b). Huatabampo Oro C2009 is a spring-type durum wheat cultivar that originated from hybridizations made in the Durum Wheat Breeding Program of CIMMYT. The cross number and history selection is CDSS02B00562S-0Y-0M-2Y-1M-04Y-0B. Shuttle breeding was carried out between the experimental stations of El Batán, state of Mexico (B) (19°30'N and 2,249 msnm); San Antonio Atizapán, state of Mexico (M) (19°17'N and 2,640 msnm); and the Yaqui Valley

(Y) (27°20'N and 40 msnm), in Sonora (Table 7).

Table 7. Selection history and localities where cultivar Huatabampo Oro C2009 was evaluated. Yield trials at INIFAP were at the following plant dates: 15, 30 November, 15 December, and 1 January. For season, F–W = autumn–winter, S–S = spring–summer; For irrigation conditions, RR = regular rainfed, NI = normal irrigation.

Activity	Locality	Season	Irrigation conditions
Simple genetic cross	El Batan, Mexico	S–S / 2002	RR
F_1 generation	Cd. Obregon, Sonora	F–W / 2002–03	NI
F_2 generation	Cd. Obregon	F–W / 2003–04	NI
F_3 generation	Atizapan, Mexico	S–S / 2004	RR
F_4 generation	Cd. Obregon	F–W / 2004–05	NI
F_5 generation	Atizapan	S–S / 2005	RR
F_6 generation	Cd. Obregon	F–W / 2005–06	NI
F_7 generation yield trials by CIMMYT	El Batan	S–S / 2006	RR
Yield trials by INIFAP	Cd. Obregon	F–W / 2007–08	NI
		F–W / 2008–09	NI

The most important phenotypic characteristics of this cultivar, according to the International Union for the Protection of New Varieties of Plants (UPOV 1994), are given in Table 8 (p. 69). Cultivar Huatabampo Oro C2009 has an average of 78 days-to-heading with a range of 68 to 86. The cultivar has an average of 118 days to physiological maturity; however, the cycle may be shortened due to the lack of cold hours if planting is late, and may average 107 days when sowing is done at the end of December. Huatabampo Oro C2009 has an average height of 86 cm (Fig. 7), a maximum of 100 and minimum of 75. Plant growth habit is erect,and shows no or low frequency of recurved flag leaves.

Fig. 7. Huatabampo Oro C2009 durum wheat cultivar has an average height of 86 cm. Plants are erect and present no or very low frequency of recurved flag leaves.

Fig. 8. The grain shape of Huatabampo Oro C2009 durum wheat cultivar is elongated. In the dorsal view, pubescence is of medium length. Grain coloratin after treatment with phenol is absent or very light.

Spike shape in profile view is tapering, density is medium, and the length excluding awns is medium; awns are longer than the spikes. Spike glaucosity is strong, and awns are distributed the whole length and have a brown color. At maturity, spikes become pigmented. Glume shape is ovoid (spikelet in mid-third of spike), and hairiness on the external surface is present. The shape of the shoulder is rounded and the width is narrow; length of the beak is short and slightly curved. Grain shape is elongated (Fig. 8), and the length of brush hair in dorsal view is medium. Grain coloration when treated with phenol is absent or very light.

Acknowledgements. The authors wish to thank Dr. Karim Ammar, Head of the Durum Wheat Breeding Progam of the International Maize and Wheat Improvement Center (CIMMYT), for providing the advanced lines from which Huatabampo Oro C2009 originated.

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Table 8. Characteristics and description of phenotypic components of cultivar Huatabampo Oro C2009.

Structure	Characteristic	Description
Coleoptile	Anthocyanin coloration	Strong
First leaf	Anthocyanin coloration	Absent or very weak
Plant	Growth habit	Erect
	Frequency of plants with recurved flag leaves	Absent or very low
	Seasonal type	Spring
Spike	Time of emergence	Early
	Glaucosity	Strong
	Length (stem, ear and awns)	Medium
	Distribution of awns	Whole length
	Awns at tip of spike in relation to spike	Longer
	Length excluding awns	Medium
	Hairiness of margin of first rachis segment	Absent or very weak
	Color (at maturity)	Pigmented
	Shape in profile view	Tapering
	Density	Medium
Flag leaf	Glaucosity	Strong
	Glaucosity of blade	Weak
Awn	Anthocyanin coloration	Absent or very weak
	Color	Brown
Culm	Hairiness of uppermost node	Weak
	Glaucosity of neck	Medium
Lower glume	Shape (spikelet in mid-third of ear)	Ovoid
	Shape of shoulder	Rounded
	Shoulder width	Narrow
	Length of beak	Short
	Shape of beak	Slightly curved
	Hairiness on external surface	Present
Straw	Pith in cross section (half way between base of ear and stem node below)	Medium
Grain	Shape	Elongated
	Length of brushhair in dorsal view	Medium
	Coloration with phenol	Absent or very light

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Evaluation of grain yield of durum wheat cultivar Movas C2009.

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Introduction. Northwest Mexico, comprised by the states of Sonora, Sinaloa, and South and North Baja California, is the main wheat-producing region of Mexico with approximately 460,000 ha. In this region, wheat producers have a high

demand for cultivars with important agronomic and quality characteristics; this, in turn, forces and maintains dynamic breeding programs that evaluate experimental germ plasm under different environments. Every crop season, wheat lines that show stability in main parameters, such as grain yield, quality, and disease resistance, are proposed for commercial release. After several crop seasons of evaluation, the experimental spring durum wheat CIMMYT line 'CMH83.2578/4/ D88059//WARD/ YAV79/3/ACO89/5/2*SOOTY_9/RASCON_37/6/1A.1D5+106/3*MOJO/3/AJAIA_12/ F3LOCAL (SEL.ETHIO. 135.85)//PLATA_13' was released as the commercial cultivar Movas C2009 (Félix-Fuentes et al. 2010). The cross number and selection history is CDSS02B00720S-0Y-0M-8Y-1M-04Y-0B. Evaluations of grain yield of Movas C2009 and the check cultivar Júpare C2001 are presented here.

Materials and methods. This study was at the Norman E. Borlaug Experimental Station (CENEB), which belongs to the Northwest Regional Research Center (CIRNO) of the Mexican National Institute for Forestry, Agriculture and Livestock Research (INIFAP), located in block 910 of the Yaqui Valley (27°22' latitude north, 109°55' longitude west, at 38 masl). Grain yield of Movas C2009 and the check cultivar Júpare C2001 was evaluated in four sowing dates with two and three complementary irrigations during the crop season autumn–winter 2008–09 (Table 9), with two and four complementary irrigations during the 2009–10 crop season (Table 10), and with drip irrigation (full irrigation) during crop seasons 2005–06 to 2008–09 on one sowing date (1 December), in block 810 at CIMMYT area. Experimental plots were 5-m long on two beds with two rows; space between beds was 0.8 m. Sowing dates were 15 November, 1 and 15 December, and 1 January, in dry clay soil using 100 kg of seed/ha. Fertilization consisted of 100 units of N (as urea) and 100 units of P (as monomonium phosphate) before seeding. The trial was irrigated right after seeding and later during the season complementary irrigations were provided as indicated (Tables 9 and 10). Also, 100 units of N were applied before the first complementary irrigation and 50 before the second. The herbicide Situi® xl at 25 g/ha of commercial product was sprayed over the trial 30 days after sowing. Statistical analysis was performed using SAS, and mean comparison with Tukey's test (0.05).

Table 9. Dates of application of the two and three complementary irrigations for cultivars Movas C2009 and Júpare C2001 at four sowing dates during the autumn–winter crop season 2008–09, at the Norman E. Borlaug Experimental Station in Sonora, Mexico (D = sowing, IR = two and three complementary irrigations, days after sowing are indicated in parentheses following date).

1D 2IR	6 January (50)	17 February (92)	
1D 3IR	31 December (44)	5 February (80)	2 March (107)
2D 2IR	23 January (53)	3 March (90)	
2D 3IR	14 January (44)	18 February (79)	12 March (103)
3D 2IR	6 February (53)	10 March (87)	
3D 3IR	28 February (44)	4 March (81)	27 March (104)
4D 2IR	26 February (56)	26 March (86)	
4D 3IR	13 February (43)	10 March (67)	3 April (93)

Table 10. Dates of application of the two and three complementary irrigations for cultivars Movas C2009 and Júpare C2001 at four sowing dates during the autumn–winter crop season 2009–10, at the Norman E. Borlaug Experimental Station in Sonora, Mexico (D = sowing, IR = two and three complementary irrigations, days after sowing are indicated in parentheses following date).

1D 2IR	6 January (50)	18 February (93)		
1D 4IR	24 December (37)	22 January (67)	18 February (93)	5 March (110)
2D 2IR	10 January (50)	3 March (90)		
2D 4IR	8 January (38)	9 February (70)	4 March (95)	19 March (110)
3D 2IR	10 February (57)	23 March (100)		
3D 4IR	22 January (38)	24 February (71)	19 March (96)	29 March (106)
4D 2IR	23 February (54)	26 March (91)		
4D 4IR	11 February (42)	17 March (76)	29 March (91)	15 April (107)

Results and discussion. The results of the evaluation during the 2008–09 crop season with two and three complementary irrigations indicated that the best sowing date, in order to obtain the highest yield potential of both cultivars Movas C2009 and Júpare C2001, was 1 December, which produced an average of 6.1 ton/ha, followed by the first sowing date with 5.8 (Table 11, p. 71). In general, sowing between 15 November and 1 December 1 allows the accumulation of more cold units (CU) that render better grain yield by wheat cultivars in the Yaqui Valley. Félix-Valencia et al. (2009)

reported that with an accumulation of 340 CU, wheat grain yield would be approximately 4,630 kg/ha, and for each increment of 100 CU, yield will increase by 330 kilograms.

Table 11. Average grain yield of cultivars Movas C2009 and Júpare C2001 with two and three complementary irrigations during autumn-winter 2008–09 crop season, at the Norman E. Borlaug Experimental Station in Sonora, Mexico. For grain yield, columns with the same letter are statistically similar (Tukey, p = 0.05).

Sowing date	Grain yield (ha)
1st	5.8 ab
2nd	6.1 a
3rd	5.4 bc
4th	5.1 c

The average grain yield of Movas C2009 in four sowing dates with two complementary irrigations registered 0.7 ton/ha greater than that of the check cultivar Júpare C2001, although the highest yield difference was recorded in the 1st sowing date with 0.9 ton/ha (Table 12). The average difference in grain yield was 0.8 ton/ha in favor of Movas C2009 with three complementary irrigations, and the highest difference was recorded again in the 1st sowing date with 2.6 ton/ha. The effect generated by water stress on a wheat crop depends on the phenological stage of the plant, pre- and post-anthesis being the most susceptible to this abiotic factor. During the evaluation in 2008–09, the average temperature during this stage was 16°C (Fig. 9). Most of the assimilates that are stored in the grain are generated during grain filling, therefore, a preanthesis reserve does not increase with water stress, as expressed as the proportion of dry weight of the crop during anthesis, but increases as yield proportion.

Table 12. Grain yield of cultivars Movas C2009 and Júpare C2001 in four sowing dates with two and three complementary irrigations during autumn-winter 2008–09 crop season, at the Norman E. Borlaug Experimental Station in Sonora, Mexico.

Number / date of irrigation	Cultivar	
	Movas C2009	Júpare C2001
Two irrigations		
15 November	6.8	5.9
1 December	6.2	5.4
15 December	6.0	5.6
1 January	5.3	4.7
Average	6.1	5.4
Three irrigations		
15 November	6.7	4.1
1 December	7.0	5.9
15 December	4.4	5.7
1 January	5.4	4.8
Average	5.9	5.1

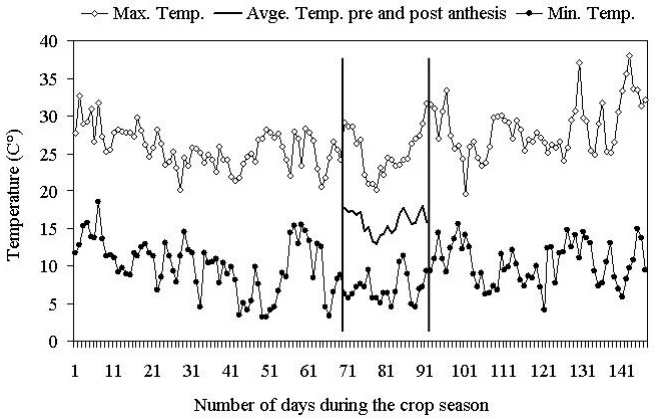

Fig. 9. Maximum, minimum, and average termerature during pre- and post-anthesis during the 2008–09 autumn-winter wheat season at the Norman E. Borlaug Experimental Station, Sonora, Mexico.

Table 13. Grain yield of cultivars Movas C2009 and Júpare C2001 in four sowing dates with two and four complementary irrigations during autumn-winter 2009–10 crop season, at the Norman E. Borlaug Experimental Station in Sonora, Mexico.

Number / date of irrigation	Cultivar	
	Movas C2009	Júpare C2001
Two irrigations		
15 November	6.6	6.6
1 December	7.1	6.5
15 December	6.4	5.5
1 January	6.3	5.3
Average	6.6	6.0
Four irrigations		
15 November	7.0	6.7
1 December	8.4	7.9
15 December	7.7	7.3
1 January	7.2	5.7
Average	7.6	6.9

Movas C2009 expressed its grain yield potential with four complementary irrigations during the 2009–10 crop season with an average of 7.6 ton/ha and a maximum of 8.4 in the second sowing date (Table 13). The yield difference ranged from 1 to 1.7 t/ha when Movas C2009 had two or three complementary irrigations during crop seasons 2008–09 and 2009–10. Movas C2009 showed a higher grain yield than that of Júpare C2001, with an average difference of 0.65 t/ha with two and four complementary irrigations during 2009–10.

The difference in grain yield for Movas C2009 between the average of the first two sowing dates and the average of the third and fourth ones, was 0.850 t/ha with two irrigations in 2008–09 and 0.500 in 2009–10 in favor of the first two sowing dates. The same trend was found in 2008–09 with three irrigations (1.950 t/ha difference) and in 2009–10 with four ir-

rigations (0.250 t/ha). The low grain yield obtained on the dates considered as late (third and fourth) can be attributed to the high temperatures registered in the region when plants were in a vegetative stage and under this stress and represents a decrease in grain number. Fokar et al. (1998) and Savin et al. (1997) have reported significant variation in reduction of grain number and weight/spike under heat stress. The environmental stress may be different but most have a common effect on the hydric status of the plant (Bohnert et al. 1995).

Moderate water stress in a wheat plant causes a foliar reduction and, according to Abbate et al. (1997), anthesis takes place earlier than normal. Anthesis is delayed when a more severe stress occurs, being able to be modified on the day spike growth ends, however, Abbate and Cantarero (2001) reported that the duration of spike growth is not affected in a significant way by drought. The way in which a plant responds under such conditions depends on the species, because the mechanisms that confer tolerance to stress in many instances have evolved in a specific way for certain plant groups. Ortiz (2009) reported that only the first complementary irrigation can be delayed without affecting normal plant development; this irrigation is applied during tillering, 35 to 40 days after sowing. The second irrigation is applied during heading or flowering, 74 to 85 days after sowing, and can affect grain yield if delayed. The third and fourth irrigations are applied during the milky stage; the number of days to reach this stage is about 100 days, depending on the sowing date.

The grain yield of Movas C2009 and the check cultivar Júpare C2001 was similar during the different crop seasons of evaluation under drip irrigation (Fig. 10). Movas C2009 showed a greater grain yield than that of Júpare C2001 in a range of 0.14 to 0.28 t/ha during 2008–09 and 2006–07, respectively. The highest yield by Movas C2009 was 7.17 t/ha during crop seasons 2007–08 and 2005–06. Grain yield of Júpare C2001 was greater than that of Movas C2009, 0.170 to 0.290 t/ha, respectively. The highest yield by Júpare C2001 was 8.79 t/ha. Although this type of irrigation maintains a hydric status in the soil, which avoids water stress in the plant, environmental conditions vary from season to season and may have an effect on grain yield, as it was shown in contrasting crop seasons 2007–08 and 2008–09; grain yield difference in Movas C2009 in both seasons was 1.92 t/ha and 2.23 t/ha for Júpare C2001.

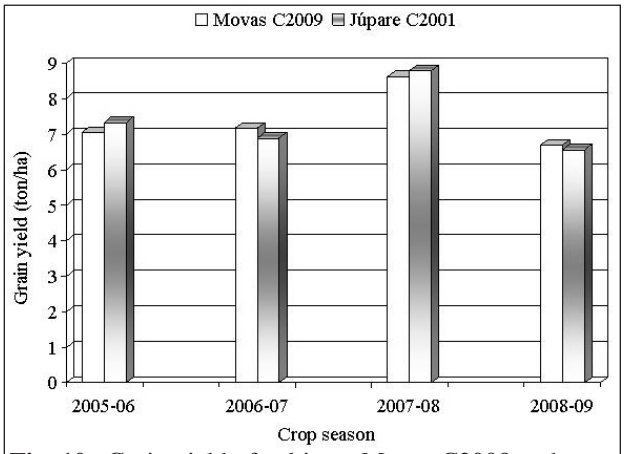

Fig. 10. Grain yield of cultivars Movas C2009 and Júpare C2001 under drip irrigation in block 810 at CIMMYT, during the autumn–winter 2005–06 to 2008–09 crop seasons in the Yaqui Valley, Sonora, Mexico.

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Effect of green manure crops and inoculation with Glomus intraradices on the quality and yield of wheat in the Yaqui Valley, Sonora, Mexico.

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Abstract. The effect of inoculating wheat seed with *Glomus intraradices* and the interaction with incorporation of maize (*Zea mays*), *Sesbania exaltata*, *Clitoria ternatea*, and sorghum (*Sorghum bicolor*) as green manure on wheat grain yield and quality was studied. Green manure treatments were compared with a control treatment that consisted of a fallow plot during the summer. A randomized complete block split-plot design with three replications was used to evaluate the treatments. Significant statistical differences were detected for grain yield, between green manure treatments, and the interaction between green manure and inoculation treatments. Grain yield was 7.690, 7.653, 7.590, 7.433, and 7.115 t/ha for *Clitoria*, sorghum, *Sesbania*, the control, and maize, respectively. There was a significant and positive interaction between *Glomus* and sorghum. The average grain yield of the biofertilizer treatment was 7.632 t/ha and 7.36 for the control. Wheat grain yield was 7.394 t/ha when green manure crops were established under irrigation, and 7.597 t/ha under rainfed conditions. For grain protein, the only significant difference was between irrigation treatments for green manure crops; a greater grain protein content (10.32%) was found in treatments where green manure crops were irrigated than those where green manure crops grew under rainfed conditions (9.67%). An average of 10.16% was obtained when seed was inoculated with *Glomus*, and 9.83% when it was not.

Introduction. The use of biological fertilizers is a practice of great interest in the last few years. The practice consists in inoculating seed with beneficial, natural soil microorganisms, increasing its concentration in the rhizosphere (Ferraris and Couretot 2006). Macias (2004) evaluated the use of biofertilizers in wheat during three crop seasons in northern Sinaloa, Mexico, and reported a 700 to 1,280 kg/ha increase with the use of the rhizobacterium *Azospirillum brasilense*, and from 300 to 820 kg/ha with the use of the fungal mycorrhiza *Glomus intraradices*, with respect to a control without nitrogen fertilization. In soil in the Yaqui Valley with 166 kg/ha of nitric nitrogen and 30 kg/ha of phosphorus available, Cortés (2000) did not find significant differences between the inoculation with *A. brasilense* and *G. intraradices*, fertilization with the formula NPK 200-52-0, and the absolute control; grain yield was 6.406, 6.696, and 6.128 t/ha, respectively. When *G. intraradices* or *A. brasilense* were used separately, grain yield was lower than that of the absolute control. Treatment with the rhizobacterium accumulated 28.3 kg/ha of additional nitrogen in relation to the absolute control. According to the information available, associations with *A. brasilense* are capable of fixing from 12 to 313 kg of nitrogen per ha per year depending on the conditions. In the case of the *Glomus* spp., it is generally accepted that this type of microorganisms increases the absorption of those nutrients that have very low mobility in the soil, such as phosphorus (Marschner 1986). Ferraris and Couretot (2006) reported an additive behavior without the interaction of inoculation by chemical fertilization in relation to yield, which coincides with the results obtained in northwest Mexico (Manjarrez 2002; Manjarrez et al. 2002; Macias 2002).

On the other hand, green manure is a type of cover crop grown primarily to add nutrients and organic matter to the soil. Typically, a green manure crop is grown for a specific period and then plowed under at the flowering stage and incorporated into the soil. In general, green manure crops are decomposed in and on the soil and are an ideal food-stuff for soil microorganisms (Kulmans and Vásquez 1999). They also increase the resistance to abrupt pH modification, provide substances such as phenols that contribute to plant respiration, and facilitate greater absorption of phosphorus and a better plant health (Guerrero 1993). Incorporation of green manure crops also is very important in crop rotation, because they increase production, incorporate residues, improve the soil cover, and interrupt the life cycles of pests, diseases, and weeds (Altieri and Nicholls 2000). The use of green manure is an option that will depend upon the objectives proposed, the area, weather conditions, and the main crop to be cultivated. In the case of the Yaqui Valley, it is possible to establish a green manure leguminous crop after wheat harvest, from July to September, in order to take advantage of the rainy period, by which the production of green material rises and nitrogen is delivered into the soil (García and Martínez 2011). This study evaluated the effect of inoculating wheat seed of durum cultivar CIRNO C2008 with the fungal mycorrhiza *G. intraradices* and the incorporation of green manure crops during the summer on grain yield and quality of the same cultivar.

Materials and methods. A study on the effect of green manure crops maize, *S. exaltata*, *C. ternatea*, sorghum, and a control treatment on wheat grain yield and quality was carried out at the Norman E. Borlaug Experimental Station during 2009–10. A randomized complete block split-plot design with three replications was used to evaluate treatments. The main plot corresponded to the green manure crops, the subplot to the irrigation treatments in the green manure crops, and the sub-subplot to seed inoculation with *G. intraradices*. The experimental plot consisted of four beds with two 50-m

rows each with a separation of 0.80 m (160 m^2), whereas the experimental unit consisted of two 3-m long beds. Mean comparison was performed with Tukey's multiple range test (p = 0.01 and 0.05). Weed control was carried out manually.

Crops were established in the month of June and incorporated as green manure in September of 2009. They were irrigated for germination and, later, half the area of each plot was irrigated twice on 30 July and 14 August, and the other half was left under rainfed conditions. The durum wheat cultivar CIRNO C2008 was sown in humid soil on 7 December, 2009, in those plots where the green manure crops had previously been incorporated. The seed that was inoculated with *G. intraradices* was treated at the rate of 1.0 kg/ha/30 kg of seed. Three complementary furrow irrigations were applied 46, 75, and 94 days after sowing.

Results and discussion. Significant statistical differences were detected between the green manure treatments, and the interaction between green manure and inoculation treatments for grain yield. In all cases, greater yield was detected in plots where the seed was inoculated with *G. intraradices*, except when maize was established as green manure crop under rainfed conditions. Incorporation of leguminous crops grown under irrigation or rainfed conditions, produced greater wheat grain yield with or without inoculation with the mycorrhiza; this phenomenom was not observed with incorporation of gramineous crops. In the case of maize, its incorporation as green manure caused a reduction in grain yield under all the different conditions of evaluation, whereas sorghum caused a reduction in yield when CIRNO C2008 was not inoculated with *G. intraradices*, but it significantly increased when inoculated with the mycorrhiza. The treatment with the greatest average wheat grain yield (7.690 t/ha) was obtained with the incorporation of *C. ternatea*, whereas the lowest yield was obtained with incorporation of maize. The significant statistical interaction between green manure crops and inoculation treatments indicated that inoculation with *G. intraradices* produced greater wheat grain yield, only when the green manure crop incorporated was sorghum (Table 14).

Table 14. The effect of green manure crops and inoculation with *Glomus intraradices* on the grain yield (t/ha) of durum wheat cultivar CIRNO C2008. Inoculation x green manure crop, Tukey 0.05 = 0.536; green manure crop, Tukey 0.05 = 0.473.

Green manure crop	Without *G. intraradices*		With *G. intraradices*		Mean
	Irrigated	Rainfed	Irrigated	Rainfed	
Sorghum	7.127 a	7.167 a	8.153 b	8.163 b	7.653 a
Clitoria	7.523 a	7.700 a	7.587 a	7.950 a	7.690 a
Control	7.290 a	7.497 a	7.320 a	7.623 a	7.433 ab
Sesbania	7.363 a	7.660 a	7.367 a	7.970 a	7.590 ab
Maize	7.017 a	7.257 a	7.197 a	6.990 a	7.115 b
Mean	7.264 a	7.456 a	7.525 a	7.739 a	

For grain protein, the only significant difference was between irrigation treatments for green manure crops; there was a positive effect when crops were established under irrigation compared to rainfed conditions, because the percentage of protein increased (Table 15). During this first study, the grain yield obtained without fertilizers, including the control, indicated a great amount of residual nitrogen in the soil from trials carried out in previous wheat seasons. This also indicates the low efficiency of wheat for taking up this element. The greater wheat grain yield obtained when green manure crops were established under rainfed conditions could be explained by the fact that under this condition they produce a small amount of biomass, which in turn requires less time to be mineralized, and the nitrogen becomes immovable for a shorter period of time.

Table 15. The effect of green manure crops and inoculation with *Glomus intraradices* on the gran protein content (%) of the durum wheat cultivar CIRNO C2008. Inoculation x irrigation, Tukey 0.05 = 0.634.

Green manure crop	Without *G. intraradices*		With *G. intraradices*		Mean
	Irrigated	Rainfed	Irrigated	Rainfed	
Sorghum	9.94	9.71	10.12	10.07	9.96
Clitoria	10.12	9.25	10.45	10.08	9.97
Control	10.44	9.85	10.71	9.82	10.24
Sesbania	9.91	8.08	10.28	9.87	9.54
Maize	10.68	10.25	10.46	9.67	10.27
Mean	10.22 a	9.43 b	10.41 a	9.90 a	

Conclusions. The incorporation of leguminous crops as green manure helps to increase wheat grain yield. The use of mycorrhizae such as *G. intraradices* as seed inoculants must continue being investigated in order to determine the interactions that provide its optimum use on wheat, as well as the use of irrigation on the production of green manure.

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Evaluation of the biological effectiveness of BTN+ in rainfed wheat.

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Introduction. Intensive agricultural activities constantly deteriorate soil fertility, therefore, the theories of minimum tillage and the use of plant residues after harvest aim to partially reëstablishing the fertile condition of soils. Soil bacteria form part of this biological complex and have a key role in production of organic matter. The soil is an ecosystem that harbors five main groups of microorganisms: bacteria, actinomycetes, fungi, algae, and protozoa are considered inhabitants of the community. Bacteria have a wide biochemical diversity, so they are the most abundant of the groups. The bacterial population in the soil is large, although individuals measure a few micrometers in length.

The commercial product BTN+ is distributed and commercialized by the company GrowGreen Mexico, a subsidiary of Bio Tech Nutrients LLC, from Las Vegas, NV, U.S., and it is publicized as 'plant feed'. BTN+ is composed of carbon, hydrogen, oxygen, micronutrients, humic acid, fulvic acid, kelp, soil microbia, and enzymes. BTN+ utilizes energized carbon and bacteria, which according to the company, reduce salts in the soil and consequently reduce the soil electrical conductivity (EC), making nutrients available to the plant. Our objective was to evaluate the biological effectiveness of BTN+ on wheat cultivar Arandas F90 under rainfed conditions.

Materials and methods. A randomized complete block design with three treatments and six replication was used for this study, using bread wheat cultivar Arandas F90 under rainfed conditions. The study was carried out at the Centro-Altos de Jalisco Experimental Station, in Tepatitlan, Jalisco, Mexico, during the summer 2009. The soil type where the experiment was established was a loam-clay, pH 5.0–5.6, with a deficient organic matter content of 0.84–0.90%. The

sowing date was 9 July, 2009, once the rainfall period was established. The treatments were as follows: 1. BTN+, 2. fertilization formula according to INIFAP`s technical recommendation, and 3. control without any fertilization (Table 16).

Table 16. Application of BTN+ and INIFAP recommended fertilizer formula on bread wheat cultivar Arandas F90 at the Centro-Altos de Jalisco Experimental Station, in Tepatitlan, Jalisco, Mexico, during summer 2009.

Treatment	Application	Date
BTN+	1st application: 41 L/ha of the liquid product, sprayed during sowing and on the seed.	9 July
	2nd application: 18 L/ha of Carbon Burst solution to the foliage.	14 August
	3rd application: 25 oz/ha (750 mL/ha) of fungicide Quadris two weeks after the 2nd application.	27 August
	4th application: two weeks later, 18 L/ha of Carbon Burst + 10 oz (300 mL) of Quadris.	14 September
INIFAP's technical recommendation (160-60-00)	The formula 80-60-00 was applied during sowing.	9 July
	Complementary application 80-00-00	9 August
Control	No fertilizer application.	

Foliar applications were made with a manual sprayer with a 20 L capacity and a Tee Jeet 8004 flat nozzle using a rate proportional to 200 L/ha of water. For the INIFAP treatment, the fertilization formula 180-60-00 was obtained by a physical mixture of 130.5 kg of the formula 18-46-00 + 145 kg of urea. The experimental plot was 8.0 m x 8.0 m with a proportional quantity of fertilizer (835.2 g + 928 g of 18-46-00 + urea/experimental plot (64 m^2), for the first application, and 1,248 g of urea for the second application. The experimental unit was 4.0 m x 4.0 m (16 m^2), according to the protocol.

The variables evaluated were days to flowering, days to physiological maturity, and grain yield (kg/ha). Harvest was carried out with a Pullman stationary thresher. Three soil samples were taken randomly during sowing; they were made up of six sub-samples obtained at 0–15 cm depth, which represents the arable horizon.

Results and discussion. Although the experiment was established once the rainfall period started, three weeks later there was a two week interval of drought, which somewhat effected the overall development of the wheat plant, with a consequent delay in the application of treatments. Because of this drought, weed control practices were limited, but days to flowering, heading, height, and physiological maturity were the same, because the same cultivar was used in all treatments; therefore, data on those parameters is not presented.

Table 17. Grain yield (kg/ha) of the bread wheat cultivar Arandas F90 under different nutrient treatments, at the Centro-Altos de Jalisco Experimental Station, in Tepatitlan, Jalisco, Mexico, during summer 2009.

Treatment	Replication					
	I	II	III	IV	V	VI
BTN+	3,687.50	4,859.38	4,218.75	3,765.63	2,468.75	3,750.00
INIFAP (160-60-00)	3,250.00	3,187.50	1,531.25	1,765.63	2,937.50	5,500.00
Control	937.50	3,250.00	2,187.50	2,000.00	2,000.00	1,875.00
Mean	2,625.00	3,765.63	2,645.83	2,510.42	2,468.75	3,708.33

Grain yield with BTN+ ranged from 2,468.75 to 4,859.38 kg/ha, INIFAP's treatment ranged from 1,531.25 to 5,500, and the control was 937.50 to 3,250.00 (Table 17). BTN+ showed the highest yield in four of the six replications; whereas INIFAP's treatment was highest in two, which included the overall highest yield of 5,500 kg/ha in the sixth replication. The yield average of the six replications ranged from 2,468.75 to 3,765.63 kg/ha. Average grain yield of the BTN+ treatment was 3,791.67 kg/ha (Fig. 11), but it was not statistically different from INIFAP's treatment (3,028.65) (Table 18, p. 77). Average yield of the control was 2,041.67 kg/ha, statistically different from the BTN+ treatment, but not from the INIFAP treatment. The grain yield of the control

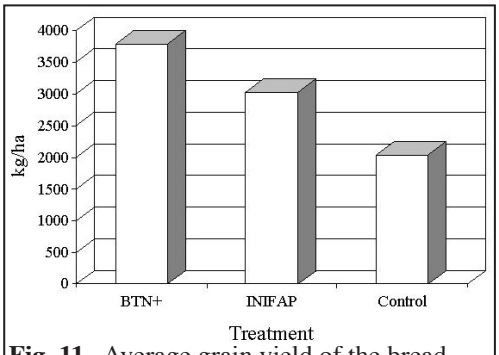

Fig. 11. Average grain yield of the bread wheat cultivar Arandas F90 under three different nutrient treatments at the Centro-Altos de Jalisco Experimental Station in Tepatitlan, Jalisco, Mexico, during summer 2009.

indicated a normal soil fertility, either due to residue from the previous crop or other factors not considered in this study.

Table 18. Analysis of variance and mean comparison of grain yield (kg/ha) of the bread wheat cultivar Arandas F90 under different nutrient treatments at the Centro-Altos de Jalisco Experimental Station, in Tepatitlan, Jalisco, Mexico, during summer 2009.

SV	df	SS	MS	Fc	Pr>F	
Treatments	2	9,237,657.335	4,818,828.668	4.50	0.0403	*
Replications	5	5,589,586.046	1,117,917.209	1.09	0.4225	NS
Error	10	10,255,506.730	1,025,550.670			
Total	17	25,082,750.110				

Treatment	kg/ha	Significance
BTN+	3,791.67	a
INIFAP	3,028.65	ab
Control	2,041.67	b

The study of the rhizosphere is complicated, because three important components converge: soil, plants, and microorganisms. Microorganisms are highly influenced by plant exudates, soil pH, and the physico-chemical condition. Exudates reported include carbohydrates of different types, nucleotides, flavonoids, enzymes, plant hormones, and aminoacids. These compounds are generated by the photosynthetic and metabolic activity of the plant (carbon compounds, H^+, inorganic ions, organic acids, or reducing agents). To conclude that BTN+ was the best treatment for wheat grain yield under rainfed conditions in Tepatlitan, Jalisco, Mexico would be biased, because it is not known its composition and the specific effects on the wheat plant or on the microorganisms present in the soil at the experimental station. Although, the average yield obtained with the BTN+ treatment was the highest, we do not know which factors or elements are induced or those that are inhibited or eliminated. On the other hand, the highest yield in this study was obtained with the INIFAP treatment (5,500 kg/ha).

Because several aspects were not included in this study, such as the pH behavior in the soil through time in the different treatments, the identification of population dynamics of the soil microorganisms more representative of the location, or the characterization with greater precision of the plant phenology under the different treatments, repeating the experiment taking into consideration the parameters that were not recorded in this study would be important.

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ITEMS FROM PAKISTAN

NUCLEAR INSTITUTE OF AGRICULTURE (NIA)
Tando Jam, Pakistan.

Karim Dino Jamali.

Breeding for semidwarf and high grain yield wheats.

Wheat is an excellent food crop for Pakistan. The production of wheat always has been the main occupation of the farmer in the diversified agroclimatic conditions of Pakistan. The evolution of cultivars with high grain yield potential and a desirable combination of traits have always been the major objectives of our wheat breeding programs. During 2009-10, a production of 23.8 x 10^6 tons was achieved from an area of 9.0 x 10^6 hectares. The average yield during the year was 2,639 kg/ha (Table 1).

Table 1. Area, production, and average yield (2009–10) of wheat in Pakistan (Source: Ministry of Food, Agriculture and Livestock, Islamabad Pakistan).

Province	Area (x 10^6 ha)	Production (x 10^6 ha)	Yield (kg/ha)
Punjab	6.894	18.240	2,646
Sindh	1.028	3.650	3,551
Khyber Pakhtunkhwa (NWFP)	0.752	1.184	1,574
Baluchistan	0.368	0.790	2,147
Pakistan	9.042	23.864	2,639

Wheat breeding at NIA, Tando Jam. The objective of the wheat breeding program is to develop high-yielding wheat cultivars endowed with good quality characteristics. These cultivars must possess tolerance to biotic and abiotic stresses. The NIA has released 11 cultivars, including two new cultivars, NIA-Sunhari and NIA-Amber for Sindh province. NIA–Sunhari and NIA–Amber were released on 3 February, 2010.

Salient features of NIA–Sunhari. NIA-Sunhari carries the *Rht1* gene and ranges from 90–100 cm. This cultivar has dark green leaves and possesses a high tillering capacity. NIA–Sunhari was developed for irrigated areas but can produce better yields under drought conditions. The cultivar has excellent quality characteristics, having high protein content (14.92%), a higher percentage of wet gluten (32.86%), dry gluten (11.02%), and an SDS value of 30 CC.

Salient features of 22-03, a candidate cultivar. The candidate wheat cultivar was tested in National Uniform Wheat Yield Trial (NUWYT) during 2008–09. The NUWYT results suggested that 22-03 is completely resistant to leaf and yellow rusts. The relative rateindex for leaf rust was 8.5 and yellow rust 8.7. Line 20-33 also is moderately resistant against a local stem rust race. The line yielded 4,267 kg/ha compared with those of the check cultivars (4,098 kg/ha) under normal sowing conditions. Line 22-30 has a high protein content of 16.42%, a higher percentage of wet gluten (35.19%), a higher percentage of dry gluten (12.4%), and a high SDS value of 35 CC.

Cooperation with the National Institute of Biology and Genetic Engineering (NIBGE), Faisalabad. A new advanced line (C7-98-4) has been sent to NIBGE scientists for wheat transformation (genes for phosphorus use efficiency) during 2008. We are still waiting for the performance of the line.

Collaboration for wheat breeding and genetics during the year 2009–10. Genotypes NIA–Sunhari, 22-03, 54-03, 6-12, and C7-98-4 were sent to the National Agriculture Research Council Islamabad, Pakistan for rust disease screening Genotypes DTSN-06, DTSN-23, DTNS-26, DTNS-29, and DTSN-33 were sent to the Barani Agriculture Research Institute, Chakwal, Pakistan, for drought screening. For plant physiological studies related to drought, the genotypes 54-03, 5-02, NIA–Sunhari, 22-03, and 17-02 were given to the Plant Physiology Division, Nuclear Institute of Agriculture, Tando Jam.

Zonal/regional trial studies. Two candidate lines, 6-12 and CIM-04-10, were grown in eight sites for zonal trial studies during the year 2009–10 in the Sindh province.

Advance Station Trials (Trial I, II, III, and IV). Four trials were grown during the 2008–09 crop year for yield and yield component studies. Trial I, Trial II, and Trial III each consisting of 16 genotypes including the two common check cultivars Sarsabz and Kiran. Trial-IV (isolines) consisted of 34 genotypes including the two checks Sarsabz and Anmol. The trials had three replicates, six rows with a 4-m row length.

Advance Station Trial I. This trial was sown on 21 November, 2008, and consisted of 14 advanced station lines and two check cultivars. In this trial, line 10 produced the highest grain yield (1,850 g/plot). Other lines with high grain yields were 7 (1,817 g/plot), 5 (1,800 g/plot), 9 (1,717 g/plot), 1 (1,692 g/plot), 11 and 13 (1,583 g/plot), and 2 (1,567 g/plot). The possible reasons for the high grain yield in line 10 could be due to an early heading date (70) and better 1,000-kernel weight (42.01 g).

Advance Station Trial II. The trial was sown on 21 November, 2008, and consisted of 14 advanced station lines and two check cultivars. Line 7 had the highest grain yield (1,817 g/plot) followed by line 9 (1,817 g/plot). Subsequent lines with high grain yields were 13 (1,600 g/plot), 5 (1,583 g/plot), 2 and 6 (1,550 g/plot), and 3 (1,542 g/plot). Possible reasons for the high grain yield in line 7 could include that it had the highest main spike grain yield and a better 1,000-kernel weight (40.4 g).

Advance Station Trial III. The trial was sown on 4 December, 2008, and consisted of 14 advanced station lines and two check cultivars. In this comparison, line 11 had the highest grain yield (1,500 g/plot), followed by lines 4 (1,433 g), 2 (1,350 g/plot), 5 and 12 (1,325 g/plot), and 9 (1,233 g/plot). The high grain yield in line 11 could due to its high number of spikelets/spike (20.6).

Advance Station Trial IV (isoline studies). This trial was sown on 13 November, 2008, and consisted of 32 advanced station lines and two check cultivars. In this comparison, line 30 had the highest grain yield (2,083 g/plot). Other lines with high grain yields were 29 (2,033g/plot), 7 (1,967 g/plot), 22 (2,025 g/plot), and 7 (1,967 g/plot).

Mutation breeding studies.

Radiation studies in the M_3 generation. Selected M_3 plants were grown in progeny rows under normal soil conditions from irradiated material of cultivars Bhittai and Kiran-95. A total of 97 M_3 progenies of mutated breeding material were sown in two replicates with 1-m rows. Data were recorded for morphological characters and days-to-heading under field conditions. The data for yield and its components are being recorded. Mutant M_3 plants were selected for M_4 generation.

Selected M_3 bulk material also was grown under saline soil conditions; the salinity ranging from 17 to 41 ECe ds/m. The trial consisted of irradiated breeding material of the cultivars Bhittai and Kiran-95 planted in six 2-m rows in three replicates. Data were recorded for morphological characters and days-to-heading under field conditions. The data for yield and yield components are in progress to be recorded. Mutant M_3 progenies were selected for M_4 studies.

Drought tolerance studies.

Thirty-six genotypes of wheat were selected for drought studies during 2009–10. The trial consisted of three replicates; each entry had two 1.5-m rows. Four treatments were used; treatment 1 had zero/no irrigation, treatment 2 had two irrigations, treatment 3 had three irrigations, and treatment 4 received four irrigations. The data were recorded for days-to-heading and plot grain yield (g). Genotype C6-98-7 had an earlier heading date (63 days) under zero/no irrigation than the check cultivar Margalla (65 days). Genotypes that had a comparatively higher grain yield than the best check cultivar Margalla (202 g) were 29-02 and C7-98-4 (222 g), C3-98-8 (213 g), CIM-03-2 and C6-98-5 (208 g), CIM-04-1 (212 g), and C2-98-7 (242 g) under zero/no irrigation. The genotype C2-98-7 (317 g) with two irrigation had a higher grain yield than best check cultivar Margalla (314 g). Other genotypes that had higher grain yields than that of Margalla (320 g) under three irrigations were 4-03 (322 g), CIM-04-1 (345 g), C2-98-7 (330 g), and C6-98-5 (347 g). With four irrigations, genotypes with a higher grain yield than Margalla (386 g) were CIM-04-1 (427 g) and C2-98-7 (413 g). The mean performance over the four treatments showed that the check Margalla was early heading; 70 days. The grain yield for check cultivars were Margalla (306 g), Khirman (182 g), and Chakwal (182 g). Genotypes with higher grain yiel/plot were CIM-04-1 (311 g), C2-98-8 (326 g) ,and C6-98-5 (308 g).

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NATIONAL AGRICULTURAL RESEARCH CENTER (NARC), ISLAMABAD WHEAT WIDE CROSSES AND CYTOGENETICS AND COLLABORATING NATIONAL PROGRAMS
Islamabad, Pakistan.

Wheat wide crosses and general wheat improvement trends: initiatives and the course ahead.

Mujeeb-Kazi and Alvina Gul Kazi.

Wheat production in 2010 reached near 24 x 10^6 tons at approximately 2.6 t/ha. The yield projection for the approaching harvest in 2011 has been projected between 24.5 to 25 x 10^6 tons, and this is primarily due to congenial environmental conditions across the country. No change in the production constraints that prevail to achieve projection targets was observed. Abiotic stresses of drought and salinity/sodicity remain with heat merging as a major concern due to the cropping systems that are in place. The rusts still rank as number one biotic stress priority, with yellow and leaf rust the biggest. Stem rust, around the local race prevalent in lower Punjab and in the province of Sindh, is carefully monitored because, if confounded by Ug99 when it reaches Pakistan, will pose a serious hazard. National scientists have released varieties that are Ug99 resistant based upon screening in Kenya and advanced breeding materials in conventional national breeding programs also are added sources of new resources. Extensive new genetic diversity is crucial for achieving security against this biotic stress and an on-base research program is a dire need.

A strong prebreeding program firmly in place in Pakistan is paramount and has been initially planned by mid-2010. Unfortunately, both CIMMYT and ICARDA leadership have set in place an operational plan where the CIMMYT Pakistan representative has stated that all prebreeding under the Pak-U.S. bilateral alliance will be done in U.S. This is a set-back to our national efforts, where the forward direction should be to evolve and upgrade the developing country programs promoting scientific advancement integrated with U.S. elite scientific institutions, which was the spirit earlier advocated by the Pak/U.S. partners in 2009 and 2010. Our current program is actively involved in prebreeding and has made impact. International center decisions have not helped our national cause in moving ahead swiftly around volatile young, human, resource strength that is being generated progressively. Despite this temporary constraint, our wide crossing program is moving ahead and has rapidly restructured around new partners hoping that the earlier linkages will fall back in place.

Our new Wheat Wide Crosses Program has identified Ug99 resistant lines through crosses involving D-genome synthetic hexaploid germ plasm. Furthermore, the derivatives also are resistant against the local race of stem rust identified upon screening in Sindh. The nature of the local race has to be elucidated and the Cereal Disease Program of NARC is on the front line for this informational sharing. Resistant, derived lines from Wheat Wide Crosses to Ug99 are shown in Table 1 (p. 82).

Table 1. Advanced Ug99 stem rust resistant derivatives from bread wheat cultivars recombined with D-genome synthetic hexaploid wheats screened in Kenya under the BGRI initiated facilitation at the Kenyan Agricultural Research Institute. Reactions are R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlap of MR–MS, MSS = moderately susceptible to susceptible, and S = susceptible; control disease 90–100S.

Pedigree	Stripe rust	Stem rust	
	25 February	4 March	17 March
Altar 84/*Ae. tauschii* (224)//2*YACO/3/ Mayoor//TKSN1081/*Ae. tauschii* (222)/4/ Kukun/5/Altar 84/*Ae. tauschii* (221)/YACO	15M	10M	20M
KAUZ/5/68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (431)	5MR	10M	15M
Opata//DOY 1/*Ae. tauschii* (255)	10M	5MR	10MR
BKH93/Flycatcher	30MSS	20M	30M
Bakhtawar 94/5/68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (431)	15M	15M	20M
CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (208)/5/OAPTA/5/68.111/RGB-U// WARD RESEL/3/STIL/4/*Ae. tauschii* (783)	30S	5MR	10MR
Mayoor//TK SN1081/*Ae. tauschii* (222)/3/ OPATA/6/68.111/RGB-U//WARD/3/ FGO/4/RABI/5/*Ae. tauschii* (878)	40M	15M	20M
Opata//CETA/*Ae. tauschii* (1027)	0	15M	20M
Worrakatta/Pastor//SHR	50S	10M	15M
PFAU/Weaver*2//Kiritati/3/WAFAQ	5MR	5M	10M
WL6736/5/2*BR12*3/4/IAS55*4/CI14123/3/ WAFAQ	5MR	10M	15M

Our Wheat Wide Crosses Program, due to prevalent circumstances, has shifted its major focus towards intensive prebreeding areas exploiting novel alien genomic diversity that could be readily adapted to national environmental regimes. Our main breeding effort now is structured around alliances with the private sector and the four agricultural centers of the Pakistan Atomic Energy Commission (PAEC). The PAEC has centers in Sindh and two in Punjab (Upper) and KPK (former NWFP). The Sindh alliance will allow the province of Baluchistan to be covered and then other selected provincial partners shall be tapped to facilitate. Selected locations across the country allow for hotspot sites to be tapped that permit screening for heat, drought, salinity, stem rust local race (SINDH) plus bread-making quality aspects, leaf and stem rust, spot blotch, drought (Lower Punjab), drought (Upper Punjab), yellow rust, aphids, BYDV (KPK), and drought (Baluchistan).

The pivot location where Wheat Wide Crosses Program is located (Islamabad) concentrates on prebreeding plus basic research to feed material to all locations and maintain wider international ties in addition to those with CIMMYT/ICARDA and embrace all regional programs that surround Pakistan to the west, east, and northeast. This modified structure allows the wide cross group to concentrate on basic prebreeding and strategic aspects of genetic recombinations with the applied parts exploited by other location partners through their major expertise on breeding.

Our group now focusses on screening for karnal bunt, biochemical quality aspects, all in vitro testings for abiotic stresses, molecular diagnostics, doubled haploidy, micronutrient assays and cytogenetics plus maintenance of genetic stocks and wild species with depositions of appropriate categorized germplasms in the national gene bank also in NARC in PGRI at Islamabad.

Current progress in the Wide Cross Program during mid-2006 to mid-2010, via the support of three major research projects, led to the modest development of an infrastructure including greenhouses, screenhouses, field, and laboratories that undertake activities on stress physiology, cytogenetics, biochemical genetics, molecular diagnostics, doubled haploidy, growth rooms and seed storage capacity around the programs working with the germ plasm collection.

The second major output has been a human resource development from internees, degree holders at the M. Phil and Ph.D. levels, research fellows and assistants, plus trained support staff that hold high school degrees (ayudantes in Spanish or skilled labor). The total output number has been 70 in approximately four years (September 2006 until June 2010).

The third component of the program has been research output, and the current status is the generation of advanced F_7 lines (KAZI 1–9, 11–13) that have seed distributed across the country for testing and increase. These are introduced and adapted lines from international nurseries and also those generated from wheat/synthetic hexaploid crosses made within our program. The SSR-based diversity profiles of these lines will allow us to differentially deploy cultivars in the near future across the country and safeguard our food security through possessed genetic variation across a wide genetic base. The line KAZI 11 is early maturing, possesses multiple resistances, and is a good candidate for the province of Sindh. KAZI 11 is resistant to both the local stem rust race and Ug99. A field plot at a private partner location in Punjab (RCA Seeds) exemplifies our applied effort (Fig. 1).

Fig. 1. A collaborating scientist from the RCA seeds in the KAZI 11 plot at Khanewal, Punjab, during the 2010–11 crop cycle.

In addition, 1,000 elite selections from the F_5 to F_6 generations, derived from our main recombination programs where hexaploids of the A and D genome have been crossed onto elite bread wheat cultivars, are being studied for various attributes. We also have 60,000 derivatives from F_2 to F_4 generations, various mapping populations, cytogenetic stocks, and wild species from all three Triticeae gene pools.

Students who have been involved in the program are major contributors and the articles that follow this introduction show the potential of the germ plasm that has been generated for various production stress constraints. These introductory perceptions address investigations conducted by our young human resource talent on resistance/tolerance to rust, Karnal bunt, powdery mildew, spot blotch, heat, salinity, drought, DNA fingerprint diversity using RAPDs and SSRs, and bread-making quality. The outputs are based upon national testing, collaborative alliances (national/international), and field and controlled environment testing.

The way forward: some perceptions.

National organizational changes have set in and will be implemented by mid-2011. Food security will remain a key concern and, as wheat research progresses, a substantial strategic change is advocated. The immediate major benefit will come from management aspects and these could pay off swift dividends that appear unimaginable if set in place appropriately. The research program alliances of interest will have to be formulated that can address and exploit at least some of the following:

– exploit the global elite durum cultivar diversity for improving bread wheat via pentaploid breeding,
– target tetraploids identified for heat and drought tolerance for bread wheat improvement, e.g., *T. turgidum* subsp. *dicoccum*,
– incorporate bread wheats with large spikes in the breeding program with a selection sieve for optimum grain filling, grain number/spike, and improved tillering capacity,
– investigate early maturity to address climate change and global warming,
– micronutrient enrichment, an interest for wheat breeders, requires greater attention,
– encourage cotton and rice breeders to produce early maturing types as these two crops fall in the wheat cropping system of rice/wheat and cotton/wheat cycles,
– give greater attention to wheat/alien chromosome translocations on the applied dimensions through earlier available stocks or by producing new products mediated by cytogenetic protocols of manipulation,
– have in place a volatile program on doubled haploidy to assist national breeding partners for applying the protocol at least by the F_3 and,
– infuse molecular diagnostics for adding efficiency to breeding to allow marker-assisted trait incorporation to flourish.

There is interest in hybrid wheat and transgenics; two areas that could be contemplated upon and addressed through multidisciplinary integration of expertise. Double haploidy has a role in both programs where for heterotic F_1s to be fixed or transgenics made homozygous on T_0 plants, a massive effort is required. At present, using the maize protocol is the key, but for the future, microspore culture if genotype nonspecific could do wonders for wheat breeding efficiency. Other aspects that can augment yield need to be observed and should be integrated into programs as these

become available. Some are experimental but a C4 wheat or bringing the rice resistance for rust into wheat may be a long shot. However, innovative means of using genomic diversity through gene pyramiding, another look at Triticale or even durum as a new crop addition. should be within our national reach to address when we are projecting to the national vision of 2050 based upon prebreeding, genetic diversity, and the 'Green-to-Gene Revolution'.

Evaluation of Elite-I synthetic hexaploid germ plasm for various phenological, molecular, and disease attributes.

Alvina Gul Kazi, Awais Rasheed, Farrukh Bashir, Hadi Bux, Abdul Aziz Napar, and Abdul Mujeeb-Kazi.

In the primary gene pool of wheat, the species included are hexaploid landraces, cultivated tetraploids (2n=4x=28, AABB), wild *T. turgidum* subsp. *dicoccoides*, and the diploid (2n=2x=14) donors of the A and D genomes to durum/bread wheats. In this gene pool, genetic transfers result through direct hybridization, homologous recombination, and relatively simple breeding strategies. Some combinations requirethe assistance of embryo rescue and are of greater interest for enhancing diversity in bread wheat. The goat grass *Ae. tauschii* (2n=2x=14, DD) currently occupies a very high priority in wheat breeding.

Conventional wheat breeding programs are built around diverse cross combinations of germ plasm residing in the same gene pool that undergo genetic recombination followed by trait segregation, evaluation, and ultimately cultivar release. In order to amplify the genetic diversity of the crop, novel genetic resources become a focus and the close progenitors of wheat are preferred; these are the numerous accessions of the A, B, and D genomes. Within this spectrum, the A and D genomes have greater advantage than B essentially because of their proximity to the A and D sets present in bread wheat and also based upon cytogenetic test analyses that indicate greater closeness of the seven chromosomes of the D-genome wild diploids than the A-genome chromosomes with their respective D and A genomes. Accessions of these two diverse sources reside in the primary gene pool, can be hybridized with ease, allow for swift gene transfer via homologous recombination, and have extensive diversity for global biotic/abiotic stress/constraints that limit wheat production.

Greater genetic proximity tilts the optimum choice towards the exploitation of the D-genome diploid *Ae. tauschii* and also because few accessions were involved in the natural hybridization/amphiploidization event, thus giving rise to a crop with an extremely narrow genetic base. Complementary to this are observations associated with the *Ae. tauschii* role that have enabled current investigators to focus their wheat improvement efforts around this wild diploid via various protocols.

Elite-I subset advance. The 95 primary synthetics were studied for their phenotypic and molecular characterization together with screening against Karnal bunt, stripe rust, and powdery mildew. The phenotypic characters were days-to-flowering, days-to-physiological maturity, height at maturity, presence or absence of pubescence and pigmentation, and 1,000- kernel weight. Molecular characterization for establishing DNA diversity profiles was done via RAPDs and SSR microsatellite markers.

All the 95 Elite-I entries were screened in pot trials in the greenhouse at Murree. Fourty-four accessions of 95 the Elite-1 SH wheats showed a resistant reaction at seedling stage (Table 2, pp. 84-86). Infection type ranged from 0–6 at the seedling stage indicating the presence of major genes for resistance. Some of these resistant accessions exhibited different reaction types against powdery mildew under field conditions. The Elite-I entries also were screened under field conditions at Kaghan and majority showed APR and were found to be resistant to completely resistant (immune).

In the Elite-I, 44 accessions showed resistance against powdery mildew at both seedling and adult-plant stages, including 6, 7, 8, 11, 14, 25, 27, 32, 34, 36, 37, 38, 40, 42, 43, 44, 45, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 59, 60, 62, 64, 68, 69, 70, 71, 78, 79, 81, 83, 84, 90, 91, and 93. All these lines with excellent resistance against powdery mildew can be used in direct crosses with elite commercial wheat cultivars for further exploitation as sources of resistance against powdery mildew for wheat improvement.

Another category of the germ plasm included the accessions with APR but susceptible at the seedling stage. This high value APR is needed by breeders and agronomists for introducing durable powdery mildew resistance in elite commercial cultivars and is controlled by different minor genes independently or group of genes working together mak-

Table 2. Phenological and disease characterization of the D-genome synthetic hexaploids in the Elite-I set. FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown); PMA = days-to-physiological maturity; TKW = 1,000-kernel weight (g); G/S = number of grains/spike; SL = spike length (cm); KB = Karnal bunt (– = immune, + = susceptible); Pm (S) = powdery mildew screening at the seedling stage; Pm (A) = powdery mildew screening at the adult-plant stage; Yr (S) = stripe rust screening at the seedling stage; Yr (A) = stripe rust screening at the adult-plant stage where R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible.

No.	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Pm (A)	Yr (S)	Yr (A)
1	104	100	LB	144	52.3	22	12.0	–	1-1	6	1	R
2	89	110	LB	130	59.6	43	12.0	–	1-1	7	1	0
3	102	95	LB	136	59.7	31	12.0	–	2-1	6	0	5MRR
4	85	115	W	120	43.0	23	8.0	+	1-1	6	78	20MR
5	99	120	LB	140	57.0	38	12.0	+	0-0	5	78	5R
6	99	100	DB	136	54.4	20	12.2	+	0-0	3	1	5R
7	96	105	W	132	46.7	10	10.2	–	1-1	2	0	20S
8	100	110	W	132	59.4	25	7.2	–	1-1	3	0	0
9	96	135	W	134	53.7	14	8.0	–	1-1	4	78	0
10	117	85	DB	152	52.4	9	14.0	–	1-1	4	12	TMS
11	100	110	DB	144	55.6	13	12.0	–	3-1	2	12	10S
12	85	115	DB	127	62.2	14	11.0	+	1-1	4	56	20MS
13	110	105	DB	148	55.5	48	7.0	–	1-1	4	7	10MS
14	93	115	W	130	59.0	42	14.0	–	1-1	3	0	40S
15	106	115	B	144	60.0	10	11.0	–	1-1	4	7	40MS
16	100	95	W	134	55.9	9	9.0	–	1-1	5	4	40S
17	99	100	DB	134	60.0	54	13.7	–	1-1	4	78	50S
18	110	105	B	148	58.8	10	13.2	–	3-2	5	7	20MSS
19	96	105	B	134	57.7	15	12.0	–	1-1	5	1	30MR
20	99	100	W	136	50.8	14	10.0	+	2-1	5	12	20MRMS
21	110	105	W	144	59.6	12	10.5	–	2-1	4	34	MSS
22	110	105	LB	148	53.1	15	9.0	–	2-1	4	89	S
23	106	105	DB	148	55.9	18	12.3	–	1-1	4	67	40MRMS
24	99	90	LB	134	54.8	16	12.0	–	1-1	4	12	40MS
25	100	105	LB	136	52.6	12	13.0	–	1-1	3	0	10MS
26	85	125	DB	127	60.5	49	9.2	–	1-1	6	67	40MSS
27	117	90	B	152	53.2	28	7.3	–	1-1	3	1	10R
28	119	100	LB	152	49.5	11	12.5	–	1-1	7	34	20MSS
29	100	105	W	132	47.5	6	11.0	+	1-1	4	12	20MRMS
30	110	100	B	148	38.0	12	14.0	–	1-1	5	12	40MRMS
31	96	115	LB	134	55.6	23	14.2	–	1-1	5	45	60MRMS
32	99	100	W	134	54.0	16	14.0	+	1-1	3	0	0
33	96	120	W	134	33.4	14	13.0	+	1-1	4	89	50S
34	96	110	LB	130	58.1	10	14.0	–	1-1	2	0	20S
35	106	100	LB	148	32.5	17	14.3	–	1-1	4	0	10R
36	96	110	LB	144	60.1	13	14.5	–	1-1	2	0	20MRR
37	96	125	LB	134	58.9	15	12.0	–	1-1	2	12	40MS
38	99	110	LB	136	52.1	23	14.0	–	1-1	3	56	50MS
39	99	100	LB	134	30.2	38	14.0	–	1-1	5	12	40MS
40	100	115	LB	138	51.0	10	15.5	+	2-1	2	0	TR
41	99	120	LB	136	48.7	16	14.2	–	1-1	4	0	TR
42	96	105	LB	134	46.5	9	14.8	+	1-1	3	12	20RMR
43	104	120	LB	144	50.7	13	11.0	–	1-1	3	12	40MRMS
44	93	125	B	134	58.2	17	12.0	–	1-1	3	12	20MRMS
45	93	125	B	130	55.4	28	9.0	–	1-1	2	23	60MSS

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No.	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Pm (A)	Yr (S)	Yr (A)
46	96	100	LB	144	57.4	18	12.0	–	2-1	6	45	20MS
47	96	125	LB	130	55.9	20	12.0	–	1-1	2	45	40MS
48	100	100	LB	148	54.9	22	12.0	+	1-1	2	1	0
49	76	135	DB	115	44.7	5	10.0	–	1-1	3	1	0
50	85	110	LB	127	57.8	20	10.0	–	1-1	3	0	0
51	85	110	LB	127	51.2	6	12.3	–	1-1	2	1	5MRR
52	99	105	LB	134	54.2	12	14.0	–	1-1	3	0	0
53	96	90	LB	127	53.4	8	14.2	–	1-1	3	4	40MSS
54	110	120	LB	148	42.3	23	14.0	–	0-0	3	0	40MSS
55	99	125	LB	144	54.7	23	14.0	+	0-0	3	8	5R
56	112	115	LB	148	54.8	9	10.0	–	1-1	3	1	30MS
57	112	110	LB	148	50.0	5	12.0	–	2-1	1	45	50S
58	110	115	LB	144	49.0	8	12.0	–	1-1	3	78	10MS
59	99	90	B	134	49.5	11	10.2	+	0-0	4	45	40MS
60	96	120	B	134	52.4	16	14.0	–	1-1	3	1	20MR
61	100	115	LB	144	54.1	61	14.2	–	1-1	3	1	70S
62	96	110	LB	136	52.8	46	13.0	–	2-1	5	67	5MRMS
63	96	115	LB	136	52.7	8	11.0	–	1-1	2	12	10R
64	100	115	LB	152	38.8	58	9.3	+	1-1	4	0	0
65	117	125	LB	152	43.8	22	15.2	–	2-1	3	78	0
66	106	115	LB	152	41.4	15	14.0	+	1-1	5	4	60MS
67	106	110	B	144	67.6	14	12.0	–	1-1	5	8	40MS
68	117	105	LB	150	58.3	4	8.0	–	1-1	5	8	30MS
69	112	120	LB	144	59.5	10	14.0	–	1-1	2	8	0
70	99	115	LB	134	57.9	15	10.2	–	1-1	2	34	60S
71	110	105	LB	144	47.1	30	12.0	–	1-1	3	12	10MS
72	100	105	LB	136	60.8	21	14.3	–	1-1	1	12	80S
73	96	120	LB	130	56.8	9	13.3	–	1-1	5	78	80S
74	96	105	LB	130	57.6	18	11.2	–	1-1	6	34	10R
75	99	95	LB	130	53.7	17	14.3	–	2-1	4	89	50S
76	96	90	LB	134	48.7	18	14.3	–	1-1	5	0	40MS
77	99	95	LB	134	49.3	5	12.0	–	1-1	6	1	40MSS
78	100	95	LB	136	49.1	15	14.0	–	1-1	5	78	0
79	108	90	DB	140	55.7	12	16.0	+	1-1	1	89	0
80	99	140	LB	134	59.0	12	16.0	–	1-1	1	0	0
81	115	110	LB	152	46.8	18	16.0	–	1-1	1	89	70S
82	115	105	LB	152	45.0	20	16.0	–	1-1	5	0	50R
83	96	135	LB	130	60.4	14	15.2	–	1-1	2	0	20MRMS
84	89	95	LB	127	56.9	13	16.0	–	1-1	6	78	5R
85	102	100	LB	138	56.8	19	15.0	–	1-1	3	1	10MR
86	99	105	LB	136	55.7	15	15.0	–	1-1	2	0	10MR
87	96	100	LB	138	54.4	16	15.0	–	1-1	5	0	10MR
88	96	120	LB	134	49.0	18	14.0	–	1-1	5	0	5R
89	108	110	DB	146	58.1	15	14.0	–	1-1	5	0	0
90	84	140	B	137	63.2	16	16.0	–	1-1	4	12	50S
91	96	90	LB	134	57.1	13	15.2	–	1-1	4	0	0

Table 2. Phenological and disease characterization of the D-genome synthetic hexaploids in the Elite-I set. FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown); PMA = days-to-physiological maturity; TKW = 1,000-kernel weight (g); G/S = number of grains/spike; SL = spike length (cm); KB = Karnal bunt (– = immune, + = susceptible); Pm (S) = powdery mildew screening at the seedling stage; Pm (A) = powdery mildew screening at the adult-plant stage; Yr (S) = stripe rust screening at the seedling stage; Yr (A) = stripe rust screening at the adult-plant stage where R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible.

No.	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Pm (A)	Yr (S)	Yr (A)
92	96	115	LB	134	57.2	14	15.0	–	1-1	2	78	0
93	77	127	145	119	48.4	16	15.0	–	1-1	3	12	40MS
94	106	105	LB	138	56.1	30	15.0	–	1-1	5	12	20MS
95	99	105	LB	138	62.0	28	15.0	–	1-1	2	0	0

ing it difficult for a new race of pathogen to overcome the plant resistance. The 49 Elite-I accesions were 2, 3, 4, 5, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 29, 30, 31, 33, 35, 39, 41, 46, 52, 61, 63, 65, 66, 67, 72, 73, 74, 75, 76, 77, 80, 82, 85, 86, 87, 88, 89, and 92.

The third category had moderate resistance or was susceptible to powdery mildew at both seedling and adult-plant stages. The Elite-I accessions with an intermediate resistance or susceptible to powdery mildew at the seedling stage are 1, 3, 4, 5, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 29, 30, 31, 33, 35, 39, 41, 46, 58, 61, 63, 65, 66, 67, 72, 73, 74, 75, 76, 77, 80, 82, 85, 86, 87, 88, 89, and 92.

Stripe rust studies. Seedling screening showed that 63 out of 95 (66.3%) in Elite-I exhibited seedling resistance to stripe rust (Table 2, pp. 84-86). These genotypes also were screened for APR under field conditions at NARC; 40 of the 95 (42.1%) were resistant genotypes. Thirty-one (32.6%) genotypes had both seedling and APR (1, 2, 3, 6, 8, 19, 27, 32, 35, 36, 40, 41, 42, 48, 49, 50, 51, 52, 55, 63, 64, 74, 80, 82, 85, 86, 87, 88, 89, 91, and 95). All this germ plasm represents the presence of major genes against stripe rust and can be exploited further in breeding programs.

Adult-plant resistance involving susceptibility at the seedling stage and resistance only at the adult-plant stage indicates the presence of minor genes, which are considered of great importance against rust diseases in acquiring durable resistance. In the Elite-I, nine lines (9%), including 4, 5, 9, 65, 69, 78, 79, 84, and 92, showed APR and are good candidates for providing durable resistance to wheat cultivars.

Karnal bunt studies. Karnal bunt evaluation was done by examining the grains following artificial inoculation. Grains from each entry were examined separately after hand threshing. The rating scale was from 0 to 5 (Fig 2). Only a rating of 0 was considered acceptable and 1–5 as susceptible. In the Elite-I, 79 entries (83.1%) were found to be completely immune to Karnal bunt, including 1, 2, 3, 7, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 25, 26, 27, 28, 30, 31, 34, 35, 36, 37, 38, 39, 41, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 56, 57, 58, 60, 61, 62, 63, 65, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 80, 81,82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, and 95 (Table 2, pp. 84-86).

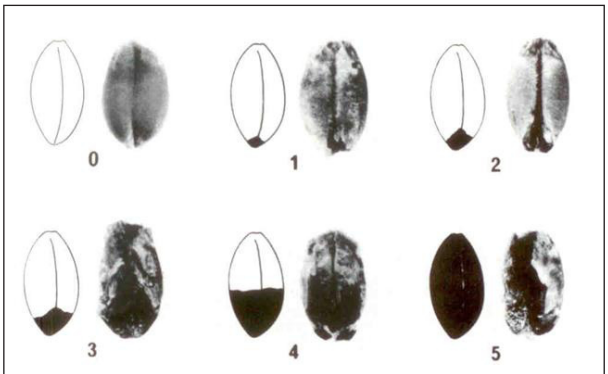

Fig. 2. Infection severity scale caused by Karnal bunt, 0 = zero infection to 5 = a completely bunted grain (Warham et al. 1986).

Molecular studies. ***Genetic diversity evaluation using random amplified polymorphic DNA RAPD primers.*** RAPD primers were used for genetic diversity evaluation of these D-genome synthetic hexaploids. All 520 RAPD primers of the Operon Series were screened, and working primers were identified and applied to detect genetic polymorphism at DNA level. Samples that did not amplify were not included in the analysis.

Genetic analysis was performed only on the scorable bands. Each single band was considered as a single locus/allele. The loci were scored as present/absent. Bivariate data 1–0 were used to estimate genetic distances (GD). Un-

weighted pair group of arithmetic means (UPGMA) function estimated genetic distances between the genotypes as follows: $GD_{xy} = 1 - d_{xy}/d_x + d_y - d_{xy}$, where GD_{xy} = genetic distance between two genotypes, d_{xy} = total number of common loci (bands) in two genotypes, d_x = total number of loci (bands) in genotype 1, and d_y = total number of loci (bands) in genotype 2.

The efficiency of primers to amplify the genotypes ranged from a maximum of 41 genotypes (OPG-12) to a minimum of two genotypes (OPH-4) in Elite-I (Table 3). Scorable bands ranged from five (OPF-3) to 92 (OPG-6) (Table 3). Genetic analysis of the population showed that the total number of loci for Elite-I was 92, of which 82 were polymorphic with a percentage of 89.13% (Table 3). The range of scorable bands was from 250–3,000 bp.

Table 3. Molecular fingerprinting pattern by RAPD analysis in the Elite-I D-genome synthetic hexaploid set.

Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable Bands	Amplification product range (bp)
OPF-1	3	3	100%	24	36	500–1,500
OPF-3	2	2	100%	5	5	500–1,000
OPF-4	2	2	100%	21	37	1,500–2,000
OPF-8	4	4	100%	14	19	500–1,500
OPF-10	4	4	100%	6	11	1,000–2,000
OPF-13	7	7	100%	28	70	500–2,000
OPF-18	5	5	100%	10	14	500–2,000
OPF-20	5	3	60%	8	14	500–2,500
OPG-2	5	5	100%	33	58	750–2,000
OPG-4	1	1	100%	14	14	1,500–2,000
OPG-5	2	0	0%	6	12	250–750
OPG-6	9	9	100%	36	92	250–2,500
OPG-9	4	4	100%	15	30	750–2,000
OPG-11	4	4	100%	7	13	750–2,500
OPG-12	8	8	100%	41	89	250–2,500
OPG-13	3	3	100%	7	17	250–1,000
OPG-17	1	1	100%	5	5	250–500
OPG-18	2	2	100%	8	8	250–1,000
OPG-19	5	5	100%	18	47	750–1,500
OPH-2	2	0	0%	3	6	250–1,000
OPH-3	5	5	100%	5	12	500–2,000
OPH-4	5	3	60%	2	6	500–1,500
OPH-9	4	2	50%	6	16	500–2,000

Similarity matrix.
A bivariate analysis generated a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. The value of the similarity matrix ranged from 63.0% (minimum), between genotypes 49 and 51 and 51 and 53, and 100% (maximum), between genotypes 18 and 68, 18 and 89, 18 and 91, 18 and 93, 68 and 89, 68 and 92, 68 and 94, 80 and 83, 80 and 84, 89 and 92, 89 and 94, and 92 and 94, in the Elite-I.

Dendrogram interpretation. The genetic distance between genotypes were used to construct a dendrogram by UPGMA analysis for determining the grouping of the lines on the basis of similarities and differences. In the Elite-I, the dendrogram represents one main cluster with subclusters A, B, and C (Fig. 3, p.88). Subcluster A has 15 genotypes containing genotype 15 as the most diverse line in the entire Elite-I. Other good lines in subcluster A are 46, 47, and 49. In subcluster B, there are 21 entries of which 73 is the most diverse; lines 81, 83 and 84, and 78 and 80 are 100% similar to each other. Line 73 is the most diverse line in this subcluster and 69, 70, and 77 are other good lines. Subcluster C can be further divided into five groups, from C1 to C5. Group C1 contains four genotypes with entry 3 as the most diverse line. Group C2 has seven genotypes of which 25 and 30 are the best to recommend. Group C3 has seven genotypes, again with 11 and 14 as the best genotypes. Group C4 represents the largest group in subcluster C with 32 genotypes, lines 18, 68, 89, 92, and 94 show 100% similarity. Line 59 stands out as the best line, followed by 23, 37, and 42. Subcluster C5 has nine genotypes of which 1 and 4 represent the best lines.

Molecular studies. ***Evaluation of genetic diversity using simple sequence repeat (SSR) primers.*** SSR primers were used for genetic diversity evaluation of A-, B-, and D-genome synthetic hexaploids. All 275 SSR primers were applied to each set to detect genetic polymorphism at DNA level (Table 4, pp. 89-90). Samples that did not amplify were not included in the analysis.

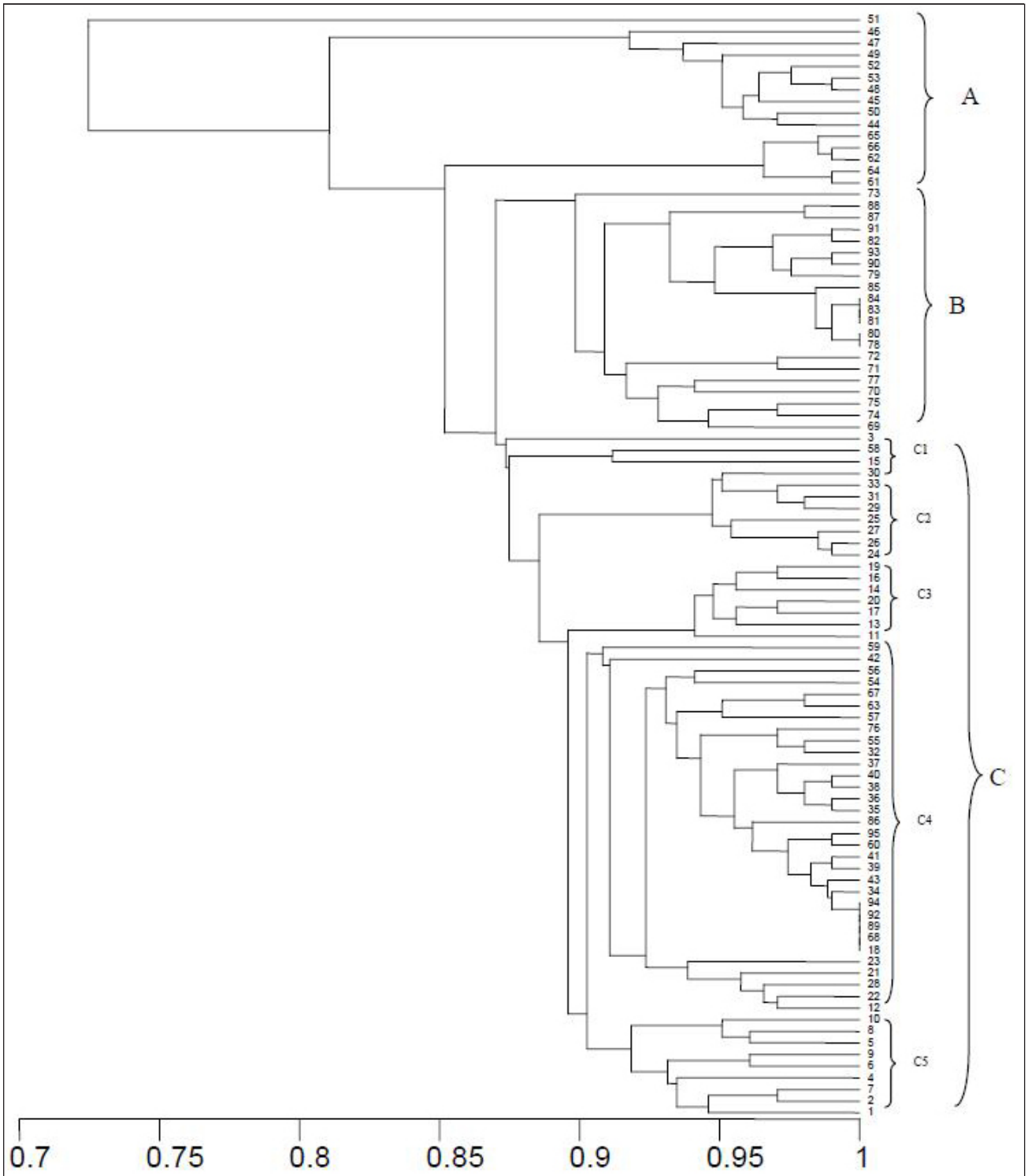

Fig. 3. A dendrogram of the genetic diversity in the Elite-I synthetic hexaploids, evaluated using random amplified polymorphic DNA (RAPD) primers, with one main cluster and three subclusters A, B, and C.

Genetic analysis was performed only on the scorable bands. Each single band was considered as a single locus/allele. The loci were scored as present/absent. Bavariate data 1–0 were used to estimate the GD as for the RAPD markers. The efficiency of the primers to amplify the genotypes ranged from maximum 92 genotypes (*Xgwm645-3D*, *Xgwm149-4B*, *Xgwm550-1B*, *Xgwm264-1B*, *Xgwm169-6A*, and *Xgwm4-4A*) to the minimum of two genotypes (*Xgwm459-6A*) in the Elite-I (Table 4, pp. 89-90). Scorable bands ranged from two (*Xgwm459-6A*) to 430 (*Xgwm219-6B*) (Table 4, pp. 89-90). A genetic analysis of the population showed that the total number of alleles for the Elite-I was 452, of which 431 were polymorphic (95.35%).

Table 4. Molecular fingerprinting pattern using SSR markers in Elite-I set of D-genome synthetic hexaploids.

Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
Xgwm33-1A	8	8	100%	90	185	50–250	0.14
Xgwm99-1A	7	7	100%	86	175	50–150	0.54
Xgwm135-1A	4	4	100%	27	44	150	0.53
Xgwm136-1A	6	6	100%	72	86	250–400	0.90
Xgwm164-1A	4	4	100%	80	131	100–150	0.39
Xgwm497-1A	4	4	100%	46	85	100	0.42
Xgwm71.1-2A	5	5	100%	86	257	50–150	0.90
Xgwm359-2A	2	2	100%	8	8	250	0.72
Xgwm497-2A	4	4	100%	77	148	100–150	0.41
Xgwm558-2A	5	5	100%	85	183	50–150	0.55
Xgwm2-3A	7	3	33.33%	82	109	50–100	0.82
Xgwm391-3A	6	6	100%	28	39	150	0.65
Xgwm4-4A	10	10	100%	92	304	50–600	0.75
Xgwm160-4A	6	6	100%	75	115	50–250	0.72
Xgwm610-4A	4	4	100%	81	175	50–150	0.73
Xgwm126-5A	5	5	100%	12	24	800–1,000	0.55
Xgwm617-5A	7	7	100%	89	212	50–150	0.62
Xgwm169-6A	4	4	100%	92	114	200	0.87
Xgwm459-6A	2	2	100%	2	2	50	0.73
Xgwm494-6A	2	2	100%	78	124	100–150	0.67
Xgwm570-6A	4	4	100%	29	122	200	0.71
Xgwm130-7A	4	4	100%	27	44	50–150	0.05
Xgwm332-7A	9	9	100%	90	230	50–500	0.57
Xgwm350-7A	3	3	100%	35	38	50–150	0.51
Xgwm635-7A	4	4	100%	25	38	50–100	0.73
Xgwm140-1B	8	8	100%	86	107	50–400	0.28
Xgwm264-1B	8	8	100%	92	313	50–200	0.69
Xgwm403-1B	2	2	100%	19	20	100	0.57
Xgwm550-1B	12	12	100%	92	359	50–200	0.75
Xgwm47-2B	8	8	100%	81	149	200	0.62
Xgwm210-2B	5	3	100%	90	225	50–200	0.86
Xgwm257-2B	12	12	100%	91	216	200–400	0.72
Xgwm112-3B	5	5	100%	89	159	50–100	0.40
Xgwm264-3B	11	11	100%	74	224	150–1000	0.84
Xgwm284-3B	4	4	100%	37	99	500–1000	0.75
Xgwm493-3B	4	4	100%	85	113	150–200	0.22
Xgwm533.1-3B	3	3	100%	36	36	100–150	0.46
Xgwm6-4B	6	6	100%	36	105	50–300	0.06
Xgwm149-4B	4	4	100%	92	104	150	0.14
Xgwm191-5B	10	10	100%	82	138	50–150	0.54
Xgwm234-5B	16	16	100%	87	346	200–1,000	0.90
Xgwm371-5B	3	3	100%	65	126	50–150	0.39
Xgwm193-6B	6	6	100%	91	137	50–150	0.42
Xgwm219-6B	16	16	100%	88	430	50–1,000	0.90
Xgwm508-6B	5	5	100%	63	120	150–200	0.72
Xgwm613-6B	3	3	100%	7	11	150	0.41
Xgwm626-6B	4	4	100%	86	163	50–150	0.55
Xgwm43-7B	5	5	100%	90	160	50–1,000	0.82

Table 4. Molecular fingerprinting pattern using SSR markers in Elite-I set of D-genome synthetic hexaploids.

Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
Xgwm46-7B	5	5	100%	15	23	200	0.65
Xgwm68-7B	5	5	100%	90	286	50–200	0.75
Xgwm146-7B	4	4	100%	76	162	50–200	0.72
Xgwm344-7B	6	6	100%	64	93	100–150	0.73
Xgwm106-1D	4	4	100%	81	124	50–150	0.55
Xgwm232-1D	5	5	100%	84	123	50–150	0.62
Xgwm458-1D	4	4	100%	67	93	50–100	0.53
Xgwm642-1D	11	11	100%	80	301	50–1,000	0.87
Xgwm102-2D	6	6	100%	64	69	150–200	0.73
Xgwm261-2D	6	6	100%	91	184	50–200	0.67
Xgwm515-2D	4	4	100%	30	85	50–150	0.71
Xgwm645-3D	2	2	100%	92	104	50–300	0.05
Xgwm3-3D	3	3	100%	24	28	50–100	0.57
Xgwm183-3D	7	7	100%	75	128	50–150	0.51
Xgwm383-3D	8	5	62.5%	75	153	50–150	0.73
Xgwm608-4D	8	8	100%	85	216	100–1,000	0.28
Xgwm182-5D	5	5	100%	79	106	50–200	0.69
Xgwm190-5D	5	5	100%	88	135	150–200	0.57
Xgwm292-5D	6	6	100%	23	27	50–200	0.75
Xgwm565-5D	10	10	100%	78	332	50–1,000	0.62
Xgwm583-5D	4	4	100%	91	115	150–200	0.86
Xgwm55-6D	4	4	100%	87	152	50–100	0.72
Xgwm325-6D	4	4	100%	69	90	50–150	0.40
Xgwm469-6D	13	11	84.61%	87	253	50–1,000	0.84
Xgwm44-7D	8	8	100%	88	276	50–1,000	0.75
Xgwm428-7D	12	2	16.66%	79	100	50–1,000	0.22
Xgwm437-7D	5	5	100%	86	102	50–100	0.46

Similarity matrix. A bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient (1979) to estimate genetic diversity (Fig 4, p. 91). The value of similarity matrix ranged from 64.9 (minimum) between genotypes 55 and 40, 79 and 28, 80 and 40 and 81 and 20 while 92.6% (maximum) between genotypes 52 and 51 in the Elite-I.

Dendrogram interpretation. Genetic distances between the genotypes were used to construct a dendrogram by UPGMA analysis for determining grouping of the lines on the basis of similarities and differences. The dendrogram for Elite-I represents only one main cluster with six subclusters (Fig. 4, p. 91). Subcluster 1 has only six genotypes in which 78 and 88 are the most diverse lines. Subcluster 2 has 18 genotypes in which 20, 21, and 29 are the best lines. Subcluster 3 has 18 genotypes also, with 39, 40, 45, and 53 as the genetically diverse lines. Subcluster 4 has 17 genotypes of which 65 is truly the best line. Subcluster 5 also includes some lines that are 100% similar, such as 55 and 80. A total 22 genotypes in this and 8, 9, 28, 82, 86 and 95 are highly diverse lines in this subcluster 5. Subcluster 6 has 14 genotypes of which 3, 6, 7, and 16 are comparatively better lines.

The Elite-I set of synthetic hexaploids. All SH entries were tall, late maturing, hard to thresh, and showed phenology characteristics that exhibited enormous diversity for various traits analyzed (Table 2, pp. 84-86). Important parameters for breeding generally are days-to-flowering, days-to-physiological maturity, plant height at maturity, spike length, grains/spike, and, most significantly, 1,000-kernel weight. These traits figured in the selection of SHs in crossing with bread wheat. Synthetics are generally tall with a range from over 85 cm to a maximum of 140 cm. The tall height does not negate their utilization in crossing, because height can be rectified via the genetic contribution of the wheat involved. This holds true for the other parameters such as days-to-flowering and physiological maturity, which are, in essence, crucial indices for successful utilization in crossing. If these two traits are later than wheat, having various planting

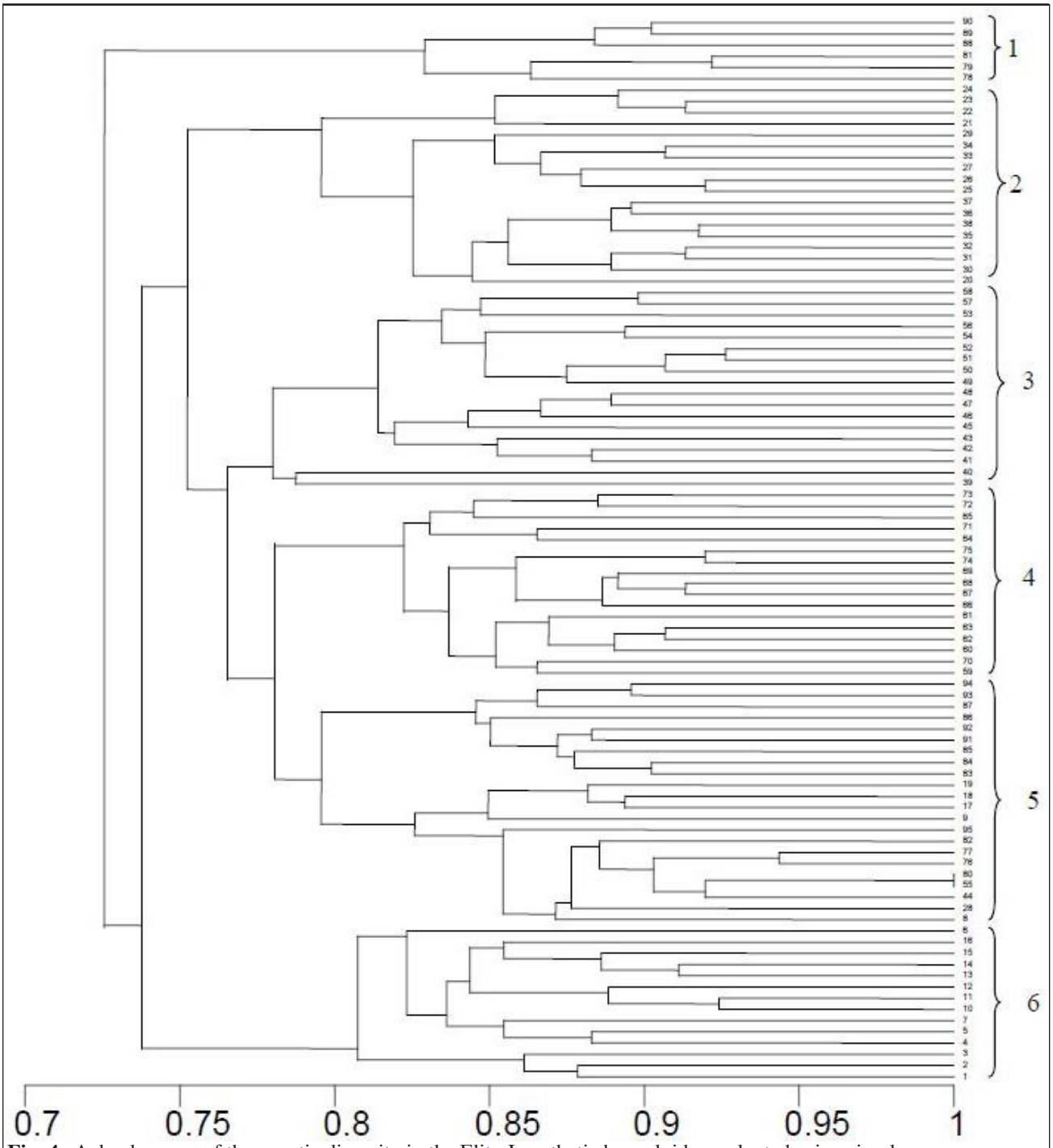

Fig. 4. A dendrogram of the genetic diversity in the Elite-I synthetic hexaploids, evaluated using simple sequence repeat (SSR) primers, with one main cluster and three subclusters A, B, and C.

dates overrides the constraint of lateness. Of greater significance for yield enhancement is the spike detail, where a 1,000-kernel weight greater than 45 g is highly desirable. The variation in 1,000-kernel weight is between 30.2 to 67.6 g (Table 2). The molecular differences within the germ plasm delineated the materials and can be useful for selecting entries useful as breeding resources. Narrowing down the SH parents for a crossing program requires a diagnostic step that permits smart selections to be made; and for this, the molecular diversity is crucial. The diversity exhibited in the Elite-I after RAPD and SSR analyses is shown (Figs. 3 (p. 88) and 4). From this data, desired SHs were identified as parents for a crossing effort. Elite-I lines 1, 3, 4, 11, 13, 15, 23, 25, 30, 37, 42, 46, 47, 49, 59, 69, 70, 73, and 77 were the best SHs according to their diversity status based upon RAPD analysis. Lines 3, 6, 7, 8, 9, 16, 20, 21, 28, 29, 39, 40, 45, 53, 65, 78, 82, 86, 88, and 94 exhibited greater diversity when screened by SSRs. Narrowing these down to a limited number was made possible by the phenology data (Table 2, pp. 84-56) and stringent evaluation of their screening data.

A characteristic spike variation demonstrates the co-dominant genetic expression of the two parents in the SH product (Fig. 5). The tough glumes of *Ae. tauschii* are dominant as are the awns of the durum parent. Spike architecture is modified; awns are inherited and seed has a boldness that is linked with the durum parent. A 1,000-kernel weight much higher (50–65 gm) than that of breadwheat (40–44 g) is common. The Elite-I entries expressed a wide diversity and several emerged as donors for Karnal bunt, powdery mildew, and stripe rust resistance, desirable yield components, and unique plant morphology traits such as leaf waxiness, pubescence, and stay green attributes. The germ plasm tillered well and per plant seed output ranged from 200 to 350 under field increase conditions.

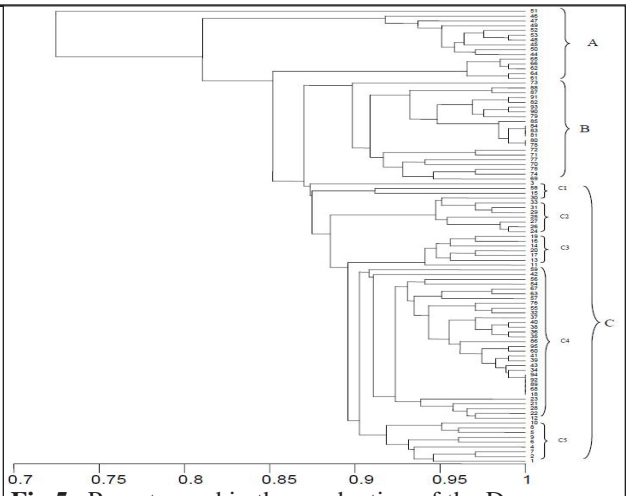

Fig 5. Parents used in the production of the D-genome synthetic hexaploid wheats showing (from left to right): dorsal and ventral spike morphology views of (a) *T. turgidum* subsp. *turgidum* (2n=4x=28; AABB); (b) the synthetic hexaploid (2n=6x=42, AABBDD), and (c) *Ae. tauschii* (2n=2x=14, DD).

The Elite-I SH wheats have been internationally exploited by wheat breeders for the incorporation of biotic and abiotic stress resistances. Often a single trait of interest gives reason to use a SH in a program, but this has been modified as many positive traits are present in a single synthetic, which makes achieving the breeding targets more efficient. Lines with multiple stress resistance are not uncommon, and the screening done in this study has allowed for selecting such elite SHs for breeding utilization. Apart from the stress factors, emphasis also has been given to the molecular diversity within the selected SHs, which serves as a guide for selecting only those SHs in a recombination program that possess the desired traits and also have molecular uniqueness (diversity).

From a holistic perceptive, various traits enable breeders to a select few of the best SHs. A major trait was earliness (days-to-flowering), which is linked with days-to-maturity, height at maturity, and 1,000-kernel weight. A satisfactory number of grains/spike and spike length also were factors. Too many grains/spike was avoided, because a heavier head would promote lodging and the 1,000-kernel weight was heavy in most lines selected. We favored selections that ranged in flowering time, between 76 to 89 days, and had a 1,000-kernel weight between 60.0 and 67.6 g. A maximum spike length of 16 cm was observed in entries 79, 80, 81, 82, 84, and 90. The maximum grains/spike were 64 in entry 58. The maximum 1,000-kernel weight was 67.6 g was in entry number 67 and the minimum days to anthesis was 76 days for entry 49, which reached physiological maturity in 115 days. Seven entries selected for breeding from the Elite-I set of 95 that possessed multiple interesting practical attributes based on phenology alone; 17, 26, 67, 72, 90, 93, and 95. These lines had CIMMYT *Ae. tauschii* accession numbers 220, 309, 629, 877, 502, 1027, and 1030 in their pedigrees. A DNA polymorphic profile was established and stringent utility deduced for application in recombination breeding. Supportive disease data was an additional facet that was considered. For powdery mildew resistance at the seedling and adult-plant stages, entries 90 and 93 indicated the presence of major genes. Adult-plant resistance alone was observed in entries 17, 26, 67, and 72. For stripe rust resistance, entry 95 was identified with both seedling and APR, whereas no line had APR alone. All the seven lines possessed excellent Karnal bunt resistance. These data have enabled the use of these seven lines for location-specific breeding efforts in Pakistan. Powdery mildew resistance is a prerequisite for wheat breeding materials grown in off-season locations where natural prevalence facilitates natural selection on all breeding materials. To this base, by adding in other attributes, one can deploy the best into other sites.

A-genome based diversity status and its practical utilization in wheat.

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One avenue of using the A-genome diversity is via bridge-crossing of AABBAA amphiploids (Fig. 6, p. 93). The 'durum wheat/A-genome accession' crosses are simple and of high frequency. The durum cultivars in these amphiploids are susceptible for the stresses being addressed and a resistant amphiploid implies that a particular A-genome accession contributed the expressed resistance. So far, some diversity has been identified in the AABBAA amphiploids for *Cochliobolus sativus*, *Fusarium graminearum*, and leaf rust resistance but is more extensively observed for *Septoria tritici* resistance.

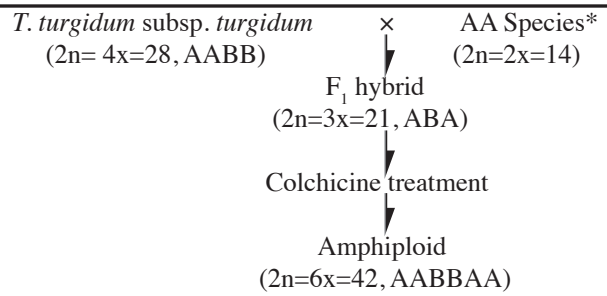


Fig. 6. Schematic showing the production of A-genome 2n = 6x = 42 chromosome stocks as a consequence of hybridizing durum cultivars with A-genome diploid accessions. The A-genome strategy resembles that of the D genome, which demonstrates the utilization of the AABBDD synthetics. Crossing the resistant synthetic hexaploids (SH) with elite but susceptible bread wheat (BW) cultivars yield resistant BW/SH derivatives. *A-genome species include *T. monococcum* subsps. *monococcum* and *aegilopoides* and *T. urartu*.

A set of 194 A-genome synthetics was acquired from the Wheat Wide Crosses Program at CIMMYT, Mexico, and the seed increased in the Wheat Wide Crosses Program based at NARC (Table 6, pp. 94-97). This germ plasm, as a part of the study conducted in Pakistan, was cytologically validated, phenologically characterized, genetically evaluated and screened against Karnal bunt, stripe rust, and powdery mildew during the crop cycles of 2005–06, 2006–07, 2007–08, and 2008–09 (Table 5). The A-genome diploid accessions (2n=2x=14) were *T. monococcum* subsp. *monococcum* and *aegilopoides* and *T. urartu*.

Table 5. The A-genome synthetic hexaploid entries utilized in the study. Synthetic hexaploid entry numbers are the same as those used in the CIMMYT, Mexico, Wide Crosses Program data base. Pedigree details are given in Table 6, pp. 95-97).

Group	A-genome synthetic hexaploid entry	Durum parent	Total entries
1	1, 2	21	2
2	3, 36	28	2
3	4, 6, 10, 16, 21, 23, 24, 26, 29, 30, 31, 106, 113	17	13
4	7, 8, 13, 15	23	4
5	5, 9, 11, 12, 48, 53	34	6
6	14, 27, 49, 63	35	4
7	17, 19, 20, 22, 68, 69, 70, 76, 77, 78, 125, 128, 129	22	13
8	18, 37, 40, 44, 46, 55, 173	45	7
9	25, 32, 33, 34, 41, 42, 45, 47, 51, 52, 54, 56, 57, 58, 59, 64	27	16
10	28, 50, 176, 179, 185, 187, 188, 191, 192	12	9
11	35	37	1
12	38, 39	40	2
13	43, 62, 71, 72, 73, 74, 75	9	7
14	60, 61, 65	25	3
15	66, 67	33	2
16	79, 83	26	2
17	80, 84, 88, 90, 92, 163	5	6
18	81, 82, 85, 89, 91, 93, 94, 101, 102, 103, 104, 105, 111, 112, 119, 120, 123	20	17
19	86, 87, 95, 96, 98, 99, 100, 107, 108, 109, 110, 114, 131, 132, 134, 135, 138, 139, 140, 142, 175, 97, 115, 116, 121, 122, 146, 183, 190, 193, 194	11	31
20	117, 118	14	2
21	124, 170, 156, 160, 161	1	5
22	126	4	1
23	127, 130, 165, 167, 169, 172, 137, 155, 158, 177	13	10
24	133, 136, 141, 143, 157, 159, 174, 178, 144, 145, 147, 148, 149, 150, 151, 152, 153, 154, 162, 180, 181, 182, 184, 186, 164, 166, 168, 171, 189	2	29

The mean crossability data for the production of ABA hybrids across all three categories of diploid progenitors (*aegilopoides*, *monococcum*, and *urartu*) were based on embryos plated from the crosses. The average of all these crosses was 13.0 percent (Table 7, p. 98) for which regeneration and colchicine induced doubling ranged between 90 and 98 percent (Mujeeb-Kazi, unpublished data). Conventional cytological validation protocols provided evidence that the production of F_1 hybrids and their amphiploid production was normal. The F_1 hybrids have 21 chromosomes at mitosis (Fig. 7a, p. 94) and at meiosis show nine univalents + three rod bivalents + three ring bivalents (Fig.

Table 6. Pedigrees of the A-genome synthetic hexaploids.

Number	Parentage / Pedigree
1	YUK/T.BOEOTICUM (1)
2	YUK/T.BOEOTICUM (2)
3	STY-US/CELTA//PALS/3/SRN_5/4/T.BOEOTICUM (3)
4	SCA/T.BOEOTICUM (3)
5	ALG86/4/FGO/PALES//MEXI_1/3/RUFF/FGO/5/ENTE/6/T. BOEOTICUM (3)
6	SCA/T.BOEOTICUM (10)
7	GARZA/BOY//T.BOEOTICUM (10)
8	GARZA/BOY//T.BOEOTICUM (12)
9	ALG86/4/FGO/PALES//MEXI_1/3/RUFF/FGO/5/ENTE/6/T. BOEOTICUM (13)
10	SCA/T. BOEOTICUM (14)
11	ALG86/4/FGO/PALES//MEXI_1/3/RUFF/FGO/5/ENTE/6/T. BOEOTICUM (14)
12	ALG86/4/FGO/PALES//MEXI_1/3/RUFF/FGO/5/ENTE/6/T. BOEOTICUM (15)
13	GARZA/BOY//T.BOEOTICUM (16)
14	BOTNO/T.BOEOTICUM (20)
15	GARZA/BOY//T.BOEOTICUM (21)
16	SCA/T.BOEOTICUM (23)
17	DOY1/T.BOEOTICUM (23)
18	SHAG/T.BOEOTICUM (24)
19	DOY1/T.BOEOTICUM (26)
20	DOY1/T.BOEOTICUM (27)
21	SCA/T.BOEOTICUM (28)
22	DOY1/T.BOEOTICUM (28)
23	SCA/T.BOEOTICUM (31)
24	SCA/T.BOEOTICUM (33)
25	SCOOP_1/T.BOEOTICUM (33)
26	SCA/T.BOEOTICUM (34)
27	BOTNO/T.BOEOTICUM (35)
28	D 67. 2/P66. 270//T.BOEOTICUM (35)
29	SCA/T.BOEOTICUM (36)
30	SCA/T.BOEOTICUM (39)
31	SCA/T.BOEOTICUM (40)
32	SCOOP_1/T.BOEOTICUM (40)
33	SCOOP_1/T.BOEOTICUM (46)
34	SCOOP_1/T.BOEOTICUM (50)
35	LCK59. 61/T.BOEOTICUM (52)
36	STY-US/CELTA//PALS/3/SRN_5/4/T.BOEOTICUM (54)
37	SHAG_22/T.BOEOTICUM (55)
38	AJAIA/T.BOEOTICUM (55)
39	AJAIA/T.BOEOTICUM (56)
40	SHAG_22/T.BOEOTICUM (56)
41	SCOOP_1/T.BOEOTICUM (59)
42	SCOOP_1/T.BOEOTICUM (60)
43	68.111/RBG-U//WARD/3/T.BOEOTICUM (61)
44	SHAG_22/T.BOEOTICUM (68)
45	SCOOP_1/T.BOEOTICUM (69)
46	SHAG_22/T.BOEOTICUM (70)
47	SCOOP_1/T.BOEOTICUM (71)
48	ALG86/4/FGO/PALES//MEXI_1/3/RUFF/FGO/5/ENTE/6/T. BOEOTICUM (74)

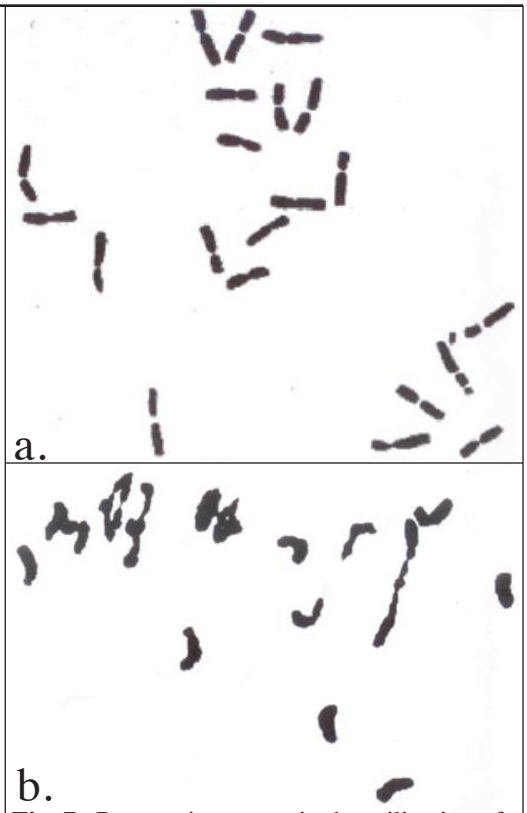


Fig. 7. Progressive stages in the utilization of the A-genome variation showing its cytological validation details as follows: (a) F_1 (2n=3x=21, ABA) hybrid at mitotic metaphase and (b) An F_1 meiocyte at metaphase I with associations of nine univalents + three rod bivalents + three ring bivalents.

7b). The F_1 hybrids after colchicine doubling led to a generation of fertile amphiploids with 2n=6x=42 chromosomes (Fig. 8a, p. 95), AABBAA, that were associated at metaphase I as five rod bivalents + 16 ring bivalents (Fig. 8b, p. 95). Despite the four doses of A-genome chromosomes, bivalency prevailed for most of the AABBAA hexaploids where association of the 42 chromosomes express maximum bivalency; the association is three rod bivalents + 19 ring bivalents (Fig. 9a, p. 96) and two rod bivalents + 19 ring bivalents (Fig. 9b, p. 96). Another line had eight rod bivalents + 13 ring bivalents (Fig. 10a, p. 97), similar to other amphiploids analyzed) at anaphase I with a 21/21 split (Fig. 10b, p. 97).

Mean meiotic associations of several AABBAA amphiploids that were produced involving diverse elite durum wheats and accessions where determined for *T. monococcum* subsp. *aegilopoides* (Table 8, pp. 98-99), *T. monococcum* subsp. *monococcum* (Table 9, p. 100), and *T. urartu* (Table 10, p. 101). The

Table 6. Pedigrees of the A-genome synthetic hexaploids.

Number	Parentage / Pedigree
49	BOTNO/T.BOEOTICUM (75)
50	D 67. 2/P66. 270//T.BOEOTICUM (75)
51	SCOOP_1/T.BOEOTICUM (79)
52	SCOOP_1/T.BOEOTICUM (80)
53	ALG86/4/FGO/PALES//MEXI_1/3/RUFF/FGO/5/ENTE/6/T. BOEOTICUM (83)
54	SCOOP_1/T.BOEOTICUM (87)
55	SHAG_22/T.BOEOTICUM (88)
56	SCOOP_1/T.BOEOTICUM (89)
57	SCOOP_1/T.BOEOTICUM (90)
58	SCOOP_1/T.BOEOTICUM (91)
59	SCOOP_1/T.MONOCOCCUM (98)
60	AOS/T.MONOCOCCUM (98)
61	AOS/T.MONOCOCCUM (111)
62	68.111/RGB-U//WARD/3/T.MONOCOCCUM (112)
63	BOTONO/T.MONOCOCCUM (112)
64	SCOOP _ 1/T.MONOCOCCUM (118)
65	AOS/T.MONOCOCCUM (118)
66	FGO/USA2111//T.MONOCOCCUM (119)
67	FGO/USA2111//T.MONOCOCCUM (122)
68	DOY1/T.URARTU (542)
69	DOY1/T.URARTU (543)
70	DOY1/T.URARTU (550)
71	68.111/RGB-U//WARD/3/T.URARTU (550)
72	68.111/RGB-U//WARD/3/T.URARTU (551)
73	68.111/RGB-U//WARD/3/T.URARTU (553)
74	68.111/RGB-U//WARD/3/FGO/4/RABI/5/T.URARTU (554)
75	68.111/RGB-U//WARD/3/FGO/4/RABI/5/T.URARTU (555)
76	DOY1/T.URARTU (560)
77	DOY1/T.URARTU (563)
78	DOY1/T.URARTU (564)
79	GAN/T.BOEOTICUM (7)
80	DVERD_2/T.BOEOTICUM (18)
81	YAV_2/TEZ//T.BOEOTICUM (18)
82	YAV_2/TEZ//T.BOEOTICUM (25)
83	GAN/T.BOEOTICUM (29)
84	DVERD_2/T.BOEOTICUM (37)
85	YAV_2/TEZ//T. BOEOTICUM (37)
86	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (38)
87	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (41)
88	DVERD_2/T.BOEOTICUM (43)
89	YAV_2/TEZ//T.BOEOTICUM (43)
90	DVERD_2/T.BOEOTICUM (44)
91	YAV_2/TEZ//T.BOEOTICUM (44)
92	DVERD_2/T.BOEOTICUM (45)
93	YAV_2/TEZ//T.BOEOTICUM (45)
94	YAV_2/TEZ//T.BOEOTICUM (47)
95	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (48)
96	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (49)
97	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (53)
98	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (57)
99	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (58)

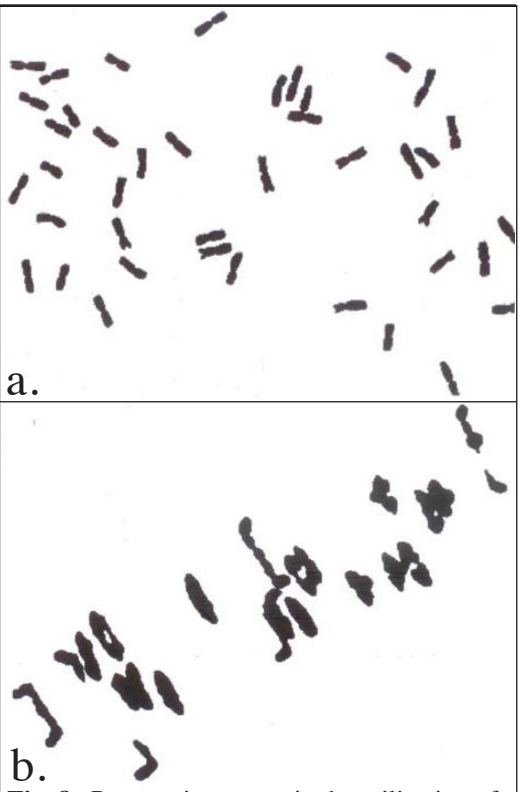


Fig. 8. Progressive stages in the utilization of the A-genome variation showing its cytological validation details as follows: (a) an amphiploid (2n=6x=42; AABBAA) at mitotic metaphase and (b) a 2n=6x=42 meiocyte showing five rod bivalents + 16 ring bivalents.

high frequency of bivalent associations are evident within each group and euploids dominate. These parameters are crucial to fertility and good seed finish, which was the case for all derivatives studied.

Plant morphology characteristics show variation across the amphiploids (Table 11, p. 101). This variation is more pronounced at the spike level (Figs. 11-12, p. 102). The spike characteristics across all accessions of the diploid A-genome resources are subtle (partially listed in Table 11, p. 101). Those for spike length and nodes/spike have priority because these traits determine seed number/spike and the degree of compactness/laxness of the florets.

Powdery mildew studies. All 194 A-genome synthetic hexaploids entries and their 24 durum parents were screened for powdery mildew resistance in pot trials in the greenhouse at Murree; 88 synthetic hexaploids and nine of the durum wheat parents showed resistance reaction at seedling stage. Infection type ranged from 0–6 at the seedling stage indicating the presence of

Table 6. Pedigrees of the A-genome synthetic hexaploids.

Number	Parentage / Pedigree
100	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (58)
101	YAV_2/TEZ//T.BOEOTICUM (62)
102	YAV_2/TEZ//T.BOEOTICUM (64)
103	YAV_2/TEZ//T.BOEOTICUM (65)
104	YAV_2/TEZ//T.BOEOTICUM (67)
105	YAV_2/TEZ//T.BOEOTICUM (73)
106	SCA/T.BOEOTICUM (75)
107	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (76)
108	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (77)
109	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (78)
110	CPI/GEDIZ/3/GOO//JO/ CRA/4/T.BOEOTICUM (81)
111	YAV_2/TEZ//T.BOEOTICUM (82)
112	YAV_2/TEZ//T.BOEOTICUM (83)
113	SCA/T.BOEOTICUM (92)
114	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (93)
115	CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (99)
116	CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (101)
117	STN/T.MONOCOCCUM (111)
118	STN/T.MONOCOCCUM (112)
119	YAV_2/TEZ//T.MONOCOCCUM (112)
120	YAV_2/TEZ//T.MONOCOCCUM (113)
121	CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (114)
122	CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (115)
123	YAV_2/TEZ//T.MONOCOCCUM (121)
124	CROC_1/T.URARTU (548)
125	DOY1/T.URARTU (552)
126	ALTAR 84/T.URARTU (558)
127	CETA/T.URARTU (558)
128	DOY1/T.URARTU (559)
129	DOY1/T.URARTU (561)
130	CETA/T.URARTU (562)
131	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (4)
132	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (5)
133	ARLIN_1/T.BOEOTICUM (6)
134	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (9)
135	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (30)
136	ARLIN_1/T.BOEOTICUM (32)
137	CETA/T.BOEOTICUM (42)
138	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (51)
139	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (63)
140	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (72)
141	ARLIN_1/T.BOEOTICUM (84)
142	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (85)
143	ARLIN_1/T.BOEOTICUM (86)
144	ARLIN_1/T.MONOCOCCUM (94)
145	ARLIN_1/ T.MONOCOCCUM (96)
146	CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (100)
147	ARLIN_1/T.MONOCOCCUM (102)
148	ARLIN_1/T.MONOCOCCUM (103)
149	ARLIN_1/T.MONOCOCCUM (104)
150	ARLIN_1/T.MONOCOCCUM (105)
151	ARLIN_1/T.MONOCOCCUM (109)

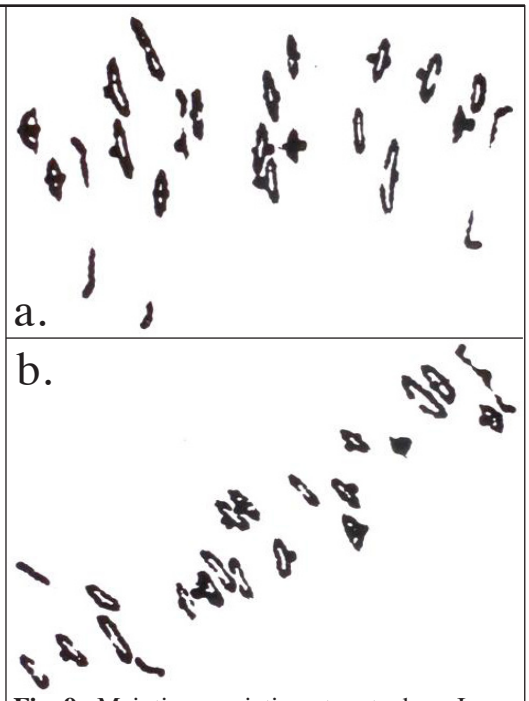


Fig. 9. Meiotic association at metaphase I of some A-genome synthetic amphiploids (hexaploids) with 42 chromosomes and genomically AABBAA: (a) 21 bivalent meiocyte associated as three rod bivalents + 18 rings and (b) 21 bivalent meiocyte associated as two rod bivalents + 19 rings.

major genes for resistance. Some of these resistant accessions exhibited different reaction types against powdery mildew under field conditions.

The A-genome synthetic hexaploids that showed resistance at seedling stage are 1, 4, 6, 18, 19, 24, 25, 26, 27, 28, 37, 39, 40, 42, 43, 45, 47, 48, 50, 53, 54, 55, 56, 57, 58, 60, 62, 68, 72, 75, 76, 78, 79, 81, 85, 87, 88, 93, 95, 96, 97, 98, 101, 102, 103, 105, 106, 107, 108, 109, 110, 113, 115, 116, 117, 118, 119, 124, 126, 127, 129, 131, 133, 134, 135, 136, 138, 144, 145, 150, 155, 156, 157, 162, 167, 168, 169, 177, 179, 182, 183, 185, 186, 188, 192, and 194. The durum parents included 5, 7, 9, 10, 11, 15, 16, 19 and 23.

Stripe rust studies. Seedling screening showed that 29 out of 194 (14.9%) of the synthetics (Table 12, p. 103-107) and 22 out of 23 (95.6%) of the durum wheat parents (Table 13, p. 108) exhibited seedling resistance to strip rust. These genotypes also were screened for APR under field conditions at NARC, which separated 82 out of 194 (42.3%) synthetics and 20 out of 23 (86.9%) of the durum wheat parents as resistant genotypes.

Table 6. Pedigrees of the A-genome synthetic hexaploids.

Number	Parentage / Pedigree
152	ARLIN_1/T.MONOCOCCUM (116)
153	ARLIN_1/T.MONOCOCCUM (117)
154	ARLIN_1/T.MONOCOCCUM (120)
155	CETA/T.BOEOTICUM (72)
156	CROC_1/T.BOEOTICUM (8)
157	ARLIN_1/T.BOEOTICUM (8)
158	CETA/T.BOEOTICUM (8)
159	ARLIN_1/T.BOEOTICUM (11)
160	CROC_1/T.BOEOTICUM (19)
161	CROC_1/T.MONOCOCCUM (97)
162	ARLIN_1/T.MONOCOCCUM (97)
163	DVERD_2/T.MONOCOCCUM (122)
164	ARLIN_1/T.URARTU (544)
165	CETA/T.URARTU (544)
166	ARLIN_1/T.URARTU (546)
167	CETA/T.URARTU (546)
168	ARLIN_1/T.URARTU (547)
169	CETA/T.URARTU (547)
170	CROC_1/T.URARTU (549)
171	ARLIN_1/T.URARTU (549)
172	CETA/T.URARTU (549)
173	SHAG_22/T.URARTU (549)
174	ARLIN_1/T.BOEOTICUM (19)
175	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (19)
176	D67.2/P66.270//T.BOEOTICUM (19)
177	CETA/T.BOEOTICUM (19)
178	ARLIN_1/T.BOEOTICUM (66)
179	D67.2/P66.270//T.BOEOTICUM (66)
180	ARLIN_1/T.MONOCOCCUM (95)
181	ARLIN_1/T.MONOCOCCUM (97)
182	ARLIN_1/T.MONOCOCCUM (107)
183	CPI/GEDIZ/3/GOO//JO/CRA/4/T.BOEOTICUM (107)
184	ARLIN_1/T.MONOCOCCUM (108)
185	D67.2/P66.270//T.MONOCOCCUM (108)
186	ARLIN_1/T.MONOCOCCUM (110)
187	D67.2/P66.270//T.URARTU (542)
188	D67.2/P66.270//T.URARTU (543)
189	ARLIN_1/T.URARTU (548)
190	CPI/GEDIZ/3/GOO//JO/CRA/4/T.URARTU (548)
191	D67.2/P66.270//T.URARTU (550)
192	D67.2/P66.270//T.URARTU (553)
193	CPI/GEDIZ/3/GOO//JO/CRA/4/T.URARTU (553)
194	CPI/GEDIZ/3/GOO//JO/CRA/4/T.URARTU (556)

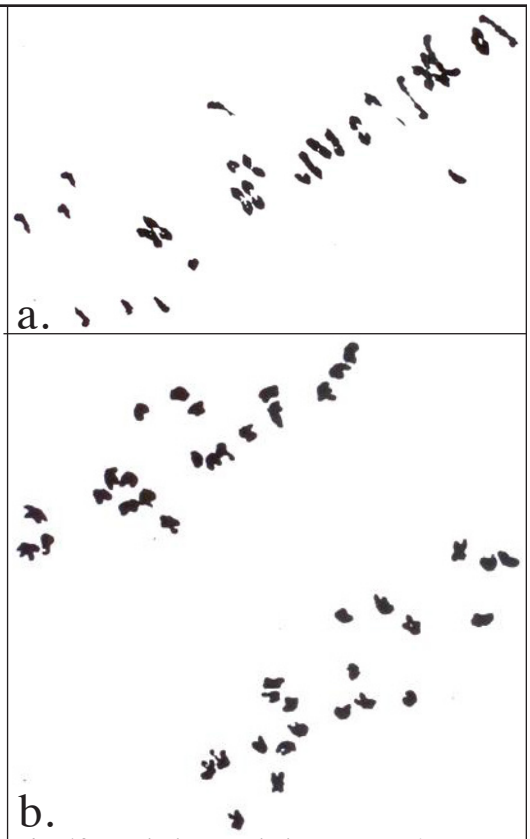


Fig. 10. Meiotic association at metaphase I of some A-genome synthetic hexaploids with 42 chromosomes and genomically AABBAA: (a) 21 bivalents with eight rods + 13 ring associations and (b) anaphase I separation with a 21 + 21 split in a meiocyte.

Seventeen synthetic genotypes (8.7%) were resistant at both seedling and adult-plant stages (5, 15, 19, 20, 24, 30, 32, 35, 58, 59, 60, 61, 95, 108, 109, 119, and 128) and 19 (82.6%) of the durum wheat parents (1, 2, 4, 5, 8, 9, 11, 12, 13, 14, 17, 20, 21, 22, 26, 27, 28, 37, and 40). All this germ plasm represents the presence of major genes against stripe rust and can be exploited further in breeding programs.

Adult-plant resistance involving susceptibility at the seedling stage and resistance only at the adult-plant stage indicates the presence of minor genes, which are considered of great importance against rust diseases in acquiring durable resistance. Sixty-five (33.5%) of the A-genome synthetic hexaploids (1, 8, 10, 11, 14, 17, 21, 25, 29, 31, 33, 34, 38, 40, 41, 45, 49, 50, 51, 55, 56, 62, 64, 67, 68, 69, 88, 89, 96, 103, 104, 105, 114, 115, 116, 117, 118, 120, 121, 122, 123, 125, 126, 127, 135, 136, 137, 139, 141, 142, 143, 148, 150, 151, 159, 161, 168, 169, 178, 179, 182, 187, 189, and 191) and only one (4.35%) durum wheat parent (45) showed APR and are good candidates for providing durable resistance to wheat cultivars.

Molecular studies. ***Genetic diversity evaluation using random amplified polymorphic DNA (RAPD) primers.*** RAPD primers were used to evaluate the genetic diversity of the A-genome synthetic hexaploids. All 520 RAPD primers of

Table 7. The mean crossability data of some *T. turgidum* subsp. *turgidum*/A and B genome diploid species accessions.

Cross combination (AA-genome species)	Florets pollinated	Seed set	Embryos plated
/ *T. monococcum subsp. aegilopoides*	58.5	27.2	25.5
/ *T. monococcum* subsp. *monococcum*	42.0	6.80	6.00
/ *T. urartu*	58.7	12.5	7.50
Average of all three diploid genomes	53.1	15.5	13.0

Table 8. Mean meiotic chromosome associations at metaphase I in AABBAA synthetic hexaploids (amphiploids) involving *Triticum turgidum* subsp. *turgidum* cultivars and A-genome diploid accessions of *T. monococcum* subsp. *aegilopoides*. Abbreviations in table are as follows: I = univalent, rII = rod bivalent, oII = ring bivalent, III = trivalent, cIV = chain quadrivalent, oIV = ring quadrivalent, and Xta = chiasmata.

AABBAA number	Number of cells	I	rII	oII	III	cIV	oIV	Xta	Chromosome number
3	20	1.20	2.05	13.90	0.60	0.80	1.00	37.9	42
5	20	0.20	0.80	13.90	0.00	0.70	2.40	40.3	42
6	20	0.00	2.10	15.50	0.00	0.10	1.60	39.8	42
7	20	1.40	6.20	10.30	0.00	1.00	0.60	33.0	42
8	20	0.00	4.60	13.00	0.00	0.60	1.10	36.8	42
12	20	0.10	3.50	11.30	0.10	1.10	1.90	37.2	42
14	20	0.10	3.80	11.20	0.10	0.90	2.00	37.1	42
16	20	0.00	2.60	13.40	0.00	1.20	1.30	38.2	42
17	20	0.00	1.00	13.40	0.00	1.00	2.30	40.0	42
19	20	0.00	1.80	15.00	0.00	0.20	1.90	40.0	42
20	20	0.10	3.50	11.30	0.10	1.10	1.90	37.2	42
21	20	0.00	2.80	15.80	0.00	0.10	1.10	39.1	42
22	20	0.20	2.90	12.30	0.20	0.80	1.90	37.9	42
23	20	0.20	2.90	13.40	0.00	0.30	2.00	38.6	42
24	20	0.20	2.20	14.00	0.20	0.60	1.60	38.8	42
25	20	0.10	2.10	14.30	0.10	0.50	1.70	39.2	42
26	20	0.30	2.10	12.50	0.90	1.30	1.40	38.4	43
27	20	0.20	3.10	15.80	0.00	0.40	0.60	38.3	42
29	20	0.50	4.10	14.50	0.10	0.40	0.60	36.9	42
30	20	0.30	2.90	15.00	0.10	0.40	1.00	38.3	42
31	20	1.20	3.80	13.40	0.40	0.60	0.70	36.00	42
34	20	0.70	3.60	15.10	0.10	0.40	0.50	37.20	42
36	20	0.60	4.60	12.30	0.00	0.60	1.30	36.20	42
38	20	0.10	3.90	14.70	0.10	0.40	0.70	37.50	42
39	20	1.20	2.60	12.90	0.20	1.10	1.20	36.90	42
40	20	0.40	3.90	13.70	0.00	0.60	1.00	37.10	42
41	20	0.00	2.80	14.40	0.00	0.40	1.50	38.80	42
44	20	0.00	2.80	15.20	0.00	0.50	1.00	38.70	42
45	20	0.00	2.40	15.60	0.00	0.60	0.90	39.00	42
46	20	1.00	5.10	12.60	0.40	0.60	0.50	34.90	42
48	20	0.00	3.10	15.10	0.00	0.50	0.90	38.40	42
49	20	0.50	2.60	15.60	0.10	0.40	0.80	38.40	42
50	20	0.10	3.20	15.20	0.10	0.60	0.60	38.00	42
51	20	0.10	2.80	14.40	0.10	0.50	1.30	38.50	42
52	20	0.20	2.10	16.00	0.00	0.40	1.00	39.30	42
53	20	0.10	2.40	15.60	0.10	0.40	1.00	39.00	42
54	20	0.70	3.30	14.60	0.10	0.50	0.80	37.40	42
55	20	0.20	2.40	15.20	0.20	0.60	0.90	38.60	42

Table 8. Mean meiotic chromosome associations at metaphase I in AABBAA synthetic hexaploids (amphiploids) involving *Triticum turgidum* subsp. *turgidum* cultivars and A-genome diploid accessions of *T. monococcum* subsp. *aegilopoides*. Abbreviations in table are as follows: I = univalent, rII = rod bivalent, oII = ring bivalent, III = trivalent, cIV = chain quadrivalent, oIV = ring quadrivalent, and Xta = chiasmata.

AABBAA number	Number of cells	I	rII	oII	III	cIV	oIV	Xta	Chromosome number
79	20	3.60	6.20	7.700	0.20	1.10	1.40	30.90	42
82	20	0.20	3.20	14.90	0.00	0.50	0.90	38.10	42
83	20	0.00	3.50	14.50	0.00	0.60	0.90	37.90	42
85	20	0.40	4.30	13.90	0.00	0.50	0.80	36.80	42
86	20	0.00	2.50	15.50	0.00	0.40	1.10	39.10	42
87	20	8.80	6.20	6.000	1.60	0.70	0.30	24.70	42
89	20	0.20	3.50	14.60	0.00	0.50	0.90	37.80	42
91	20	0.20	3.20	14.00	0.20	0.80	0.90	37.60	42
94	20	0.50	3.90	16.70	0.10	0.00	0.00	37.50	42
95	20	0.20	4.70	13.40	0.00	0.70	0.70	36.40	42
96	20	0.10	3.10	15.50	0.10	0.50	0.60	38.20	42
97	20	0.00	1.80	16.80	0.00	0.50	0.70	39.70	42
98	20	1.56	6.33	10.11	0.44	0.78	0.78	32.89	42
99	20	0.30	3.20	14.50	0.10	0.40	1.10	38.00	42
103	20	0.00	2.50	16.50	0.00	0.30	0.70	39.20	42
104	20	0.20	3.00	15.40	0.20	0.40	0.70	38.20	42
106	20	0.00	2.50	15.50	0.00	0.50	1.00	39.00	42
108	20	0.20	2.60	15.60	0.20	0.40	0.80	38.60	42
109	20	0.00	2.80	15.20	0.00	0.40	1.10	38.80	42
133	20	0.10	2.40	17.40	0.10	0.00	0.50	39.40	42
134	20	0.10	1.80	17.20	0.10	0.30	0.60	39.70	42
135	20	0.00	1.70	17.20	0.20	0.30	0.60	39.80	42
136	20	0.30	2.80	16.70	0.10	0.30	0.30	38.50	42
137	20	0.10	1.80	16.20	0.10	0.40	1.00	39.60	42
139	20	0.10	3.40	14.40	0.10	0.40	1.10	38.00	42
142	20	0.70	4.30	13.80	0.10	0.40	0.80	36.50	42
143	20	0.50	3.70	14.40	0.30	0.70	0.40	36.80	42
101	20	0.60	3.10	13.80	0.60	0.60	1.10	38.10	43
102	20	0.60	3.30	13.30	0.20	0.50	1.40	37.40	42
110	20	1.50	3.60	13.20	0.40	0.50	0.80	35.90	42
111	20	0.50	2.80	15.30	0.30	0.20	0.90	38.20	42
112	20	0.40	4.20	14.60	0.00	0.40	0.60	37.00	42
113	20	0.20	1.90	15.80	0.00	0.20	1.40	39.70	42
114	20	0.10	2.50	14.70	0.10	0.60	1.20	38.70	42
131	20	0.40	3.80	13.40	0.00	0.40	1.40	37.40	42
132	20	0.30	1.20	15.00	0.30	0.10	2.00	40.10	42
138	20	2.80	3.50	10.80	1.20	0.60	0.90	32.90	41
156	20	1.00	2.70	13.40	0.40	0.40	1.50	37.50	42
157	20	1.60	3.20	12.90	0.20	0.90	1.00	36.10	42
158	20	0.70	3.40	11.30	0.10	1.40	1.50	36.40	42
159	20	0.20	2.50	13.20	0.00	0.40	2.20	38.90	42

the Operon Series were screened, working primers identified, and applied to detect genetic polymorphism at DNA level. The samples that did not amplify were not included in the analysis. Genetic analysis was performed only on the scorable bands. Every single band was considered as a single locus/allele. The loci were scored as present/absent. Bivariate data 1–0 were used to estimate the genetic diversity (GD). The unweighted pair group of arithmetic means (UPGMA) func-

Table 9. Mean meiotic chromosome associations at metaphase I in AABBAA synthetic hexaploids (amphiploids) involving *Triticum turgidum* subsp. *turgidum* cultivars and A-genome diploid accessions of *T. monococcum* subsp. *monococcum*. Abbreviations in table are as follows: I = univalent, rII = rod bivalent, oII = ring bivalent, III = trivalent, cIV = chain quadrivalent, oIV = ring quadrivalent, and Xta = chiasmata.

AABBAA number	Number of cells	I	rII	oII	III	cIV	oIV	Xta	Chromosome number
18	20	0.00	1.90	16.9	0.00	0.20	0.90	39.9	42
59	20	0.10	3.30	14.3	0.10	0.60	1.00	37.0	42
64	20	0.20	2.80	14.8	0.20	0.50	1.00	38.3	42
65	20	0.30	2.80	14.3	0.10	0.60	1.20	38.2	42
115	20	1.60	2.20	15.4	0.00	0.40	0.90	37.8	42
116	20	1.90	3.30	14.1	0.30	0.40	0.70	36.1	42
117	20	0.70	3.20	14.3	0.10	0.70	0.70	37.2	42 (one VI)
119	20	0.80	2.80	14.5	0.20	0.40	1.10	37.8	42
120	20	0.30	2.20	14.5	0.50	0.40	1.30	38.6	42
121	20	1.70	3.10	12.6	0.30	0.60	0.40	36.3	42
122	20	1.00	3.70	14.1	0.20	0.40	0.80	36.7	42
123	20	1.20	5.30	13.3	0.40	0.40	0.20	34.7	42
144	20	0.30	2.60	15.3	0.20	0.30	1.00	38.7	42
145	20	0.80	3.40	15.3	0.20	0.60	0.20	37.0	42
146	20	0.20	3.20	15.6	0.20	0.20	0.70	38.2	42
147	20	0.40	2.80	16.0	0.00	0.30	0.70	38.5	42
148	20	0.80	4.70	14.3	0.40	0.30	0.20	35.8	42
149	20	1.80	5.40	13.2	0.20	0.40	0.20	34.2	42
150	20	1.80	4.60	13.3	0.40	0.60	0.20	34.6	42
151	20	0.90	3.90	14.3	0.10	0.30	0.80	36.8	42
152	20	0.80	4.20	14.8	0.40	0.10	0.40	36.5	42
153	20	0.70	3.20	14.2	0.10	0.70	0.70	37.2	42
154	20	0.00	2.20	16.8	0.00	0.60	0.40	39.2	42
161	20	0.20	2.20	15.5	0.00	0.30	1.30	39.3	42
162	20	1.90	4.00	12.7	0.50	0.20	1.10	35.4	42
163	20	0.20	2.90	13.2	0.00	0.40	2.00	38.5	42

tion estimated the GDs between the genotypes as follows: $GD_{xy} = 1 - d_{xy}/d_x + d_y - d_{xy}$, where GD_{xy} = GD between two genotypes, d_{xy} = total number of common loci (bands) in two genotypes, d_x = total number of loci (bands) in genotype 1, and d_y = total number of loci (bands) in genotype 2.

The efficiency of primers to amplify the genotypes ranged from 124 (OPE-3 and OPR-8) to one (OPG-10, OPG-17, OPH-11, OPI-2, OPI-4, OPM-14, and OPN-1) in A-genome synthetic hexaploids (Table 14, pp. 109-111) and from nine (OPN-6) to one (OPA-4, OPE-11, OPJ-1, OPW-5, OPX-2, and OPY-8) in B-genome synthetic hexaploids (Table 15, pp. 111-112). Scorable bands ranged from 1 (OPI-4 and OPM-14) to 666 (OPE-3) in A-genome synthetic hexaploids (Table 14, pp. 109-111).

A genetic analysis of the population showed that the total number of loci for A-genome synthetic hexaploids equaled 1,095 of which 1.062 were polymorphic (Table 14, pp. 109-111). The percentage of polymorphism was very high (96.68%). The range of scorable bands was from 250–3,000 bp in A-genome synthetic hexaploids.

Similarity matrix. A bivariate analysis was conducted to generate a similarity matrix and dendrogram to estimate genetic diversity. The A-genome synthetic hexaploids exhibited a minimum value of similarity matrix of 68.9% between 1 and 107 and the maximum value of 98.8% between 121 and 152.

Dendrogram interpretation. The GD between genotypes was used to construct a dendrogram by UPGMA analysis for determining grouping of the lines on the basis of similarities and differences. In A-genome synthetic hexaploids, the

Table 10. Mean meiotic chromosome associations at metaphase I in AABBAA synthetic hexaploids (amphiploids) involving *Triticum turgidum* subsp. *turgidum* cultivars and A-genome diploid accessions of *T. urartu*. Abbreviations in table are as follows: I = univalent, rII = rod bivalent, OII = ring bivalent, III = trivalent, cIV = chain quadrivalent, OIV = ring quadrivalent, and Xta = chiasmata.

AABBAA number	Number of cells	I	rII	oII	III	cIV	oIV	Xta	Chromosome number
52	20	5.20	5.10	9.80	1.40	0.20	0.00	28.1	40
70	20	0.60	2.10	17.6	0.00	0.30	0.20	39.0	42
72	20	0.00	2.90	14.7	0.00	0.80	0.90	38.3	42
74	20	0.00	3.50	14.5	0.00	0.80	0.70	37.7	42
75	20	0.00	4.00	14.4	0.00	0.60	0.70	37.4	42
76	20	2.00	5.00	9.60	0.20	0.90	1.40	32.9	41
77	20	0.40	2.50	15.3	0.00	0.60	0.90	38.5	42
78	20	1.70	6.80	8.60	0.30	1.00	0.90	31.2	41
125	20	1.50	4.00	10.5	0.50	1.20	1.30	34.8	42
126	20	0.70	3.30	14.8	0.10	0.30	0.90	37.6	42
127	20	1.20	2.60	12.6	0.00	0.20	2.40	38.0	42
128	20	1.80	5.60	9.90	0.60	0.20	1.40	32.8	41
129	20	1.10	5.20	10.6	0.30	0.60	1.50	34.8	42
130	20	0.50	3.60	11.6	0.10	1.20	1.50	36.8	42
165	20	1.20	3.40	12.6	0.00	0.60	1.60	36.8	42
166	20	0.70	3.70	10.1	0.30	1.30	1.90	36.0	42
168	20	0.00	2.20	14.0	0.00	0.20	2.20	39.6	42
169	20	0.40	2.60	15.2	0.40	0.40	0.80	38.2	42
170	20	1.30	2.30	12.4	1.50	0.40	0.80	34.5	40
172	20	0.00	2.40	15.4	0.00	0.40	1.20	39.2	42
173	20	0.10	2.70	14.1	0.10	1.00	1.00	38.1	42
154	20	0.00	2.20	16.8	0.00	0.60	0.40	39.2	42
161	20	0.20	2.20	15.5	0.00	0.30	1.30	39.3	42
162	20	1.90	4.00	12.7	0.50	0.20	1.10	35.4	42
163	20	0.20	2.90	13.2	0.00	0.40	2.00	38.5	42

Table 11. Mean phenotypic characteristics of selected AA-genome amphiploids involving *Triticum monococcum* subsps. *aegilopoides* and *monococcum* and *T. urartu*.

	Spike				Spikelet				Glume		Lemma		
No.	Length (cm)	Width (cm)	Nodes /spike	Internode length (cm)	Length (cm)	Width (cm)	/spike	Florets /spikelet	Length (cm)	Awn length (cm)	Body length (cm)	Awn length (cm)	Anther length (cm)
T. monococcum* subsp. *aegilopoides													
28	21.45	1.21	22.00	0.44	11.13	0.65	22.00	4.00	0.91	0.24	1.17	9.17	0.35
86	20.60	1.25	22.00	0.46	11.48	0.81	22.00	4.00	1.12	0.44	1.23	10.58	0.32
133	20.40	1.01	26.00	0.57	10.83	0.81	26.00	4.50	1.22	0.40	1.29	9.15	0.35
T. monococcum subsp. monococcum													
185	14.90	1.70	26.00	0.30	8.33	1.02	26.00	3.75	1.05	0.21	1.16	6.97	0.32
115	20.65	1.10	24.50	0.41	12.18	0.72	24.50	3.25	1.01	0.31	0.93	10.33	0.40
148	17.65	1.21	27.00	0.43	10.73	0.87	27.00	4.25	1.24	0.41	1.06	7.99	0.33
185	14.90	1.70	26.00	0.30	8.33	1.02	26.00	3.75	1.05	0.21	1.16	6.97	0.32
T. urartu													
191	15.40	1.41	19.50	0.61	9.08	0.89	19.50	4.00	0.96	0.35	1.26	8.43	0.31
193	17.85	1.08	24.50	0.46	9.25	0.81	24.50	4.00	0.87	0.28	1.06	6.88	0.21
189	19.60	1.31	26.00	0.40	11.50	0.84	26.00	4.00	1.17	0.80	1.26	9.96	0.40

Fig. 11. Spike morphology of some AABBAA synthetic hexaploids involving the diploid progenitor species *T. monococcum* subsp. *aegilopoides* and *monococcum* and *T. urartu*, (a) *T. turgidum*/accession 086; (b) *T. turgidum*/accession 115; (c) *T. turgidum*/accession 133; (d) *T. turgidum*/accession 148 and (e) *T. turgidum*/accession 185.

exhibited minimum value of similarity matrix of 73.3% between 34 and 130 and the maximum value of 100% in 314 different combinations.

Phenotypic characterization and disease screening. From the wide array of AAAABB synthetic wheats produced, field plantings were utilized to establish descriptive parameters and seed increase. The descriptor characteristics demonstrated extensive genetic diversity for plant height, flowering date, and 1,000-kernel weight (Table 12, pp. 103-107). Utilizating this germ plasm for durum wheat improvement will be an advantage selecting synthetics that are trait positive and agronomically superior. The targeted variation also can be tapped for direct crossing with durum wheat cultivars as shown for bread wheat improvement. Because bread wheat in Pakistan is the main cereal crop, the diversity of the A genome can be exploited via bridge crossing of the AAAABB hexaploid with the AABBDD bread wheat as recombination events across the AA genomes will permit the donor variation to be introgressed. Alternatively, after the durum wheats are screened and resistance sources identified, the desired A-genome accession also can enter into direct hybridization with bread wheat.

only main cluster has three subclusters, A, B, and C (Fig. 13, p. 113). Subcluster A has five genotypes and also contains the most diverse line of the group, 107. Other good lines in this subcluster include 3, 68, 92, and 111. The highly diverse lines in subcluster B include 20, 39, 82, 95, 118, and 177 in total of 188 genotypes. Subcluster C has only one genotype, 1.

Genetic diversity evaluation using simple sequence repeat (SSR) Primers. SSR primers were used for to evaluate the GD of the A-genome synthetic hexaploids. All 275 SSR primers were applied to detect genetic polymorphism at DNA level. The samples which did not amplify were not included in the analysis. Genetic analysis was similar to that for the RAPD primers.

The efficiency of primers to amplify the genotypes ranged from 68 (*Xgwm312-2A*) to six (*Xgwm473-2A*) in the A-genome synthetic hexaploids (Table 16, p. 112) and scorable bands ranged from six (*Xgwm473-2A*) to 112 (*Xgwm311-2A*) (Table 16, p. 112).

A genetic analysis of the population showed that the total number of alleles for A-genome synthetic hexaploids scored equaled 126, all of were polymorphic; the the percentage of polymorphism was 100% (Table 16, p. 112). The range of scorable bands was from 50–250 bp.

Similarity matrix. Bivariate analysis was conducted to generate a similarity matrix and dendrogram to estimate genetic diversity. The A-genome synthetic hexaploids

Fig. 12. Spike morphology of some AABBAA synthetic hexaploids involving the diploid progenitor species *T. monococcum* subsps. *aegilopoides* and *monococcum* and *T. urartu*, (a) *T. turgidum*/accession 189; (b) *T. turgidum*/accession 191; (c) *T. turgidum*/accession 193; (d) Altar84/accession 015; (e) Decoy/accession 036 and (f) *T. turgidum*/accession 028.

Table 12. Phenotypic and disease characterization of the 194 A–genome synthetic hexaploids (2n=6x=42; AABBAA). FLOW = days–to–flowering, HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), P MA = days to physiological maturity, TKW = 1,000–kernel weight (g), G/S = number of grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Pm (S) = reaction to powdery mildew at the seedling stage (– indicates missing data), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult-plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Synthetic number	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Yr (S)	Yr (A)
1	125	104	LB	175	46.0	18	13.5	–	2	89	5R
2	136	99	LB	169	59.0	18	12.0	–	–	89	30S
3	141	97	LB	171	65.0	2	13.0	–	–	89	30S
4	128	95	LB	173	72.0	4	13.0	–	4	89	30S
5	125	98	LB	179	44.0	29	13.8	–	4	23	5R
6	116	105	LB	180	60.0	15	13.2	–	2	23	30S
7	134	117	LB	174	40.0	30	12.0	–	1	89	30S
8	133	129	LB	184	60.0	40	10.3	–	3	56	5R
9	117	127	LB	179	58.0	39	14.0	–	4	7	30S
10	125	125	LB	185	38.0	5	14.1	–	4	7	10R
11	135	124	LB	181	38.0	7	11.1	–	3	89	10R
12	135	127	LB	184	48.0	33	14.1	–	3	89	90S
13	116	112	LB	181	40.0	1	13.1	–	4	89	90S
14	154	104	LB	186	32.0	7	12.1	–	3	78	10R
15	143	104	LB	186	22.6	24	12.3	–	4	1	5R
16	136	116	LB	184	39.5	3	12.1	–	–	23	30MRMS
17	131	128	LB	187	35.2	2	12.3	–	–	89	10R
18	133	139	DB	180	41.4	7	12.0	–	3	89	30S
19	133	125	LB	186	40.6	13	11.5	–	–	0	10R
20	135	135	LB	186	38.4	4	12.1	–	–	1	10R
21	143	125	LB	185	43.8	18	12.6	–	5	89	10R
22	129	145	LB	181	20.0	2	13.0	–	–	89	30S
23	142	92	LB	181	50.0	11	11.0	–	–	0	30S
24	140	121	LB	187	50.0	5	12.3	–	4	4	10R
25	135	133	LB	187	44.0	9	12.8	–	4	78	10R
26	125	124	LB	181	55.2	8	11.1	–	4	78	10S
27	145	151	LB	176	69.0	5	8.0	–	–	78	30S
28	124	130	LB	175	13.7	7	18.0	–	3	89	30S
29	128	125	LB	181	49.0	21	13.0	–	5	78	10MR
30	108	119	LB	176	43.5	9	12.1	–	4	0	10R
31	133	100	LB	181	44.0	2	11.1	–	–	78	10R
32	135	104	LB	186	42.6	12	10.1	–	3	0	10R
33	133	101	DB	186	48.2	22	10.1	–	2	78	10R
34	147	129	LB	190	27.2	29	11.5	–	2	89	10R
35	135	118	LB	187	48.0	6	10.1	–	–	12	5R
36	127	133	LB	176	43.8	6	8.0	–	3	89	30S
37	128	129	LB	175	52.0	8	9.0	–	–	89	30S
38	135	125	LB	181	42.6	9	11.1	–	1	89	10R
39	127	133	LB	179	56.0	18	15.0	–	1	89	30S
40	145	121	LB	190	60.0	4	13.5	–	1	89	10R
41	149	104	LB	190	40.6	24	11.0	–	2	78	10R
42	118	102	LB	176	54.2	16	10.0	–	1	0	30S

Table 12. Phenotypic and disease characterization of the 194 A–genome synthetic hexaploids (2n=6x=42; AABBAA). FLOW = days–to–flowering, HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), P MA = days to physiological maturity, TKW = 1,000–kernel weight (g), G/S = number of grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Pm (S) = reaction to powdery mildew at the seedling stage (– indicates missing data), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult-plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Synthetic number	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Yr (S)	Yr (A)
43	134	118	LB	179	42.8	18	11.0	–	–	56	30S
44	116	106	LB	178	47.5	4	10.0	–	2	34	30S
45	125	94	LB	175	45.2	24	9.5	–	2	89	10R
46	127	112	LB	176	30.0	32	10.5	–	4	89	30S
47	127	113	LB	180	45.0	4	11.0	–	–	89	30S
48	135	115	LB	193	37.8	13	11.1	–	3	89	40S
49	133	102	Y	189	23.5	4	13.3	–	–	89	5R
50	145	80	LB	191	29.0	32	12.1	–	5	89	10R
51	126	110	Y	182	40.0	33	13.5	–	2	89	10R
52	125	126	LB	186	68.0	35	12.0	–	–	89	30MS
53	140	124	LB	180	40.0	33	9.0	–	2	89	30S
54	125	123	LB	181	44.4	21	10.0	–	0	89	30S
55	131	119	DB	187	32.2	21	11.0	–	1	89	30MR
56	146	130	DB	193	37.0	16	11.1	–	1	89	10R
57	126	110	LB	179	56.4	3	8.0	–	4	89	30S
58	136	116	LB	189	56.2	27	11.1	–	4	1	10R
59	131	117	LB	171	56.4	37	12.3	–	–	1	10R
60	127	105	LB	150	55.6	21	11.6	–	3	0	10R
61	127	103	LB	151	41.6	16	11.1	–	1	0	5R
62	121	108	LB	158	24.0	6	12.8	–	3	89	10R
63	127	110	LB	156	30.0	5	8.0	–	4	89	30S
64	139	113	LB	154	50.0	26	11.3	–	5	89	10MR
65	137	127	Y	156	48.0	6	14.0	–	–	89	30S
66	124	141	LB	150	50.0	1	11.5	–	5	89	30MS
67	125	108	LB	146	50.0	1	12.3	–	–	89	5 MR
68	122	114	LB	140	52.2	7	11.6	–	–	89	10MR
69	125	120	LB	150	46.0	43	13.1	–	2	89	5R
70	126	144	LB	179	43.4	31	12.3	–	–	12	10S
71	127	146	LB	171	53.2	22	14.6	–	–	9	90S
72	129	146	LB	173	32.6	6	13.5	–	–	1	10S
73	133	127	LB	172	37.6	16	10.0	–	4	9	30S
74	133	108	LB	185	46.0	26	14.6	–	3	12	20S
75	120	112	LB	172	17.4	21	7.0	–	–	9	30S
76	127	145	LB	175	63.0	11	15.0	–	3	89	40S
77	119	75	LB	171	49.6	20	14.0	–	1	89	30S
78	141	75	LB	183	42.8	33	8.0	–	6	45	30S
79	126	126	DB	176	32.8	33	11.0	–	6	56	90S
80	129	122	LB	180	33.2	18	9.0	–	4	89	30S
81	131	124	LB	179	32.0	17	14.0	–	–	9	30S
82	133	123	LB	176	31.0	4	13.0	–	1	12	30S
83	120	125	LB	175	37.0	35	10.0	–	0	89	30S
84	122	125	LB	173	50.0	11	12.0	–	0	89	30S

Table 12. Phenotypic and disease characterization of the 194 A–genome synthetic hexaploids (2n=6x=42; AABBAA). FLOW = days–to–flowering, HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), P MA = days to physiological maturity, TKW = 1,000–kernel weight (g), G/S = number of grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Pm (S) = reaction to powdery mildew at the seedling stage (– indicates missing data), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult-plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Synthetic number	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Yr (S)	Yr (A)
85	125	127	LB	178	41.2	15	13.0	–	3	89	20MS
86	136	112	LB	178	40.0	7	8.0	–	0	9	30S
87	141	110	LB	175	46.0	17	11.0	–	1	9	30S
88	128	115	LB	178	38.0	15	11.0	–	2	9	10MR
89	128	104	LB	183	31.0	6	12.0	–	2	9	10R
90	131	109	LB	172	31.6	5	9.0	–	1	9	30S
91	131	114	LB	180	57.4	19	11.0	–	7	9	30S
92	134	119	LB	175	51.8	25	10.0	–	1	9	30S
93	134	118	LB	176	40.0	17	11.0	–	2	9	30S
94	139	120	LB	180	40.0	13	13.0	–	3	9	30S
95	134	123	LB	184	71.0	6	10.0	–	3	1	10MRMS
96	148	114	LB	191	59.0	6	12.5	–	1	56	10R
97	125	108	LB	177	49.6	7	7.0	–	–	89	30S
98	126	109	LB	178	38.0	16	9.0	–	–	67	30S
99	142	106	LB	184	35.0	14	10.0	–	6	89	30S
100	131	131	LB	183	35.4	23	14.0	–	0	89	30S
101	124	118	LB	179	43.4	6	13.0	–	1	89	30S
102	133	108	LB	180	65.6	13	7.0	–	0	9	30S
103	134	116	LB	183	56.6	38	12.0	–	0	9	5R
104	133	89	LB	181	61.6	14	9.8	–	5	89	5R
105	133	85	LB	179	50.2	51	10.0	–	4	89	5R
106	135	82	LB	176	31.0	1	12.0	–	0	89	30S
107	145	81	LB	179	30.8	21	9.0	–	–	89	30S
108	150	79	LB	188	72.0	36	9.0	–	2	1	10R
109	145	128	LB	186	44.6	21	11.0	–	1	0	10R
110	120	123	DB	178	46.2	14	10.0	–	4	9	80S
111	120	110	LB	182	47.0	1	15.0	–	0	9	40S
112	125	105	LB	185	48.0	15	13.0	–	5	9	30S
113	127	109	LB	182	48.0	21	10.0	–	5	9	30S
114	135	100	LB	187	44.0	20	13.0	–	7	89	10R
115	135	102	LB	187	26.6	9	11.0	–	5	89	10R
116	137	120	LB	186	45.4	10	12.0	–	4	89	10R
117	145	114	LB	188	38.2	26	8.0	–	4	89	5R
118	143	107	LB	188	32.6	7	14.0	–	4	9	5R
119	141	117	LB	189	53.8	34	12.0	–	6	12	10R
120	126	117	LB	189	48.0	27	12.6	–	0	89	10R
121	139	87	LB	187	44.0	7	13.0	–	4	89	10R
122	143	137	LB	191	45.6	10	12.0	–	7	89	10R
123	143	124	LB	191	32.4	8	11.0	–	1	89	5R
124	134	95	LB	186	59.8	32	14.0	–	2	89	30S
125	127	100	DB	189	45.3	6	8.0	–	3	89	5R
126	132	100	LB	183	46.2	19	10.0	–	3	9	5R

Table 12. Phenotypic and disease characterization of the 194 A–genome synthetic hexaploids (2n=6x=42; AABBAA). FLOW = days–to–flowering, HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), P MA = days to physiological maturity, TKW = 1,000–kernel weight (g), G/S = number of grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Pm (S) = reaction to powdery mildew at the seedling stage (– indicates missing data), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult-plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Synthetic number	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Yr (S)	Yr (A)
127	127	120	LB	176	36.6	9	7.0	–	2	78	5R
128	131	131	LB	173	35.8	20	6.0	–	2	1	5R
129	138	95	LB	184	48.0	40	14.0	–	4	89	30S
130	122	119	LB	183	41.8	24	8.0	–	1	9	70S
131	147	113	DB	186	45.2	57	14.0	–	3	89	30S
132	133	111	LB	179	46.8	16	11.0	–	5	12	30S
133	128	111	LB	172	34.4	9	12.0	–	4	89	30S
134	143	110	LB	176	35.6	5	10.0	–	2	7	30S
135	140	115	LB	175	36.0	9	12.6	–	7	89	10R
136	140	137	LB	185	31.6	5	13.0	–	3	89	10R
137	140	138	LB	185	35.6	9	10.0	–	3	89	10R
138	125	133	LB	186	42.0	41	12.0	–	2	78	10R
139	140	123	LB	185	40.0	3	17.0	–	3	89	10R
140	140	120	LB	179	58.0	16	11.0	–	1	89	30S
141	140	122	LB	181	27.0	18	12.0	–	1	89	5R
142	140	143	LB	187	41.6	20	13.0	–	1	89	5R
143	139	135	LB	185	37.6	30	10.1	–	1	7	5R
144	139	125	LB	180	36.0	35	12.0	–	–	89	30S
145	137	138	LB	181	42.6	23	10.0	–	9	7	10S
146	140	135	LB	180	24.4	6	11.0	–	8	7	30S
147	127	132	LB	172	24.0	33	14.0	–	–	89	30S
148	133	135	LB	187	30.8	14	10.0	–	2	67	5R
149	142	155	LB	186	33.6	31	9.0	–	6	78	10MS
150	141	155	Y	188	24.0	13	11.0	–	2	78	30MR
151	135	111	LB	186	38.2	11	8.0	–	5	89	10R
152	125	136	LB	185	41.0	30	14.0	–	–	78	30MS
153	128	137	LB	185	40.8	29	14.0	–	3	89	30MS
154	127	137	LB	187	35.0	24	12.0	–	3	89	90S
155	136	126	DB	180	28.2	30	10.0	–	8	89	30S
156	126	115	LB	179	30.0	15	11.0	–	–	89	30S
157	128	119	LB	176	54.7	17	12.0	–	7	8	30S
158	127	122	LB	187	30.6	13	11.0	–	4	89	5S
159	151	130	LB	187	30.2	28	12.0	–	9	89	10R
160	122	125	DB	180	36.0	16	17.0	–	–	89	30S
161	141	131	LB	186	20.4	19	12.0	–	7	9	10R
162	131	104	LB	186	25.6	41	10.0	–	5	9	30S
163	139	108	LB	187	31.8	5	13.0	–	7	89	5MS
164	130	111	LB	180	36.4	18	12.0	–	5	9	30S
165	125	101	Y	187	26.2	23	8.0	–	5	9	MSS
166	144	95	LB	179	39.6	15	13.0	–	4	9	30S
167	140	95	LB	185	22.4	30	7.0	–	4	9	30S
168	141	117	LB	187	22.0	29	7.0	–	3	9	10R

Table 12. Phenotypic and disease characterization of the 194 A–genome synthetic hexaploids (2n=6x=42; AABBAA). FLOW = days–to–flowering, HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), P MA = days to physiological maturity, TKW = 1,000–kernel weight (g), G/S = number of grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Pm (S) = reaction to powdery mildew at the seedling stage (– indicates missing data), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult-plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Synthetic number	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Yr (S)	Yr (A)
169	133	119	LB	181	40.4	33	12.0	–	7	9	10R
170	141	121	LB	182	30.0	10	9.0	–	7	9	10S
171	140	120	LB	185	29.0	18	10.0	–	–	9	30S
172	146	102	LB	183	39.8	8	10.0	–	6	9	30S
173	135	112	LB	176	29.3	15	8.0	–	7	9	30S
174	122	116	LB	172	36.4	19	16.0	–	4	89	30S
175	139	112	LB	176	32.4	31	11.0	–	5	89	30S
176	132	116	LB	171	10.0	3	11.6	–	–	9	30S
177	132	108	LB	173	38.4	9	11.0	–	4	89	30S
178	133	100	LB	182	32.6	9	14.0	–	7	9	5R
179	128	108	LB	182	24.0	16	13.3	–	4	89	5R
180	141	118	LB	183	28.5	4	12.6	–	2	89	20S
181	140	131	LB	180	25.2	34	8.0	–	3	89	30S
182	129	144	LB	187	20.7	25	10.0	–	1	78	30MR
183	137	107	LB	182	33.6	12	11.0	–	0	0	30S
184	136	95	LB	180	48.9	12	14.0	–	0	9	30S
185	127	85	LB	182	24.4	18	10.0	–	0	78	30S
186	133	116	LB	186	21.4	52	12.8	–	2	8	80S
187	128	112	LB	176	42.0	32	12.8	–	7	8	5R
188	124	113	LB	175	43.0	25	10.0	–	7	89	30S
189	129	115	LB	177	44.8	22	8.0	–	0	89	5R
190	120	86	LB	182	35.6	27	13.0	–	2	9	40MS
191	122	120	LB	173	45.2	7	13.0	–	0	9	10R
192	135	98	LB	177	25.0	4	7.0	–	1	9	30MS
193	125	150	LB	177	35.8	11	17.0	–	8	9	30S
194	128	145	LB	176	32.0	18	15.0	–	–	89	30S

This study has focussed on having in stock a genetic resource in adequate seed amounts that is phenotypically characterized and molecularly typed for its diversity. Earlier investigations indicated that in the AAB F_1 hybrids (2n=3x=21), mean pairing frequency ranged between 5.5 to 6.0 bivalents across the 194 combinations produced with 25 to 50 meiocytes analyzed per F_1 sample. Because A genome recombination events were possible, the variation of the diploid progenitors could be harnessed in breeding. Producing AAAABB amphiploids provided a resource that has the merit of being globally distributed and utilized by providing a more reliable evaluation of the genetic value of the alien genes in the derived background through a permanent germ plasm base. Although amphiploid instability is a frequent occurrence, all the synthetics analyzed in our field studies in Pakistan showed exceptional cytological stability. The predominance of bivalents (Figs. 8–10, pp. 95-97) with a high seed set with well-filled grains enabled adequate production of seed for national testing against key biotic/abiotic stress production constraints.

The Karnal bunt screening of all the AAAABB synthetic hexaploids reinforced the earlier observations that have expressed durums to be generally field resistant. Bringing in additional diversity from new diploid progenitor accessions did not alter this field resistance trend. The A-genome synthetic hexaploids when tested under field conditions for yellow rust exhibited a parallel trend to the D-genome-based amphiploids. Conclusions drawn in the above study were that the germ plasm tested fell into two categories:

Table 13. Phenotypic and disease characterization of the 194 A–genome synthetic hexaploids (2n=6x=42; AABBAA). FLOW = days–to–flowering, HT = plant height at maturity (cm); AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), P MA = days to physiological maturity, TKW = 1,000–kernel weight (g), G/S = number of grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Pm (S) = reaction to powdery mildew at the seedling stage (– indicates missing data), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult–plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Entry	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Pm (S)	Yr (S)	Yr (A)
1	87	86	LB	101	45	45	9	–	7	0	10R
2	86	86	LB	105	18.5	16	9	–	5	0	5RMR
4	89	78	LB	108	33.0	26	6	–	7	0	TR
5	87	76	LB	112	37.6	18	6	–	3	0	10R
8	95	103	LB	108	32.2	30	9	–	3	0	0
9	88	103	LB	103	41.6	38	8	–	3	0	5R
11	85	102	LB	99	46.0	28	6	–	2	0	0
12	98	96	LB	110	37.0	41	10	–	4	0	5R
13	88	102	LB	100	41.1	28	7	–	5	0	10R
14	87	85	LB	106	46.5	31	7	–	6	0	10MR
17	92	83	LB	112	32.0	42	11	–	6	0	40R
20	89	85	LB	114	38.4	47	10	–	–	0	10R
21	87	90	LB	102	35.1	34	9	–	5	0	5R
22	89	103	LB	115	34.8	48	9	–	7	0	0
23	100	68	LB	115	12.5	9	8	–	2	0	20MRMS
25	89	75	LB	100	42.5	36	8	–	–	0	40MS
26	82	104	LB	98	35.5	41	9	–	–	0	5R
27	82	90	LB	95	41.2	45	8	–	–	0	20RMR
28	88	92	LB	93	44.2	28	8	–	–	0	TR
33	92	93	LB	105	32.1	30	5	–	–	0	20MRMS
34	102	104	LB	115	34.3	34	5	–	–	0	20MRMS
35	102	97	LB	116	32.4	23	7	–	–	0	20MRMS
37	100	96	LB	112	29.7	9	9	–	–	0	TR
40	100	78	LB	118	34.2	30	9	–	–	0	0
45	89	87	LB	103	42.7	15	7	–	–	78	TR

1. Dual resistance, where the durum wheat parent and the corresponding synthetic hexaploid entry were resistant. Because the diploid donor was not tested, the resistance of the synthetic could be due to the durum parent alone or the durum parent complimented by the resistance in the diploid donor accession.
2. Resistance in the synthetic and susceptibility in the durum wheat parent. This category provided unequivocal support that the resistance was a contribution of diversity that was expressed from the diploid donor accession.

By analogy, the stripe rust resistance present in the AAAABB synthetics is inferred to emanate either from the durum wheat parent if that was resistant or the A-genome diploid if the durum wheat was susceptible, or as a consequence of both the durum wheat parent and the A-genome parent where both parents were resistant.

Systematic discussion is now built upon addressing the phenology, disease, and genetic diversity of the 194 A-genome synthetics that have been used. The synthetics have been grouped into various categories based upon the durum wheat parent used (Table 5, p. 93) where group 1 has two synthetics with the same durum wheat cultivar entry 21; YAR-MUK. From the various groups, number 19 contributed to 31 AABBAA synthetics and the durum wheat parent is entry number 11 (CPI/GEDIZ/3/GOO//JO/CRA). In this group, the synthetics have been separated according to the diploid parent used, thus the categories discussed are *T. monococcum* subsp. *aegilopoides* with 23 synthetics, *T. monococcum* subsp. *monococcum* with five, and *T. urartu* with three (Table 11, p. 101).

Table 14. Molecular fingerprinting pattern by random amplified polymorphic DNA (RAPD) primers in the A-genome synthetic hexaploids (2n=6x=42; AABBAA).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
1	OPD-20	14	14	100%	84	448	250–3,000
2	OPE-1	12	12	100%	73	321	500–2,500
3	OPE-2	9	9	100%	34	119	500–2,500
4	OPE-3	12	12	100%	124	666	250–2,500
5	OPE-4	12	12	100%	113	476	250–3,000
6	OPE-5	5	5	100%	35	37	750–3,000
7	OPE-6	12	12	100%	63	187	500–2,500
8	OPE-7	13	13	100%	85	422	500–3,000
9	OPE-12	12	12	100%	49	150	500–2,500
10	OPE-14	11	11	100%	79	289	500–2,500
11	OPE-15	14	14	100%	80	382	250–2,500
12	OPE-16	13	13	100%	46	115	250–2,500
13	OPE-19	11	11	100%	35	112	250–2,500
14	OPF-10	10	10	100%	47	152	500–2,500
15	OPF-12	11	11	100%	40	133	500–2,500
16	OPF-13	12	12	100%	65	275	250–2,500
17	OPF-14	13	13	100%	60	292	250–2,500
18	OPF-15	11	11	100%	42	184	500–2,500
19	OPF-16	3	3	100%	3	4	1,000–3,000
20	OPF-20	11	11	100%	41	190	500–2,500
21	OPG-2	10	10	100%	9	27	500–2,500
22	OPG-3	11	11	100%	13	49	500–2,500
23	OPG-8	9	9	100%	74	233	750–2,500
24	OPG-10	8	0	0%	1	8	750–2,500
25	OPG-17	6	0	0%	1	6	1,000–2,000
26	OPG-18	13	13	100%	18	81	250–2,500
27	OPG-19	11	11	100%	52	270	500–2,500
28	OPH-1	8	8	100%	2	10	500–2,500
29	OPH-2	14	14	100%	12	46	250–3,000
30	OPH-4	10	10	100%	51	159	500–2,500
31	OPH-5	12	12	100%	12	57	500–2,500
32	OPH-11	2	0	0%	1	2	500–1,000
33	OPH-12	8	8	100%	10	30	250–1,000
34	OPH-13	11	11	100%	15	48	500–2,500
35	OPH-15	10	10	100%	11	28	250–2,000
36	OPH-17	5	5	100%	6	10	500–2,500
37	OPH-19	10	10	100%	15	37	500–2,500
38	OPI-2	6	0	0%	1	6	500–1,500
39	OPI-4	1	1	100%	1	1	1,500
40	OPI-6	12	12	100%	29	159	250–2,500
41	OPI-7	9	9	100%	8	23	250–2,000
42	OPI-9	14	14	100%	69	200	250–3,000
43	OPI-10	11	11	100%	69	218	250–2,000
44	OPI-12	15	15	100%	121	643	250–3,000
45	OPI-14	11	11	100%	41	138	250–2,500
46	OPI-16	10	10	100%	27	69	250–2,000
47	OPI-17	12	12	100%	53	245	1,000–1,500

Table 14. Molecular fingerprinting pattern by random amplified polymorphic DNA (RAPD) primers in the A-genome synthetic hexaploids (2n=6x=42; AABBAA).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
48	OPI-18	1	1	100%	3	3	1,000–1,500
49	OPI-20	11	11	100%	25	87	250–2,500
50	OPJ-1	12	12	100%	14	50	250–2,000
51	OPJ-6	11	11	100%	21	63	750–2,500
52	OPJ-9	12	11	91.67%	48	124	500–3,000
53	OPJ-17	11	11	100%	13	47	500–3,000
54	OPJ-19	11	11	100%	54	235	250–2,000
55	OPJ-20	12	12	100%	116	536	250–2,500
56	OPK-15	5	5	100%	18	34	750–2,000
57	OPK-16	13	13	100%	101	331	250–3,000
58	OPK-19	11	11	100%	70	290	250–2,000
59	OPK-20	7	7	100%	3	14	250–1,500
60	OPL-7	8	8	100%	17	25	250–3,000
61	OPL-8	8	0	0%	2	16	250–2,000
62	OPL-11	12	12	100%	62	300	250–2,500
63	OPL-12	10	10	100%	86	308	250–2,000
64	OPL-14	12	12	100%	52	135	250–3,000
65	OPL-16	11	11	100%	72	236	500–2,500
66	OPL-20	14	14	100%	71	242	250–2,500
67	OPM-1	8	8	100%	27	65	500–1,500
68	OPM-3	12	12	100%	46	184	250–2,500
69	OPM-4	10	10	100%	18	70	500–2,500
70	OPM-5	11	11	100%	11	37	250–2,500
71	OPM-7	11	11	100%	15	64	500–2,500
72	OPM-8	3	3	100%	6	7	1,000–1,500
73	OPM-10	10	10	100%	54	234	250–2,000
74	OPM-12	7	7	100%	11	32	500–2,500
75	OPM-13	12	12	100%	26	92	250–2,500
76	OPM-14	1	1	100%	1	1	500
77	OPM-15	8	8	100%	24	57	750–2,500
78	OPM-16	10	10	100%	27	89	500–2,500
79	OPM-20	14	14	1000%	17	102	500–2,500
80	OPN-1	2	0	0%	1	2	250–500
81	OPN-2	14	14	100%	40	180	250–2500
82	OPN-3	10	10	100%	7	34	250–2500
83	OPN-4	12	12	100%	69	329	250–2500
84	OPN-5	11	11	100%	33	89	250–2,500
85	OPN-7	6	6	100%	9	19	500–2,000
86	OPN-9	13	13	100%	14	53	250–2,500
87	OPN-11	9	9	100%	13	40	250–2,000
88	OPN-12	11	11	100%	34	124	250–3,000
89	OPN-13	12	12	100%	8	39	500–2000
90	OPN-14	13	13	100%	16	73	250–2,500
91	OPN-16	9	9	100%	93	381	500–2,000
92	OPN-18	13	13	100%	71	319	250–2,500
93	OPN-19	13	13	100%	22	60	250–3,000
94	OPN-20	11	11	100%	26	119	250–2,500

Table 14. Molecular fingerprinting pattern by random amplified polymorphic DNA (RAPD) primers in the A-genome synthetic hexaploids (2n=6x=42; AABBAA).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
95	OPO-12	8	8	100%	7	16	500–2,000
96	OPO-13	6	6	100%	4	12	1,000–2,500
97	OPQ-6	12	12	100%	13	63	250–2,500
98	OPQ-9	8	8	100%	9	27	250–1,500
99	OPQ-14	15	15	100%	52	277	250–3,000
100	OPQ-16	13	13	100%	72	344	250–2,500
101	OPR-1	13	13	100%	63	163	250–2,500
102	OPR-4	6	6	100%	17	24	1,000–2,000
103	OPR-8	12	12	100%	124	400	250–1,500
104	OPR-9	12	12	100%	39	149	250–3,000
105	OPR-20	13	13	100%	49	160	250–3,000
106	OPT-8	9	9	100%	28	70	250–1,500
107	OPV-3	11	11	100%	18	70	500–3,000
108	OPV-18	09	09	100%	38	110	500–2,500

Table 15. Molecular fingerprinting pattern by random amplified polymorphic DNA (RAPD) primers in the B-genome synthetic hexaploids (2n=6x=42; AABBBB(SS)).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
1	OPA-3	8	8	100%	4	15	750–2,500
2	OPA-4	1	1	100%	1	1	1,000
3	OPB-1	8	5	62.5%	5	10	750–3,000
4	OPC-2	5	5	100%	5	7	750–2,000
5	OPE-9	2	2	100%	2	2	1,500
6	OPE-11	1	1	100%	1	1	1,000
7	OPE-14	4	2	50%	2	5	750–1,500
8	OPE-15	9	8	88.88%	5	21	500–2,500
9	OPE-16	7	6	85.71%	4	15	250–2,000
10	OPG-2	3	2	66.66%	2	4	750–1,500
11	OPG-5	8	8	100%	8	26	250–1,500
12	OPG-13	1	1	100%	2	2	1,500
13	OPI-7	9	7	77.77%	4	22	250–2,000
14	OPI-19	9	4	44.44%	4	17	250–2,000
15	OPJ-1	5	1	20%	1	5	500–1,500
16	OPJ-9	3	3	100%	4	7	750–1,500
17	OPJ-20	4	2	50%	6	21	250–1,000
18	OPK-9	2	2	100%	2	2	1500–2,000
19	OPL-1	7	7	100%	4	13	500–1,500
20	OPL-2	9	9	100%	7	20	250–1,500
21	OPL-12	4	3	75%	6	15	750–1,000
22	OPL-20	8	5	62.5%	8	17	250–2,500
23	OPM17	8	8	100%	4	18	250–1,500
24	OPN-1	3	3	100%	2	3	1,000–2,000
25	OPN-2	7	7	100%	6	16	250–2,000
26	OPN-3	2	2	100%	3	4	1,500
27	OPN-4	6	4	66.66%	8	29	500–1,500
28	OPN-5	6	6	100%	7	17	250–1,500

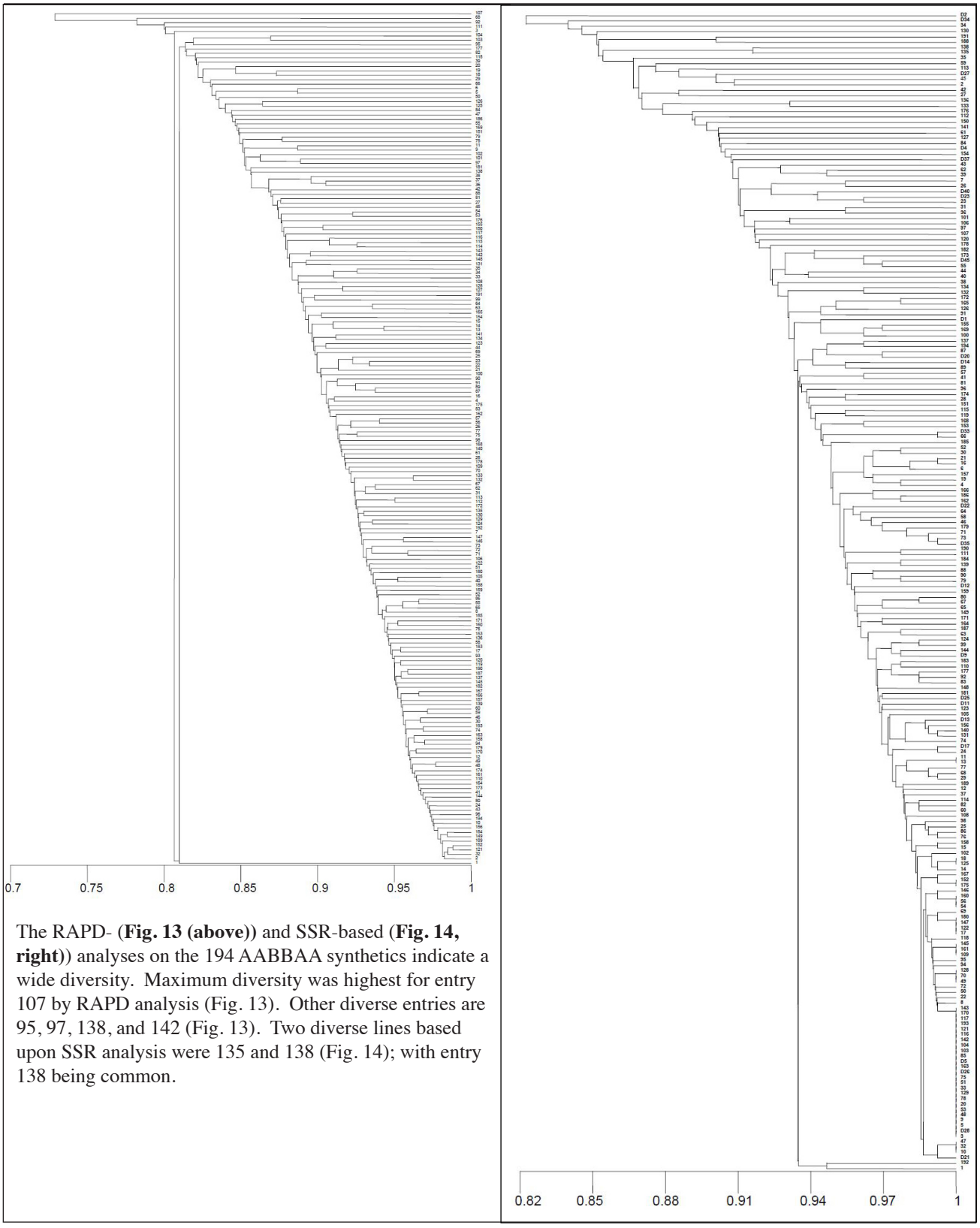
Table 15. Molecular fingerprinting pattern by random amplified polymorphic DNA (RAPD) primers in the B-genome synthetic hexaploids (2n=6x=42; AABBBB(SS)).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
29	OPN-6	7	7	100%	9	25	250–1,500
30	OPN-9	2	2	100%	2	3	250–1,500
31	OPN-12	4	1	25%	2	7	500–2,000
32	OPN-17	4	4	100%	3	9	500–1,000
33	OPP-16	3	3	100%	5	7	750–1,500
34	OPQ-5	4	4	100%	5	12	250–1,000
35	OPW-4	3	3	100%	3	6	750–2,000
36	OPW-5	1	1	100%	1	1	1,000
37	OPX-2	4	0	0%	1	4	750–1,500
38	OPX-12	4	4	100%	3	9	500–1,000
39	OPY-7	2	0	0%	2	4	1,000
40	OPY-8	3	0	0%	1	3	750-1,500

Table 16. Molecular fingerprinting pattern by simple sequence repeat (SSR) primers in A-genome synthetic hexaploids (2n=6x=42; AABBAA).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
1	*Xgwm10-2A*	7	7	100%	58	73	50–150	0.36
2	*Xgwm47.1-2A*	5	5	100%	31	36	50–200	0.57
3	*Xgwm47.2-2A*	6	6	100%	18	28	50–200	0.51
4	*Xgwm71.1-2A*	6	6	100%	34	80	50–150	0.73
5	*Xgwm71.2-2A*	6	6	100%	27	61	50–150	0.76
6	*Xgwm95-2A*	3	3	100%	56	62	50–150	0.37
7	*Xgwm122-2A*	5	5	100%	17	20	50–150	0.43
8	*Xgwm249-2A*	9	9	100%	50	92	50–200	0.78
9	*Xgwm265-2A*	4	4	100%	16	16	50–200	0.36
10	*Xgwm296-2A*	5	5	100%	15	18	50–100	0.65
11	*Xgwm311-2A*	9	9	100%	46	112	50–250	0.77
12	*Xgwm312-2A*	6	6	100%	68	85	50–150	0.57
13	*Xgwm372-2A*	3	3	100%	15	16	50–200	0.28
14	*Xgwm382-2A*	8	8	100%	25	45	50–200	0.85
15	*Xgwm473-2A*	1	1	100%	6	6	50–100	0.00
16	*Xgwm515-2A*	5	5	100%	44	65	50–150	0.75
17	*Xgwm558-2A*	6	6	100%	22	32	50–100	0.76
18	*Xgwm5-3A*	8	8	100%	31	50	50–200	0.70
19	*Xgwm30-3A*	4	4	100%	12	14	50	0.38
20	*Xgwm162-3A*	4	4	100%	34	38	50–200	0.47
21	*Xgwm391-3A*	4	4	100%	9	12	50–300	0.70
22	*Xgwm666.2-3A*	4	4	100%	25	31	50–150	0.58
23	*Xgwm397-4A*	2	2	100%	22	24	50	0.12
24	*Xgwm601-4A*	5	5	100%	42	49	50–100	0.59
25	*Xgwm637-4A*	1	1	100%	17	17	50	0.00

The *T. monococcum* subsp. *aegilopoides*-based SHs are entries 86, 87, 95, 96, 97, 98, 99, 100, 107, 108, 109, 110, 114, 131, 132, 134, 135, 138, 139, 140, 142, 175, and 183. The range for days-to-flowering in this set is 120–150 days. Among those that are considered early flowering (120–135 d) are 110 (120 d), 97 and 138 (125 d), 98 (126 d), 100



The RAPD- (**Fig. 13 (above)**) and SSR-based (**Fig. 14, right**)) analyses on the 194 AABBAA synthetics indicate a wide diversity. Maximum diversity was highest for entry 107 by RAPD analysis (Fig. 13). Other diverse entries are 95, 97, 138, and 142 (Fig. 13). Two diverse lines based upon SSR analysis were 135 and 138 (Fig. 14); with entry 138 being common.

(131 d), 132 (133 d), 95 (134 d), and 114 (135 d). The range for days to physiological maturity was 175–191 days, of which 11 matured by 180 days (86, 87, 97, 98, 107, 110, 132, 134, 135, 140, and 175). Thousand-kernel weight ranged from 30.8 to 72 g. A majority of lines were up to 50 g, and those higher than 50 g were 95 (71 g), 96 (59 g), and 190 (58 g). Grains/spike ranged from 3 to 57, with a majority between 10 to 20. A maximum of 57 grains/spike was found

in entry 131; 138 had 41 grains/spike. Spike length ranged from 7 to 17 cm, where the greatest was 17 cm in entry 139. Entrys 100 and 131 had 14-cm spikes. The detailed data is in Table 12 (pp. 103-107).

All AABBAA synthetics possessed Karnal bunt resistance (Table 12, pp. 103-107). For powdery mildew seedling resistance, entries showing a susceptible reaction were 99, 114, 132, 135, and 175. All the others were classified as resistant. Seedling resistance for stripe rust was limited to five entries; 95, 108, 109, 132, and 183. The first three entries also had APR and are favored candidates for wheat breeding. Other entries possessing seedling susceptibility but having APR were 96, 114,135, 138, 139, and 142. These lines have minor genes and are highly desirable for durable resistance breeding.

The RAPD- and SSR-based analyses on the 194 AABBAA synthetics indicated a wide diversity. Maximum diversity was highest for entry 107 by RAPD analysis. Other diverse entries are 95, 97, 138, and 142 (Fig. 13, p. 113). Two diverse lines based upon SSR analysis were 135 and 138 (Fig. 14, p. 113); with entry 138 being common. This line also possessed APR for stripe rust, had KB resistance, and some positive phenotypic traits rendering it a potent source for breeding efforts. Line 95 is resistant to Karnal bunt, powdery mildew, and strip rust and has a high 1,000-kernel weight. Such comprehensive checks identify various synthetics for exploitation.

The synthetic lines mentioned above are from five durum wheat entries (115, 116, 121, 122, and 146), and two lines (116 and 121) have multiple traits for resistance and good phenology. Three durum/*T. urartu* synthetics (190, 193, and 194) are suitable for breeding possessing multiple positive attributes (Table 12, pp. 103-107).

A stringent analysis of the phenotypic and biotic stress data across all the 194 AABBAA synthetics studied indicate that the 14 entries are elite in performance and top priority candidates for wheat improvement; 9, 12, 52, 59, 71, 95, 103 108, 111, 116, 121,124, 138, and 190. They possess a maximum of positive traits and also are molecularly diverse. Within each group, this number can be enhanced based upon fewer of positive traits (Table 12, pp. 103-107).

Of the 14 elite entries some are described in detail for their practical attributes:
Entry 9: resistant to KB and powdery mildew, early flowering (117 d), 1,000-kernel weight (58 g), grains/spike (39), spike length (14 cm),
Entry 12: resistant to KB and powdery mildew, grains/spike (33), spike length (14.1 cm),
Entry 52: resistant to KB and powdery mildew, 1,000-kernel weight (68 g), grains/spike (35),
Entry 59: resistant to KB and stripe rust (seedling and APR), 1,000-kernel weight (56.4 g), grains/spike (37),
Entry 71: resistant to KB and powdery mildew, 1,000-kernel weight (53.2 g), spike length (14.6 cm),
Entry 103: resistant to KB and stripe rust (APR), 1,000-kernel weight (56.6 g), grains/spike (38),
Entry 108: resistant to KB and stripe rust (seedling and APR), 1,000-kernel weight (72 g), grains/spike (36),
Entry 111: resistant to KB and powdery mildew, early flowering (120 d), spike length (15 cm), and
Entry 124: resistant to KB, grains/spike (32), spike length (14 cm).

Genomic diversity present in the A-genome diploids is plentiful and a boon for broadening the wheat genetic base. Often, single valuable traits of significance are exploited, but the our studies have shown that multiple traits can be harnessed simultaneously to assist efficiency of breeding. The more traits are present in the starting genetic stock, the easier to isolate recombinants where the wheat parent contributions are additive. These stocks are excellent tools for screening for other stress traits and, with the molecular diversity foundation established here, the meaningful decisions can aid the way forward in breeding.

Cytological, phenoligical, and molecular characterization of B-genome synthetic hexaploids.

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The polyploid *Aegilops* and *Triticum* species sharing one genome with wheat are included in the secondary gene pool. Also included are the diploid species of the *Sitopsis* section. Genetic transfers are routine within homologous genomes but require manipulative protocols between nonhomologous types. Embryo rescue is a complementary aid for obtaining hybrids. Although limited use exists for wheat improvement, priority has been suggested for exploiting the *Sitopsis* species *Ae. speltoides* (2n = 2x =14, SS) for durum and bread wheat improvement. Breeding protocols are more complex

because manipulation strategies associated with alien gene transfer often incorporate undesirable traits together with the target gene of interest.

We currently are exploiting *Ae. speltoides* accessions via a hexaploid–amphiploid bridge-cross (2n=6x=42, AABBSS) (Fig. 15). These newly produced amphiploids have shown initial promise for resistance to *C. sativus, F. graminearum, S. tritici*, barley yellow dwarf virus, and leaf and stripe rust. More testing together with exploiting the potential of other *Sitopsis* species diploids appears logical, recognizing that the positive outputs from *Ae. speltoides* accessions genetic is just one example.

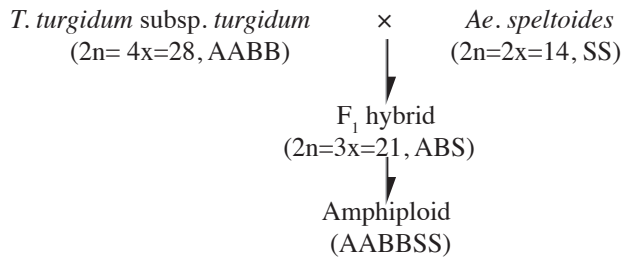

Fig. 15. Schematic for AABBSS production involving *T. turgidum* subsp. *turgidum* and *Ae. speltoides* (2n=2x=14, SS).

Table 17. The B-genome synthetic hexaploid entries utilized in the study, synthetic hexaploid entry numbers are similar to those maintained in CIMMYT, Mexico, Wide Crosses Program. Pedigrees details are given in Table 18.

Group No.	B-genome synthetic hexaploid entry Numbers	Total entries
1	7, 9, 11, 48	4
2	6, 12, 13	3
3	10, 22, 24, 25, 26, 32, 34, 36, 47, 49	10
4	18	1
5	19	1
6	23	1

Table 18. Pedigrees of the B-genome synthetic hexaploids.

Synthetic number	Parentage/pedigree
6	CETA/*Ae. speltoides* (127)
7	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (129)
9	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (133)
10	ARLIN_1/*Ae. speltoides* (134)
11	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (135)
12	CETA/*Ae. speltoides* (135)
13	CETA/*Ae. speltoides* (139)
18	ALTAR 84/*Ae. speltoides* (141)
19	CROC_1/*Ae. speltoides* (149)
22	ARLIN_1/*Ae. speltoides* (126)
23	D67.2/P66.270//*Ae. speltoides* (126)
24	ARLIN_1/*Ae. speltoides* (128)
25	ARLIN_1/*Ae. speltoides* (130)
26	ARLIN_1/*Ae. speltoides* (131)
32	ARLIN_1/*Ae. speltoides* (143)
34	ARLIN_1/*Ae. speltoides* (144)
36	ARLIN_1/*Ae. speltoides* (145)
47	ARLIN_1/*Ae. speltoides* (157)
48	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (157)
49	ARLIN_1/*Ae. speltoides* (158)

A set of 20 B-genome synthetics were cytologically and phenologically characterized and screened against powdery mildew, due to limited seed availability (Table 17).

Since the initial production of the B-genome hexaploids, the number available has decreased to 34. Several of the original 54 total were poorly adapted to the Pakistani conditions at Islamabad. In contrast to the A-genome synthetics, the B-genome synthetics are weaker plants and showed aneuploid meiotic associations (Fig. 16a and b, p. 116) and all expressed a co-dominant spike phenotype (Fig. 17a, p. 116). At meiosis, open bivalents increased in number with increased appearance of multiple chromosomal associations, trivalents, quadrivalents, and to a lesser degree pentavalents and aneuploidy (Table 19, p. 117). Like the A-genome hexaploids, those of the B genome were similar in having a tall plant habit (100–130 cm) and late maturity (145–155 days) under Islamabad conditions. Seed fertility was satisfactory in those that were adapted, but the seed was shriveled. The crossability across all combinations obtained at CIMMYT was of a high frequency (Table 19, p. 117) and regeneration of embryos was generally over 90% with colchicine-induced doubling to yield the AABB(SS) amphiploids also of a similar or higher level (Table 20, p. 118). C-banding was used to validate the presence of four B genomes in the amphiploid.

All the entries were screened in pot trials in the greenhouse at Murree. Nine of 20 B-genome synthetic hexaploids showed a resistant reaction to powdery mildew at the seedling stage (Table 21, p. 119). Infection type ranged from 0–6 in all lines at the seedling stage indicating the presence of major genes for resistance. Some of these resistant accessions exhibited different reaction types against powdery mildew under field conditions. The entries also were screened under field conditions at Kaghan and a majority of the germ plasm showed APR and were found to be resistant to completely resistant (immune). In B-genome synthetic hexaploids, the accessions were found to be completely resistant (immune) to susceptible at seedling stage. The accessions that showed resistance at seedling stage are 1, 3, 4, 5, 6, 7, 8, 13, and 18. Resistant lines at the seedling stage provide a source of major resistance genes but further evaluation at the adult-plant stage is needed for the identification of lines with novel resistance source and, thus, for further exploitation in future breeding programs.

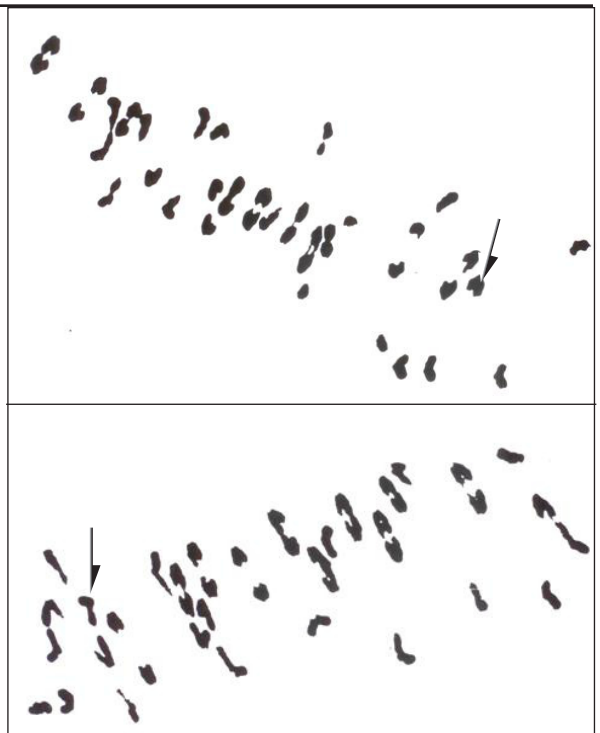

Fig. 16. Meiotic associations at metaphase I of some B-genome synthetic hexaploids, genomically AABBSS, showing (a) an aneuploid synthetic wth 41 chromosomes with one trivalent (arrow) and a mixture of ring and rod bivalents and (b) an aneuploid synthetic derivative with 41 chromosomes and univalents, ring and rod bivalents, and one quadrivalent association (arrow).

Evaluation of genetic diversity using random amplified polymorphic DNA (RAPD) primers. RAPD primers were used for genetic diversity evaluation of A-, B-, and D-genome synthetic hexaploids. All 520 RAPD primers of the Operon Series were screened and working primers were identified and applied to detect genetic polymorphism at DNA level. Samples that did not amplify were not included in the analysis.

Genetic analysis was performed only on the scorable bands. Every single band was considered as a single locus/allele. The loci were scored as present/absent. Bivariate data 1–0 were used to estimate genetic distances (GD). The unweighted pair group of arithmetic means (UPGMA) function estimated GD between the genotypes as follows: $GD_{xy} = 1 - d_{xy}/d_x + d_y - d_{xy}$, where GD_{xy} = genetic distance between two genotypes, d_{xy} = total number of common loci (bands) in two genotypes, d_x = total number of loci (bands) in genotype 1, and d_y = total number of loci (bands) in genotype 2.

Fig. 17. Spike morphology of B-genome (S) genome hexaploids derived from *T. turgidum* subsp. *turgidum* (2n=4x=28, AABB)/*A. speltoides* crosses (2n=2x=14; SS) from left to right (a) *T. turgidum* subsp. *turgidum*, (b) *T. turgidum* cv. Cerceta/*Ae. speltoides* (B-13), and (c) *T. turgidum* cv Cerceta/*Ae. speltoides* (B-02).

The efficiency of primers to amplify the genotypes ranged from nine (OPN-6) to one (OPA-4, OPE-11, OPJ-1, OPW-5, OPX-2, and OPY-8) (Table 22, p. 120). Scorable bands ranged from one (OPA-4, OPE-11, and OPW-5) to 29 (OPN-4).

Genetic analysis of the population showed that the B-genome synthetic hexaploids scored total 190 loci with 151 as polymorphic (79.47%) (Table 22, p. 120). The range of scorable bands was from 500–3,000 bp.

Similarity matrix. Bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. The similarity coefficient in B-genome synthetic hexaploids ranged from 54.7% (6 and 7) to 100% (between 6 and 47, 6 and 9, and 9 and 47).

Table 19. Mean meiotic chromosomal associations at metaphase I of AABBBB(SS) synthetic hexaploids (amphiploids) involving *T. turgidum* subsp. *turgidum* cultivars and B-genome diploid accessions of *Ae. speltoides* (I = univalent, rII = rod bivalent, oII = ring bivalent, III = trivalent, cIV = chain quadrivalent, oIV = ring quadrivalent, XTA = chiasmata).

Synthetic No.	No. cells	I	rII	oII	III	cIV	oIV	V	VI	XTA	Chromosome number
1	20	1.40	3.70	15.3	0.20	0.50	0.00	0.00	0.00	36.2	42
2	20	2.90	6.90	7.20	1.00	1.30	0.30	0.10	0.00	28.8	41
6	20	5.30	5.30	7.40	1.10	1.00	0.10	0.20	0.10	26.5	40
7	20	5.70	4.40	8.60	0.60	1.30	0.20	0.10	0.00	27.5	40
8	20	5.30	5.50	7.80	1.00	0.90	0.00	0.10	0.00	25.8	39
9	20	4.80	5.40	7.20	1.80	1.40	0.00	0.20	0.00	27.6	42
10	20	5.20	7.40	7.60	1.80	0.60	0.00	0.00	0.00	28.0	43
11	20	0.00	3.40	16.4	0.00	0.60	0.00	0.00	0.00	38.0	42
12	20	3.20	4.40	11.8	1.00	0.60	0.00	0.00	0.00	38.8	41
13	20	3.00	3.80	14.5	0.40	0.30	0.00	0.00	0.00	34.5	42
16	20	1.90	2.60	12.9	1.00	0.80	0.10	0.10	0.00	33.6	40
17	20	2.40	4.10	12.2	1.40	0.50	0.20	0.00	0.00	33.6	42
19	20	6.60	6.00	5.80	1.80	1.20	0.40	0.00	0.00	26.4	42
22	20	4.50	3.20	9.60	1.10	0.40	0.00	0.00	0.00	25.8	35
23	20	5.70	6.20	3.80	2.20	0.80	0.20	0.10	0.20	22.2	38
27	20	2.30	7.90	7.40	1.10	0.90	0.30	0.00	0.00	28.8	41
30	20	3.50	5.50	10.8	0.90	0.70	0.10	0.00	0.00	31.4	42
32	20	5.00	6.00	7.20	1.80	0.30	0.10	0.00	0.10	25.7	39
34	20	1.90	5.50	12.1	0.60	0.20	0.20	0.10	0.00	32.3	41
37	20	3.00	6.80	11.0	0.60	0.30	0.10	0.00	–	31.3	42
38	20	22.5	7.70	1.40	0.10	0.00	0.00	0.00	0.00	10.7	41
39	20	2.00	4.50	14.2	0.40	0.10	0.00	0.00	–	34.0	41
40	20	9.50	8.90	5.80	0.50	0.20	0.20	0.00	0.00	22.9	42
41	20	6.20	9.30	6.90	0.40	0.20	0.10	0.00	–	24.9	41
42	20	4.40	7.80	7.90	0.80	0.30	0.40	0.00	–	27.7	41
43	20	1.70	5.00	13.7	0.70	0.10	0.10	0.00	–	34.5	42
45	20	7.40	7.60	6.50	1.40	0.20	0.10	0.00	–	24.4	41
47	20	3.90	6.10	9.20	1.10	0.10	0.20	0.00	–	27.8	39
48	20	1.20	4.60	13.6	0.60	0.10	0.30	0.00	–	34.5	41
49	20	2.20	5.30	13.0	0.40	0.20	0.30	0.00	–	33.9	42
52	20	5.20	5.10	9.80	1.40	0.20	0.00	0.00	0.00	28.1	40

Dendrogram interpretation. The GD between genotypes was used to construct a dendrogram by UPGMA analysis for determining grouping of the lines on the basis of similarities and differences. The dendrogram of B-genome (Fig. 18, p. 118) has only one cluster with 7 as the most diverse line with 11, 18, 24, 36, and 48 as other good lines of this group. The genotypes 6, 9, and 47 are 100% similar.

Evaluation of genetic diversity using simple sequence repeat (SSR) primers. SSR primers were used for genetic diversity evaluation of B-genome synthetic hexaploids. All 275 SSR primers were applied on each set to detect genetic polymorphism at DNA level. The samples which did not amplify were not included in the analysis.

Efficiency of primers to amplify the genotypes ranged from 19 (*Xgwm257-2B*, *Xgwm319-2B*, and *Xgwm554-5B*) to one (*Xgwm11-1B*, *Xgwm148-2B*, *Xgwm540-5B*, and *Xgwm569-7B*) in B-genome synthetic hexaploids. Scorable bands ranged from one (*Xgwm11-1B*, *Xgwm148-2B*, and *Xgwm569-7B*) to 61 (*Xgwm213-5B*) (Table 23, pp. 121-122).

Population genetic analysis showed that the B-genome synthetic hexaploids scored total 327 alleles with 299 as polymorphic or 91.43% (Table 23, pp. 121-122). The range of scorable bands was 50–800 bp.

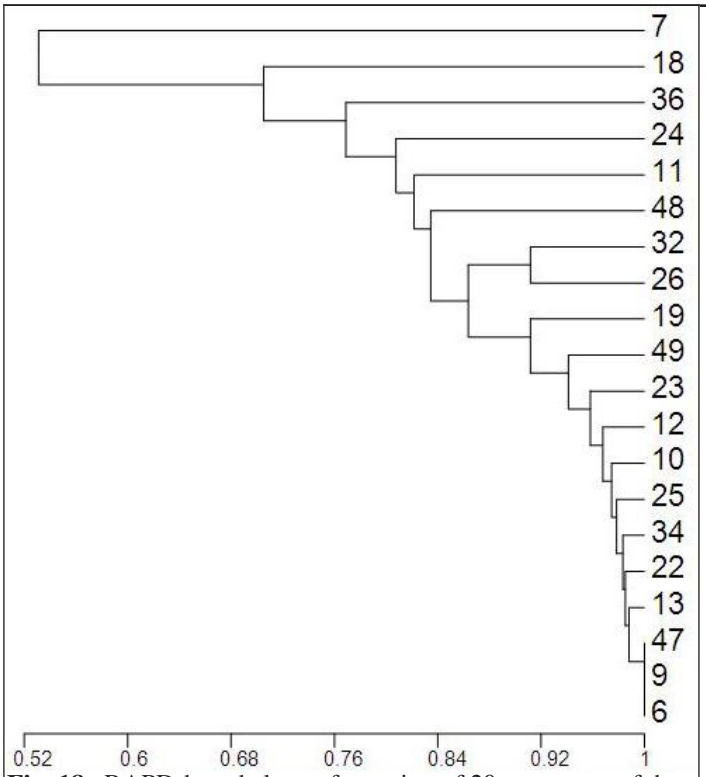

Fig. 18. RAPD-based cluster formation of 20 genotypes of the B-genome synthetic hexaploids (2n=6x=42; AABBSS).

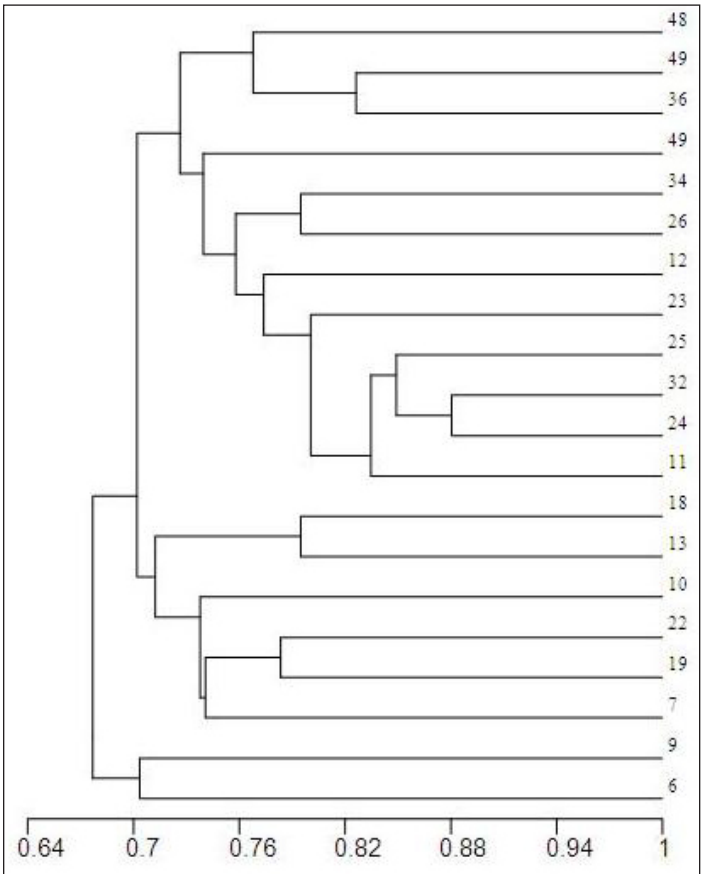

Fig. 19. SSR-based cluster formation of 20 genotypes of the B-genome synthetic hexaploids (2n=6x=42; AABBSS).

Table 20. The mean crossability data of some B-genome synthetic hexaploids (*T. turgidum* subsp. *turgidum*/*Ae. speltoides*).

Synthetic number	Florets pollinated	Seed set	Embryos rescued
22	48	14	14
23	24	15	15
24	48	14	14
25	48	7	7
26	37	20	20
27	48	20	19
28	48	17	15
29	24	16	15
30	96	33	20
31	76	14	13
32	48	20	20
33	48	10	9
34	48	20	20
35	52	2	2
36	48	5	4
37	48	20	18
38	24	21	19
39	48	27	20
40	48	20	18
41	72	21	20
42	48	20	20
43	48	20	18
44	24	20	15
45	48	23	20
46	96	16	10
47	48	26	20
48	48	12	12
49	24	11	11
50	72	3	2
51	24	21	20
52	120	47	20
53	24	11	5
54	48	20	17
55	48	11	10
56	48	4	3

Similarity matrix. A bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. The similarity coefficient in B-genome synthetic hexaploids ranged from 58.2% (13 and 49) to 88.1% present between 24 and 32.

The B-genome diploids offer another reservoir of genetic diversity that can provide wheat breeders a unique source of variation for traits that limit productivity. These lines have been limited in practical use essentially because of chromosomal

behavior. The classic example has been of the *Ph* suppression activity, and the alien transfer that has been a standard in cytogenetic manipulation studies. For applied efforts focusing on *Ae. speltoides*, researchers in CIMMYT initiated an ambitious program to make AABBSS synthetics and generated over 50 lines. Of these, 20 were used to study phenology and powdery mildew screening resistance. Four lines appeared to be useful sources for further exploitation in breeding; entries 6, 9, 10, and 11 (Table 21). All possessed seedling resistance for powdery mildew. Some phenotypic attributes of thes four lines are

Table 21. Morphological and disease characterization of 20 B-genome synthetic hexaploids (2n=6x=42; AABBSS). FLOW = days-to-flowering, HT = plant height at maturity (cm), AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), PMA = days to physiological maturity, TKW = 1,000-kernel weight (g), G/S = grains/spike, SL = spike length (cm), and Pm (S) = powdery mildew reaction at the seedling stage.

Synthetic number	FLOW	HT	AWN	PMA	TKW	G/S	SL	Pm (S)
6	113	72	Y	161	52.0	22	10.0	0
7	140	80	Y	160	40.0	40	12.5	8
9	113	75	Y	160	60.3	56	14.0	0
10	133	90	AW	164	62.7	28	15.0	0
11	112	85	AW	163	44.8	60	12.0	1
12	129	98	Y	164	18.0	5	13.0	0
13	133	93	Y	162	44.6	24	14.5	2
18	133	66	LB	166	60.0	30	13.0	1
19	139	78	AW	163	40.0	36	11.3	1
22	131	85	AW	165	40.0	34	12.6	6
23	130	89	Y	162	40.0	36	12.8	7
24	130	92	AW	164	50.0	6	9.3	6
25	145	74	AW	166	13.2	14	11.0	3
26	113	65	AW	161	44.8	42	8.5	8
32	146	90	Y	165	18.0	12	16.0	8
34	134	87	AW	160	22.4	1	13.0	8
36	141	68	Y	166	15.0	9	16.0	8
47	118	63	AW	161	28.6	46	8.0	0
48	134	77	LB	162	11.0	8	14.0	7
49	133	79	AW	164	19.5	27	18.5	7

Entry 6: days-to-flowering (113), 1,000-kernel weight (52.0 g),

Entry 9: days-to-flowering (113), 1,000-kernel weight (60.3 g), grains/spike (56), spike length (14 cm) (This was the best line in the set),

Entry 10: 1,000-kernel weight (62.7 g), spike length (15 cm), and

Entry 11: days-to-flowering (112), grains/spike (60).

The 20 synthetics (AABBSS) were tested for diversity using RAPDs (Fig. 18, p. 118) and SSRs (Fig. 19, p. 118). The maximum diversity via RAPD markers was for entry 7. Using SSR markers, entries 6 and 9 showed maximum diversity, were linked, and also have been selected for use in breeding based upon resistance plus phenotypic attributes. Entry 10 also showed good diversity and has other positive traits of interest.

The Mantel Test (Z) between RAPD and SSR similarity matrices for the population of B-genome synthetics indicates a RAPD-SSR matrix correlation (r) of –0.113 with a P value of 0.247. The Z value was used to compare the direction of diversity generated by both marker systems (RAPDs and SSRs). For this purpose, the similarity matrix for RAPDs and SSRs of each population was used. A negative diversity spectrum was shown by both markers in the population.

From the limited number of 20 B-genome synthetics studied, that four were superior for use in breeding is a fairly high frequency and encouraging. The meiotic behavior during maintenance of these stocks is a notch below that of the A-genome synthetics; more rod bivalents/aneuploidy is observed, but seed set is adequate. The trait value coupled with the molecular diversity status and a unique genetic resource sparsely used in breeding make this germ plasm important for further exploitation and additional stock production. Target practices can give precision to the efforts whereby screening of all accessions and actively pursuing the direct crossing protocols in use for the A- and D-genome diploids can be applied here also.

Table 22. Molecular fingerprinting by random amplified polymorphic DNA (RAPD) primers in B-genome synthetic hexaploids (2n=6x=42; AABBSS).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
1	OPA-3	8	8	100%	4	15	750–2,500
2	OPA-4	1	1	100%	1	1	1,000
3	OPB-1	8	5	62.5%	5	10	750–3,000
4	OPC-2	5	5	100%	5	7	750–2,000
5	OPE-9	2	2	100%	2	2	1,500
6	OPE-11	1	1	100%	1	1	1,000
7	OPE-14	4	2	50%	2	5	750–1,500
8	OPE-15	9	8	88.88%	5	21	500–2,500
9	OPE-16	7	6	85.71%	4	15	250–2,000
10	OPG-2	3	2	66.66%	2	4	750–1,500
11	OPG-5	8	8	100%	8	26	250–1,500
12	OPG-13	1	1	100%	2	2	1,500
13	OPI-7	9	7	77.77%	4	22	250–2,000
14	OPI-19	9	4	44.44%	4	17	250–2,000
15	OPJ-1	5	1	20%	1	5	500–1,500
16	OPJ-9	3	3	100%	4	7	750–1,500
17	OPJ-20	4	2	50%	6	21	250–1,000
18	OPK-9	2	2	100%	2	2	1,500–2,000
19	OPL-1	7	7	100%	4	13	500–1,500
20	OPL-2	9	9	100%	7	20	250–1,500
21	OPL-12	4	3	75%	6	15	750–1,000
22	OPL-20	8	5	62.5%	8	17	250–2,500
23	OPM17	8	8	100%	4	18	250–1,500
24	OPN-1	3	3	100%	2	3	1,000–2,000
25	OPN-2	7	7	100%	6	16	250–2,000
26	OPN-3	2	2	100%	3	4	1,500
27	OPN-4	6	4	66.66%	8	29	500–1,500
28	OPN-5	6	6	100%	7	17	250–1,500
29	OPN-6	7	7	100%	9	25	250–1,500
30	OPN-9	2	2	100%	2	3	250–1,500
31	OPN-12	4	1	25%	2	7	500–2,000
32	OPN-17	4	4	100%	3	9	500–1,000
33	OPP-16	3	3	100%	5	7	750–1,500
34	OPQ-5	4	4	100%	5	12	250–1,000
35	OPW-4	3	3	100%	3	6	750–2,000
36	OPW-5	1	1	100%	1	1	1,000
37	OPX-2	4	0	0%	1	4	750–1,500
38	OPX-12	4	4	100%	3	9	500–1,000
39	OPY-7	2	0	0%	2	4	1,000
40	OPY-8	3	0	0%	1	3	750-1500

Table 23. Molecular fingerprinting by simple sequence repeat (SSR) primers in the B-genome synthetic hexaploids (2n=6x=42; AABBSS).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
1	*Xgwm11-1B*	1	1	100%	1	1	50	0.00
2	*Xgwm18-1B*	4	4	100%	9	13	50–200	0.43
3	*Xgwm33-1B*	1	1	100%	7	7	50	0.00
4	*Xgwm124-1B*	2	2	100%	6	7	50–200	0.24
5	*Xgwm131-1B*	2	2	100%	3	4	150	0.27
6	*Xgwm140-1B*	1	1	100%	4	4	50	0.00
7	*Xgwm268-1B*	2	2	100%	9	12	100	0.65
8	*Xgwm273-1B*	4	2	50%	7	13	150–700	0.27
9	*Xgwm274-1B*	4	4	100%	8	16	150–250	0.66
10	*Xgwm403-1B*	2	0	0%	2	4	150–200	0.50
11	*Xgwm413-1B*	3	3	100%	8	10	200	0.47
12	*Xgwm550-1B*	4	2	50%	6	12	150–700	0.63
13	*Xgwm47-2B*	3	1	33.33%	6	8	50–200	0.25
14	*Xgwm16-2B*	5	3	60%	11	25	50–250	0.72
15	*Xgwm55.1-2B*	6	6	100%	5	13	50–150	0.81
16	*Xgwm55.2-2B*	3	3	100%	3	6	50–150	0.61
17	*Xgwm120-2B*	2	2	100%	7	11	50–150	0.40
18	*Xgwm129-2B*	1	1	100%	4	4	200	0.00
19	*Xgwm148-2B*	1	1	100%	1	1	150	0.00
20	*Xgwm191-2B*	2	2	100%	8	12	100	0.48
21	*Xgwm210-2B*	4	2	50%	8	11	150	0.31
22	*Xgwm257-2B*	8	5	62.5%	19	27	200–800	0.44
23	*Xgwm319-2B*	3	3	100%	19	33	50–250	0.58
24	*Xgwm374-2B*	4	4	100%	14	16	50–200	0.56
25	*Xgwm382-2B*	5	5	100%	12	33	50–200	0.75
26	*Xgwm388-2B*	3	1	33.33%	9	28	100–150	0.66
27	*Xgwm410-2B*	2	2	100%	5	6	50–250	0.61
28	*Xgwm429-2B*	4	4	100%	10	21	50–300	0.67
29	*Xgwm501-2B*	3	3	100%	8	10	50	0.38
30	*Xgwm526-2B*	5	3	60%	15	23	50–200	0.45
31	*Xgwm630-2B*	4	4	100%	17	39	50–200	0.66
32	*Xgwm72-3B*	2	2	100%	8	10	50–200	0.46
33	*Xgwm77-3B*	6	6	100%	10	23	50–250	0.78
34	*Xgwm112-3B*	3	3	100%	14	28	50–100	0.58
35	*Xgwm264-3B*	3	1	33.33%	3	5	150–200	0.66
36	*Xgwm285-3B*	2	2	100%	8	9	500	0.30
37	*Xgwm340-3B*	2	2	100%	13	22	100–200	0.45
38	*Xgwm376-3B*	3	3	100%	14	16	50–150	0.13
39	*Xgwm389-3B*	1	1	100%	6	6	100	0.00
40	*Xgwm493-3B*	5	5	100%	16	31	50–700	0.69
41	*Xgwm547-3B*	2	2	100%	3	4	50–200	0.27
42	*Xgwm566-3B*	2	2	100%	12	12	50–100	0.23
43	*Xgwm6-4B*	5	5	100%	15	47	50–1500	0.71
44	*Xgwm66-4B*	11	9	81.81%	14	34	50–600	0.78
45	*Xgwm113-4B*	2	2	100%	16	27	50–150	0.49
46	*Xgwm149-4B*	2	2	100%	15	25	50–150	0.48

Table 23. Molecular fingerprinting by simple sequence repeat (SSR) primers in the B-genome synthetic hexaploids (2n=6x=42; AABBSS).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
47	*Xgwm165-4B*	6	1	16.66%	10	29	50–250	0.71
48	*Xgwm368-4B*	5	5	100%	10	17	50	0.48
49	*Xgwm495-4B*	1	1	100%	2	2	50–200	0.00
50	*Xgwm513-4B*	3	3	100%	8	13	50–150	0.57
51	*Xgwm66-5B*	14	14	100%	8	50	50–700	0.91
52	*Xgwm67-5B*	4	4	100%	7	17	50–100	0.72
53	*Xgwm68-5B*	1	1	100%	12	22	50–250	0.56
54	*Xgwm159-5B*	5	5	100%	18	25	200–250	0.37
55	*Xgwm191-5B*	2	2	100%	15	25	150–250	0.37
56	*Xgwm213-5B*	15	15	100%	15	61	50–500	0.87
57	*Xgwm234-5B*	3	3	100%	12	22	50–250	0.64
58	*Xgwm335-5B*	5	5	100%	15	29	50–250	0.74
59	*Xgwm371-5B*	4	4	100%	15	34	50–200	0.70
60	*Xgwm408-5B*	5	5	100%	12	17	50–200	0.45
61	*Xgwm443-5B*	7	7	100%	13	25	50–150	0.76
62	*Xgwm499-5B*	7	7	100%	10	19	50–200	0.80
63	*Xgwm540-5B*	1	1	100%	1	8	100	0.32
64	*Xgwm544-5B*	2	2	100%	13	14	150	0.19
65	*Xgwm554-5B*	3	3	100%	19	30	150	0.46
66	*Xgwm604-5B*	3	3	100%	15	25	50–100	0.53
67	*Xgwm639-5B*	6	6	100%	10	28	50–200	0.69
68	*Xgwm70-6B*	3	3	100%	6	14	100–200	0.63
69	*Xgwm88-6B*	7	7	100%	7	16	50–500	0.77
70	*Xgwm191-6B*	3	3	100%	8	9	50	0.57
71	*Xgwm193-6B*	5	5	100%	13	29	150	0.59
72	*Xgwm219-6B*	3	3	100%	15	24	50–200	0.60
73	*Xgwm361-6B*	4	4	100%	13	31	100	0.74
74	*Xgwm508-6B*	5	5	100%	3	7	100–150	0.75
75	*Xgwm518-6B*	5	5	100%	7	16	50–200	0.17
76	*Xgwm16-7B*	2	2	100%	14	19	50–200	0.31
77	*Xgwm43-7B*	2	2	100%	12	13	50–250	0.44
78	*Xgwm68-7B*	2	2	100%	16	29	100–200	0.48
79	*Xgwm146-7B*	5	5	100%	16	30	50	0.61
80	*Xgwm274-7B*	2	2	100%	4	6	100	0.37
81	*Xgwm297-7B*	2	2	100%	16	17	50	0.05
82	*Xgwm302-7B*	5	5	100%	17	31	250	0.55
83	*Xgwm333-7B*	2	2	100%	4	5	50	0.21
84	*Xgwm344-7B*	2	2	100%	2	2	150	0.50
85	*Xgwm400-7B*	1	1	100%	13	13	150–200	0.16
86	*Xgwm537-7B*	7	7	100%	15	31	50–200	0.72
87	*Xgwm569-7B*	1	1	100%	1	1	150	0.00
88	*Xgwm573-7B*	3	3	100%	8	10	250	0.32
89	*Xgwm644-7B*	5	5	100%	16	18	100–150	0.57

Molecular and phenological study and disease screening of various Aegilops tauschii accessions in a similar durum wheat background.

Alvina Gul Kazi, Sadia Latif, Bilal Haider Abbasi, Awais Rasheed, Hadi Bux, Arsalan Ahmed, and Abdul Mujeeb-Kazi.

Diseased and insect pest resistance are the most readily exploited characters in wide hybridization. This also is true for synthetic hexaploid (SH) wheats, which have many genes for resistance to the three major rusts introgressed into bread wheat. A wide array of these wheats are being globally utilized for wheat improvement either at the SH or at the 'bread wheat/SH' advanced derivative level. The SH wheats built around the D genome are known to carry a good level of resistance to Karnal bunt, *S. tritici,* and *C. sativus*. The promise also exists for resistance and tolerance in this SH germ plasm for resistance to leaf rust, stripe rust, powdery mildew, loose smut, and cereal cyst nematode; mineral toxicities; drought; salinity; heat; cold; sprouting; water logging; high-molecular-weight (HMW)/low-molecular-weight (LMW) quality subunits; and yield and yield components. The least diversity observed so far in the D genome is for *F. graminearum* (less than 1.0 percent) but, under evaluation tests conducted at one location in Mexico, the observed FHB resistance is promising and superior than that of the leading bread wheat cultivars Frontana and Sumai 3 with their assemblage of four genes.

From the primary synthetics, an experimental set was made and categorized as having same durum cultivar as the female parent crossed with different *Ae. tauschii* accessions (89 entries, Table 24; Table 25, pp. 124-125; and Table 26, p. 124). This subset was designed to study the inheritance of different genes and also to identify the effect of cytoplasmic inheritance, if any. The 89 entries were screened against two biotic stresses (Karnal bunt and stripe rust), phenotypically characterized, and analyzed with RAPD and SSR markers.

Table 24. Synthetic entries numbered from combining same durum cultivars and different *Aegilops tauschii* accessions. Synthetic hexaploid (SH) numbers are similar to those maintained in the CIMMYT, Mexico, Wide Crosses Program with the pedigrees of the durum wheat cultivars detailed in Table 25.

Group number	D-genome synthetic hexaploid number	Durum parent nuber	Total number of SH entries
1	1, 18, 30, 63, 66, 78, 83, 89	4	8
2	2, 3, 14, 19, 26, 43, 49, 51, 65	8	9
3	4, 11, 20, 35, 37, 38, 42, 47, 64	13	9
4	5, 8, 9, 10, 12, 21, 23, 27, 58	12	9
5	6, 15, 22, 31, 45, 50, 56, 74, 75	23	9
6	7, 32, 48, 53, 68, 71, 72, 76, 86	26	9
7	13, 16, 17, 25, 36, 46, 57, 61, 88	5	9
8	24, 39, 40, 41, 60, 62, 73, 85, 90	1	9
9	28, 29, 33, 34, 55, 59, 69, 79, 82	11	9
10	44, 54, 67, 70, 77, 80, 81, 84, 87	22	9

Stripe rust studies. Seedling screening showed that 34 of 90 (37.7%) synthetics and 22 of 23 (95.6%) durum wheat parents were resistant (Table 27, pp. 126-127). These genotypes also were screened for APR under field conditions at NARC, which identified 37 of 89 (41.4%) synthetics and 20 of 23 (86.9%) durum wheat parents as resistant. Genotypes with both seedling resistance and APR were 19 of 90 (21.1%) synthetics (1, 13, 14, 17, 19, 20, 34, 37, 38, 42, 62, 63, 67, 72, 74, 80, 81, 87, and 89) and 19 of 23 (82.6%) durum wheat parents (1, 2, 4, 5, 8, 9, 11, 12, 13, 14, 17, 20, 21, 22, 26, 27, 28, 37, and 40). All this germ plasm represents the presence of major genes against stripe rust and can be exploited further in breeding programs.

Adult-plant resistance involving susceptibility at seedling stage and resistance only at the adult-plant stage is an indicator of minor genes, which are considered of great importance in acquiring durable resistance. Eighteen of 90 (20%) synthetics (2, 3, 5, 7, 11, 15, 22, 23, 31, 33, 53, 55, 58, 71, 73, 82, 83, and 84) and one of 23 (4.35%) durum wheat parents (45) had APR and are good candidates for providing durable resistance to wheat cultivars.

Karnal bunt (KB) studies. The KB evaluation was done by examining the grains following artificial inoculation. Grains from each entry were examined separately after hand threshing. The rating scale was from 0 to 5 (see Fig. 2, p. 86). Only a rating of 0 was considered acceptable and all others, from 1 to 5, as susceptible. In the first experiment, 30 of 90 entries (33.3%), including 4, 9, 10, 11, 13, 14, 16, 17, 29, 31, 32, 39, 40, 42, 45, 47, 49, 53, 59, 66, 67, 68, 81, 82, 83, 84, 86, 87, 89, and 90 were completely immune (Table 27, pp. 126-127).

Table 25. Pedigree/Parentage of the *Ae. tauschii* synthetic germ plasm used in this study.

Number	Pedigree
1	ALTAR 84/*Ae. tauschii* (191)
2	68.111/RGB-U//WARD/3/*Ae. tauschii* (328)
3	68.111/RGB-U//WARD/3/*Ae. tauschii* (321)
4	CETA/*Ae. tauschii* (540)
5	D67.2/P66.270/*Ae. tauschii* (213)
6	GARZA/BOY//*Ae. tauschii* (286)
7	GAN/*Ae. tauschii* (268)
8	D67.2/P66.270//*Ae. tauschii* (220)
9	D67.2/P66.270//*Ae. tauschii* (222)
10	D67.2/P66.270//*Ae. tauschii* (308)
11	CETA/*Ae. tauschii* (1016)
12	D67.2/P66.270//*Ae. tauschii* (221)
13	DVERD_2/*Ae. tauschii* (1027)
14	68.111/RGB-U//WARD/3/*Ae. tauschii* (329)
15	GARZA/ BOY//*Ae. tauschii* (467)
16	DVERD_2/*Ae. tauschii* (221)
17	DVERD_2/*Ae. tauschii* (214)
18	ALTAR 84/*Ae. tauschii* (220)
19	68.111/RGB-U//WARD/3/*Ae. tauschii* (452)
20	CETA/*Ae. tauschii* (327)
21	D67.2/P66.270//*Ae. tauschii* (633)
22	GARZA/BOY//*Ae. tauschii* (276)
23	D67.2/P66.270//*Ae. tauschii* (218)
24	CROC_1/*Ae. tauschii* (205)
25	DVERD_2/*Ae. tauschii* (295)
26	68.111/RGB-U//WARD/3/*Ae. tauschii* (463)
27	D67.2/P66.270//*Ae. tauschii* (257)
28	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (215)
29	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (223)
30	ALTAR 84/*Ae. tauschii* (333)
31	GARZA/ BOY//*Ae. tauschii* (265)
32	GAN/*Ae. tauschii* (182)
33	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (273)
34	CPI/GEDIZ/3/GOO// JO/CRA/4/*Ae. tauschii* (296)
35	CETA/*Ae. tauschii* (661)
36	DVERD_2/*Ae. tauschii* (402)
37	CETA/*Ae. tauschii* (174)
38	CETA/*Ae. tauschii* (1024)
39	CROC_1/*Ae. tauschii* (886)
40	CROC_1/*Ae. tauschii* (444)
41	CROC_1/*Ae. tauschii* (518)
42	CETA/*Ae. tauschii* (256)
43	68.111/RGB-U//WARD/3/*Ae. tauschii* (325)
44	DOY 1/*Ae. tauschii* (188)
45	GARZA/BOY//*Ae. tauschii* (307)

Table 26. Pedigrees of durum wheat parents in the *Ae. tauschii* synthetic germ plasm.

Number	Pedigree
D-1	CROC_1
D-4	ALTAR84
D-5	DVERD_2
D-8	68.111/RGB-U//WARD
D-11	CPI/GEDIZ/3/GOO//JO/CRA
D-12	D67.2/P66.270
D-13	CERCETA
D-22	DECOY1
D-23	GARZA/BOY
D-26	GAN

Molecular studies. ***Genetic diversity evaluation using random amplified polymorphic DNA (RAPD) primers.*** RAPD primers were used for genetic diversity evaluation of A-, B-, and D-genome synthetic hexaploids. All 520 RAPD primers of the Operon Series were screened and working primers were identified and applied to detect genetic polymorphism at DNA level. The samples which did not amplify were not included in the analysis.

Genetic analysis was performed only on the scorable bands. Every single band was considered as a single locus/allele. The loci were scored as present/absent. Bivariate data 1–0 were used to estimate genetic distances (GD). Unweighted Pair Group of Arithmetic Means (UPGMA) function estimated genetic distances between the genotypes as follows: $GD_{xy} = 1 - d_{xy}/d_x + d_y - d_{xy}$, where GD_{xy} = genetic distance between two genotypes, d_{xy} = total number of common loci (bands) in two genotypes, d_x = total number of loci (bands) in genotype 1, and d_y = total number of loci (bands) in genotype 2.

The efficiency of primers to amplify the genotypes ranged from a maximum of 36 genotypes (OPE-16) to four genotypes (OPE-6) in this experiment (Table 28, p. 128). The scorable bands ranged from six (OPE-6) to 86 (OPE-12) (Table 28, p. 128). The total number of loci was 197 with 186 polymorphic showing a percentage of 94.41% (Table 28, p. 128) and the range of scorable bands was from 250–3,000 bp.

Similarity matrix. A bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. The value of the similarity matrix ranged from 73.9% (minimum) between entries 8 and 66 to 100% (maximum) between genotypes 48 and 18, 6 and 18, 2 and 18, 6 and 48, 2 and 6, and 2 and 48.

Dendrogram interpretation. The GD between genotypes were used to construct a dendrogram by UPGMA analysis for determining grouping of the lines on the basis of similarities and differences. Only one main cluster is in the dendrogram with two subclusters, A and B (Fig. 20, p. 129). In subcluster-A, 2, 6, 18, and 40 show 100% similarity and 8 is the most diverse line overall, followed by 13, 35, 36, 63, 65, and 87. The total number of genotypes in this cluster is 96. The B subcluster has only three genotypes in which D-4 represents the most diverse line.

Genetic diversity evaluation using simple sequence repeat (SSR) primers. SSR primers were used for genetic diversity evaluation of D-genome synthetic hexaploids. All 275 SSR primers were used to detect genetic polymorphism at the DNA level. Samples that did not amplify were not included in the analysis.

Genetic analysis was performed similar to that for the RAPD primers. The efficiency of primers to amplify the genotypes ranged from maximum 39 genotypes (*Xgwm129-5A*) to two (*Xgwm68-5B* and *Xgwm284-3B*) in this experiment (Table 29, p. 130). The scorable bands ranged from two (*Xgwm68-5B*) to 66 (*Xgwm129-5A*) in this experiment (Table 29, p. 130).

Genetic analysis of the population showed that the total number of alleles was 191, with 185 polymorphic showing a percentage of 96.85% (Table 29, p. 130). The range of scorable bands was 50–600 bp in this experiment.

Similarity matrix. The bivariate analysis was conducted to generate a similarity matrix and dendrogram using similar to that for the RAPD primers. The value of similarity matrix ranged from 75.5% (minimum) between 2 and 90 ans was 100% (maximum) in 33 different combinations.

Dendrogram interpretation. In this experiment, only one main cluster with two subclusters A and B; A has 38 and B has 61 genotypes (Fig. 21, p. 131). Subcluster A carries the most diverse line of the group, 27. Other highly diverse lines in this subcluster include 14, 54, and 61. In subcluster B, genotype 1 is the most diverse line and 4, 5, and 41 are other good examples.

The same durum wheats and different *Ae. tauschii* accessions. Other researchers have recognized that the interaction of the A and B genomes of durum wheat with the D genome of *Ae. tauschii* plays a significant role in gene expression and suppression for the traits under study. To delineate the genomic effects using same durum wheat cultivars with diverse D-genome accessions, we identified ten sets to study; 10 durum

Table 25. Pedigree/Parentage of the *Ae. tauschii* synthetic germ plasm used in this study.

Number	Pedigree
46	DVERD_2/*Ae. tauschii* (1022)
47	CETA/*Ae. tauschii* (796)
48	GAN/*Ae. tauschii* (236)
49	68.111/RGB-U//WARD/3/*Ae. tauschii* (326)
50	GARZA/BOY//*Ae. tauschii* (270)
51	68.111/RGB-U//WARD/3/*Ae. tauschii* (316)
52	ALTAR 84/*Ae. tauschii* (332)
53	GAN/*Ae. tauschii* (180)
54	DOY 1/*Ae. tauschii* (255)
55	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (453)
56	GARZA/BOY//*Ae. tauschii* (278)
57	DVERD_2/*Ae. tauschii* (333)
58	D67.2/P66.270//*Ae. tauschii* (217)
59	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (193)
60	CROC_1/*Ae. tauschii* (170)
61	DVERD_2/*Ae. tauschii* (1031)
62	CROC_1/*Ae. tauschii* (213)
63	ALTAR 84/*Ae. tauschii* (304)
64	CETA/*Ae. tauschii* (235)
65	68.111/RGB-U//WARD/3/*Ae. tauschii* (322)
66	ALTAR 84/*Ae. tauschii* (507)
67	DOY 1/*Ae. tauschii* (510)
68	GAN/*Ae. tauschii* (163)
69	CPI/GEDIZ/3/GOO// JO69/CRA/4/*Ae. tauschii* (633)
70	DOY 1/*Ae. tauschii* (349)
71	GAN/*Ae. tauschii* (408)
72	GAN/*Ae. tauschii* (201)
73	CROC_1/*Ae. tauschii* (333)
74	GARZA/BOY//*Ae. tauschii* (439)
75	GARZA/BOY//*Ae. tauschii* (350)
76	GAN/*Ae. tauschii* (285)
77	DOY 1/*Ae. tauschii* (333)
78	ALTAR 84/*Ae. tauschii* (219)
79	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (208)
80	DOY 1/*Ae. tauschii* (1030)
81	DOY 1/*Ae. tauschii* (515)
82	CPI/GEDIZ/3/GOO// JO69/CRA/4/*Ae. tauschii* (637)
83	ALTAR 84/*Ae. tauschii* (502)
84	DOY 1/*Ae. tauschii* (517)
85	CROC_1/*Ae. tauschii* (224)
86	GAN/*Ae. tauschii* (890)
87	DOY 1/*Ae. tauschii* (458)
88	DVERD_2/*Ae. tauschii* (1029)
89	ALTAR 84/*Ae. tauschii* (211)
90	CROC_1/*Ae. tauschii* (879)

Table 27. Phenotypic and disease characterization of D-genome synthetic hexaploids. FLOW = days-to-flowering, HT = plant height at maturity (cm), AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), PMA = days to physiological maturity, TKW = 1,000-kernel weight (g), G/S = grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult–plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Entry	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Yr (S)	Yr (A)
1	66	73	LB	105	44.1	13	9.5	+	1	10MRR
2	60	105	LB	99	33.5	19	12.0	+	89	TR
3	66	77	LB	105	38.2	15	10.5	+	89	TR
4	60	90	LB	99	36.6	12	9.0	–	8	70S
5	66	113	LB	110	32.0	13	8.5	+	67	30MR
6	70	103	LB	109	29.7	19	12.0	+	8	70S
7	73	91	LB	112	39.2	18	12.0	+	78	10R
8	67	118	LB	107	32.2	14	10.5	+	8	90S
9	70	121	LB	109	35.4	14	12.0	–	8	90S
10	65	98	LB	105	31.0	13	9.0	–	89	70S
11	65	104	LB	105	27.0	13	9.5	–	89	0
12	70	104	LB	109	31.0	14	10.0	+	78	70S
13	66	96	LB	106	34.0	14	10.1	–	1	10R
14	70	120	LB	109	52.9	15	10.3	–	1	0
15	149	108	LB	179	28.8	17	9.0	+	56	10MR
16	71	102	LB	110	33.0	16	11.5	–	56	70S
17	70	110	LB	109	49.9	14	10.0	–	12	5R
18	70	103	LB	109	27.9	12	8.0	+	56	70S
19	70	86	LB	109	32.0	16	12.0	+	1	0
20	70	102	LB	108	49.8	15	11.5	+	1	0
21	70	115	LB	109	24.0	13	9.0	+	78	90S
22	70	90	LB	110	25.0	13	10.0	+	9	TR
23	75	90	LB	113	26.2	14	8.5	+	8	10R
24	74	88	LB	112	27.0	15	13.0	+	56	30MSS
25	69	90	LB	107	23.7	13	10.5	+	78	30MSS
26	73	90	LB	112	28.5	14	10.5	+	78	30MSS
27	141	117	LB	168	33.5	8	11.0	+	89	70S
28	66	73	LB	105	25.4	21	14.0	+	78	90S
29	92	103	LB	105	41.0	14	9.5	–	0	30MSS
30	70	82	LB	108	37.5	16	10.5	+	23	70S
31	73	75	LB	112	26.0	13	11.0	–	8	TR
32	62	100	LB	101	32.5	12	7.0	–	8	90S
33	59	100	LB	97	34.6	14	13.0	+	8	0
34	60	110	LB	100	35.5	13	13.0	+	0	0
35	62	110	LB	101	27.3	12	9.5	+	8	90S
36	65	90	LB	106	35.2	13	10.0	+	0	30MSS
37	146	90	LB	178	25.0	22	9.0	+	0	10MR
38	126	135	LB	175	30.0	20	13.0	+	0	10MRR
39	77	93	LB	113	37.0	13	10.0	–	8	30MSS
40	77	90	LB	113	35.2	13	10.5	–	7	40MS
41	68	83	LB	106	55.7	14	10.0	+	67	40MS
42	62	80	LB	101	46.2	12	8.5	–	0	10R
43	72	99	LB	109	49.8	14	8.5	+	78	10MS
44	65	109	LB	105	59.2	15	10.0	+	1	30MSS
45	64	85	LB	103	30.5	13	9.0	–	9	30MS
46	70	97	LB	106	44.0	14	9.5	+	9	70S

Table 27. Phenotypic and disease characterization of D-genome synthetic hexaploids**.** FLOW = days-to-flowering, HT = plant height at maturity (cm), AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), PMA = days to physiological maturity, TKW = 1,000-kernel weight (g), G/S = grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult–plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Entry	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Yr (S)	Yr (A)
47	79	69	LB	114	31.0	14	10	–	78	90S
48	72	97	LB	109	34.6	15	11	+	78	90S
49	70	89	LB	109	35.7	12	7.5	–	3	90S
50	72	76	LB	109	39.2	13	11	+	89	30MSS
51	68	102	LB	106	45.0	12	9.5	+	1	70S
53	68	100	LB	106	37.2	14	9.5	–	67	10R
54	70	100	LB	110	37.0	12	8	+	0	90S
55	140	153	DB	182	40.0	13	12	+	78	10R
56	72	80	LB	111	43.2	15	10	+	9	90S
57	141	104	LB	177	40.0	15	12	+	56	90S
58	71	75	LB	110	31.0	15	13	+	78	10R
59	70	113	LB	108	32.5	19	12	–	1	30MRMS
60	65	97	LB	105	53.4	18	10	+	78	30MRMS
61	129	113	LB	177	40.0	19	10	+	89	90S
62	72	96	LB	112	39.8	20	11	+	1	10R
63	79	62	LB	116	37.9	12	7	+	1	10R
64	73	100	LB	109	35.5	14	10	+	89	30MSS
65	77	109	LB	115	32.2	15	12	+	1	90S
66	75	120	LB	113	35.2	16	12	–	78	90S
67	146	120	LB	172	41.0	30	13	–	0	0
68	68	113	LB	106	41.0	15	11	–	89	70S
69	63	104	LB	101	40.0	12	9	+	0	70S
70	149	100	LB	181	40.0	14	12	+	1	90S
71	66	100	LB	106	36.6	15	13	+	78	10R
72	140	95	LB	121	35.0	15	10	+	0	10R
73	142	72	LB	181	35.0	20	10	+	78	10R
74	144	128	LB	176	30.0	2	11	+	0	10R
75	150	97	LB	180	16.0	8	10	+	0	70S
76	141	102	LB	161	33.0	37	13	+	67	70S
77	133	114	LB	178	37.0	26	12	+	78	90S
78	136	99	LB	172	31.0	7	11	+	0	70S
79	74	119	LB	112	28.7	14	10	+	0	70S
80	139	110	LB	182	30.0	15	10	+	0	10MR
81	78	100	LB	116	35.9	15	11	–	0	0
82	72	109	LB	109	36.6	14	10	–	78	0
83	73	103	LB	110	26.1	12	9	–	45	10R
84	143	119	LB	175	40.0	12	13	–	45	0
85	74	112	LB	112	52.3	12	10	+	9	70MSS
86	67	86	LB	105	41.0	13	10	–	89	70MSS
87	76	72	LB	113	31.1	12	10	–	0	0
88	144	184	LB	184	30.0	13	10	+	89	90S
89	75	117	LB	112	27.3	14	10	–	0	10R
90	74	103	LB	112	32.1	16	13	–	78	90S

Table 28. Molecular fingerprinting pattern by RAPD primers in the D–genome synthetic hexaploids.

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
1	OPA–3	12	12	100%	14	23	1,000–3,000
2	OPA-4	9	7	77.77%	5	21	750–2,500
3	OPA-13	5	5	100%	31	63	500–1,500
4	OPA-18	10	10	100%	7	26	1,000–2,000
5	OPB-1	9	9	100%	24	62	750–1,500
6	OPB-4	9	9	100%	15	35	500–2,500
7	OPB-5	7	7	100%	18	33	750–3,000
8	OPB-6	13	13	100%	15	59	500–3,000
9	OPB-12	7	5	71.42%	7	17	750–1,000
10	OPB-17	9	9	100%	10	33	50–1,500
11	OPC-5	8	8	100%	13	34	750–2,000
12	OPC-10	7	7	100%	6	14	500–2,000
13	OPC-15	9	9	100%	25	81	250–1,500
14	OPD-2	10	10	100%	13	46	750–2,500
15	OPD-5	8	5	62.5%	32	64	500–3,000
16	OPD-7	11	11	100%	14	41	250–2,000
17	OPD-13	5	3	100%	5	11	500–1,000
18	OPE-4	6	6	100%	11	23	500–1,500
19	OPE-6	5	3	60%	4	6	1,500
20	OPE-7	10	10	100%	35	76	500–2,000
21	OPE-12	12	12	100%	20	86	500–25,00
22	OPE-15	8	8	100%	6	22	1,000–2,500
23	OPE-16	8	8	100%	36	83	750–2,500
24	OPE-18	4	4	100%	11	15	250–1,500
25	OPE-19	2	2	100%	9	10	250–2,000

wheats with various *Ae. tauschii* accessions. The first durum wheat cultivar (Table 25, pp. 124-125), Altar 84, has a combination with eight D-genome accessions. Focussing on the major characters that play a key role in breeding aspects, plant height at maturity was 73–120 cm, days to physiological maturity was 105–172 days, and 1,000-kernel weight was 26.1–44.1 g (Table 27, pp. 126-127). Biotic stress data indicted susceptibility to Karnal bunt in all except in two entries (83 and 89). Stripe rust resistance (seedling and adult) was present in entries 63 and 89. The durum parent Altar 84 was immune to KB and also possessed stripe rust resistance. The observations across these parameters where eight different D-genome accessions were involved show a significant performance variation based upon the expression of the genomes influenced by accessions. The trend seen elucidates why appropriate synthetic entries should be selected in breeding, because trait masking across genomes is a common phenomenon and, hence, an extended analytical focus is helpful. Variable expression trends can be seen with other durum wheat cultivars and strengtens the view that accession diversity can be used to target the right synthetic for wheat improvement.

Wee selected the following synthetics to use: 27, 34, 44, 67 and 76 (Table 27, pp. 126-127). Entry 67 has both stripe rust resistance (seeding and adult) and also KB; hence the best line. The data in Table 27 (pp. 126-127) will identify accessions to be used for direct crossing, where exchanges will be restricted to only the D genome. Because the durum wheat parent Altar 84 was immune to KB and resistant to strip rust, varied results upon crossing with *Ae. tauschii* accessions indicated that the accessions were overriding the durum cultivars resistance. Hence, only selection of those accessions in which the corresponding synthetic showed KB and strip rust resistance would be ideal for use in direct crossing because their influence on the A and B genomes of bread wheat would, hopefully, not be penalizing. If the bread wheat is susceptible to KB and stripe rust, selecting resistant derivatives would unequivocally demonstrate that the *Ae. tauschii* carried the desired genes. This trend also is well expressed in other groups where other durum cultivars and *Ae. tauschii* accessions are used (Table 27, pp. 126-127).

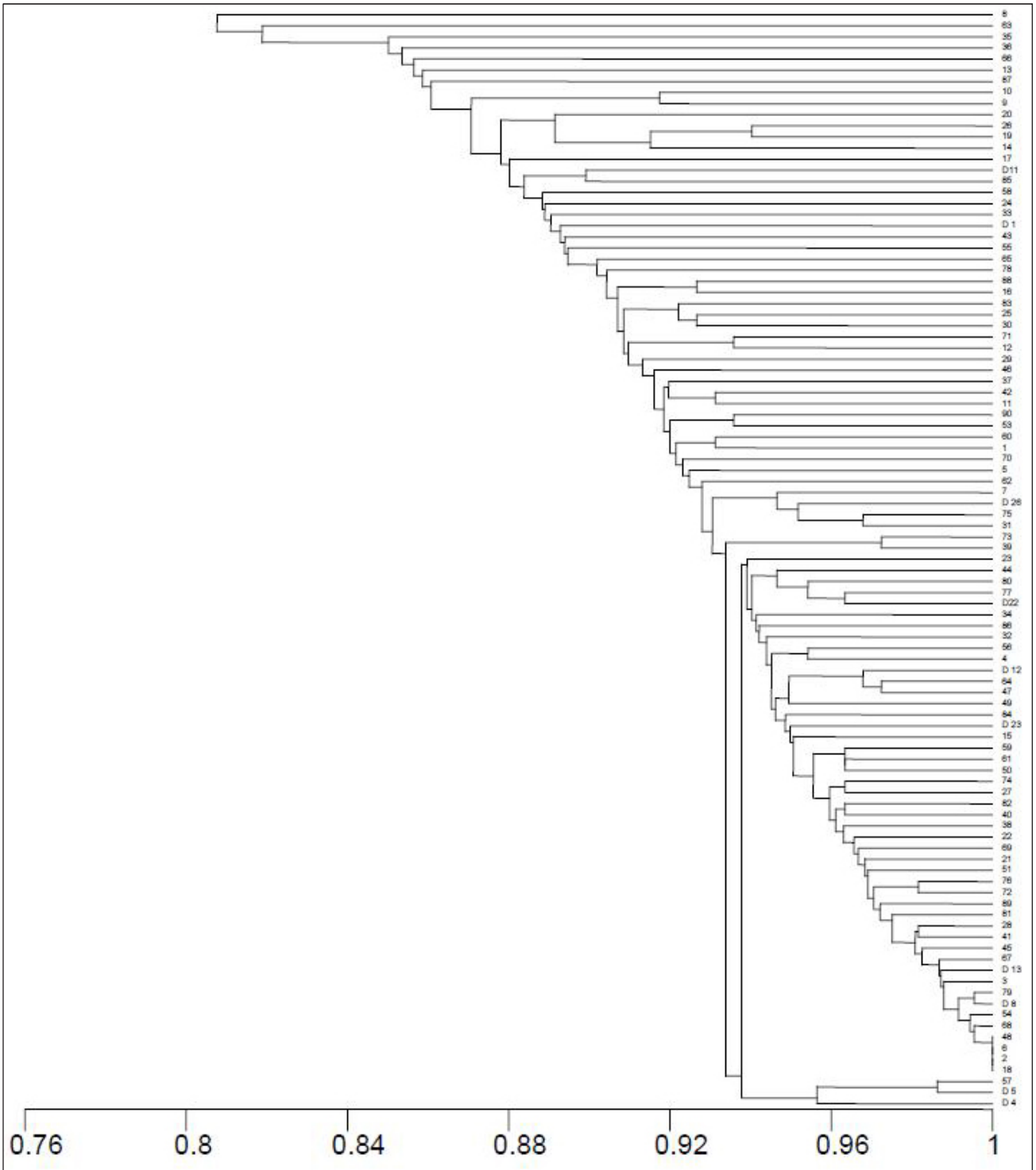

Fig. 20. A RAPD-based cluster formation of genotypes of various *Aegilops tauschii* accessions in a similar durum wheat background.

The synthetic combinations from group 1 involving Altar 84 and eight *Ae. tauschii* accessions showed diversity in molecular analysis also. Using RAPDs, 63 was most diverse line and next was 66. Using SSRs, entries 1, 63, 78, and 83 grouped together; next were entries 13 and 18, with entry 89 being the most diverse. Incorporating the stress resistance data, entries 63 and 89 possessed both seedling and adult-plant resistance, and entry 89 had KB resistance. Hence entry 89 possesses ideal KB and stripe rust resistance and also is the most diverse line based upon SSR-based polymorphism. This strategy enables tge integration of various components for adding efficiency to a breeding program.

Table 29. Molecular fingerprinting pattern by SSR primers in the D-genome synthetic hexaploids (experiment 1, same durum with different *Ae. tauschii* accessions).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
1	*Xgwm99-1A*	4	4	100%	15	19	50–150	0.34
2	*Xgwm666-1A*	3	3	100%	8	8	100–150	0.53
3	*Xgwm249-2A*	4	4	100%	7	13	50–150	0.64
4	*Xgwm294-2A*	4	4	100%	10	10	50–100	0.70
5	*Xgwm558-2A*	5	5	100%	11	12	50–200	0.76
6	*Xgwm614-2A*	4	4	100%	13	20	50–200	0.67
7	*Xgwm5-3A*	8	8	100%	16	33	50–300	0.78
8	*Xgwm30-3A*	3	3	100%	6	9	50–100	0.54
9	*Xgwm32-3A*	7	7	100%	22	46	50–200	0.67
10	*Xgwm666.2-3A*	4	4	100%	15	16	50–200	0.39
11	*Xgwm610-4A*	7	7	100%	34	62	50–200	0.86
12	*Xgwm129-5A*	6	6	100%	39	66	50–200	0.78
13	*Xgwm179-5A*	2	2	100%	4	4	50–150	0.37
14	*Xgwm617-5A*	7	5	71.42%	16	21	50–200	0.69
15	*Xgwm617-6A*	8	6	75%	13	18	50–200	0.68
16	*Xgwm63-7A*	4	4	100%	12	13	50–500	0.60
17	*Xgwm18-1B*	5	5	100%	21	26	50–200	0.64
18	*Xgwm33-1B*	4	4	100%	4	8	50–100	0.67
19	*Xgwm124-1B*	7	7	100%	24	38	50–200	0.78
20	*Xgwm550-1B*	7	7	100%	14	23	50–200	0.55
21	*Xgwm16-2B*	7	7	100%	17	27	50–200	0.50
22	*Xgwm610-2B*	3	3	100%	11	13	50–100	0.36
23	*Xgwm257-2B*	6	6	100%	9	11	50–200	0.77
24	*Xgwm131-3B*	2	2	100%	2	2	50–150	0.50
25	*Xgwm284-3B*	3	3	100%	5	8	50–600	0.62
26	*Xgwm66-4B*	6	6	100%	9	14	50–100	0.72
27	*Xgwm149-4B*	8	8	100%	8	16	50–250	0.73
28	*Xgwm66-5B*	2	2	100%	9	13	50–150	0.34
29	*Xgwm68-5B*	1	1	100%	2	2	50	0.00
30	*Xgwm213-5B*	4	4	100%	12	14	50–150	0.64
31	*Xgwm132-6B*	4	4	100%	6	8	100–150	0.58
32	*Xgwm232-1D*	4	2	50%	4	5	50–150	0.65
33	*Xgwm157-2D*	5	5	100%	26	31	50–300	0.63
34	*Xgwm212-2D*	3	3	100%	20	20	50–150	0.60
35	*Xgwm455-2D*	6	6	100%	19	34	50–100	0.65
36	*Xgwm3-3D*	1	1	100%	20	20	50	0.00
37	*Xgwm183-3D*	2	2	100%	21	21	100–150	0.69
38	*Xgwm314-3D*	4	4	100%	10	19	100–200	0.67
39	*Xgwm608-4D*	1	1	100%	9	9	100	0.00
40	*Xgwm16-5D*	6	6	100%	28	47	50–150	0.69
41	*Xgwm192-5D*	7	7	100%	23	40	150–250	0.77
42	*Xgwm55-6D*	6	6	100%	9	23	50–150	0.75

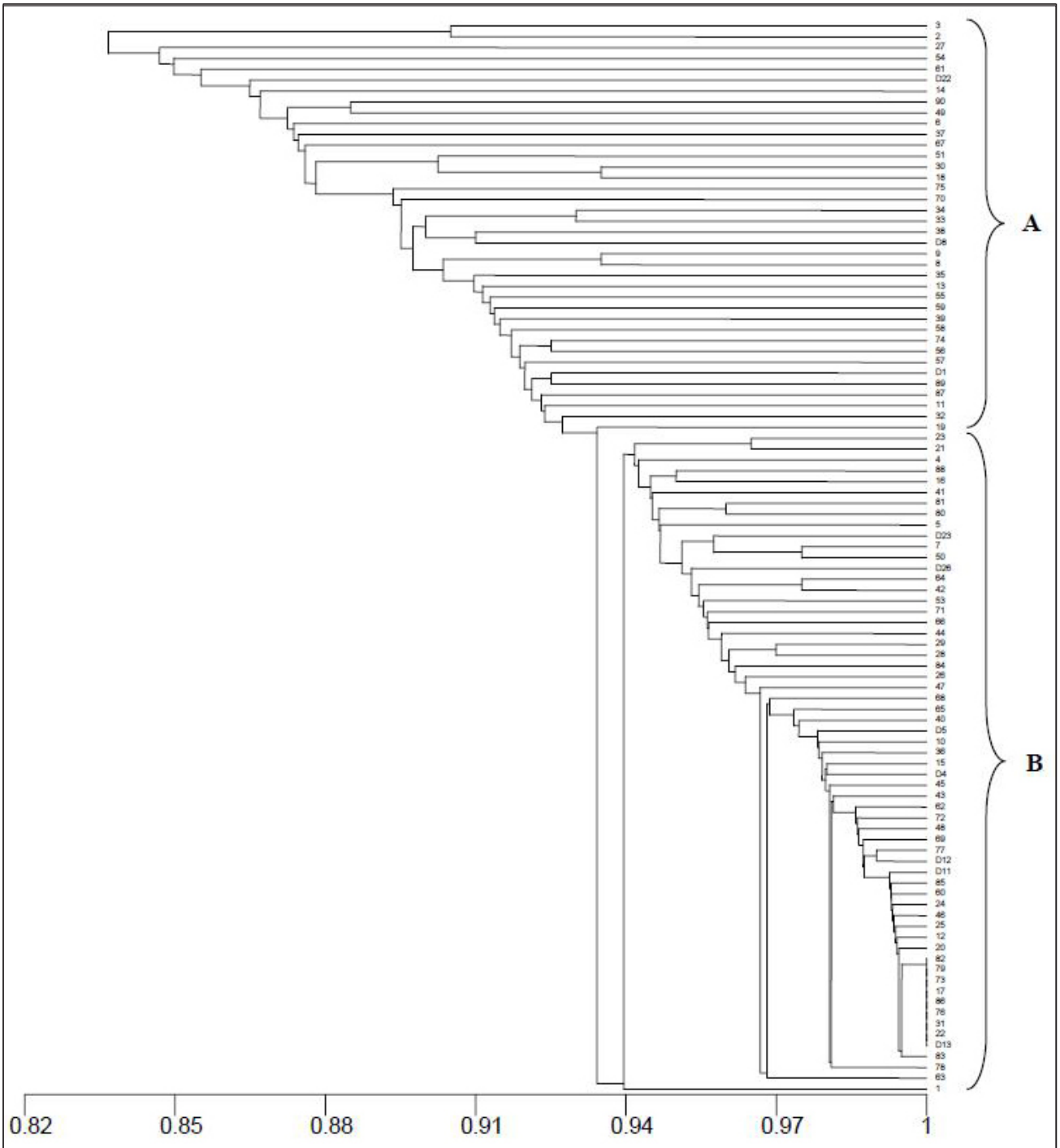

Fig. 21. An SSR-based cluster formation of genotypes of various *Aegilops tauschii* accessions in a similar durum wheat background.

Phenotypic and molecular characterization of synthetic hexaploids derived from the same Ae. tauschii accessions and diverse durum cultivars.

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This study with same *Ae. tauschii* accession used as the female parent in crosses with different durum cultivars as the pollen parent (78 entries) is designed to study the inheritance of different genes and also identify the effect of cytoplasmic inheritance if any. The total of 78 entries was screened against two biotic stresses (Karnal bunt and stripe rust), phenotypically characterized, and analyzed with RAPD and SSRs for molecular characterization (Table 30 and Table 31, pp. 132-133).

Stripe rust studies. Seedling screening showed that 51 of 78 (65.4%, Table 32, pp. 134-135) exhibited resistance. These genotypes also were screened for APR under field conditions at NARC, which identified 51 of the 95 (65.4%) as resistant genotypes. Genotypes with both seedling and adult-plant resistance were 15 of 78 (19.2%), including entries 9, 11, 12, 13, 14, 15, 16, 31, 32, 33, 39, 42, 50, 54, and 66. All this germ plasm represents the presence of major genes against stripe rust and can be exploited further in breeding programs.

Adult-plant resistance involving susceptibility at seedling stage and resistance only at the adult-plant stage is an indicator of presence of minor genes, which are considered of great importance against rust diseases in acquiring durable resistance. Nine of 78 entries (11.5%) had APR, including entries 21, 22, 25, 29, 36, 49, 62, 63, and 64 and are good candidates for providing durable resistance to wheat cultivars.

Karnal bunt studies. Karnal bunt (KB) evaluation was done by examining the grains following artificial inoculation. Grains from each entry were examined separately after hand threshing. The rating scale was from 0 to 5; only a rating of 0 was considered acceptable and all others as susceptible (See Fig. 2, p. 86). In this experiment, 29 of the 78 genotypes (37.2%) were found to be immune, including 2, 5, 7, 8, 9, 13, 17, 20, 21, 22, 23, 25, 26, 28, 29, 30, 41, 42, 43, 44, 45, 48, 49, 53, 54, 68, 72, 73, and 77 (Table 32, pp. 135-136).

Molecular studies. ***Genetic diversity evaluation using random amplified polymorphic DNA (RAPD) primers.*** RAPD primers were used for genetic diversity evaluation of A-, B-, and D-genome synthetic hexaploids. All 520 RAPD primers of the Operon Series were screened and working primers were identified and applied to detect genetic polymorphism at DNA level. The samples which did not amplify were not included in the analysis.

Genetic analysis was performed only on the scorable bands. Every single band was considered as a single locus/allele. The loci were scored as present/absent. Bivariate data 1–0 were used to estimate genetic distances (GD). The unweighted pair group of arithmetic means (UPGMA) func-

Table 30. Synthetic hexaploid entries derived from combining durum wheat cultivars with *Aegilops tauschii* accessions and their respective reciprocal cross combinations. Entry numbers are similar to data base maintained in CIMMYT Wide Crosses program in Mexico.

Group number	D-genome synthetic hexaploid entry	Total number of entries
1	1, 39, 45, 49	4
2	2, 20, 78	3
3	3, 10, 47	3
4	4, 19, 30	3
5	5, 27, 46	3
6	6,17, 24	3
7	7, 41, 68	3
8	8, 15, 33	3
9	9, 26, 28, 43, 59, 74	6
10	11, 40, 63	3
11	12, 50, 76	3
12	13, 69, 75	3
13	14, 16, 52	3
14	18, 60, 73	3
15	21, 25, 66	3
16	22, 29, 42, 56	4
17	23, 35, 38, 71	4
18	31, 61, 67, 77	4
19	32, 48, 65	3
20	34, 44, 57	3
21	36, 51, 54, 58	4
22	37, 53, 55, 62, 64, 70, 72	7

Table 31. Pedigrees of the genotypes used in this study that combined durum wheat cultivars with *Aegilops tauschii* accessions.

Synthetic number	Pedigree
1	DVERD_2/*Ae. tauschii* (1026)
2	ARLIN/*Ae. tauschii* (665)
3	ARLIN/*Ae. tauschii* (295)
4	ALTAR 84/*Ae. tauschii* (221)
5	RASCON/*Ae. tauschii* (314)
6	D67.2/ P66.270//*Ae. tauschii* (633)
7	D67.2/ P66.270//*Ae. tauschii* (223)
8	STY-US/CELTA//PALS/3/SRN_5/4/*Ae. tauschii* (174)
9	CROC_1/*Ae. tauschii* (507)

Table 31. Pedigrees of the genotypes used in this study that combined durum wheat cultivars with *Aegilops tauschii* accessions.

Synthetic number	Pedigree
10	ROK/KML//*Ae. tauschii* (295)
11	RABI//GS/CRA/3/*Ae. tauschii* (457)
12	GAN/*Ae. tauschii* (446)
13	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (205)
14	CROC_1/*Ae. tauschii* (215)
15	CETA/*Ae. tauschii* (174)
16	SORA/*Ae. tauschii* (215)
17	SNIPE/YAV79//DACK/TEAL/3/*Ae. tauschii* (633)
18	YAV_2/TEZ//*Ae. tauschii* (170)
19	D67.2/P66.270//*Ae. tauschii* (221)
20	6973/WARD.7463//74110/3/*Ae. tauschii* (665)
21	ALTAR 84/*Ae. tauschii* (211)
22	ARLIN_1/*Ae. tauschii* (1018)
23	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (629)
24	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (633)
25	SORA/*Ae. tauschii* (211)
26	LARU/*Ae. tauschii* (507)
27	SCOT/MEXI_1//*Ae. tauschii* (314)
28	ALTAR 84/*Ae. tauschii* (507)
29	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (1018)
30	DVERD_2/*Ae. tauschii* (221)
31	YAR/*Ae. tauschii* (783)
32	LCK59.61/*Ae. tauschii* (308)
33	ALTAR 84/*Ae. tauschii* (174)
34	DVERD_2/*Ae. tauschii* (1031)
35	SNIPE/YAV79//DACK/TEAL/3/*Ae. tauschii* (629)
36	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (1029)
37	DVERD_2/*Ae. tauschii* (333)
38	68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (629)
39	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (1026)
40	YAV79//DACK/RABI/3/SNIPE/4/*Ae. tauschii*(457)
41	ALTAR 84/*Ae. tauschii* (223)

Table 31. Pedigrees of the genotypes used in this study that combined durum wheat cultivars with *Aegilops tauschii* accessions.

Synthetic number	Pedigree
42	DOY 1/*Ae. tauschii* (1018)
43	DOY 1/*Ae. tauschii* (507)
44	CETA/*Ae. tauschii* (1031)
45	CETA/*Ae. tauschii* (1026)
46	KAPUDE/*Ae. tauschii* (314)
47	DVERD_2/*Ae. tauschii* (295)
48	D67.2/ P66.270//*Ae. tauschii* (308)
49	DOY 1/*Ae. tauschii* (1026)
50	DOY 1/*Ae. tauschii* (446)
51	DVERD_2/*Ae. tauschii* (1029)
52	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (215)
53	ARLIN_1/*Ae. tauschii* (333)
54	DOY 1/*Ae. tauschii* (1029)
55	ALTAR 84/*Ae. tauschii* (333)
56	CETA/*Ae. tauschii* (1018)
57	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (1031)
58	CETA/*Ae. tauschii* (1029)
59	ROK/ KML//*Ae. tauschii* (507)
60	CROC_1/*Ae. tauschii* (170)
61	CETA/*Ae. tauschii* (783)
62	LARU/*Ae. tauschii* (333)
63	YAV_2/ TEZ//*Ae. tauschii* (457)
64	CROC_1/*Ae. tauschii* (333)
65	ARLIN/*Ae. tauschii* (308)
66	D67.2/ P66.270//*Ae. tauschii* (211)
67	68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (783)
68	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (223)
69	ALTAR 84/*Ae. tauschii* (205)
70	DOY 1/*Ae. tauschii* (333)
71	CIT71/ CPT//*Ae. tauschii* (629)
72	ROK/ KML//*Ae. tauschii* (333)
73	CETA/*Ae. tauschii* (170)
74	DVERD_2/*Ae. tauschii* (507)
75	CROC_1/*Ae. tauschii* (205)
76	SRN/*Ae. tauschii* (446)
77	LCK59.61/*Ae. tauschii* (783)
78	CETA/*Ae. tauschii* (665)

Table 32. Phenotypic and disease characterization of D-genome synthetic hexaploids that combined durum wheat cultivars with *Aegilops tauschii* accessions. FLOW = days-to-flowering, HT = plant height at maturity (cm), AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), PMA = days to physiological maturity, TKW = 1,000-kernel weight (g), G/S = grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult–plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Entry	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Yr (S)	Yr (A)
1	75	92	LB	112	30.0	15	12	+	1	10MRMS
2	76	90	LB	114	30.0	17	13	-	1	10MRMS
3	74	88	LB	112	31.2	14	11	+	1	30MRMS
4	79	100	LB	118	29.5	12	9	+	45	30MSS
5	72	109	LB	109	23.6	14	10	-	0	90S
6	79	115	LB	115	55.7	13	9	+	23	90S
7	75	113	LB	113	69.2	14	11	-	89	30MSS
8	89	91	LB	123	38.6	13	11	-	1	90S
9	92	93	LB	101	31.5	15	12	-	0	30MR
10	84	107	LB	101	25.4	18	14	+	89	30MSS
11	70	112	LB	112	39.7	12	11	+	1	0
12	76	102	LB	113	29.4	13	11	+	1	0
13	78	100	LB	116	31.2	12	11	-	1	10R
14	76	109	LB	113	32.5	14	11	+	1	0
15	70	123	LB	107	35.2	15	13	+	89	5MR
16	72	100	LB	108	36.6	16	13	+	89	10MR
17	72	99	LB	109	55.0	14	9	-	34	90S
18	68	124	LB	106	39.5	16	11	+	89	70S
19	71	112	LB	109	26.0	13	11	+	89	50S
20	73	114	LB	112	37.0	14	11	-	1	50S
21	75	107	LB	113	36.2	16	12	-	78	10R
22	73	104	LB	111	32.5	12	8	-	78	10R
23	73	110	LB	101	17.6	12	9	-	78	90S
24	70	111	LB	108	25.6	16	13	+	78	90S
25	77	92	LB	116	39.9	14	12	-	98	10R
26	79	75	LB	118	33.5	13	11	-	45	90S
27	128	112	LB	181	37.0	9	10	+	34	90S
28	144	82	LB	180	35.0	20	15	-	89	90S
29	83	109	LB	123	37.6	23	18	-	89	0
30	79	109	LB	118	25.0	15	11	-	89	90S
31	80	105	LB	113	26.0	15	12	+	12	10R
32	82	98	LB	112	26.0	15	11	+	12	10R
33	81	99	LB	118	27.0	14	10.5	+	12	5R
34	75	110	LB	112	31.0	16	11	+	34	90S
35	74	112	LB	112	29.5	14	10	+	89	30MRMS
36	87	85	LB	123	39.0	13	10	+	89	10R
37	70	109	LB	105	31.0	14	10	+	1	90S
38	70	110	LB	106	32.5	13	9.5	+	1	90S
39	69	84	LB	105	42.0	12	8	+	34	5R
40	73	104	LB	112	40.6	18	14	+	1	90S
41	129	128	LB	173	33.0	15	11	+	34	10MSS
42	83	102	LB	120	37.6	15	11	-	34	5R
43	83	107	LB	118	29.8	13	9.5	-	0	30MSS
44	84	76	LB	119	25.3	12	8.5	-	0	90S
45	83	122	LB	115	27.3	15	10.5	-	1	90S

Table 32. Phenotypic and disease characterization of D-genome synthetic hexaploids that combined durum wheat cultivars with *Aegilops tauschii* accessions. FLOW = days-to-flowering, HT = plant height at maturity (cm), AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), PMA = days to physiological maturity, TKW = 1,000-kernel weight (g), G/S = grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult–plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Entry	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Yr (S)	Yr (A)
46	72	98	LB	112	25.5	14	10	+	1	90S
47	72	96	LB	109	38.5	16	12	+	1	90S
48	74	120	LB	112	29.6	15	10	-	34	90S
49	76	103	LB	114	29.5	12	9	-	89	0
50	76	99	LB	113	30.5	14	10.5	+	0	0
51	72	100	LB	109	31.5	13	11.5	+	0	70S
52	66	106	LB	106	36.5	12	9.5	+	0	70S
53	70	98	LB	106	37.0	14	11	-	78	90S
54	83	108	LB	118	36.5	16	11	-	0	10R
55	70	104	LB	106	31.5	14	10	+	34	90S
56	138	114	LB	167	30.5	14	10	+	78	90S
57	72	111	LB	106	32.6	15	10.5	+	0	90S
58	83	92	LB	115	32.5	13	9.5	+	0	30MSS
59	66	111	LB	108	31.2	12	9	+	34	70S
60	66	98	LB	105	30.5	13	9	+	0	30MRMS
61	83	92	LB	114	29.5	16	12	+	23	90S
62	69	96	LB	106	37.3	15	10	+	89	10R
63	72	111	LB	109	35.3	13	9.5	+	89	10R
64	72	121	LB	113	34.5	12	10	+	89	10R
65	73	120	LB	112	40.0	11	10	+	1	90S

tion estimated genetic distances between the genotypes as follows: $GD_{xy} = 1 - d_{xy}/d_x + d_y - d_{xy}$, where GD_{xy} = genetic distance between two genotypes, d_{xy} = total number of common loci (bands) in two genotypes, d_x = total number of loci (bands) in genotype 1, and d_y = total number of loci (bands) in genotype 2. The efficiency of primers to amplify the genotypes ranged from maximum from 34 (OPC-5) to one (OPA-9) (Table 33, p. 136). Scorable bands ranged from four (OPG-18, OPI-11, OPJ-9, OPJ-13) to 185 (OPC-15) (Table 33, p. 136). Genetic analysis of the population showed that the total number of loci reached 194, out of which 164 were polymorphic, and the percentage of polymorphism was 84.53% (Table 33, p. 136). The range of scorable bands was from 250-3,000 bp.

Similarity matrix. Bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. The value of similarity matrix ranged from 70.3% (minimum) between genotypes 6 and 49 and was 100% (maximum) in 33 combinations.

Dendrogram interpretation. The GD between genotypes were used to construct a dendrogram by UPGMA analysis for determining grouping of the lines on the basis of similarities and differences. The dendrogram shows only one main cluster with two subclusters, A and B (Fig. 22, p. 137). Subcluster A has 66 genotypes of which 16 is the most diverse line and 2, 18, 50, 54, 61, 69, 71, 72, and 73 have 100% similarity to each other. Some other good lines in subcluster A include 3, 13, 15, 19, 23, 24, 57, and 76. Subcluster B has 12 genotypes of which 1, 25, and 41 are the best lines.

Evaluation of genetic diversity using simple sequence repeats (SSR) primers. SSR primers were used for genetic diversity evaluation of A-, B-, and D-genome synthetic hexaploids. All 275 SSR primers were applied to detect genetic polymprphism at the DNA level. Samples that did not amplify were not included in the analysis, The genetic analysis was similar to that for RAPD primers. The efficiency of primers to amplify the genotypes ranged from a maximum of 60 (*Xgwm437-7D*) to two (*Xgwm18-1B*, *Xgwm210-2B*, *Xgwm257-2B*, *Xgwm285-3B*, and *Xgwm102-2D*) (Table 34, pp. 139-140).

Table 33. Molecular fingerprinting pattern by RAPDs in D–genome wynthetic hexaploids (Same *Ae. tauschii* accessions with different durums)

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples qmplified	Scorable bands	Amplification product 4ange (bp)
1	OPA–2	4	4	100%	13	26	500–1,500
2	OPA-3	7	5	71.42%	9	21	1,000–2,000
3	OPA-4	1	1	100%	5	5	7,50–1,000
4	OPA-7	8	6	75%	8	18	1,000–2,500
5	OPA-9	5	0	0%	1	5	750–3,000
6	OPA-13	8	6	75%	16	40	750–3,000
7	OPB-5	2	2	100%	13	14	1,000–2,500
8	OPC-1	3	3	100%	7	13	1,000–2,000
9	OPC-2	10	10	100%	20	59	750–3,000
10	OPC-5	12	12	100%	34	137	750–2,500
11	OPC-15	12	12	100%	33	185	500–2,500
12	OPC-18	12	8	66.66%	22	45	500–3,000
13	OPD-19	8	0	0%	1	8	500–2,500
14	OPE-19	9	9	100%	12	98	250–2,000
15	OPE-20	9	7	77.77%	28	52	750–2,000
16	OPF-1	10	10	100%	7	25	250–2,500
17	OPG-9	6	6	100%	7	14	750–2,000
18	OPG-15	7	7	100%	11	21	1,000–3,000
19	OPG-18	4	1	25%	2	4	500–2,000
20	OPH-4	6	6	100%	4	12	500–2,500
21	OPH-15	9	9	100%	11	28	500–2,500
22	OPI-4	10	10	100%	11	27	250–2,000
23	OPI-11	3	1	33.33%	2	4	500–2,000
24	OPJ-9	4	4	100%	4	4	1,000–1,500
25	OPJ-12	6	6	100%	4	18	250–15,00
26	OPJ-13	3	3	100%	3	4	500–750
27	OPK-19	6	6	100%	14	34	500–2,000
28	OPK-20	10	10	100%	11	25	500–2,500

The scorable bands ranged from two (*Xgwm210-2B*, *Xgwm257-2B*, and *Xgwm157-2D*) to 120 (*Xgwm192-5D*) (Table 34, pp. 138-139). A genetic analysis of the population showed that the total number of alleles reached 208, of which 204 were polymorphic, and the percent polymorphism was 98.07% (Table 34, pp. 138-139). The range of scorable bands was from 50–500 bp.

Similarity matrix. Bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. The value of similarity matrix ranged from 60.5% (minimum) between genotypes 7 and 1 and 7 and 49 and 98.6% (maximum) between 75 and 78 and 74 and 75.

Dendrogram interpretation. The dendrogram (Fig. 23, p. 137) shows one main cluster with subclusters A and B. Subcluster A can further be divided into two groups A1 and A2, with 10 and 57 genotypes, respectively. Group A1 has the most diverse genotype, 7, and other good lines include 9, 53, and 64. In group A2, 5, 39, 46, 63, and 77 are highly diverse genotypes. Subcluster B has 11 genotypes with 1 as the most diverse and 8 and 15 as highly diverse lines.

Same *Ae. tauschii* accession and different durum wheat cultivars. Contrary to the previous study (this issue: pp. 123-131), the influence of the same *Ae. tauschii* accession across diverse durum cultivars was observed across some group categories. This set of materials involved 22 groups with a total number of 78 entries that were studied for phenotypic, biotic stress, and molecular parameters. Across the entire group, days-to-flowering ranged from 66 days (entries 52, 59, 60, 68, and 71), spike length was satisfactory (line 71 was 14 cm), and a 1,000-kernel weight of 69.2 g was observed for entry 7. The best entries on the basis of overall phenotype were 7, 40, 71, and 77 with the most desirable being 71, because it is the earliest flowering and has the longest spike length. Karnal bunt resistance was found in entries 7 and 77.

The molecular diversity of these 78 entries was deduced from RAPD and SSR analysis. Entries 1, 3, 13, 15, 16, 19, 23, 24, 25, 41, 57, and 76 exhibited higher levels of diversity when analyzed by RAPDs. The most diverse were 1, 5, 7, 8, 9, 15, 39, 46, 53, 63, 64, and 77. Entries 1 and 15 were highly diverse for both RAPDs and SSRs. For biotic stress, entries 7 and 77 were the best for KB resistance, possessed good phenotypic traits, and are good candidates for future breeding efforts.

For some specific same *Ae. tauschii*/ durum wheat cultivar groups, synthetic groups 1 of 4 (entries 1, 39, 45, and 49) involved accession 1026. Entries 45 and 49 have KB resistance, entry 1 has stripe rust resistance at the seedling and adult-plant level and also is the most diverse genetically (RAPD/SSR). Entries 39 and 49 have APR and with the overall picture it is concluded that entry 49 possessing KB, APR for stripe rust, and good phenotype will be the ideal candidate for breeding.

Group 2, where the alien accession was 665, was comprised of three synthetics (2, 20, and 78). Of these entries, 2 and 20 are immune to KB and 2 has seedling and adult-plant strip rust resistance. Entry 2 is a desirable breeding parent with highest genetic diversity in the group based on SSR analysis.

Group 9 has six synthetics structured on the alien accession number 507, including SH 9, 26, 28, 43, 59, and 74. All entries except 59 and 74 are immune to KB; none are resistant to stripe rust. The diversity was high in entries 26 and 43 through RAPDs and 9 and 26 through SSRs. Because of its diversity, entry 26 is a preferred candidate for breeding utilization with KB resistance as an added positive attribute.

In group 22, seven synthetics involved *Ae. tauschii* accession 333, including 37, 53, 55, 62, 64, 70, and 72. All except 53 and 72 were susceptible to KB and entries 62, 64 had APR for stripe rust. Entry 64 had the maximum molecular diversity based upon RAPD and SSR analysis and possesses more positive attributes to give it high priority in breeding.

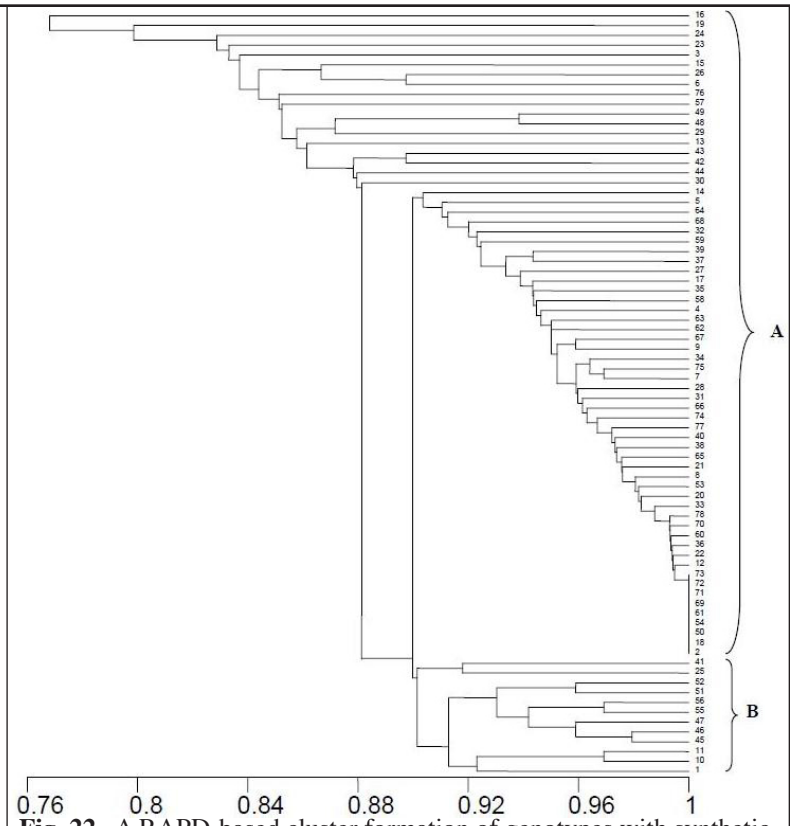

Fig. 22. A RAPD-based cluster formation of genotypes with synthetic hexaploids derived from the same *Ae. tauschii* accessions and diverse durum cultivars.

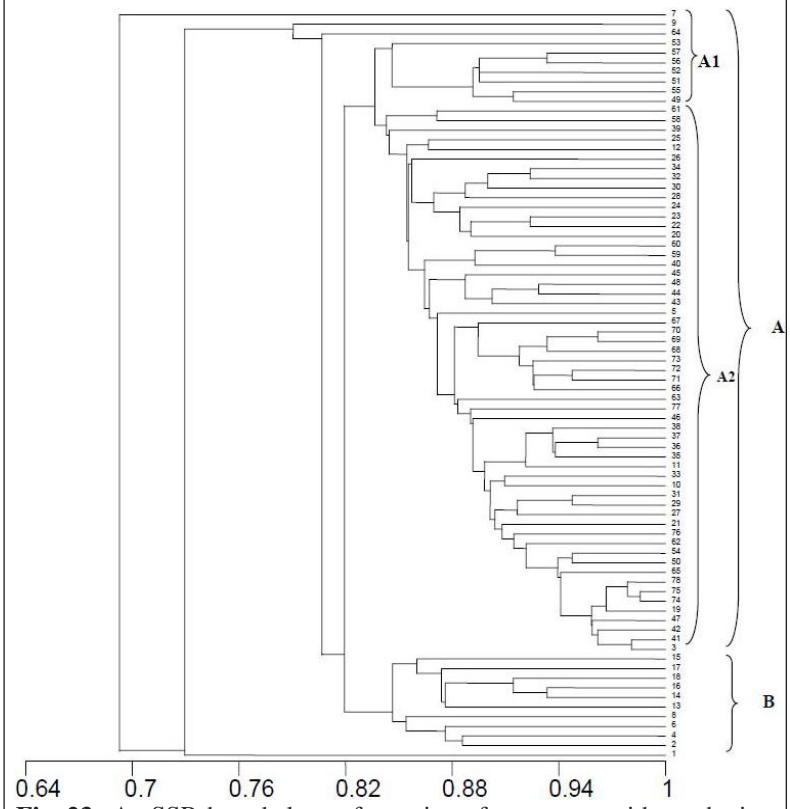

Fig. 23. An SSR-based cluster formation of genotypes with synthetic hexaploids derived from the same *Ae. tauschii* accessions and diverse durum cultivars.

Table 34. Molecular fingerprinting pattern by SSRs in D-genome synthetic hexaploids derived from the same *Ae. tauschii* with different durums).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
1	*Xgwm99-1A*	3	3	100%	5	7	50-150	0.31
2	*Xgwm10-2A*	4	4	100%	8	11	50-150	0.44
3	*Xgwm47.1-2A*	4	4	100%	20	23	50-200	0.41
4	*Xgwm47.2-2A*	2	2	100%	4	5	50-200	0.21
5	*Xgwm71.1-2A*	18	18	100%	23	60	50-100	0.78
6	*Xgwm95-2A*	3	2	66.67%	6	7	50-100	0.84
7	*Xgwm296-2A*	6	6	100%	17	28	50-200	0.75
8	*Xgwm312-2A*	1	1	100%	12	12	200	0.00
9	*Xgwm558-2A*	2	2	100%	5	5	50-200	0.32
10	*Xgwm205-5A*	1	1	100%	7	7	150	0.00
11	*Xgwm291-5A*	3	3	100%	4	4	100-150	0.62
12	*Xgwm169-6A*	2	2	100%	10	11	100-200	0.09
13	*Xgwm494-6A*	4	4	100%	17	20	50-200	0.42
14	*Xgwm11-1B*	5	4	80%	8	11	50-150	0.47
15	*Xgwm18-1B*	5	5	100%	2	6	100-200	0.77
16	*Xgwm124-1B*	4	4	100%	3	6	50-150	0.69
17	*Xgwm131-1B*	2	2	100%	3	3	200	0.00
18	*Xgwm140-1B*	3	3	100%	8	10	50-150	0.21
19	*Xgwm210-2B*	1	1	100%	2	2	200	0.54
20	*Xgwm257-2B*	1	1	100%	2	2	100	0.00
21	*Xgwm319-2B*	6	6	100%	4	11	50-200	0.78
22	*Xgwm284-3B*	1	1	100%	7	7	500	0.00
23	*Xgwm285-3B*	5	5	100%	2	6	50-200	0.73
24	*Xgwm66-4B*	5	5	100%	12	18	50-200	0.43
25	*Xgwm113-4B*	1	1	100%	4	4	50	0.00
26	*Xgwm149-4B*	1	1	100%	4	4	50	0.00
27	*Xgwm102-2D*	2	2	100%	2	2	150-200	0.50
28	*Xgwm157-2D*	5	5	100%	13	21	50-150	0.73
29	*Xgwm249-2D*	6	6	100%	8	23	50-150	0.76
30	*Xgwm261-2D*	6	6	100%	26	33	50-200	0.54
31	*Xgwm296-2D*	5	5	100%	47	53	150-200	0.62
32	*Xgwm301-2D*	4	4	100%	50	51	50-150	0.45
33	*Xgwm320-2D*	3	3	100%	24	24	200-250	0.55
34	*Xgwm455-2D*	3	2	66.67%	16	17	100-200	0.06
35	*Xgwm484-2D*	7	7	100%	17	35	50-250	0.80
36	*Xgwm539-2D*	5	5	100%	58	65	50-150	0.47
37	*Xgwm608-2D*	4	4	100%	23	30	100-200	0.61
38	*Xgwm3-3D*	3	3	100%	57	62	50-100	0.29
39	*Xgwm383-3D*	4	4	100%	51	51	200-250	0.45
40	*Xgwm456-3D*	2	2	100%	43	56	50-150	0.28
41	*Xgwm190-5D*	5	5	100%	35	37	200-250	0.48
42	*Xgwm192-5D*	4	4	100%	54	120	100-250	0.70
43	*Xgwm269-5D*	6	6	100%	35	70	100-250	0.73
44	*Xgwm272-5D*	3	3	100%	6	6	50-150	0.50
45	*Xgwm292-5D*	4	4	100%	28	28	150-500	0.56
46	*Xgwm358-5D*	7	7	100%	37	43	50-500	0.49

Table 34. Molecular fingerprinting pattern by SSRs in D-genome synthetic hexaploids derived from the same *Ae. tauschii* with different durums).

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
47	*Xgwm565-5D*	5	4	80%	51	101	150-250	0.66
48	*Xgwm55-6D*	5	5	100%	51	86	100-200	0.74
49	*Xgwm325-6D*	4	4	100%	13	13	50-200	0.48
50	*Xgwm469-6D*	7	7	100%	48	68	150-250	0.73
51	*Xgwm295-7D*	2	2	100%	3	3	50-250	0.44
52	*Xgwm350-7D*	2	2	100%	8	8	100-150	0.37
53	*Xgwm428-7D*	1	1	100%	25	25	150	0.00
54	*Xgwm437-7D*	1	1	100%	60	60	100	0.00

In the absence of the involved *Ae. tauschii* accession in each synthetic, the precise answers of genomic interactions cannot be obtained. From each group, it is apparent that this intergenomic phenomenon is present because the KB immunity of the durum wheat cultivars is differentially expressed in each group's derived synthetic combination. Those giving susceptible SHs indicate that the D genome has masked the expression of the durum genomes. This experiment allows the selection of SH parents for use in breeding and at the same time has opened up avenues that will be interesting to follow in the future to unravel how the D genome acts in different durum wheat backgrounds. For greater precision, it may be appropriate to purify each *Ae. tauschii* accession and then design a study that targets the purified accessions influence upon trait expression.

Analysis of cytoplasmic influence across durum and Ae. tauschii pairs for diversity and other traits.

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From the primary set of synthetics an experimental set was made consisting of crosses 'durum wheat cultivar / *Ae. tauschii* accession' and their reciprocal cross combinations, which comprised four combinations and eight entries. This subset was designed to study the inheritance of different genes and also to identify the effect of any cytoplasmic inheritance. The eight entries were screened for Karnal bunt and stripe rust resistance, phenotypically characterized, and analyzed with RAPD and SSR primerss for molecular characterization (Tables 35 and 36).

Table 35. The primary set of synthetics consisting of crosses 'durum wheat cultivar/*Ae. tauschii* accession' and their reciprocal cross combinations.

Group number	D-genome synthetic hexaploid entry	Total number of entries
1	1, 6	2
2	2, 5	2
3	3, 4	2
4	7, 8	2

Table 36. Pedigrees of the *Ae. tauschii* lines used in the crosses with durum wheats.

Entry number	Pedigree
1	*Ae. tauschii* (1026)/DOY 1
2	*Ae. tauschii* (1018)/DOY 1
3	*Ae. tauschii* (1029)/DVERD_2
4	DVERD_2/*Ae. tauschii* (1029)
5	DOY 1/*Ae. tauschii* (1018)
6	DOY 1/*Ae. tauschii* (1026)
7	DVERD_2/*Ae. tauschii* (1031)
8	*Ae. tauschii* (1031)/ DVERD_2

Stripe rust studies. Seedling screening showed that five of the eight (62.5%) were resistant (Table 37, p. 140). These genotypes were also screened for APR under field conditions at NARC; again, five of eight (62.5%) lines were resistant. Two of the eight genotypes (entries 4 and 5, 255) possess both seedling and adult-plant resistance. This germ plasm represents presence of major genes against stripe rust and can be exploited further in breeding programs.

Adult plant resistance involving susceptibility at seedling stage and resistance only at the adult-plant stage is an indicator of the presence of minor genes that are considered of great importance against rust diseases in acquiring durable resistance. Three genotyps (1, 2, and 3) out of eight (37.5%) had APR and are good candidates for providing durable resistance to wheat cultivars.

Karnal bunt studies. Karnal bunt (KB) evaluation was done by examining the grains following artificial inoculation. Grains from each entry were examined separately after hand threshing and rated on a scale was from 0 to 5 (see Fig. 2, p. 87). Only rating scale of 0 was considered acceptable and all others as susceptible. We found that five of the eight entries (62.5%), including lines 1, 2, 3, 5 and 8, were completely immune (Table 37).

Table 37. Phenotypic and disease characterization of D-genome synthetic hexaploids involved in crosses 'durum wheat cultivar/*Ae. tauschii* accession' and their reciprocals (see Table 36, p. 139 for pedigree information). FLOW = days-to-flowering, HT = plant height at maturity (cm), AWN = awn color (LB = light brown, AW = amery white, Y = yellow, and DB = dark brown), PMA = days to physiological maturity, TKW = 1,000-kernel weight (g), G/S = grains/spike, SL = spike length (cm), KB = Karnal bunt reaction (– = immune, + = susceptible), Yr (S) = reaction to stripe rust at the seedling stage, Yr (A) = reaction to stripe rust at the adult–plant stage (R = resistant, TR = trace resistant, MR = moderately resistant, MS = moderately susceptible, M = overlapping of MR–MS types, MSS = moderately susceptible to susceptible, S = susceptible, and TS = trace susceptible).

Entry	FLOW	HT	AWN	PMA	TKW	G/S	SL	KB	Yr (S)	Yr (A)
1	85	119	LB	117	32.5	15	13	-	78	10R
2	91	116	LB	123	36.6	13	13	-	67	5R
3	85	125	LB	119	35.3	12	10	-	89	10MR
4	76	95	LB	112	45.8	14	10	+	0	10MR
5	65	100	LB	105	37.5	15	12	-	0	10MR
6	70	123	LB	109	33.5	15	12	+	0	30S
7	75	102	LB	113	29.5	12	11	+	0	30MS
8	88	110	LB	122	34.9	15	12	-	0	90S

Molecular studies. ***Genetic diversity evaluation using random amplified polymorphic DNA (RAPD) primers.*** RAPD primers were used for genetic diversity evaluation of D-genome synthetic hexaploids. All 520 RAPD primers of Operon Series were screened and working primers were identified and applied to detect genetic polymorphism at DNA level. Samples that did not amplify were not included in the analysis.

Genetic analysis was performed only on the scorable bands. Every single band was considered as a single locus/allele. The loci were scored as present/absent. Bivariate data 1–0 were used to estimate genetic distances (GD). The unweighted pair group of arithmetic means (UPGMA) function was used to estimate the GD between the genotypes as follows: $GD_{xy} = 1 - d_{xy}/d_x + d_y - d_{xy}$, where GD_{xy} = genetic distance between two genotypes, d_{xy} = total number of common loci (bands) in two genotypes, d_x = total number of loci (bands) in genotype 1, and d_y = total number of loci (bands) in genotype 2.

Efficiency of primers to amplify the genotypes ranged from maximum from eight (OPD-13 and OPI-19) to one (OPA-7, OPA-11, OPA-13, OPB-3, OPB-12, OPB-13, OPB-16, OPC-14, OPE-4, OPG-7, OPH-12, OPI-17, OPM-9, OPM-12, OPQ-7, OPQ-8, OPR-11, OPS-5, OPS-7, OPT-14, OPT-15, OPW-16, OPW-17, and OPX-12) (Table 38, pp. 142-144). Scorable bands ranged from one (OPA-7, OPA-11, OPA-13, OPB-3, OPB-12, OPC-14, OPE-4, OPI-17, OPM-9, and OPV-14) to 33 (OPQ-9) (Table 38, pp. 141-143).

Genetic analysis of the population showed that the total number of loci was 419, of which only 217 were polymorphic; 51.78% polymorphism (Table 38, pp. 141-143). The range of scorable bands was from 500–3,000 bp.

Similarity matrix. A bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. In this experiment, the minimum value of 41.9% was found between genotypes 3 and 5 and the maximum value of 73.8% was present between genotypes 7 and 8.

Dendrogram interpretation. The genetic distances between genotypes were used to construct a dendrogram by UPGMA analysis for determining grouping of the lines on the basis of similarities and differences. In case of this experiment, the dendrogram shows one main cluster with two more sub-clusters A and B (Fig. 24, p. 144). Subcluster A has only two genotypes 5 and 6 and subcluster B is divided into two groups with three genotypes each.

Genetic diversity evaluation using simple sequence repeat (SSR) primers. SSR primers were used for genetic diversity evaluation of A-, B-, and D-genome synthetic hexaploids. All 275 SSR primers were applied to detect genetic poly-

Table 38. Molecular fingerprinting pattern by RAPDs in D-genome synthetic hexaploids (durum/D-genome accessions and reciprocal)

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
1	OPA-3	2	2	100%	2	3	1,000–1,500
2	OPA-7	1	1	100%	1	1	30,00
3	OPA-9	2	2	100%	3	3	1,500–2,000
4	OPA-11	1	1	100%	1	1	2,000
5	OPA-13	1	1	100%	1	1	1,500
6	OPB-3	1	1	100%	1	1	500
7	OPB-12	1	1	100%	1	1	1,000
8	OPB-13	3	0	0%	1	3	1,000–2,000
9	OPB-16	2	0	0%	1	2	250–500
10	OPC-10	3	1	33.33%	2	3	1,000–2,000
11	OPC-12	1	1	100%	5	5	3,000
12	OPC-13	1	1	100%	5	5	3,000
13	OPC-14	1	1	100%	1	1	3,000
14	OPC-15	1	1	100%	6	6	3,000
15	OPC-16	1	1	100%	6	6	3,000
16	OPC-17	1	1	100%	5	5	3,000
17	OPC-18	1	1	100%	7	7	3,000
18	OPC-19	1	1	100%	2	2	3,000
19	OPC-20	2	2	100%	7	8	1,000–3,000
20	OPD-1	2	2	100%	7	8	1,000–3,000
21	OPD-2	1	1	100%	5	5	3,000
22	OPD-3	2	2	100%	4	4	2,500–3,000
23	OPD-4	1	1	100%	3	3	3,000
24	OPD-5	1	1	100%	2	2	3,000
25	OPD-9	1	1	100%	5	5	3,000
26	OPD-10	1	1	100%	5	5	3,000
27	OPD-12	1	1	100%	7	7	3,000
28	OPD-13	1	1	100%	8	8	3,000
29	OPE-4	1	1	100%	1	1	3,000
30	OPE-5	1	1	100%	5	5	3,000
31	OPE-7	6	2	33.33%	3	14	500–2,000
32	OPE-11	3	0	0%	2	6	750–2,000
33	OPF-10	1	1	100%	5	5	3,000
34	OPF-11	1	1	100%	3	3	3,000
35	OPF-12	1	1	100%	3	3	3,000
36	OPF-13	1	1	100%	4	4	3,000
37	OPF-14	1	1	100%	3	3	3,000
38	OPF-16	1	1	100%	4	4	3,000
39	OPF-17	1	1	100%	5	5	3,000
40	OPG-2	4	1	25%	4	13	3000
41	OPG-7	8	0	0%	1	8	750–2,000
42	OPG-8	4	4	100%	6	16	750–2,000
43	OPG-13	5	5	100%	3	8	750–2,000
44	OPG-16	1	1	100%	6	6	500–1,500
45	OPG-17	1	1	100%	3	3	3,000
46	OPH-2	3	3	100%	6	10	3,000

Table 38. Molecular fingerprinting pattern by RAPDs in D-genome synthetic hexaploids (durum/D-genome accessions and reciprocal)

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
47	OPH-3	2	2	100%	4	4	2,500–30,00
48	OPH-4	3	1	33.33%	2	4	1,000–3,000
49	OPH-12	3	0	0%	1	3	500–1,000
50	OPH-15	1	1	100%	2	2	750–1,500
51	OPI-13	1	1	100%	2	2	3,000
52	OPI-15	6	3	50%	4	12	1,000
53	OPI-17	1	1	100%	1	1	750–2,000
54	OPI-18	1	1	100%	2	2	1,000
55	OPI-19	10	7	70%	8	32	750–3,000
56	OPI-20	1	1	100%	3	3	3,000
57	OPJ-5	1	1	100%	4	4	3,000
58	OPJ-7	1	1	100%	4	4	3,000
59	OPJ-8	1	1	100%	4	4	3,000
60	OPJ-20	3	0	0%	2	6	750–1,500
61	OPK-1	1	1	100%	4	4	3,000
62	OPK-2	1	1	100%	6	6	3,000
63	OPK-3	1	1	100%	5	5	3,000
64	OPK-4	1	1	100%	6	6	3,000
65	OPK-16	1	1	100%	2	2	3,000
66	OPK-17	3	0	0%	2	6	250–500
67	OPL-4	1	1	100%	2	2	1,000
68	OPL-11	6	3	50%	2	10	250–1,000
69	OPL-12	7	5	71.42%	5	25	250–1,500
70	OPL-15	7	2	28.57%	5	32	250–1,500
71	OPL-17	6	0	0%	3	12	500–1,500
72	OPL-18	5	3	60%	3	10	1,000–2,000
73	OPL-20	8	4	50%	5	22	250–2,000
74	OPM-1	5	3	60%	6	23	500–1,500
75	OPM-2	6	6	100%	6	23	250–1,500
76	OPM-9	1	1	100%	1	1	750–1,500
77	OPM-10	4	3	75%	3	11	1,500
78	OPM-11	1	1	100%	3	3	1,500
79	OPM-12	5	0	0%	1	5	750–1,500
80	OPM-13	7	5	71.42%	4	10	250–1,500
81	OPM-15	5	2	40%	2	8	250–1,500
82	OPM-16	6	3	50%	3	12	500–1,500
83	OPM-19	1	1	100%	3	3	3,000
84	OPN-19	4	2	50%	3	7	500–1,500
85	OPN-20	6	1	16.66%	3	16	500–1,500
86	OPP-15	4	2	50%	2	7	750–2,000
87	OPP-16	6	3	50%	6	24	500–2,500
88	OPP-17	4	0	0%	2	6	750–1,500
89	OPQ-3	2	0	0%	1	2	1,000–2,000
90	OPQ-7	2	0	0%	1	2	750–1,500
91	OPQ-8	3	3	100%	6	10	250–1,000
92	OPQ-9	8	1	12.5%	5	33	250–1,500

Table 38. Molecular fingerprinting pattern by RAPDs in D-genome synthetic hexaploids (durum/D-genome accessions and reciprocal)

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)
93	OPQ-10	6	0	0%	2	10	250–1,500
94	OPQ-11	4	1	25%	6	23	250–1,500
95	OPQ-12	4	2	50%	5	12	250–2,000
96	OPQ-13	8	3	37.5%	5	30	250–1,500
97	OPQ-14	9	4	44.44%	3	25	500–2,000
98	OPQ-18	4	0	0%	2	8	750–1500
99	OPR-1	2	2	100%	3	4	250–750
100	OPR-2	5	5	100%	3	9	250–1,500
101	OPR-8	1	1	100%	3	3	500
102	OPR-11	2	0	0%	1	2	500–750
103	OPR-12	3	3	100%	4	8	500–1,000
104	OPR-16	5	3	60%	3	6	250–1,500
105	OPR-17	4	4	100%	6	17	250–1,000
106	OPR-19	8	8	100%	5	18	250–2,000
107	OPR-20	3	3	100%	5	5	500–1,000
108	OPS-5	2	0	0%	1	2	1,000
109	OPS-7	5	0	0%	1	5	500–2,000
110	OPT-10	3	0	0%	3	9	750–1,500
111	OPT-12	2	2	100%	3	6	1,000–1,500
112	OPT-13	3	3	100%	3	6	500–1,500
113	OPT-14	4	0	0%	1	4	750–1,500
114	OPT-15	4	0	0%	1	4	1,000–2,000
115	OPU-13	2	2	100%	5	8	1,000–1,500
116	OPU-18	3	0	0%	4	12	500–2,000
117	OPU-20	3	3	100%	6	16	500–1500
118	OPV-3	6	3	50%	3	13	750–2,000
119	OPV-5	2	0	0%	3	6	750–2,000
120	OPV-8	2	2	100%	3	4	500–750
121	OPV-14	1	1	100%	1	1	500–750
122	OPV-15	2	0	0%	3	6	500–750
123	OPW-11	4	1	25%	2	7	250–1,000
124	OPW-12	4	2	50%	3	8	250–1,000
125	OPW-13	5	4	80%	4	13	500–2,500
126	OPW-16	4	0	0%	1	4	500–1,500
127	OPW-17	3	0	0%	1	3	500–3,000
128	OPW-18	3	3	100%	4	5	500–3,000
129	OPW-19	4	1	25%	3	6	500–1,500
130	OPX-1	3	0	0%	2	6	1,000–1,500
131	OPX-4	6	3	50%	4	15	250–2,000
132	OPX-9	4	2	50%	5	17	750–2,000
133	OPX-11	3	3	100%	6	12	750–1,500
134	OPX-12	2	0	0%	1	2	500–1,500
135	OPX-13	5	0	0%	4	18	250–1,500
136	OPX-14	1	1	100%	2	2	2,000
137	OPY-7	3	3	100%	3	6	750–2,000
138	OPY-8	4	0	0%	3	12	500–2,000

morphism at DNA level. Samples that did not amplify were not included in the analysis. Genetic analysis was similar to that for the RAPD primers.

Primer efficiency to amplify the genotypes ranged from a maximum of eight (82 primers in total; 41 in A, 30 in B, and 11 in D) to one (*Xgwm445-2A*, *Xgwm512-2A*, *Xgwm160-4A*, *Xgwm459-6A*, *Xgwm210-2B*, *Xgwm325-6D*, and *Xgwm469-6D*) in this experiment (Table 39, pp. 145-149). Scorable bands ranged from one (*Xgwm445-2A*, *Xgwm459-6A*, *Xgwm325-6D*, and *Xgwm469-6D*) to 33 (*Xgwm63-7A*) (Table 39, pp. 144-148).

Genetic analysis of the popluation showed that the total number of alleles was 502, of which only 399 were polymorphic; 79.48% (Table 39, pp. 144-148). The range of scorable bands was from 50–1,000 bp.

Similarity matrix. A bivariate analysis was conducted to generate a similarity matrix and dendrogram using Nei and Li's coefficient to estimate genetic diversity. A minimum value of 18.7% was found between genotypes

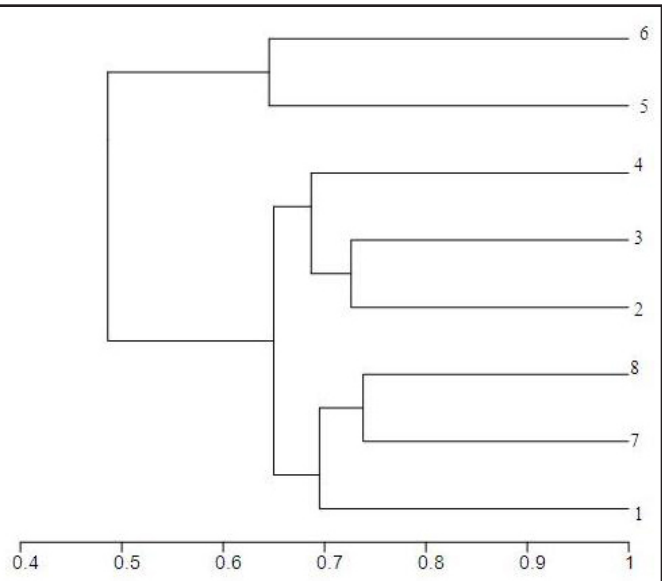

Fig. 24. SSR-based cluster formation of eight synthetic hexaploid genotypes of the same durum wheat cultivar with different *Aegilops tauschii* and the reciprocal crosses.

Table 39. Molecular fingerprinting pattern by SSRs in the D-genome synthetic hexaploids of 'durum wheat/D-genome accessions' and their reciprocal crosses.

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
1	*Xgwm33-1A*	4	4	100%	8	17	50	0.66
2	*Xgwm99-1A*	5	3	60%	8	18	50–150	0.64
3	*Xgwm135-1A*	3	1	33.33%	8	17	100–150	0.55
4	*Xgwm164-1A*	4	2	50%	7	14	100–250	0.57
5	*Xgwm357-1A*	1	1	100%	8	8	100	0.00
6	*Xgwm497-1A*	2	0	0%	8	16	100–150	0.50
7	*Xgwm666-1A*	2	2	100%	4	4	100–150	0.37
8	*Xgwm10-2A*	1	1	100%	3	8	150	0.00
9	*Xgwm47.1-2A*	2	2	100%	7	7	50–200	0.40
10	*Xgwm47.2-2A*	1	1	100%	4	4	50–200	0.00
11	*Xgwm71.1-2A*	3	1	33.33%	7	16	50–150	0.64
12	*Xgwm71.2-2A*	3	1	33.33%	7	20	50–150	0.67
13	*Xgwm95-2A*	2	2	100%	8	10	50–150	0.50
14	*Xgwm122-2A*	2	2	100%	6	6	100–200	0.44
15	*Xgwm249-2A*	2	2	100%	7	12	100–150	0.45
16	*Xgwm265-2A*	4	2	50%	8	22	50–150	0.68
17	*Xgwm275-2A*	2	2	100%	8	9	100–150	0.11
18	*Xgwm294-2A*	1	1	100%	8	8	150	0.00
19	*Xgwm311-2A*	2	2	100%	6	11	100–150	0.48
20	*Xgwm312-2A*	2	2	100%	8	13	50–250	0.42
21	*Xgwm328-2A*	1	1	100%	8	8	100	0.00
22	*Xgwm339-2A*	2	2	100%	6	6	150–200	0.27
23	*Xgwm356-2A*	1	1	100%	8	8	150	0.00
24	*Xgwm359-2A*	1	1	100%	8	8	150–200	0.11
25	*Xgwm382-2A*	4	0	0%	8	32	50–200	0.75

Table 39. Molecular fingerprinting pattern by SSRs in the D-genome synthetic hexaploids of 'durum wheat/D-genome accessions' and their reciprocal crosses.

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
26	*Xgwm425-2A*	3	0	0%	8	24	50–150	0.67
27	*Xgwm445-2A*	1	1	100%	1	1	200	0.37
28	*Xgwm473-2A*	1	1	100%	3	3	200	0.00
29	*Xgwm497-2A*	2	2	100%	7	7	200–250	0.24
30	*Xgwm512-2A*	1	1	100%	1	1	150	0.00
31	*Xgwm515-2A*	3	0	0%	3	24	50–150	0.67
32	*Xgwm558-2A*	4	2	50%	7	16	50–150	0.64
33	*Xgwm614-2A*	2	2	100%	8	12	50–150	0.37
34	*Xgwm2-3A*	1	1	100%	4	4	100	0.00
35	*Xgwm5-3A*	3	3	100%	8	11	100–500	0.41
36	*Xgwm32-3A*	2	2	100%	6	9	150–200	0.37
37	*Xgwm155-3A*	2	2	100%	8	12	100–250	0.37
38	*Xgwm162-3A*	2	2	100%	3	3	50–200	0.44
39	*Xgwm391-3A*	3	3	100%	7	13	50–800	0.65
40	*Xgwm462-3A*	1	1	100%	6	6	100–250	0.47
41	*Xgwm666.2-3A*	2	2	100%	4	4	50–100	0.37
42	*Xgwm4-4A*	1	1	100%	8	8	250	0.00
43	*Xgwm160-4A*	1	1	100%	1	7	200	0.33
44	*Xgwm397-4A*	1	1	100%	8	8	200	0.00
45	*Xgwm601-4A*	3	3	100%	7	15	50–200	0.58
46	*Xgwm610-4A*	2	2	100%	8	9	50–200	0.42
47	*Xgwm637-4A*	2	2	100%	8	15	500–800	0.49
48	*Xgwm126-5A*	3	3	100%	8	20	600–1000	0.64
49	*Xgwm129-5A*	1	1	100%	2	2	900	0.00
50	*Xgwm154-5A*	2	0	0%	8	16	50–100	0.50
51	*Xgwm156-5A*	2	2	100%	8	10	150–300	0.21
52	*Xgwm179-5A*	2	2	100%	8	10	150	0.21
53	*Xgwm186-5A*	3	3	100%	5	8	50–700	0.62
54	*Xgwm205-5A*	2	2	100%	5	5	50–150	0.32
55	*Xgwm291-5A*	1	1	100%	4	4	150	0.00
56	*Xgwm293-5A*	1	1	100%	8	8	200	0.00
57	*Xgwm304-5A*	1	1	100%	4	4	200	0.00
58	*Xgwm410-5A*	4	0	0%	7	28	200–300	0.75
59	*Xgwm415-5A*	1	1	100%	8	8	100	0.00
60	*Xgwm617-5A*	5	5	100%	8	28	50–800	0.80
61	*Xgwm639-5A*	2	0	0%	6	12	150	0.50
62	*Xgwm666-5A*	2	0	0%	8	16	50–100	0.50
63	*Xgwm169-6A*	2	2	100%	8	13	50–200	0.42
64	*Xgwm334-6A*	1	1	100%	3	3	150	0.00
65	*Xgwm459-6A*	1	1	100%	1	1	50	0.00
66	*Xgwm494-6A*	2	2	100%	8	10	50–200	0.21
67	*Xgwm570-6A*	1	1	100%	8	8	100	0.00
68	*Xgwm617-6A*	4	2	50%	8	22	50–400	0.66
69	*Xgwm60-7A*	2	0	0%	2	4	150–200	0.67
70	*Xgwm63-7A*	5	2	40%	8	33	300–1000	0.67
71	*Xgwm130-7A*	3	3	100%	8	11	50–100	0.53

Table 39. Molecular fingerprinting pattern by SSRs in the D-genome synthetic hexaploids of 'durum wheat/D-genome accessions' and their reciprocal crosses.

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
72	*Xgwm233-7A*	1	1	100%	8	8	50	0.00
73	*Xgwm276-7A*	3	3	100%	8	17	50–100	0.62
74	*Xgwm332-7A*	3	1	33.33%	7	20	50–400	0.66
75	*Xgwm471-7A*	2	2	100%	8	8	100–150	0.46
76	*Xgwm635-7A*	1	1	100%	8	8	100	0.00
77	*Xgwm666-7A*	3	1	33.33%	8	23	50–300	0.66
78	*Xgwm11-1B*	2	2	100%	5	6	50–250	0.18
79	*Xgwm18-1B*	4	4	100%	8	14	50–300	0.58
80	*Xgwm33-1B*	3	3	100%	8	15	50–100	0.53
81	*Xgwm107-1B*	3	1	33.33%	6	16	200–300	0.65
82	*Xgwm124-1B*	3	3	100%	8	20	50–1000	0.65
83	*Xgwm131-1B*	3	1	33.33%	8	21	100–300	0.65
84	*Xgwm140-1B*	2	2	100%	5	5	50–400	0.32
85	*Xgwm153-1B*	4	4	100%	8	18	50–600	0.66
86	*Xgwm259-1B*	1	1	100%	2	2	100	0.00
87	*Xgwm264-1B*	3	1	33.33%	8	20	50–200	0.64
88	*Xgwm268-1B*	2	2	100%	2	2	200–250	0.50
89	*Xgwm274-1B*	2	2	100%	3	4	150–800	0.27
90	*Xgwm413-1B*	1	1	100%	3	3	100	0.00
91	*Xgwm498-1B*	4	4	100%	4	10	50–150	0.67
92	*Xgwm550-1B*	4	2	50%	4	8	150–250	0.68
93	*Xgwm582-1B*	2	2	100%	6	7	150–1000	0.48
94	*Xgwm16-2B*	3	3	100%	7	13	50–200	0.53
95	*Xgwm47-2B*	2	2	100%	8	11	50–200	0.29
96	*Xgwm55.1-2B*	3	3	100%	8	20	50–150	0.64
97	*Xgwm55.2-2B*	1	1	100%	6	6	100	0.00
98	*Xgwm129-2B*	2	2	100%	4	4	50–250	0.37
99	*Xgwm210-2B*	3	0	0%	1	3	50–150	0.66
100	*Xgwm257-2B*	3	3	100%	5	6	50–150	0.61
101	*Xgwm319-2B*	3	1	33.33%	3	6	50–200	0.61
102	*Xgwm374-2B*	3	3	100%	8	17	150–500	0.62
103	*Xgwm382-2B*	3	3	100%	8	11	50–250	0.75
104	*Xgwm388-2B*	2	2	100%	8	15	50–200	0.49
105	*Xgwm429-2B*	1	1	100%	5	5	250	0.00
106	*Xgwm501-2B*	2	2	100%	8	8	50–200	0.37
107	*Xgwm526-2B*	1	1	100%	3	3	150	0.00
108	*Xgwm630-2B*	3	1	33.33%	7	13	50–200	0.64
109	*Xgwm77-3B*	2	0	0%	7	14	50–150	0.50
110	*Xgwm112-3B*	3	1	33.33%	5	12	50–300	0.65
111	*Xgwm114-3B*	2	2	100%	7	11	50–150	0.48
112	*Xgwm131-3B*	3	3	100%	7	20	100–300	0.66
113	*Xgwm181-3B*	2	2	100%	7	8	50–100	0.45
114	*Xgwm247-3B*	2	2	100%	4	4	50–150	0.37
115	*Xgwm264-3B*	4	2	50%	7	17	50–500	0.74
116	*Xgwm284-3B*	2	2	100%	7	8	50–500	0.33
117	*Xgwm299-3B*	4	2	50%	4	7	50–300	0.67

Table 39. Molecular fingerprinting pattern by SSRs in the D-genome synthetic hexaploids of 'durum wheat/D-genome accessions' and their reciprocal crosses.

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
118	*Xgwm340-3B*	4	4	100%	7	14	50–500	0.71
119	*Xgwm376-3B*	3	3	100%	7	11	150–400	0.56
120	*Xgwm389-3B*	2	2	100%	8	8	50–150	0.37
121	Xgwm493-3B	3	3	100%	7	10	50–200	0.64
122	Xgwm547-3B	2	2	100%	8	9	50–200	0.30
123	Xgwm566-3B	4	4	100%	7	12	50–300	0.64
124	Xgwm6-4B	3	3	100%	6	15	50–250	0.64
125	Xgwm66-4B	4	1	25%	8	18	50–300	0.69
126	Xgwm113-4B	1	1	100%	5	5	50	0.00
127	Xgwm149-4B	1	1	100%	5	5	50	0.00
128	Xgwm165-4B	4	1	25%	4	9	150–500	0.64
129	Xgwm251-4B	4	4	100%	7	9	50–250	0.65
130	Xgwm368-4B	1	1	100%	8	8	50	0.00
131	Xgwm495-4B	2	2	100%	8	8	50–150	0.37
132	Xgwm513-4B	2	2	100%	7	10	50–150	0.33
133	Xgwm538-4B	2	2	100%	8	14	50–150	0.50
134	Xgwm66-5B	5	5	100%	8	28	50–300	0.78
135	Xgwm68-5B	2	2	100%	8	11	50	0.49
136	Xgwm159-5B	2	2	100%	8	9	50–150	0.30
137	Xgwm191-5B	4	4	100%	8	18	50–300	0.70
138	Xgwm234-5B	2	2	100%	5	5	150	0.48
139	Xgwm335-5B	3	3	100%	5	6	50–150	0.46
140	Xgwm371-5B	9	7	77.77%	6	31	50–700	0.87
141	Xgwm499-5B	2	2	100%	8	13	50–200	0.49
142	Xgwm408-5B	2	0	0%	5	10	150–200	0.50
143	Xgwm540-5B	3	3	100%	7	9	50–250	0.25
144	Xgwm544-5B	3	3	100%	4	8	50–150	0.64
145	Xgwm554-5B	2	0	0%	8	16	50–200	0.50
146	Xgwm604-5B	2	2	100%	5	7	100–200	0.32
147	Xgwm639-5B	2	3	100%	4	7	50–400	0.46
148	Xgwm70-6B	4	2	50%	8	12	50–100	0.37
149	Xgwm88-6B	3	3	100%	8	12	50–150	0.40
150	Xgwm132-6B	4	4	100%	8	19	50–300	0.72
151	Xgwm191-6B	2	2	100%	7	11	100–800	0.40
152	Xgwm193-6B	1	1	100%	7	7	100	0.00
153	Xgwm219-6B	4	1	25%	8	26	50–900	0.73
154	Xgwm361-6B	3	3	100%	8	20	50–250	0.64
155	Xgwm508-6B	4	2	50%	7	17	50–200	0.74
156	Xgwm518-6B	5	5	100%	5	14	50–400	0.75
157	Xgwm613-6B	1	1	100%	6	6	150	0.00
158	Xgwm644-6B	2	2	100%	2	3	150–900	0.37
159	Xgwm43-7B	6	1	16.66%	5	10	150–1000	0.56
160	Xgwm46-7B	1	1	100%	4	4	150	0.00
161	Xgwm68-7B	1	1	100%	5	5	100	0.00
162	Xgwm146-7B	2	2	100%	8	13	50–150	0.42
163	Xgwm297-7B	4	4	100%	6	14	50–250	0.70

Table 39. Molecular fingerprinting pattern by SSRs in the D-genome synthetic hexaploids of 'durum wheat/D-genome accessions' and their reciprocal crosses.

Primer number	Primer	Total loci	Polymorphic loci	% polymorphism	Samples amplified	Scorable bands	Amplification product range (bp)	PIC
164	*Xgwm302-7B*	1	1	100%	5	5	50–250	0.00
165	*Xgwm333-7B*	2	2	100%	4	5	200	0.21
166	*Xgwm344-7B*	1	1	100%	3	3	150	0.00
167	*Xgwm400-7B*	1	1	100%	3	3	150	0.00
168	*Xgwm537-7B*	2	2	100%	3	3	50–200	0.44
169	*Xgwm577-7B*	3	1	33.33%	5	13	50–250	0.65
170	*Xgwm611-7B*	2	2	100%	3	3	50–200	0.44
171	*Xgwm644-7B*	2	2	100%	3	5	200–700	0.44
172	*Xgwm33-1D*	3	1	33.33%	8	23	50–100	0.64
173	*Xgwm232-1D*	2	2	100%	4	4	50–200	0.50
174	*Xgwm458-1D*	2	2	100%	8	9	50–100	0.49
175	*Xgwm642-1D*	2	2	100%	8	14	50–100	0.46
176	*Xgwm30-2D*	2	2	100%	3	4	150–700	0.00
177	*Xgwm102-2D*	2	2	100%	8	8	150–200	0.50
178	*Xgwm157-2D*	2	2	100%	5	5	150–200	0.32
179	*Xgwm210-2D*	3	3	100%	6	8	50–150	0.50
180	*Xgwm249-2D*	6	6	100%	6	18	50–1000	0.79
181	*Xgwm261-2D*	4	4	100%	8	21	50–200	0.72
182	*Xgwm296-2D*	1	1	100%	8	8	200	0.00
183	*Xgwm320-2D*	1	1	100%	2	2	100	0.00
184	*Xgwm455-2D*	2	2	100%	6	8	200–400	0.44
185	*Xgwm515-2D*	3	3	100%	8	17	50–200	0.62
186	*Xgwm539-2D*	4	2	50%	8	21	50–100	0.71
187	*Xgwm608-2D*	2	2	100%	5	5	150	0.48
188	*Xgwm2-3D*	2	2	100%	8	9	50–250	0.11
189	*Xgwm52-3D*	1	1	100%	4	4	100	0.00
190	*Xgwm71-3D*	2	2	100%	3	5	150–300	0.44
191	*Xgwm497-3D*	1	1	100%	6	6	100	0.00
192	*Xgwm645-3D*	2	2	100%	5	6	100–150	0.18
193	*Xgwm664-3D*	2	2	100%	6	6	150	0.18
194	*Xgwm194-4D*	4	2	50%	5	7	50–800	0.73
195	*Xgwm609-4D*	2	2	100%	5	8	50–1000	0.50
196	*Xgwm174-5D*	3	3	100%	7	11	50–150	0.65
197	*Xgwm292-5D*	1	1	100%	4	4	150	0.00
198	*Xgwm358-5D*	6	6	100%	7	22	150–900	0.79
199	*Xgwm565-5D*	1	1	100%	5	5	150	0.00
200	*Xgwm583-5D*	4	2	50%	8	24	50–150	0.71
201	*Xgwm654-5D*	3	3	100%	7	10	50–200	0.64
202	*Xgwm325-6D*	1	1	100%	1	1	100	0.00
203	*Xgwm469-6D*	1	1	100%	1	1	100	0.00
204	*Xgwm37-7D*	4	4	100%	8	17	50–250	0.63
205	*Xgwm44-7D*	2	2	100%	4	6	50–200	0.37
206	*Xgwm111-7D*	1	1	100%	3	3	100	0.00
207	*Xgwm295-7D*	4	4	100%	7	14	50–200	0.69

3 and 4 and the maximum value of 68.4% was present between genotypes 2 and 7. Only in one cluster so 1 and 2 represent the most diverse lines (Fig. 25); genotype 1 forms a group with 2, 3 with 6, 4 with 5 and 7 with 8.

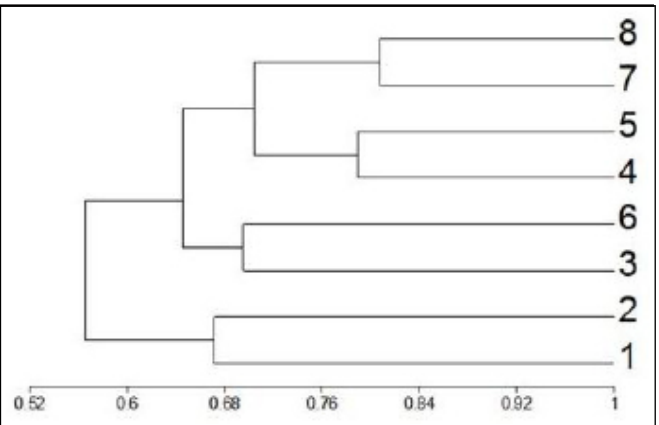

Fig. 25. SSR-based cluster formation of eight synthetic hexaploid genotypes of (same durum wheat cultivar with different *Aegilops tauschii* and the reciprocal crosses).

'Durum wheat / *Ae. tauschii*' and the reciprocal cross combinations. Four durum wheat cultivars were involved with four alien accessions; the pairs were entries 6 and 1, 5 and 2, 4 and 3, and 7 and 8. Individual pairs were structured around the durum wheat cultivar as the female parent and the *Ae. tauschii* accession as the male parent to allow cytoplasmic influences to be analyzed across each pair for diversity and other observed traits.

The overall comparison of each set was based upon eight traits; five phentypic (days-to-flowering, days to physiological maturity, 1,000-kernel weight, number of grains/spike, and spike length) and three biotic stress (Karnal bunt and seedling and adult-plant stripe rust resistance. For combination 6 and 1. no remarkable differences were seen phenotypically even though a cytoplasmic difference was introduced into the synthetic pair. Entry 1 was immune to KB but entry 6 was susceptible. Entry 1 was seedling susceptible to stripe rust, but 6 was immune. Entry 1 had APR, but 6 was susceptible. These differences indicate differential trait response around genomic interactions in which the cytoplasm may be a factor. The susceptibility of entry 6 suggests that the durum wheat attribute is suppressed by the *Ae. tauschii* parent. In entry 1, the KB resistance appears to be a consequence of expression of the durum wheat genomes and the inability of the D genome to mask the resistance effect or also contribute towards the resistance in a manner not well identified. For the 5 and 2 combination, entry 2, with the alien cytoplasm flowered 26 days later and days to physiological maturity (18 day delay); clear cytoplasmic effects. The 1,000-kernel weight, grains/spike, and spike length did not differ within the two categories. Both entries were KB resistant. Stripe rust resistance was seen in entry 5 at the seedling and adult-plant stage, but in entry 2, only APR was exhibited.

These trends were scattered across the other two sets that with entries 4 and 3 and, 7 and 8 (Table 37, p. 140). Remarkable in these sets, and similar to set 6 and 1, was KB resistance. Field resistance of the durum wheats is the normal expectation in synthetics derived from their parentage. However, when resistance is suppressed and the SH becomes susceptible is a clear indication to suggest that the expression is suppressed, which was seen in entries 6, 4, and 7. Their reciprocal crosses in entries 1, 3, and 8 are all KB resistant, suggesting that trait expression with the alien diploid parent as the female is preferred for breeding. Across all the eight combinations, lines 1, 5, and 6 are suitable for phenotypic attributes and KB and sripe rust resistance. Entry 1 was the most diverse based upon RAPD and SSR analysis and is a good candidate for breeding.

It would be logical to expect the diversity profiles to place both combinations of each set in close proximity. The trends do not seem to follow this perfectly. Sets 7 and 8 and 4 and 3 are linked as expected according to RAPD analysis. Entries 6 and 1 form a set that is the most diverse, and entries 5 and 2 fell in different clusters. Based upon SSR analysis, entries 7 and 8 were linked, but the other three sets were unrelated. In 3 and 4, entry 3 was more diverse, entry 1 was more diverse than entry 6, and entry 2 was more diverse than 5.

The question now arises as to why do reciprocal combinations show varied trends. A plausible answer may be due to structural genomic modifications that are ongoing during the maintenance of the individual SH entries. This implies that when the SH is first produced (C_0), its molecular profile would provide the relationship attribute similarity within its partners; e.g., 6 and 1. After generation advance, structural changes occur and consequently variations emerge to give the trend that is seen and which separates the set partners from each other. If the SH set variation occurs at the C_0 stage, then the variation is undoubtedly from the *Ae. tauschii* utilized in SH production is a population seed and not individual purified single accession seed used to develop the SHs. Variation in individual seedlings of an accession for traits have offered evidence that variation within an accession is prevalent and for precision experimentation, seed from individual alien seedlings must be obtained, utilizedc and used for comparative deductions.

The practicality of transferring alien genes to wheat.

Alvina Gul Kazi, Rabia Sultan, Awais Rasheed, Farrukh Bashir, Hadi Bux, Arsalan Ahmed, and Abdul Mujeeb-Kazi.

Diploid and polyploid species with nonhomologous genomes to those of wheat are included in the tertiary gene pool. Alien genetic transfers require complex cytogenetic manipulation protocols that facilitate homoeologous exchanges. Irradiation or tissue culture is another option when homoeologous exchanges are not possible. Protocols promoting homoeologous exchanges are preferred, because the introduced alien segments would be placed in the best location in the recipient chromosomes. Wheat–alien chromosome translocations are the general output of irradiation or tissue/callus culture and are less favored because compensating exchange products are rarely obtained. Hybridization requires embryo rescue and the frequency of success is low with practical agricultural output being time consuming unless modified approaches are incorporated. In essence, the choice of the parental alien species is crucial for successful wheat improvement programs that require several prerequisites beyond just producing novel hybrid combinations.

Genes can be transferred from primary and secondary gene pools to *T. aestivum* directly by hybridization, back crossing, and selection via chromosome recombination. From the tertiary gene pool, genetic transfers cannot be made easily by recombination and to obtain practical end-products, some transfer prerequisites include hybrid production, embryo rescue, plant regeneration, cytological diagnostics, breeding methodology, and stress screening, culminating in stability of the advanced derivatives as contributed by homozygosity. Wide hybridization, including both interspecific and intergeneric hybridization, is the first step to introduce alien variation and transfer desirable traits from wild species into cultivated wheat. The strategies encompass diversity resources across all gene pools.

Translocations have contributed significantly to disease resistance transfers with the major impact from the T1A·1R and T1B·1R translocations (presumably greater for T1B·1R because it influences *T. aestvum* cultivar yields). For the transfer of whole chromosome arms, the centric breakage-fusion mechanism of univalent at meiotic metaphase can be exploited. Univalents have a tendency to break at the centromere, followed by fusion of the broken arms. When an alien target chromosome and its homoeologous wheat chromosome are simultaneously univalent, compensating, whole-arm translocations can be recovered at fairly high frequencies. The first stable cytological transfer of a T1BL·1RS translocation from the bread wheat was from th eadvanced line Veery to the durum wheat Cando. The noncompensating translocations are genetically unbalanced and lead to reduced agronomic performance, whereas all wheat–alien translocations produced by induced homoeologous recombination are of compensating type and thus have greater agronomic potential.

The two categories of investigations on translocations are

1. Tapping existing global resources. Following the success of the T1BL·1RS spontaneous translocation in bread wheat, some such wheats were utilized to have a well documented base in Pakistan. In addition, a thrust was made to transfer some translocations globally available into elite bread wheat background with wide adaptation. The translocations selected include TT1AL·1RS, T5AL·5RS, T4BS·4BL-2R, T7DS·7DL-7Ag, and some Thatcher-based leaf rust stocks that include translocations carrying the *Lr* genes. The limited backcross route was used and germ plasm in each category advanced to BC_2. Translocation validation was aided by Giemsa C-banding.
2. New translocations focussed on the 'bread wheat/*Th. bessarabicum*' amphiploid where manipulating the *Ph* genetic control was exploited. This collaborative effort is still underway with partners in CIMMYT, Mexico. Eight translocation lines were produced that are monosomic or disomic euploid for a wheat–*Th. bessarabicum* translocation product. Our focus in Pakistan has been on the cytological validation of the new translocation lines, their phenotypic evaluation, and seed increase for subsequent biotic/abiotic stress analyses.

Exploiting translocations in wheat improvement. Translocations fall into two categories for utilization in wheat improvement and these are separated according to their origin.

1. Old translocations that are predominantly in genetic backgrounds that prevent their global exploitation readily, because the wheat involved is not widely adapted. Very few old translocation stocks are in extensive use. Thus, there is a need to transfer the ill-adapted translocations into good agronomic wheat backgrounds. Of the translocations that have been utilized here, some in extensive use and others are not in general use: T1AL·1RS, T5AL·5RS, T1BL·1RS, T4BS·4BL-2R, T7DS·7DL-7Ag, T2BS·2RL, T4BS·4BL-5RL, T6BS·6RL, and T2AS-2RS·2RL.

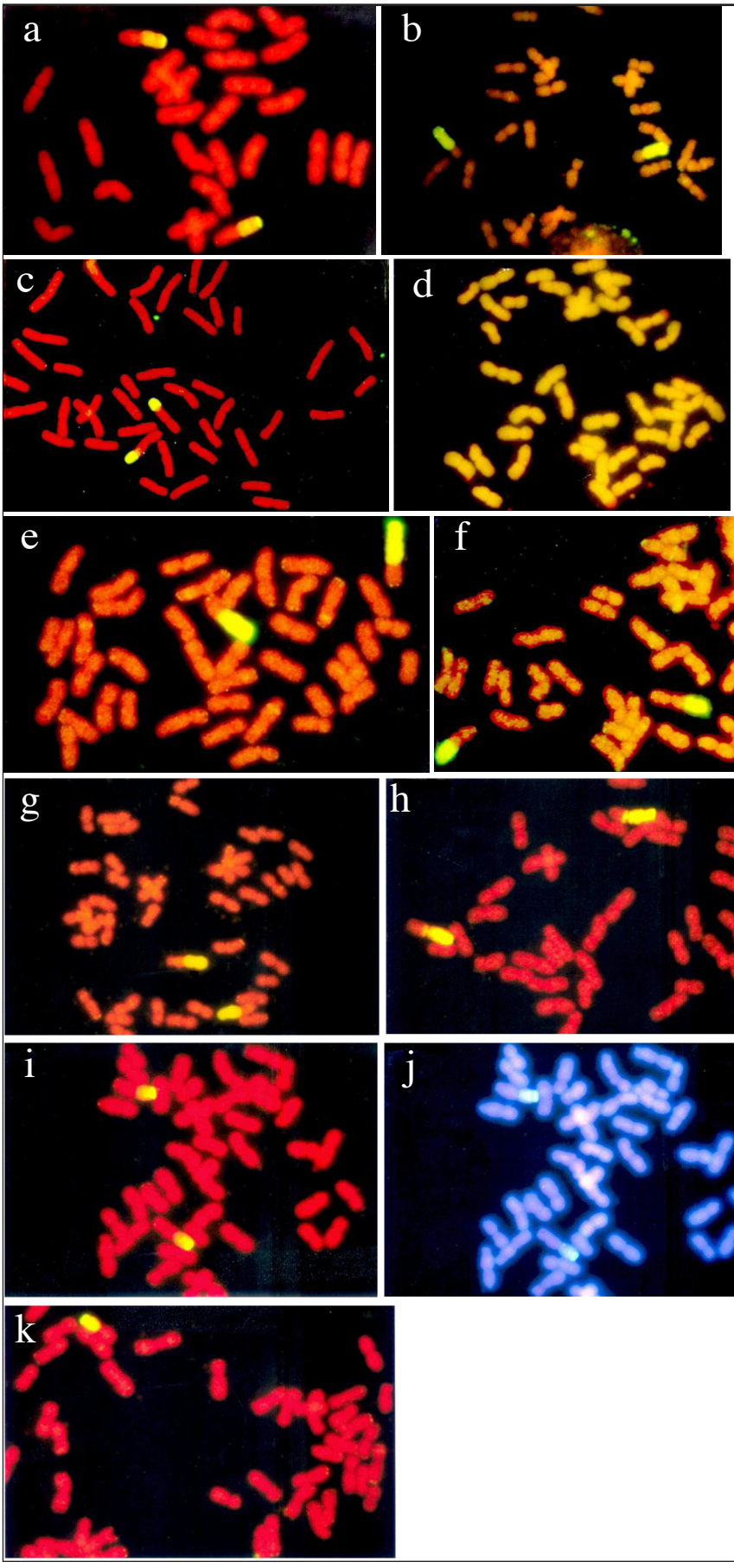

Fig. 26. Fluorescent *in situ* hybridization (wheat DNA and E^b DNA for blocking) demonstrating the usage of old wheat–alien chromosome translocations incorporated into nationally adapted, elite bread wheat cultivars and/or stocks: (a) T1AL·1RS (2n=4x=28) translocation in durum wheat, (b) T5AS·5RL (2n=4x=28) translocation in durum wheat, (c) T4BS·4BL-2R translocation in bread wheat, (d) T7DS·7DL-7Ag translocation in bread wheat, (e)T2BS·2RL translocation in bread wheat, (f) T4BS·4BL-6RL translocation in bread wheat, (g) T6BS·6RL translocation in bread wheat, (h) T2AS-2RS·2RL translocation in bread wheat, (i) T1BL·1RS translocation in bread wheat, (j) T1BL·1RS translocation in bread wheat (DAPI), and (k) T1AL·1RS (heterozygous) translocation in bread wheat.

Their status after backcrossing to elite wheats either durum or bread wheat has yielded advanced derivatives of which adequate seed amounts are available for exploitation in breeding for various stress factors after characterization. Details of the translocations transferred following reciprocal backcrossing to commercial wheats are elucidated (Figs. 26, p. 151; T1AL·1RS (a) and T5AL·5RS in durum wheat (b), T4BS·4BL-2R (c) and T7DS·7DL-7Ag in bread wheat (d), T2BS·2RL in bread wheat (e), T4BS·4BL-4RL in bread wheat (f), T6BS·6RL in bread wheat (g), T2AS-2RS·2RL in bread wheat (h), T1BL·1RS in bread wheat (i and j; two filters), and T1AL·1RS in bread wheat (a heterozygote (k) from which a homozygous form was obtained).

2. New Translocations. By utilizing the recessive *ph1b* genetic stock the CS–*Th. bessarabicum* amphiploid with the *Ph1bPh1b* locus was manipulated cytogenetically to set up a wheat–alien recombination system that would induce homoeologous translocations.

The generation of new translocations is schematically shown (Fig. 27). The protocol is elucidated in the steps described below accompanied by characterization. The use of the molecular diagnostics identifies the selfed BC_1 derivatives that are *ph1bph1b* homozygous (Fig. 28a, p. 153). These plants are then selfed to maximize the chances of obtaining wheat–alien translocation events. Once these are observed, the dominant *Ph1b* system is restored by backcrossing the translocation plants to any elite wheat cultivar. The process ends with the recovery of euploid, 42-chromosome derivatives that carry the translocation. This stock is maintained for subsequent use in agriculture via trait identification.

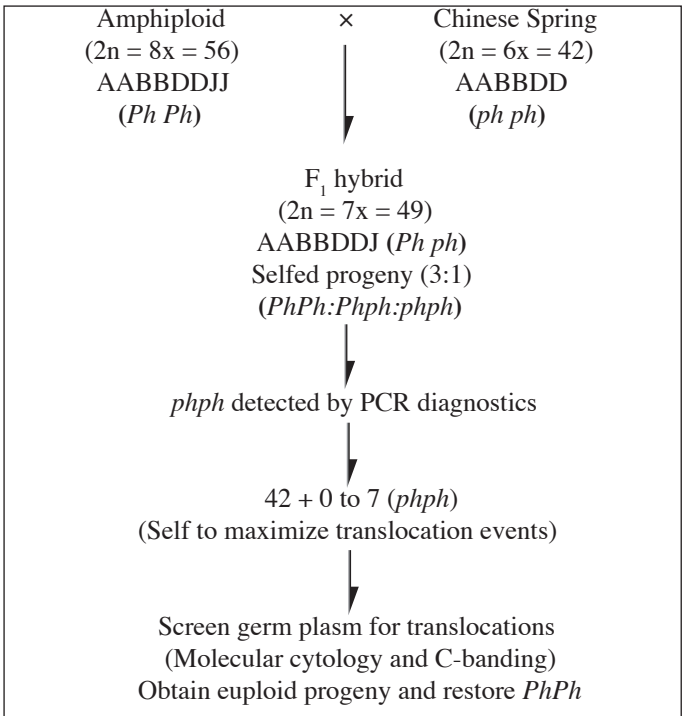

Fig. 27. Schematic elucidating the recurrent backcrossing steps used to transfer the existent wheat/alien chromosome translocations into agronomically superior wheat cultivars.

In the initiation of the translocation, six E^b chromosomes are visible in FISH and two are translocated; one is a Robertsonian and one has a terminal exchange with more of an E^b constitution (Fig. 28b, p. 153).

Additional plants where a varying number of translocations are present need to be separated as single events and turned into euploids for subsequent screening and practical utilization; two translocated chromosomes and three complete alien chromosomes (Fig. 28c, p. 153) and a desirable alien exchange (Fig. 28d, p. 153). Further backcrossing of such plants will give rise to derivatives with reduced chromosome number. Ultimately, plants with one alien and one translocation chromosome(Fig 28e, p. 153) and one translocation chromosome (Fig. 28f, p. 153) are obtained. These plants are ideal for sources of restoring the *Ph* system by backcrossing and obtaining euploids that will have 40 wheat chromosomes and a disomic pair that is translocated (Fig. 28g, p. 153). Translocations that are undesirable also are obtained and discarded as they have too much alien chromatin (Fig. 28h, p. 153).

Over the course of producing these new translocations, some euploid derivatives have been obtained that are *Ph1bPh1b* homozygous (Table 40, p. 154). All plants have 42 chromosomes and the translocations have been identified by the conventional Giemsa C-banding (Fig. 29, p. 154) for T6BS·6BL-6E^b(J), T5DL·5DS-5JS, T1DS·1JS, and T3BL·3JS. The translocations advanced to the 42-chromosome, euploid level are characterized as homoeologous, nonhomoeologous, Robertsonian, and smaller exchanges. Some characteristics of these translocations also are of good fertility and acceptable agronomic plant type.

Translocations in wheat breeding. Cytogeneticists have produced wheat–alien chromosome translocations over past several decades that hold the tremendous potential of utilization in wheat improvement programs. Globally, The main translocation in practical use is the spontaneous T1BL·1RS Robertsonian exchange that occurred as a consequence of a centric breakage-fusion event. CIMMYT put this translocation to maximum use in spring habit wheat emanating from

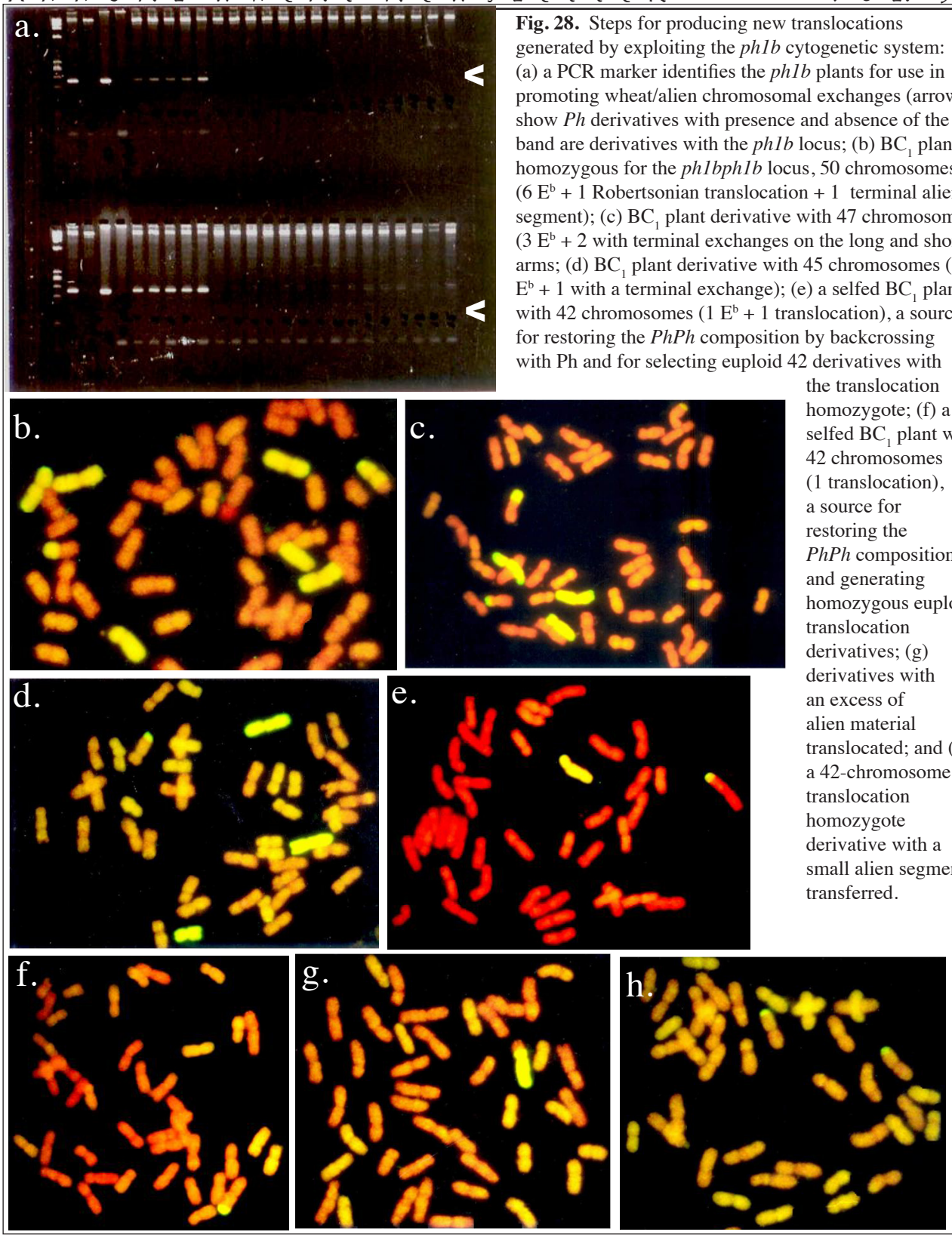

Fig. 28. Steps for producing new translocations generated by exploiting the *ph1b* cytogenetic system: (a) a PCR marker identifies the *ph1b* plants for use in promoting wheat/alien chromosomal exchanges (arrows show *Ph* derivatives with presence and absence of the band are derivatives with the *ph1b* locus; (b) BC_1 plants homozygous for the *ph1bph1b* locus, 50 chromosomes (6 E^b + 1 Robertsonian translocation + 1 terminal alien segment); (c) BC_1 plant derivative with 47 chromosomes (3 E^b + 2 with terminal exchanges on the long and short arms; (d) BC_1 plant derivative with 45 chromosomes (3 E^b + 1 with a terminal exchange); (e) a selfed BC_1 plant with 42 chromosomes (1 E^b + 1 translocation), a source for restoring the *PhPh* composition by backcrossing with Ph and for selecting euploid 42 derivatives with the translocation homozygote; (f) a selfed BC_1 plant with 42 chromosomes (1 translocation), a source for restoring the *PhPh* composition and generating homozygous euploid translocation derivatives; (g) derivatives with an excess of alien material translocated; and (h) a 42-chromosome translocation homozygote derivative with a small alien segment transferred.

the initial spring/winter wheat crossing protocol taken up in mid-1970s. The next translocation in practical use is the T1AL·1RS Robertsonian exchange linked with the cultivar Amigo for greenbug resistance. This translocation could be a consequence of univalent misdivision and/or irradiation. Amigo has entered into wheat breeding programs but to a lesser degree than T1BL·1RS. The cultivar TAM200 charaterizes this translocation. Both of these translocations are present in good agronomic type wheat and, thus, are ready for their rapid exploitation. Other translocations involving

Table 40. Details of some new translocation euploid derivatives with 44 chromosomes involving Bread wheat/*Thinopyrum bessarabicum* exchanges

Sample	Translocation	Phenotypic detail (Mean)				
		Spike length (cm)	Days-to-flowering	Nodes/spike	Plant height at maturity (cm)	Grains/spike
WWX-1	T7DS·7DL-4J	14.2	105	26	82	58
WWX-2	T6BS·6BL-6J	14.5	100	27	78	44
WWX-3	T6JS·7DL	18.0	108	26	84	27
WWX-4	T5JS-5DS·5DL	13.5	105	24	72	40
WWX-5	T1DS·1JS	15.5	98	26	80	40
WWX-6	T1AS·1AL-1JL	15.0	100	27	75	33
WWX-7	T3JS·3BL	12.5	95	24	80	54

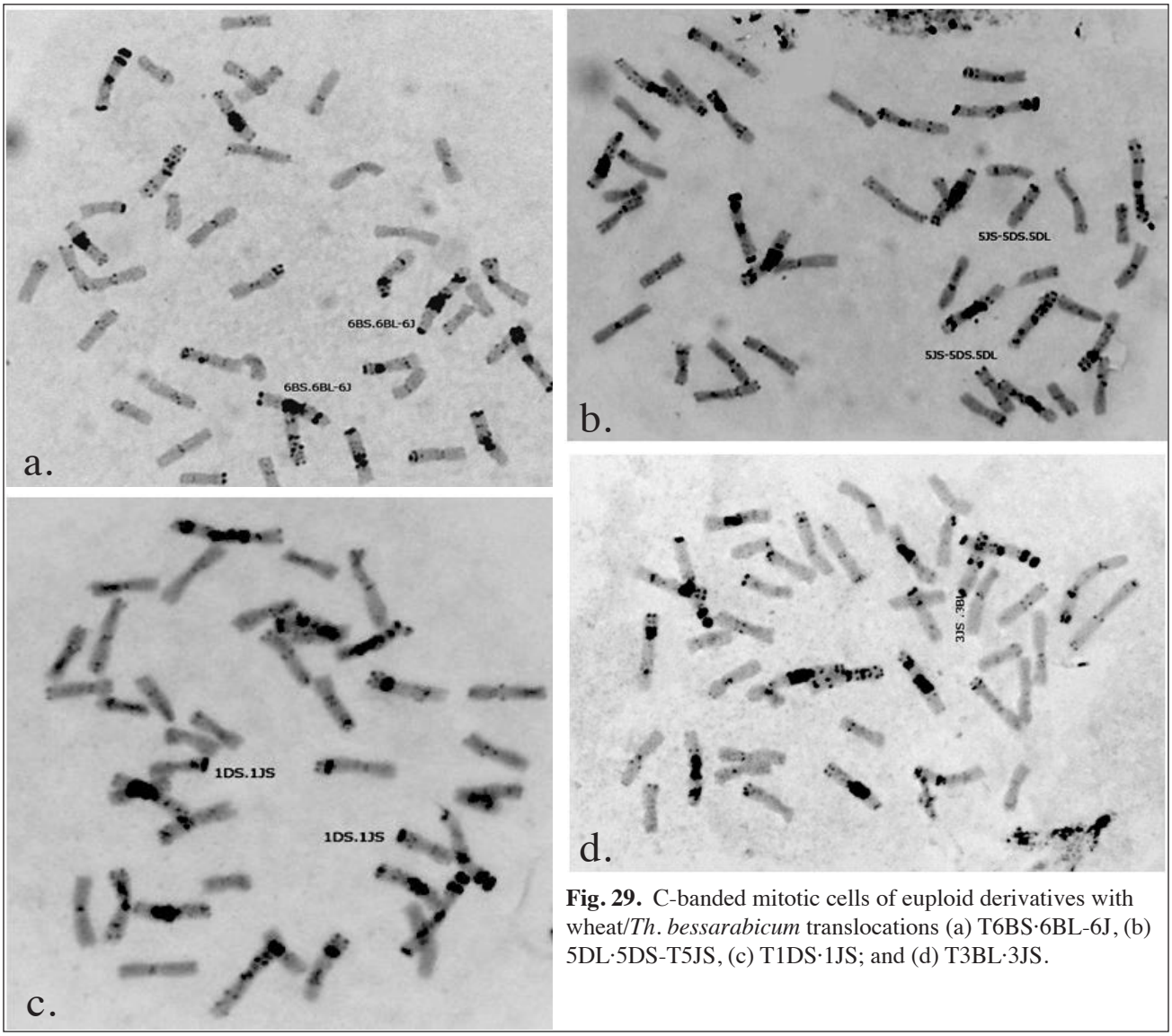

Fig. 29. C-banded mitotic cells of euploid derivatives with wheat/*Th. bessarabicum* translocations (a) T6BS·6BL-6J, (b) 5DL·5DS-T5JS, (c) T1DS·1JS; and (d) T3BL·3JS.

T5AL·5RS, T4BS·4BL-2R, T7DS·7DL-7Ag, T2BS·2RL, T6BS·6RL, and T2AS-2RS·2RL as some examples have been slow to exploit as they are present in wheat backgrounds that are poorly adapted globally. Several rust genes associated with translocations are either present in the cultivars Chinese Spring or Thatcher both of those are not amenable for appropriate field screening. A strategy is to transfer these translocations into well adapted wheat cultivars and was an effort taken on in this study. Backcrossing elite widely adapted national wheat onto the globally available translocations twice

followed by a selfing has given a usable stock of all the above translocations in an improved wheat phenotype that can be screened for various stresses under field situations. With an additional two crosses, the phenotype would be significantly improved and resemble the recurrent wheat cultivar used in backcrosses around 93%. The possibility of enriching the durum wheat was explored and, from a pentaploid F_1 followed by backcrosses with durum, recovering a durum wheat with the translocation was routine T1AL·1RS and T5AS·5RL.

Production of new wheat–alien chromosome translocations. With the success of the existing translocations, and the anticipated promise of exploiting those that are being transferred into elite agronomically superior widely adapted wheat cultivars during the last decade efforts have emerged that target wheat genetic stocks using cytogenetic manipulation systems to promote chromosomal exchanges. The options available for targeting on homoeologous exchanges are favoured by the use of *Ph*^{I} or the *ph1b* stocks. The focus in this study has been on the latter and exploited has been the CS/*Th. bessarabicum* amphiploid combination that is *PhPh* in its genetic control structure. We have shown how the crossing of this amphiploid with the *phph* stock could become a source of new translocations. In Pakistan, this directional exploitation was maximized around a collaboration with CIMMYT over the last five years. The various steps for the initiation of multiple translocations (Fig. 28, p. 153) culminate with disomic translocation stocks that are identified after C-banding (Table 40, Fig. 29, p. 154). The protocol is ideal for improvement of plant type and also for forcing exchanges within homoeologous groups. When the *Ph1bph1b* derivatives are produced, options are to either produce polyhaploids or self the heterozygote. In the first case, haploids will be obtained that are *Ph1b:ph1b* in a 1:1 ratio. In the *Ph1bph1b* selfs, the derivatives will have a 1:2:1 segregation progeny of plants that are *Ph1bPh1b* ; *Ph1bph1b* : *ph1bph1g*. Only the *ph1b* or *ph1bph1b* derivatives will be the candidate plants to give rise to translocated progeny upon advance (Fig. 27, p. 152).

The *ph1b* haploids upon doubling give derivatives that are *phph* and these upon several selfings will generate progeny that have translocations (Fig. 27, p. 152). The progress is similar with the *ph1bph1b* plants from selfing of the *Ph1bph1b* source. Once the translocations are detected, a backcross with an elite *Ph1bPh1b* wheat cultivar that is the first step to restore the *Ph1bPh1b* system. Backcrosses and cytology are required to deliver the final euploid product that is 2n=6x=42 (AABBDD) and has the translocation as a disomic homozygote. The most advanced euploid derivatives generated are validated with Giemsa C-banding (Table 40, p. 154).

Of the numerous wheat–alien translocations that were initiated during the selfing of the *ph1bph1b*-derived constitutions, seven euploid events are described that have various homozygous exchanges, are euploid and possess acceptable seed fertility plus plant types. These are:

1. T7DS·7DL-4E^{b} is a nonhomoeologous translocation where the 4E^{b} presence may possibly disturb the group 7 wheat homoeology,
2. T6BS·6BL-6E^{b} is an ideal homoeologous euploid exchange derivative with good compensation anticipated for group 6,
3. T7DL·6E^{b}S is a nonhomoeologous Robertsonian event and not preferred as it possesses a full alien arm that may add to negative aspects when used in wheat breeding, however, fortuitous benefits are possible and screening for stress factors will surely occur,

4-5. T5DL·5DS-5E^{b}S and T1AS·1AL-1E^{b}L are both highly desirable homoeologous derivatives that involve groups 5 and 1, respectively, fitting the alien chromosome exchange trait advantage value expectation, and

6-7. two other Robertsonian translocations T1DS·1 E^{b}S and T3BL·3E^{b}S are advantageous over T7DL·6E^{b}S in that both are homoeologous in nature, which may support their usage in practical agriculture for trait benefits.

All the translocations have satisfactory phenotypes that support each to be exploited in breeding programs. Plant height at maturity renders them as good donor candidates for derivatives to be targeted for irrigated agriculture with a height range of 72–84 cm. Complimenting height are spike length, satisfactory with 17–58 grains/spike coupled with 98–108 days to maturity and a nodal number range of 24–27. All alien exchanges were terminal and no interstitial exchanges were generated.

Using the amphiploid base of intergeneric hybrids is ideal for generating a high frequency of translocation events that may address traits not well defined for their inheritance or those of polygenic nature, e.g., salinity, drought, and heat. This basic effort has defined the route of how translocations can be obtained and for the future leaves behind the option to target the strategy for greater efficiency by exploiting the wheat/maize haploidy system.

Targeting individual alien chromosomes that are trait positive, each of the seven addition lines of *Th. bessarabicum* could be crossed with the CS *phbph1b* stock BC_1 progenies for each chromosome; 2n=6x=42 + 1 E^b1E^b (*Ph1bPh1b*) / CS (*ph1bph1b*) = 42 (*Ph1bph1b*) + 1 E^b to 7 E^b.

The various 43-chromosome *Ph1bph1b* derivatives would be the future candidates that lead to generating haploids that are 21 (*Ph1b*), 21 + 1E^b (*Ph1b*), 21 (*ph1b*), and 21 + 1E^b (*ph1b*). The 21+ 1E^b (*ph1b*) plants would be doubled, selfed, and progeny screened for expected translocations between 1E^b and 1A, 1B, or 1D, after which the line would be restored to *Ph1bPh1b* to recover euploid products that have 42 chromosomes, have the homoeologous exchange, are cytologically characterized, and trait positive as identified earlier in the alien disomic addition line.

Alien genetic transfers are the easiest to achieve via homologous exchanges and such are the preferred means where closely related sources are used that reside in the primary gene pool. Tapping into the secondary pool has some complexity and is the next option. The tertiary resource, due to its most complex nature of genetic transfer, reflects a challenge that researchers have pursued consistently. From producing the intergeneric hybrids to the end product are all complex steps, but the potential value of tertiary gene pool diversity are ranked extremely high. Progress is generally slow, but practical benefits are very promising. So far, the maximum benefits have been through the spontaneous T1BL·1RS translocation, but others are being incorporated. For maximizing the use of these combinations, it is imperative that they are in good agronomic backgrounds so they fit the field cropping cycles appropriately and are easier to screen and then have a days to flowering duration that is similar to that of the wheat crop. Using a reciprocal backcrossing protocol, some of the major globally available translocations have been placed in good agronomic type spring wheat that are good candidates for further practical utilization. The existing translocations have been made user friendly.

The merit of such interest on producing new forms opens up a huge arena of investigations that can enrich wheat genetic diversity. This one combination (wheat–*Th. bessarabicum*) has just scratched the surface of what lies ahead. Seven translocation products and numerous others in the research pipe line is extremely encouraging. We envision the possibility of enhancing the output, developing markers for the exchange sites, and using the gene bank wheat–alien reservoir for initiating further translocation output efforts.

Cytological and morphological characterization of a Thinopyrum bessarabicum amphiploid and its addition lines.

Alvina Gul Kazi, Rabia Sultan, Awais Rasheed, Hadi Bux, Usman Rahim, Abdul Aziz Napar, and Abdul Mujeeb-Kazi.

The three wheat genomes are believed to have been derived from single ancestral diploid species each having seven pairs of chromosomes. The haploid chromosome complement of bread wheat is made up of seven groups of three related chromosomes. These genetically related chromosomes from different genomes are referred to as homoeologous chromosomes.

Intergeneric crosses involve alien species that are extremely diverse genomically and their hybridization with wheat is complex. When hybridized, the combinations exhibit meiotic details that suggest little to no intergenomic chromosomal associations. Despite these constraints, research interest has remained high since the late 1980s and hybridization progress remained a major obstacle until the mid-1990s. Some intergeneric hybrids were easy to produce whereas others were more difficult. Subtle manipulations and careful choice of parents were a solace and widened the hybridization categories. The manuipulation categories were influenced by various factors and have been extensively reported and reviewed.

Disomic addition lines, in which single pair of homologous chromosomes from a related species is added to the wheat complement, are used to identify alien chromosomes carrying useful genes and are the starting point for the cytogenetic transfer of alien genetic material to wheat. In general, such lines have been agronomically inferior to wheat, are not entirely stable, and require cytological maintenance at each selfing generation. Stocks can degenerate quickly once the added chromosome has been lost in even a small percentage of the population, because male gametes carrying an alien chromosome are less competitive than normal wheat gametes. The method for the addition of a single, alien, chromosome pair into a recipient cultivar involves hybridization followed by backcrossing the hybrid or amphiploid to the recipient species and selecting addition lines from the backcross progeny. This procedure is now regarded as the standard method of producing alien chromosome addition lines. Using this technique, alien addition lines have been

produced in wheat with single added chromosome pairs from *Aegilops, Agropyron, Dasypyrum, Secale*, and *Hordeum*. None of the alien chromosome addition lines has become popular as a commercial cultivar, because of the instability of the alien chromosomes and the incorporation of undesirable characteristics associated with them. They are, however, a crucial starting point for allowing cytogenetic-based segmental transfers and use in wheat breeding.

Three wheat–*Th. intermedium* addition lines were developed to BC_3F_3 and showed good resistance to barley yellow dwarf virus. *Th. bessarabicum* addition lines were developed in *T. aestivum* for chromosomes of groups 1 to 7 and were identified through biochemical diagnostic markers with the help of FISH.

The diploid grass *Th. bessarabicum* (2n=2x=14 JJ or E^bE^b) is an excellent source of salt tolerance and crossing with the cultivar Chinese Spring (CS) (2n=8x=56; AABBDDE^bE^b) yielded an amphiploid from which seven disomic chromosome addition lines were developed. The first six were developed at CIMMYT, Mexico, and the seventh addition line in Pakistan. Our specific studies were

cytological characterization of the amphiploid and its disomic addition lines using conventional cytological protocols,

morphological characterization and documentation of the germ plasm, and

seed increase for the on-going projects and biotic and abiotic stress evaluations.

The parents, CS, diploid *Th. bessarabicum*, the six disomic addition lines in a Genaro or CS background, the CS–*Th. bessarabicum* amphiploid, the *ph1b* genetic stock, and selfed derivatives were the source of new translocations initiated at the 49-chromosome selfed level. Studies in Pakistan focussed on seed increase of the amphiploid and parental seed and the amphiploid was cytologically characterized. The F_1 perennial hybrid was studied in a living herbarium that is maintained at CIMMYT through exchange of F_1 clones that gave the option to characterize the F_1 hybrid in Pakistan. All acquired disomic additions and a multiple disomic addition for group 6 and 7 enabled the generation of the group-7 disomic addition. All addition liness were backcrossed with the Pakistani wheat Inquilab twice, followed by selfing to extract the respective disomic additions across all seven groups, i.e., $1E^b$ to $7E^b$. In the process, new BC_1 derivatives also emerged that are reported.

The spike morphology of various phases of exploiting the *Th. bessarabicum* variation in a CS background and the incorporation of other elite wheats in the cross combinations shows the co-dominant phenotype in all cross derivatives where the parental wheat phenotype is modified, giving evidence of alien genetic expression in a wheat background (Fig. 30). The spike structure of CS wheat and *Th. bessarabicum*, dorsal and ventral views of the F_1 hybrid (2n=4x=28, ABDE^b), the 56-chromosome amphiploid, are compared to two spikes at the BC_1 stage with cultivars Pavon and Pak-81 (CS/*Th. bessarabicum*//Pavon or Pak-81 with 2n-7x=49, AABBDDE^b chromosomes, Fig. 30f and 30g).

Fig. 30. Spike morphology of prebreeding germ plasm involving bread wheat (2n=6x=42, AABBDD) and *Thinopyrum bessarabicum* (2n=2x=14; E^bE^b): (a) Chinese Spring (CS) wheat (2n=6x=42, AABBDD), (b) *Th. bessarabicum* (2n=2x=14, E^bE^b), (c) CS/*Th. bessarabicum* F_1 hybrid (2n=4x=28, ABDE^b, dorsal view), (d) CS/*Th. bessarabicum* F_1 hybrid (2n=4x=28, ABDE^b, ventral view), (e) CS/*Th. bessarabicum* amphiploid (2n=8x=56, AABBDDE^bE^b), (f) CS/*Th. bessarabicum*//Pavon selfed BC_1 (n, 2n=7x=49; AABBDDE^b), and (g) CS/*Th. bessarabicum*//Pak81 selfed BC_1 (n, 2n=7x=49; AABBDDE^b).

Cytological validation. The amphiploid with a normal 56-chromosome complement, which was generally the case in C_0 and C_1 seed, was somatically analyzed (Fig. 31a, p. 158). All seven C_0 seed had 56 chromosomes (Fig. 31a, p. 158). Five of the C_0 derivatives bred true and had 56 chromosomes. Two C_0 derivatives gave aneuploid progeny that were hypoploid (54 and 55 chromosomes, Figs. 31b

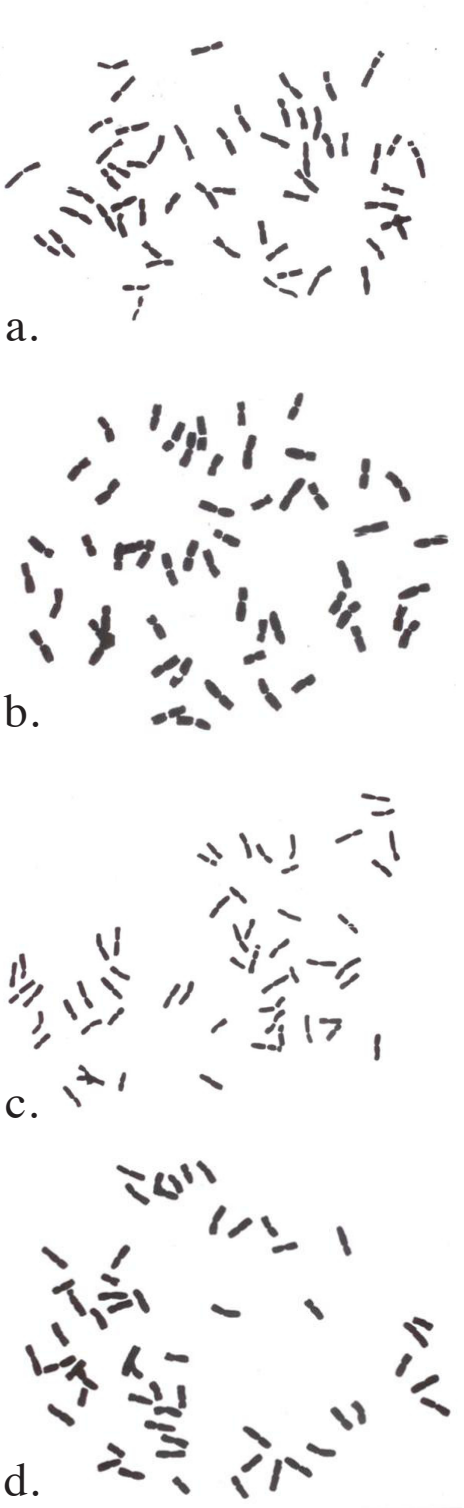

Fig. 31. Somatic chromosome numbers of various amphiploid plants of the 'bread wheat/*Thinopyrum bessarabicum*' intergeneric combination: (a) a mitotic cell with the normal chromosome number of 2n=8x=56 (AABBDDE^{b}E^{b}), (b) a hypoploid cell with 54 chromosomes, (c) a hypoploid cell with 55 chromosomes, and (d) a hypoploid cell with 57 chromosomes.

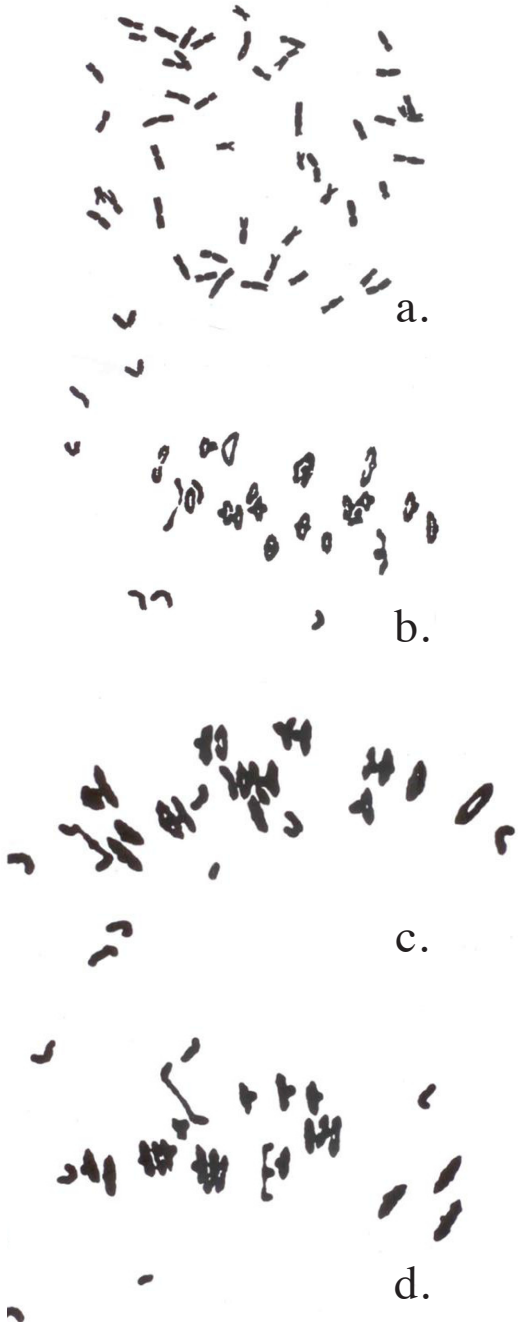

Fig. 32. Somatic and meiotic details of a BC_1 derivative from 'bread wheat/*Thinopyrum bessarabicum*//bread wheat' with 2n=7x=49 chromosomes (AABBDDE^{b}): (a) a somatic BC_1 cell with 49 chromosomes, (b) a BC_1 meiotic cell with 49 chromosomes associated at metaphase 1 as 2 rod bivalents + 19 ring bivalents + 7 univalents, (c) a BC_1 meiotic cell with 49 chromosomes associated at metaphase I as 1 rod bivalent + 20 ring bivalents + 7 univalents, and (d) a BC_1 meiotic cell with 49 chromosomes associated at metaphase I as 2 rod bivalents + 19 ring bivalents + 7 univalents.

and c, p. 158), or hyperploid (57 chromosomes), (Fig. 31d).

Crossing the CS–*Th. bessarabicum* amphiploid with Pavon or Pak-81 gave BC_1 derivatives that generally were normal, but in some cases aneuploid. In the normal derivatives, the somatic count is 49 chromosomes (Fig. 31a) and at meiosis, upto 21 bivalents (varying rods and rings) plus seven univalents (Fig. 31b, c, and d).

The aneuploid BC_1 derivatives are cytologically possess 47, 48, and 50 chromosomes (Fig. 33a, b, and c, p. 159), which were less frequent and less than 3% (6 of the 200 BC_1 observed). The aneuploid trend however became more pronounced when the aneuploid and normal BC_1s were selfed several times, but univalent retention was very high.

Exploiting the

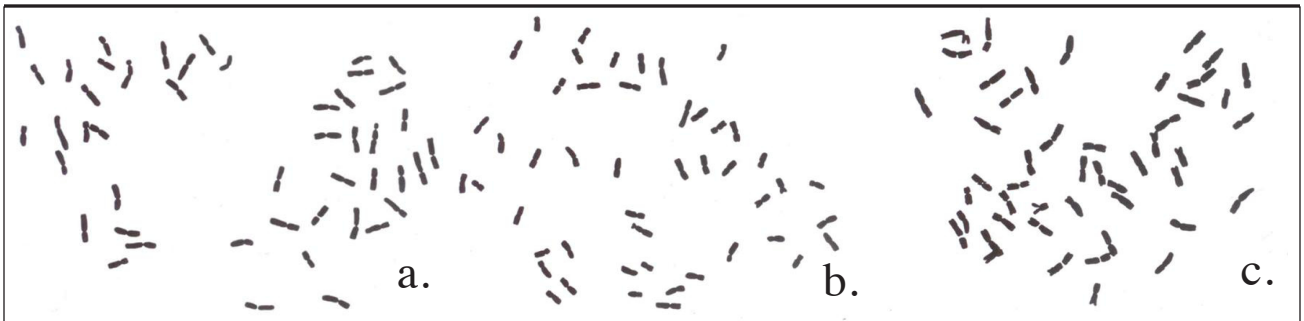

Fig. 33. Somatic details of a selfed BC_1(n) from 'bread wheat/*Thinopyrum bessarabicum*//bread wheat' (n) with retention of a high number of alien chromosomes: (a) BC_1(n) with 47 chromosomes; (b) BC_1(n) with 48 chromosomes, and (c) BC_1(n) with 50 chromosomes.

BC_1 derivatives. The normal BC_1 derivatives were advanced in a dual manner. When selfed several times, a unique gametic transmission behavior was observed where instead of a progressive loss of the alien univalents, they were retained and counts of the selfed progenies were much closer to the expected 49 chromosomes (Fig. 34a, a somatic BC_1n cell with 48 chromosomes and a meiotic association at metaphase 1 of various univalents and bivalents that characterize alien chromosome retention (Fig. 34b and c).

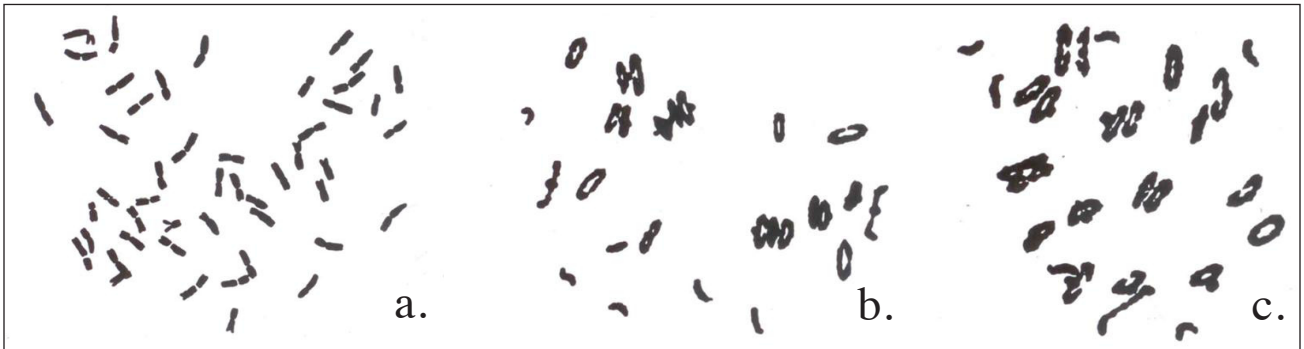

Fig. 34. Somatic and meiotic details of a 'bread wheat/*Thinopyrum bessarabicum*//bread wheat' BC_1(n) selfed derivative: (a) with 48 somatic chromosomes, (b) a meiocyte at metaphase I with 6 univalents + 1 rod bivalent + 20 ring bivalents, and (c) a meiocyte at metaphase I with 6 univalents + 2 rod bivalents + 19 ring bivalents.

Further backcrossing of the BC_1 individuals with Pavon or Pak-81 or even of the acquired disomic additions to extract new disomic addition lines with 44 chromosomes that represent the group 1–7 addition series (Fig. 35a, a somatic cell with 44 chromosomes, (b) a meiocyte with 22 bivalents associated as 3 rod and 19 ring bivalents, which separate at anaphase I normally in a 22 + 22 split (c)).

Fig. 35. Advanced BC_1(n) derivatives from 'bread wheat/*Thinopyrum bessarabicum*//bread wheat' (n) showing a disomic *Th. bessarabicum* chromosome addition line at mitosis and meiosis (a) with 44 somatic chromosomes, (b) with 44 chromosomes associated at metaphase I as 3 rod + 19 ring bivalents, and (c) with 44 chromosomes at anaphase I showing a normal 22/22 separation.

Identification and maintenance of addition lines. With the backcrossing approach, a double disomic addition stock for group-7 was extracted. The homoeology of other six groups was identified and these were backcrossed onto local cultivars from which modified phenotypic additions could be extracted for groups 1 to 6 in a nationally adapted background of Inquilab. The addition lines all had 44 chromosomes and with 22 bivalents at meiosis. Seed set was uniformally good across all the lines and from each addition line, five plants were selected as base material for subsequent advance and maintenance. The details of the seven disomic addition lines relative to plant height at maturity, days to maturity, spike length, and seed/spike are in Table 41. Homoeologous groups $2E^b$, $3E^b$, $4E^b$, and $5E^b$ are easily identified by morphology, such as tapering spike (Fig. 36a), solid stem (Fig. 36b), blue aleurone (Fig. 36c), and club-shaped spike (Fig. 36a). The status of each of the disomic lines after two cycles of increase and at the end of the current 2009–10 crop cycle is given in Table 42, including the number of individual plants that were somatically counted and found to contain 44 chromosomes.

Table 41. Mean characteristics of the *Thinopyrum bessarabicum* disomic addition lines (2n=6x=42 + $1E^bE^b$ to $7E^bE^b$).

Addition line	Characteristics			
	Height at maturity (cm)	Days to maturity	Spike length (cm)	Number of seeds/spike
$1E^bE^b$	66	110	11.0	65
$2E^bE^b$	72	110	11.0	70
$3E^bE^b$	82	113	14.0	55
$4E^bE^b$	78	114	12.0	50
$5E^bE^b$	72	112	10.0	37
$6E^bE^b$	58	104	6.5	28
$7E^bE^b$	55	114	12.0	22

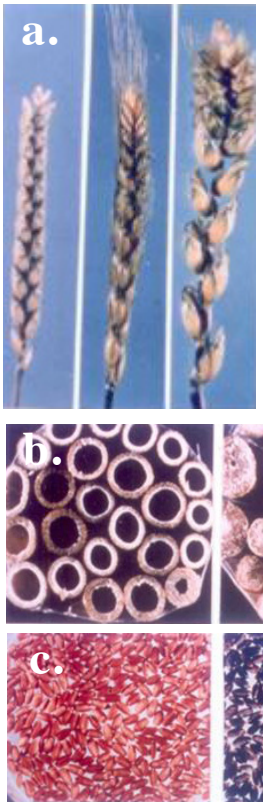

Fig. 36. Morphological markers identifying some wheat/*Thinopyrum bessarabicum* disomic addition lines (2n=6x=44): (a) Chinese Spring and homoeologous group 2 and 5 disomic addition lines with a tapering ($2E^b$) and club ($5E^b$) shaped spikes; (b) a group-3 disomic addition line ($3E^b$) with a solid stem (left) versus a normal hollow stem (right), and (c) a group-4 disomic addition line ($4E^b$) with blue aleurone (right) versus normal (left) colored wheat seed

The complete cytological details at the *in situ* hybridization level are shown (Fig. 37, p. 161). The F_1 hybrid with 28 chromosomes (Fig. 37a, p. 161) and the seven alien E^b chromosomes are differentiated due to their yellow color in the fluorescent *in situ* hybridization preparation. Wheat DNA was the blocking source and the E-genome DNA was used for blocking (Fig. 37a, p. 161). In the amphiploid somatic cell, the 14 E^b chromosomes are similarly differentiated (Fig. 37b, p. 161). The seven disomic addition lines are similarly identified ($1E^b$ (Fig. 37c, p. 161) a DAPI filter is used; $2E^b$ (Fig. 37d, p. 161), $3E^b$ (Fig. 37e, p. 162), $7E^b$ (Fig. 37f, p. 161), $4E^b$ (Fig. 37g, p. 161), $5E^b$ (Fig. 37h, p. 161), and $6E^b$ (Fig. 37i, p. 161). In all, the 42 wheat chromosomes are evident and the two alien E^b pair for each group clearly differentiated.

The germ plasm resource that is present at CIMMYT, Mexico, was investigated at NARC, Pakistan, from 2005 to 2010. The environmental conditions in Mexico were amenable for maintaining all perennial hybrids and the initial F_1 hybrid (bread wheat/*Th. bessarabicum)* was available from which clones were brought to NARC for analysis. Spike samples of the alien species from the source were used in Fig. 36. The CS spike shows a modified phenotype in the F_1 and the variation was inherited by the 2n=8x=56 $AABBDDE_bE_b$ amphiploid. The two BC_1 derivatives also have carried the modified phenotype, an important characteristic because it indicates modified expression (co-dominance) suggesting that alien characteristics can be transferred with a high chance of getting practical benefits towards improving wheat. Maintaining aneuploidy is

Table 42. Status of seed amounts produced from each *Thinopyrum bessarabicum* disomic addition lines at the end of the 2009–10 crop cycle at NARC, Pakistan. The seed number is the mean number of spikes multiplied by number of plants.

Addition line	Total plants	Seed number 2009–10	Reserve from 2008–09
$1E^bE^b$	305	19,500	500
$2E^bE^b$	90	6,300	500
$3E^bE^b$	52	2,860	500
$4E^bE^b$	310	15,500	500
$5E^bE^b$	285	10,545	500
$6E^bE^b$	4	112	100
$7E^bE^b$	173	3,806	100

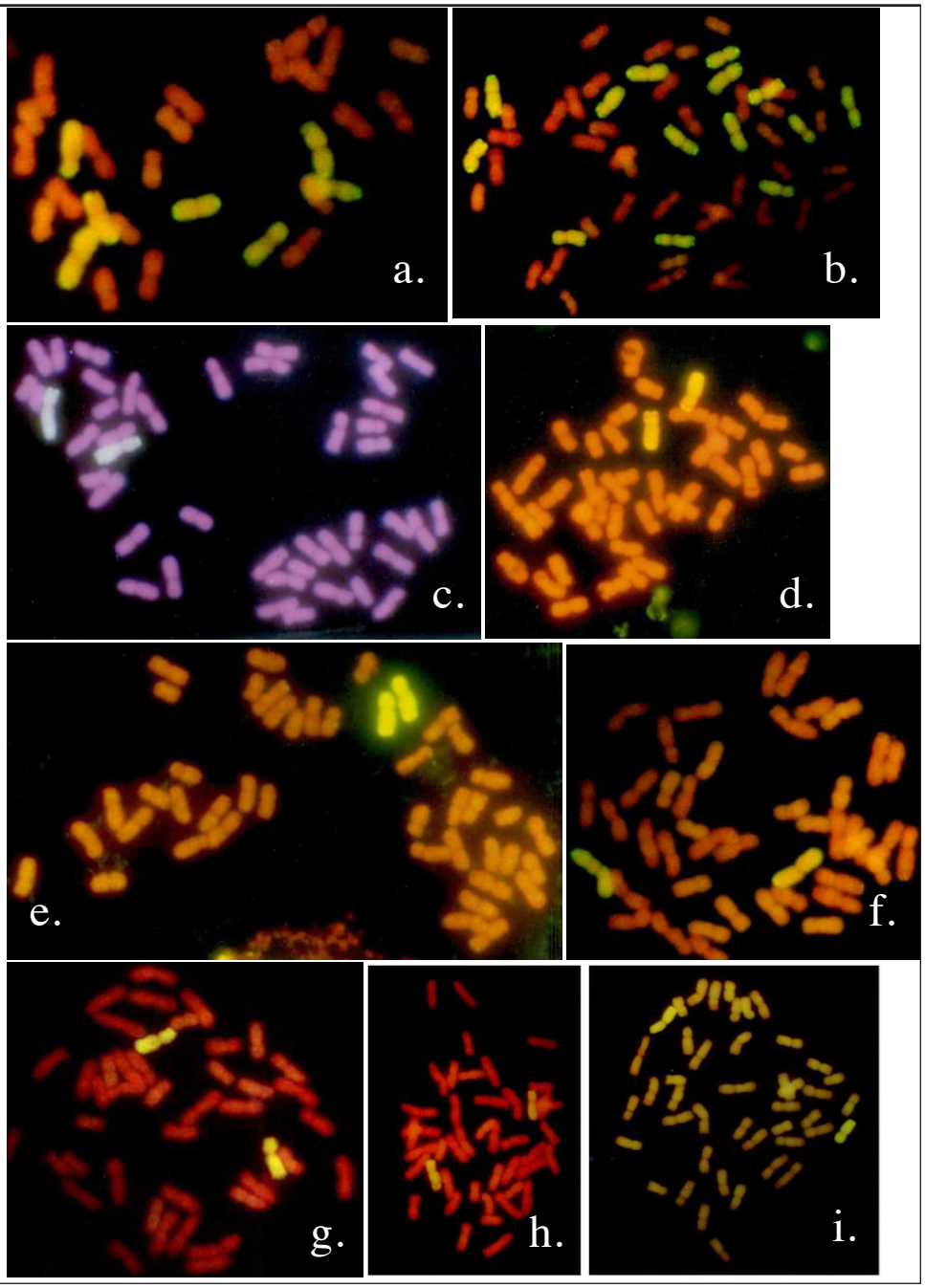

Fig. 37. Fluorescent *in situ* hybridization (wheat DNA for blocking and E^b DNA for blocking where E^b chromosomes are yellow) of somatic cells from an intergeneric hybrid combination of bread wheat/*Thinopyrum bessarabicum* at various stages of progeny development: (a) an F_1 hybrid with 2n=4x=28, ABDE^b chromosomes; (b) an amphiploid somatic cell with 2n=8x=56, AABBDDE^{b}E^b chromosomes, (14 E^{b}E^b-genome chromosomes are yellow); (c) a homoeologous group-1 E^{b}E^b disomic addition line; (d) a homoeologous group-2 E^{b}E^b disomic addition line; (e) a homoeologous group-3 E^{b}E^b disomic addition line; (f) a homoeologous group-7 E^{b}E^b disomic addition line; (g) a homoeologous group-4 E^{b}E^b disomic addition line; (h) a homoeologous group-5 E^{b}E^b disomic addition line; and (i) a homoeologous group-6 E^{b}E^b disomic addition line.

common and this trend prevailed. Hypo- and hyperploid plants were seen but euploid plants with 56 chromosomes were advanced after they were validated via C-banding and FISH (normal (Fig. 31a, p. 158) and aneuploid (Fig. 31b, c, and d, p. 158).

The utilization of the amphiploid has a two-fold advance scenario; production of addition lines and cytologically manipulating homoeologous transfer by the *ph1b* system. Systematic backcrossing and cytology (conventional and differential staining) is used to produce alien disomic alien chromosome addition lines, followed by seed increase and trait characterization. Having the addition lines in a nationally adapted wheat cultivar is an advantage for all future studies, and was incorporated in this program through the use of the high-yielding, widely adapted cultivar Inquilab. Addition lines 1 to 6 were backcrossed twice and then selfed from which plants with 44 chromosomes were increased. Addition line 7E^b was developed in Pakistan. The protocol was conventional and achieving the target goals was routine. The phenotype still requires more input using Inquilab for at least 2–3 additional backcrosses. Normal development is gauged at the BC_1 stage when the derivatives possess 2n=7x=49 chromosomes and at meiosis associate as 21 pairs (wheat) plus seven univalents (*Th. bessarabicum*) (Fig. 33, p. 159). When the disomics are generated, those showing

greater stability have normal metaphase I with 22 bivalents and anaphase I with a 22/22 split; the case in all seven addition lines (Fig. 35, p. 159). Their characterization has utilized various means covering giemsa C-banding, biochemical differentiation, molecular inputs and morphological parameters. *In situ* hybridization is an excellent, rapid means to validate the alien chromosome presence in the F_1 (Fig. 37a, p. 161), the amphiploid (Fig. 37b, p. 161), and in each disomic addition where two alien (homologous pair) chromosomes are observed (Fig. 37c–i, p. 161).

Crossing an amphiploid (2n=8x=56) with bread wheat generates a BC_1 with 2n=7x=49 chromosomes and this BC_1 is highly self-fertile with the capacity to retain alien chromosomes in a high frequency. This uniqueness allows the BC_1 derivatives to be used in stress evaluation. The two BC_1 combinations in the stocks in Pakistan have elite wheat cultivars Pavon and Pak-81 that are widely adapted wheat and amenable to field screening across the country.

Production of new bread wheat/synthetic hexaploid advanced derivatives.

Alvina Gul Kazi, Farrukh Bashir, Hadi Bux, Awais Rasheed, and Abdul Mujeeb-Kazi.

The International Maize and Wheat Improvement Center (CIMMYT), Mexico, produced 1,014 synthetic hexaploid wheats (SH) by artificially crossing elite, tetraploid wheat cultivars or their advanced breeding lines (2n=2x=28, AABB) with different accessions of *Ae. tauschii* (2n=4x=14, DD). The F_1 hybrids (2n=3x=21, ABD) were treated with colchicine, which caused chromosome doubling, and formed fertile SH wheats also known primary synthetics. All SH wheats were cytologically validated, increased, and screened against different biotic and abiotic stresses at CIMMYT. Due to varied trait diversity present in these SHs, different subsets were identified that showed resistance against diseases such as Karnal bunt, *Fusarium* head blight, *Septoria* leaf spot, *Helminthosposium* spot blotch, leaf rust, stripe rust, and abiotic stresses such as drought, water logging, and salinity and heat tolerance. We used these SHs to incorporate useful genetic traits into elite bread wheat cultivars around a major Pakistani focus to enrich and widen the narrow genetic pool of bread wheat and to combat different biotic and abiotic stresses faced by wheat production within and outside Pakistan. The desirable SHs were grown in the field at the Institute of Biotechnology and Genetic Engineering (IBGE), NWFP Agricultural University, Peshawar, in 2004–05. The IBGE planting followed cytological validation of somatic euploidy (2n=6x=42), increased the seed of all lines, and served for the production of F_1 cross combinations of elite international and nationally adapted wheat cultivars. The best bread wheats and SHs were identified and crossed, ultimately resulting in F_1 hybrid seed.

The F_1 hybrid seed was field planted in National Agricultural Research Centre (NARC), Islamabad, during the regular wheat crop cycle November 2005–May 2006. The F_2 seed produced was bulked and planted in the NARC fields in 2006–07 under artificial stripe rust stress. Only the resistant adult plants were harvested as individual spikes from selected plants and bulked. The resulting F_3 seed was planted in 2007–08 and, after artificial inoculation with stripe rust, the best plants both in terms of agronomy and disease resistance were selected (F_4 seed). These progenies were planted in the off-season at the Pakistan Agricultural Research Council (PARC) station in Kaghan (2,666 masl) for increase. The F_5 seed was harvested in September, 2008, and then planted in the NARC fields during the normal 2008–09 wheat cycle. The population was once again screened after artificial inoculation with stripe rust and single-plant selections were made on the basis of stripe rust resistance and agronomic type. The F_6 seed obtained was categorized for threshability, 1,000-kernel weight, and seed color and subsequently planted at the off-season at Kaghan near the end of May, 2009. These plants were harvested at the end of September, 2009, and then planted at NARC in '6 row × 5 m' plots for observation and seed increase and subsequently a source for national varietal testing based upon data to be gathered in May, 2010. These lines were planted again at Kaghan for seed increase. Representative samples of each combination have also been sent to the Plant Breeding Institute, Cobbity, Australia, for gene determination, a study of quality parameters, and characterization of drought tolerance. Pedigrees of these genotypes are given (Table 43, pp. 163-164).

Across all the synthetics that were increased, a natural infection of stripe rust enabled screening in the field and allowed the selection for superior agronomic performance at Peshawar. The selection criteria included plant height at maturity, no lodging, days-to-maturity, a closed crown, and spike details related mainly with spike length, grain fill, and erectness. Such synthetics from all the sets were crossed with elite, adapted, bread wheat cultivars yielding F_1 seed.

The first cycle in 2004–05 at IBGE, Peshawar. Seed increase of all synthetic sets with 25–30 grams seed/entry and crosses between SHs and elite adapted bread wheats with good agronomic traits in the various subsets in international/national cultivation to give F_1 seed.

Table 43. Pedigrees of the stripe rust-resistant F_7 produced from the CIMMYT, Mexico, collection of 1,014 synthetic hexaploid wheats.

Combination	Pedigree	Number of sister lines
1	68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)/6/CETA/… x 68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (783)	3
2	OPATA x 68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (783)	2
3	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (208)/5/OAPTA x 68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (783)	107
4	MAYOOR//TK SN1081/*Ae. tauschii*(222)/3/OPATA x 68.111/RGB-//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	22
5	149 CHAPIO/INQALAB 91 x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	1
6	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (208)/5/OAPTA x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	2
7	OPATA x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	6
8	MAYOOR//TK SN1081/AE.SQUARROSA)(222)/3/OPATA x GAN/*Ae. tauschii* (248)	6
9	ALTAR 84/*Ae. tauschii* (221)//YACO x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	3
10	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/OPATA x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	4
11	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/OPATA x CETA/*Ae. tauschii* (895)	1
12	68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)/6/CETA/… x CETA/*Ae. tauschii* (895)	2
13	CROC-1/*Ae. tauschii* (224)//KAUZ x CETA/*Ae. tauschii* (895)	1
14	TURACO/5/CHIR3/4/SIREN//ALTAR 84/*Ae. tauschii* (205)/3/3*BUC/6/OPATA x SCA/*Ae. tauschii* (518)	31
15	87 INQALAB 91/TSAPKI x SCA/*Ae. tauschii* (518)	1
16	162 CHAPIO/ INQALAB 91 x 68.111/RGB-U//WARD/3/*Ae. tauschii* (452)	6
17	YS/PASTOR x DOY1/*Ae. tauschii* (458)	5
18	CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/WEAVER/5/2*KAUZ x DOY1/*Ae. tauschii* (458)	20
19	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/PASTOR x GAN/*Ae. tauschii* (259)	2
20	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/OPATA x DOY1/*Ae. tauschii* (372)	7
21	OPATA/PASTOR x DOY1/*Ae. tauschii* (1024)	2
22	TURACO/5/CHIR3/4/SIREN//ALTAR 84/*Ae. tauschii* (205)/3/3*BUC/6/CNO x CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (273)	4
23	TURACO/5/CHIR3/4/SIREN//ALTAR 84/*Ae. tauschii* (205)/3/3*BUC/6/CNO x CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (227)	32
24	ALTAR 84/*Ae. tauschii* (224)//2*YACO/3/MAYOOR/TK SN1081/*Ae. tauschii* (222)/4/KUKUN x GAN/*Ae. tauschii* (248)	77
25	SERI x 68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (392)	1
26	BAKHTAWAR 94 x 68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (431)	3
27	OPATA x 68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (1038)	6
Using A-genome synthetic hexaploids		
28	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD x CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (101)	23
29	144 ALTAR 84/*Ae. tauschii* (221)//YACO/3/ INQALAB 91 x D67.2/P66.270//T.BOEOTICUM (66)	1
30	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD x ARLIN_1/T.MONOCOCCUM (95)	3
31	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD x CPI/GEDIZ/3/GOO//JO/CRA/4/T.MONOCOCCUM (101)	15
Drought tolerant and stripe-rust resistant F_7 produced.		
32	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/FCT x YAV_3/SCO//JO69/CRA/3/YAV/79/4/*Ae. tauschii* (498)/5/OPATA	3
33	CHIR3/CBRD x GAN/*Ae. tauschii* (897)//OPATA	2
34	GAN/*Ae. tauschii* (897)//OPATA x D67.2/P66.270//*Ae. tauschii* (223)	1
35	MAYOOR//TK SN1081/*Ae. tauschii* (222)/4/SABUF/3/BCN//CETA/*Ae. tauschii* (895) x GAN/*Ae. tauschii* (897)//OPATA	2

Table 43. Pedigrees of the stripe rust-resistant F_7 produced from the CIMMYT, Mexico, collection of 1,014 synthetic hexaploid wheats.

Combination	Pedigree	Number of sister lines
36	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/OPATA x DOY1/*Ae. tauschii* (515)	1
37	MAYOOR/TK SN1081/*Ae. tauschii* (222)/3/PASTOR x CROC_1/*Ae. tauschii* (444)	16
38	TURACO/5/CHIR3/4/SIREN//ALTAR 84/*Ae. tauschii* (205)/3/3*BUC/6/CNO x CROC_1/*Ae. tauschii* (444)	2
39	URES/PRL//BAV92 x YAV_2/TEZ//*Ae. tauschii* (249)	1
40	OPATA/PASTOR	5
41	OPATA x ALTAR 84/*Ae. tauschii* (J BANGOR)	9
42	OPATA x GAN/*Ae. tauschii* (408)	2
43	OPATA x CROC_1/*Ae. tauschii* (886)	2
44	OPATA x ROK/KML//*Ae. tauschii* (214)	1
45	OPATA x 68.112/WARD//*Ae. tauschii* (369)	1
46	OPATA x ALTAR 84/ *Ae. tauschii* (J BANGOR)	2
47	OPATA x DOY 1/*Ae. tauschii* (517)	11
48	OPATA x 68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (629)	14
49	OPATA x CETA/*Ae. tauschii* (895)	2
50	OPATA x DOY 1/*Ae. tauschii* (255)	4
51	OPATA x DOY 1/*Ae. tauschii* (1026)	2
52	OPATA x ALTAR 84/*Ae. tauschii* (205)	7
53	OPATA x INQALAB 91/AC8528	4
54	OPATA x INQALAB 91/FISCAL	1
55	OPATA x CETA/*Ae. tauschii* (1031)	8
56	OPATA x 74 INQALAB 91/TSAPKI	7
F_7 produced for bread wheat improvement using exotic germ plasm.		
57	182 SAAR/INQALAB 91 x MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD	15
58	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/PASTOR x SARSABZ	1
59	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD x KAMBARA	11
60	KAUZ x MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD	3
61	ALTAR 84/*Ae. tauschii* (224)//2*YACO/7/OPATA/6/68.111RGB-U//WARD/3/FGO/4/… x 162 SAAR/INQALAB 91	6
62	ALTAR 84/*Ae. tauschii* (224)//2*YACO/3/MAYOOR//TK SN1081/*Ae. tauschii* (222)/4/KUKUN x ALTAR 84/*Ae. tauschii* (221)//YACO	1
63	SARSABZ x CHIR3/CBRD	13
64	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/PASTOR x MH-97	2
65	KAUZ x MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD	14
66	PASTOR x MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD	15
67	BAV x (MAYOOR//TK SN1081/AE.SQUARROSA) (222)/3/CBRD	2
68	139 CHAPIO/INQALAB 91 x PICUS/3/KAUZ*2/BOW//KAUZ	100

Bread wheat/SH derivatives via advancing growth cycles. All F_1 crosses made during the 2004–05 crop cycle in Peshawar were moved to the NARC, Islamabad, as follows:

- F_1 grown at NARC during the winter 2005–06 cycle yielding F_2 seed,
- F_2 seed grown at NARC during the winter of 2006–07 yielding F_3 seed (a modified bulk procedure was adopted and plants selected for all superior agronomic traits resistant to stripe rust (artificial inoculation) and seed filling was observed prior to selection),
- F_3 seed grown at NARC during the winter of 2007–08 yielding F_4 seed (same selection criteria as in the previous section),
- F_4 modified bulk population planted at the Kaghan hill station during the summer 2008 (June to October) from which F_5 products were harvested and brought to NARC,
- F_5 progenies planted in the winter cycle of 2008–09 at NARC and observed for phenotype, stripe rust resistance (APR), and superior agronomic plant type leading to individual plant selections (F_6, the F_6 seed was

characterized for threshability, 1,000-kernel weight, and grain color),
– individual F_6 plant selections were planted at Kaghan in June, 2009, over the summer 2009 (June to October) for seed increase, and
– F_7 seed harvested at Kaghan planted at NARC in '6 row x 5 m' plots in winter 2009–10.

In general, the focus was to stringently select quality plants through modified bulks and then incorporate individual plant selection. Alternate cycles allowed for rapid seed increase and finally led to planting 2,200 '6 × 5 m' row plots of the F_7 derivatives from various bread wheat/SH combinations. Final selections were made at the end of the 2009–10 crop cycle at NARC; the number of elite selections dropped to 690 (Table 44, pp. 166-173). The best lines shall be recommended for varietal testing across Pakistan after the 2010 summer cycle at Kaghan (October, 2010).

All selected elite lines are free-threshing and have gone progressively from their tough-glumed SH parents and F_1 to free-threshing selections from the F_2 onwards. The spikes of two SH spikes of variable coloration and tough glumes, a normal free threshing bread wheat spike, and a 'bread wheat/SH' derivative that is also free-threshing are shown in Fig. 38.

Fig. 38. Spike phenotype of the utilization of the D-genome synthetic hexaploid wheats (SH) in wheat breeding: (a) two SH wheat spikes (dark and light awned) with tough glumes, (b) a free-threshing bread wheat spike, and (c) a free-threshing advanced progeny spike derived from a 'bread wheat/SH' cross.

The transfer of agronomic traits from the SHs to bread wheat developed a extensive recombination breeding effort in Pakistan around the new 'Wheat Wide Crosses and Cytogenetics' program. In general, wheats were used as the female parents for F_1 production. F_2 and F_3 advances were made around a modified bulk procedure intermixed with stress screening and selection of good agronomic plant types. From the final F_7 generation, several lines were selected. The range of variation addresses national wheat cultivation targets in both the irrigated and rainfed environments. The broad details are associated with variable heights at maturity, plant canopy intensity, early growth foliage spread, days-to-flowering, days to physiological maturity, leaf waxiness, stay-green character, spike length with terminal (apex) club shaped quality, and seed weight and appearance. Screening for resistance to stripe rust, Karnal bunt, and powdery mildew over the growing periods added information to the molecular diversity status. the national and international distribution of these advanced F_7 derivatives will permit further characterization for other factors important fornational varietal releases and deployment strategies, i.e., local and Ug99 leaf and stem rust, spot blotch, BYDV, and key quality components.

Stem rust has a unique international importance. Derivatives from this study have shown resistance to Ug99 in Kenya during the 2009 tests. Numerous crosses were made from 68 combinations that were categorized as follows:
– bread wheat/SHs resistant to rusts (27 combinations),
– bread wheat/A-genome synthetics (4 combinations),
– bead wheat/drought and rust resistant synthetics (25 combinations), and
– bread wheat/exotic synthetics, 12 combinations.

From these 68 combinations, eight were identified as resistant to Ug99 after testing in collaboration with KARI, Kenya. The entry and rust score details are 3 (5MR), 4 (15M), 9 (10M), 20 (10M), 26 (15M), 27 (20M), 50 (5MR), and 62 (10M).

Since the appearance of Ug99 in Uganda and its spread into Kenya, Ethiopia, Yemen, and Iran, Pakistan faces the danger of its entering the country. Thus, the breeding focus has shifted to test national germ plasm for Ug99 resistance and also analyze the Ug99-resistant materials within the country with a local race in lower Punjab and Sindh that has sporadic occurrence in the north. The tests against the local race were inconclusive because stem rust did not occur in the Sindh testing site during the 2009–10 cycle. The test will be repeated. Pakistan does not have race Ug99 yet, and the spores collected from minimal infections in Sindh have been sent to Australia for PCR validation to determine if Pakistan is free of Ug99 upto May 2010. The identification of resistant germ plasm moved us to have the elite synthetic-

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
1	1	1	61.08	124	163	97	16	85	42		37	33.64	118	161	103	13	74
2		2	65.58	124	163	106	16	80	43		38	38.66	118	159	104	14	78
3		3	62.22	124	162	100	14	72	44		39	39.60	118	161	100	13	72
4	2	1	46.86	124	163	114	12	55	45		40	36.02	118	161	97	13	74
5		2	39.04	124	163	120	14	62	46		41	38.76	119	159	100	13	74
6	3	1	49.28	123	164	135	12	69	47		42	40.50	119	159	106	15	84
7		2	43.50	125	173	100	14	80	48		43	39.38	119	159	99	13	80
8		3	38.84	125	173	108	14	68	49		44	43.14	119	159	109	15	90
9		4	37.56	125	168	115	16	72	50		45	39.76	119	159	100	14	86
10		5	42.26	125	169	103	15	70	51		46	45.54	119	159	116	16	96
11		6	46.86	125	168	119	14	73	52		47	41.18	119	159	101	13	82
12		7	40.96	122	162	103	13	80	53		48	37.04	119	159	124	16	92
13		8	42.04	122	162	110	13	82	54		49	34.74	119	159	113	13	76
14		9	44.96	122	162	97	13	84	55		50	41.36	119	161	110	13	72
15		10	41.40	122	162	103	13	82	56		51	43.60	119	163	125	16	109
16		11	36.20	123	162	100	13	82	57		52	44.36	119	159	122	15	94
17		12	45.00	123	159	110	14	82	58		53	37.92	118	161	103	14	78
18		13	48.22	123	159	113	13	74	59		54	41.58	118	161	100	13	76
19		14	43.74	123	159	115	18	95	60		55	42.78	118	161	126	15	78
20		15	48.04	123	159	114	17	90	61		56	41.94	118	161	123	15	76
21		16	39.42	123	159	120	18	92	62		57	43.94	118	161	108	13	68
22		17	43.38	123	164	105	16	76	63		58	40.82	118	164	115	16	68
23		18	42.04	123	164	97	13	64	64		59	43.90	118	160	101	12	68
24		19	42.36	123	164	110	15	78	65		60	43.44	118	161	126	15	96
25		20	37.06	119	164	104	13	69	66		61	41.92	118	160	120	16	90
26		21	37.04	119	164	103	13	72	67		62	38.34	118	161	119	13	74
27		22	36.68	119	164	100	14	76	68		63	35.62	118	159	113	13	78
28		23	34.04	119	164	94	13	72	69		64	44.84	118	159	114	14	86
29		24	44.10	119	164	110	14	74	70		65	43.82	118	159	125	16	86
30		25	42.10	119	164	109	14	76	71		66	39.02	118	162	101	13	80
31		26	43.30	119	164	110	14	74	72		67	40.80	118	164	109	15	96
32		27	40.78	119	165	102	14	74	73		68	41.16	118	164	121	16	84
33		28	40.50	119	165	112	15	80	74		69	42.98	118	164	107	13	78
34		29	38.10	119	165	107	17	90	75		70	41.36	118	163	114	15	84
35		30	36.26	119	165	119	18	90	76		71	39.44	118	165	125	16	90
36		31	39.98	119	165	113	18	94	77		72	39.90	118	165	109	15	82
37		32	39.12	119	165	102	11	62	78		73	40.16	118	165	116	14	72
38		33	37.60	118	161	101	12	70	79		74	36.76	118	160	106	14	70
39		34	42.54	118	161	112	13	76	80		75	43.14	118	161	101	13	76
40		35	46.66	118	161	108	15	84	81		76	38.12	118	161	113	14	80
41		36	39.16	118	161	97	14	80	82		77	37.42	118	164	110	15	93
83		78	41.00	118	165	116	15	86	129		17	53.52	121	164	130	13	76
84		79	40.18	118	160	104	14	82	130		18	50.50	121	162	128	13	78
85		80	36.48	118	164	110	14	80	131		19	42.84	121	163	125	13	70
86		81	36.66	118	166	110	14	78	132		20	52.22	121	163	130	12	75

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
87		82	40.16	118	166	113	14	89	133	5	1	41.74	125	171	92	15	77
88		83	37.88	118	164	104	13	83	134	6	1	40.64	123	177	122	12	40
89		84	41.21	119	166	112	18	95	135		2	32.18	123	176	117	15	49
90		85	37.08	119	165	113	16	82	136	7	1	48.76	120	173	125	16	87
91		86	39.94	119	165	120	16	87	137		2	51.96	120	173	116	16	86
92		87	41.32	119	166	115	17	92	138		3	38.34	120	173	130	16	84
93		88	41.28	119	166	117	18	96	139		4	50.10	120	173	109	15	82
94		89	38.52	119	164	121	16	94	140		5	46.92	124	173	111	16	74
95		90	39.64	119	165	125	17	90	141		6	41.54	124	174	121	16	72
96		91	46.88	119	165	103	16	92	142	8	1	45.24	125	165	113	14	76
97		92	42.60	119	164	118	17	100	143		2	45.06	125	165	118	12	72
98		93	36.24	119	162	120	17	98	144		3	48.66	125	165	106	10	56
99		94	40.32	119	161	116	15	94	145		4	46.46	125	167	110	10	51
100		95	41.92	119	164	114	16	85	146		5	42.80	125	169	114	11	60
101		96	38.22	119	165	113	16	88	147		6	45.64	125	165	109	11	54
102		97	39.60	119	165	111	15	86	148	9	1	41.12	124	163	100	10	35
103		98	40.90	119	166	109	16	82	149		2	36.86	124	164	112	11	77
104		99	40.12	118	165	120	16	90	150		3	51.82	124	163	122	12	80
105		100	38.48	118	165	110	16	82	151	10	1	46.22	123	167	108	14	86
106		101	40.32	118	166	118	17	96	152		2	47.66	123	165	120	13	78
107		102	37.36	118	166	113	17	94	153		3	50.74	120	163	115	14	86
108		103	39.04	118	164	110	17	96	154		4	36.82	122	163	111	13	80
109		104	34.84	119	166	107	16	88	155	11	1	44.54	132	172	130	11	58
110		105	40.22	119	166	120	17	90	156	12	1	41.98	129	167	107	11	36
111		106	43.10	119	166	114	16	86	157		2	58.50	126	172	128	13	65
112		107	37.98	119	162	103	16	90	158	13	1	47.08	119	165	10	15	89
113	4	1	46.54	125	165	130	13	80	159	14	1	33.54	123	162	104	11	84
114		2	52.52	125	168	125	13	76	160		2	34.92	121	162	116	13	86
115		3	53.44	125	165	126	14	71	161		3	39.18	121	162	120	13	71
116		4	55.26	125	165	131	13	78	162		4	35.06	121	162	124	14	64
117		5	52.86	125	164	130	13	80	163		5	37.90	121	162	101	12	79
118		6	54.86	125	166	114	13	70	164		6	32.14	121	162	97	13	84
119		7	52.00	125	166	120	13	66	165		7	34.16	121	162	103	13	86
120		8	52.54	125	168	127	13	70	166		8	35.22	121	158	100	12	70
121		9	56.78	125	169	128	12	73	167		9	38.78	125	160	102	12	82
122		10	48.22	122	164	133	14	70	168		10	36.65	125	160	105	12	76
123		11	55.28	122	162	131	13	69	169		11	35.16	123	159	98	13	92
124		12	55.82	122	163	137	12	66	170		12	41.12	123	159	109	12	80
125		13	52.60	122	166	132	13	86	171		13	32.18	123	158	106	13	72
126		14	49.88	123	169	133	13	74	172		14	41.28	122	160	97	14	86
127		15	53.88	123	164	128	13	66	173		15	35.20	122	160	104	13	90
128		16	52.10	123	165	130	13	70	174		16	37.28	122	163	100	13	94
175		17	30.04	122	159	101	13	94	221		20	36.74	123	156	96	13	72
176		18	30.88	122	159	96	13	92	222	19	1	50.72	124	172	123	14	47
177		19	35.12	122	162	100	13	86	223		2	52.36	126	169	116	11	56

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
178		20	34.22	122	159	106	15	100	224	20	1	47.16	112	167	107	11	50
179		21	36.52	120	161	119	12	92	225		2	47.72	112	168	220	14	66
180		22	38.64	121	158	100	13	80	226		3	45.44	112	167	108	13	61
181		23	41.00	121	161	106	11	72	227		4	44.74	112	167	106	13	63
182		24	36.20	121	159	97	12	78	228		5	43.88	112	167	100	11	64
183		25	31.76	121	159	104	11	76	229		6	41.92	112	170	113	10	66
184		26	42.30	121	161	122	12	82	230		7	43.88	112	167	107	16	96
185		27	38.74	121	161	119	14	79	231	21	1	49.30	121	166	120	17	90
186		28	34.92	121	159	119	13	76	232		2	47.92	121	161	122	17	86
187		29	36.00	122	159	110	14	80	233	22	1	47.86	117	164	117	16	84
188		30	39.56	122	159	118	17	97	234		2	30.08	117	164	103	19	99
189		31	33.54	122	159	110	16	98	235		3	43.72	117	163	103	18	110
190	15	1	46.24	122	157	120	13	98	236		4	41.58	117	164	105	17	98
191	16	1	38.64	115	155	100	14	90	237	23	1	45.52	125	170	118	13	76
192		2	45.28	115	156	100	14	92	238		2	42.66	125	167	120	13	78
193		3	47.20	115	156	103	13	87	239		3	42.60	125	168	128	14	72
194		4	49.26	115	156	99	12	83	240		4	41.90	125	169	124	13	78
195		5	43.88	115	156	97	14	82	241		5	44.18	125	169	129	14	76
196		6	47.30	115	156	102	11	79	242		6	46.40	125	172	120	12	68
197	17	1	44.18	114	159	120	12	62	243		7	48.40	125	171	126	13	62
198		2	45.34	114	156	125	10	56	244		8	36.36	125	169	122	13	60
199		3	47.72	114	158	105	11	62	245		9	41.70	125	172	115	13	82
200		4	45.48	114	169	103	10	54	246		10	47.16	125	166	120	12	64
201		5	41.46	114	169	110	11	50	247		11	42.74	125	172	128	15	74
202	18	1	38.12	122	157	122	14	69	248		12	42.16	125	172	122	12	90
203		2	42.42	122	157	116	14	72	249		13	42.04	125	171	110	12	62
204		3	33.24	121	156	113	13	62	250		14	40.60	124	168	120	16	110
205		4	35.40	122	155	119	13	58	251		15	47.78	124	168	126	15	72
206		5	35.06	122	155	117	16	72	252		16	47.04	124	167	114	12	68
207		6	36.80	122	157	106	16	74	253		17	43.32	124	167	128	15	78
208		7	35.58	123	163	122	17	84	254		18	43.00	124	171	112	12	86
209		8	38.90	122	156	120	14	86	255		19	42.20	124	169	115	15	78
210		9	40.44	122	156	122	14	82	256		20	44.54	124	168	120	12	66
211		10	37.16	122	161	118	16	94	257		21	44.22	124	169	118	14	76
212		11	41.86	122	161	122	15	90	258		22	49.32	124	172	106	12	74
213		12	35.28	122	156	114	13	80	259		23	44.32	124	172	115	13	78
214		13	40.46	122	156	118	14	76	260		24	43.58	124	171	120	14	80
215		14	37.44	121	157	120	16	86	261		25	43.30	124	171	123	13	78
216		15	41.42	121	158	110	15	78	262		26	43.44	124	172	124	14	78
217		16	36.18	121	158	126	15	82	263		27	45.68	124	171	110	12	64
218		17	36.42	123	157	119	16	87	264		28	42.90	124	171	130	16	83
219		18	40.42	123	157	112	14	82	265		29	44.92	124	173	108	15	80
220		19	30.82	123	156	129	16	76	266		30	43.64	124	165	120	14	74
267		31	42.52	124	167	100	10	72	313		45	50.46	116	162	105	15	76
268		32	45.04	124	167	121	14	76	314		46	49.78	116	162	102	14	74

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
269	24	1	43.58	120	157	108	14	82	315		47	48.92	116	162	103	14	76
270		2	48.88	120	164	111	15	98	316		48	45.02	125	164	100	14	82
271		3	46.82	120	164	98	15	96	317		49	48.62	125	164	99	13	83
272		4	44.30	120	164	100	13	86	318		50	49.68	125	164	110	14	90
273		5	47.40	120	164	105	14	100	319		51	45.92	125	164	98	14	86
274		6	45.52	119	164	116	15	110	320		52	45.72	119	165	110	14	80
275		7	49.44	119	164	106	15	96	321		53	45.44	119	165	110	14	84
276		8	54.92	119	164	103	15	92	322		54	46.04	119	164	99	14	80
277		9	45.56	119	164	99	12	88	323		55	49.70	119	164	103	14	82
278		10	45.20	119	164	111	12	82	324		56	43.98	119	164	102	14	84
279		11	41.96	119	164	105	13	84	325		57	48.66	119	164	100	14	82
280		12	42.30	119	164	100	13	80	326		58	50.08	119	164	105	14	86
281		13	44.56	119	164	97	13	86	327		59	43.66	120	165	100	14	82
282		14	41.76	119	164	100	13	86	328		60	44.08	120	165	105	14	82
283		15	58.58	119	164	98	13	86	329		61	48.00	120	165	103	14	80
284		16	38.66	118	164	100	13	90	330		62	49.46	120	165	103	14	78
285		17	46.70	118	164	97	13	85	331		63	47.68	120	164	115	14	86
286		18	47.66	118	164	112	12	78	332		64	46.86	120	164	115	14	80
287		19	44.10	118	164	103	13	80	333		65	47.12	120	164	104	14	84
288		20	45.76	118	164	103	12	76	334		66	41.46	120	164	100	14	82
289		21	45.28	119	164	104	11	70	335		67	43.54	120	164	103	15	84
290		22	38.66	119	164	110	12	72	336		68	43.24	120	167	110	14	86
291		23	44.90	119	164	103	13	78	337		69	47.90	120	167	110	14	80
292		24	48.64	119	164	110	14	96	338		70	41.32	120	167	108	14	89
293		25	45.60	120	164	109	13	80	339		71	48.08	117	165	120	14	88
294		26	46.48	120	164	107	12	82	340		72	48.08	117	164	103	14	79
295		27	46.12	120	164	110	13	90	341		73	45.94	117	164	115	14	68
296		28	48.86	120	167	110	15	108	342		74	48.70	117	164	100	14	68
297		29	49.34	117	164	108	13	80	343		75	48.38	117	164	104	14	72
298		30	50.62	117	164	100	13	68	344		76	45.66	117	164	125	14	76
299		31	50.60	117	164	100	13	96	345		77	41.48	117	164	106	14	78
300		32	49.52	117	164	104	12	70	346	25	1	45.78	122	160	115	14	83
301		33	49.30	116	164	102	13	80	347	26	1	45.06	122	162	92	14	82
302		34	42.88	116	164	103	12	72	348		2	55.54	125	164	93	13	84
303		35	46.60	116	164	102	12	78	349		3	55.02	125	169	90	10	70
304		36	45.68	116	164	100	10	76	350	27	1	45.20	124	157	100	13	80
305		37	36.58	125	164	104	12	72	351		2	42.16	124	157	106	14	76
306		38	54.44	125	167	103	11	70	352		3	45.20	124	157	103	15	78
307		39	43.68	125	168	105	15	88	353		4	43.48	124	156	99	15	72
308		40	40.64	125	168	103	14	78	354		5	47.46	124	157	105	15	74
309		41	51.34	116	164	100	13	60	355		6	41.50	124	157	100	14	82
310		42	47.10	116	164	99	14	74	356	28	1	46.56	119	156	95	12	62
311		43	48.24	116	164	103	14	72	357		2	42.38	123	156	96	14	100
312		44	47.64	116	164	101	14	75	358		3	41.14	126	156	98	15	60
359		4	44.18	126	156	100	12	82	405		2	48.52	129	173	120	18	106

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
360		5	42.32	126	156	95	11	72	406	36	1	42.74	122	159	107	14	75
361		6	41.08	126	156	92	13	68	407	37	1	38.00	122	164	120	15	80
362		7	42.06	126	156	96	13	68	408		2	42.46	122	164	110	14	81
363		8	39.32	126	156	96	13	73	409		3	40.14	122	162	101	12	68
364		9	47.14	126	156	95	13	66	410		4	39.22	124	162	103	13	74
365		10	38.80	126	156	92	12	62	411		5	42.82	124	160	107	11	66
366		11	43.68	126	156	96	14	86	412		6	50.12	124	159	114	12	83
367		12	43.94	126	156	96	13	53	413		7	40.82	124	160	109	11	76
368		13	42.42	126	156	94	13	66	414		8	43.96	124	160	118	13	80
369		14	41.20	126	156	96	12	67	415		9	30.18	124	159	112	13	90
370		15	46.58	126	156	96	14	84	416		10	45.18	124	159	115	12	82
371		16	43.64	126	156	98	13	72	417		11	48.62	124	160	117	13	76
372		17	42.36	126	156	95	13	70	418		12	43.64	124	160	109	11	70
373		18	43.36	125	156	99	15	76	419		13	39.36	124	160	103	12	78
374		19	42.92	125	156	100	17	110	420		14	42.84	124	160	118	13	82
375		20	42.36	125	156	98	15	90	421		15	40.76	124	160	110	12	80
376		21	43.18	125	156	101	16	92	422		16	45.76	124	160	111	14	86
377		22	45.06	125	156	100	16	86	423	38	1	55.04	112	160	100	12	66
378		23	44.18	125	156	98	15	88	424		2	54.40	112	160	104	13	68
379	29	1	46.42	118	159	99	12	71	425	39	1	36.16	112	160	104	13	68
380	30	1	43.06	121	159	118	17	100	426	40	1	38.04	120	146	94	15	92
381		2	49.94	128	159	109	18	110	427		2	29.46	120	146	97	15	88
382		3	45.18	119	160	113	15	93	428		3	37.84	120	146	95	14	80
383	31	1	38.28	123	158	117	20	80	429		4	35.28	120	168	96	14	78
384		2	35.86	123	158	110	15	64	430		5	36.24	120	169	90	14	76
385		3	45.04	123	158	90	14	70	431	41	1	41.16	120	155	118	12	60
386		4	42.58	123	158	96	15	72	432		2	49.46	120	155	120	9	45
387		5	34.28	123	158	103	14	63	433		3	41.38	120	155	125	11	60
388		6	31.77	120	160	103	14	62	434		4	44.90	110	150	100	13	76
389		7	41.88	120	160	104	15	61	435		5	50.84	110	150	120	11	60
390		8	33.96	120	160	100	13	80	436		6	37.24	110	150	110	14	72
391		9	43.04	120	164	108	14	70	437		7	37.72	110	150	116	15	80
392		10	36.48	120	164	100	13	73	438		8	49.40	110	150	113	11	64
393		11	32.98	120	164	103	13	74	439		9	42.26	110	150	99	14	72
394		12	34.96	120	167	100	11	76	440	42	1	30.28	113	161	125	14	85
395		13	42.20	120	167	96	15	82	441		2	41.26	113	161	90	13	70
396		14	53.62	120	171	99	14	62	442	43	1	22.86	112	156	87	13	70
397		15	52.18	120	170	97	14	64	443		2	43.30	107	154	90	13	79
398	32	1	43.52	116	163	121	13	74	444	44	1	47.52	125	173	106	12	46
399		2	41.60	116	160	136	13	76	445	45	1	49.00	126	174	120	12	65
400		3	41.84	116	160	123	13	78	446	46	1	57.94	120	170	115	18	90
401	33	1	52.48	123	166	134	16	79	447		2	59.06	120	170	120	15	88
402		2	33.34	123	166	114	13	72	448	47	1	37.60	133	180	119	9	65
403	34	1	41.34	135	179	122	14	86	449		2	40.72	133	180	110	9	55
404	35	1	43.00	127	168	112	18	103	450		3	44.34	133	180	125	10	48

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
451		4	42.72	133	180	116	9	49	497		5	28.72	125	172	130	15	66
452		5	46.54	132	180	118	9	52	498		6	37.16	125	172	122	15	74
453		6	45.56	132	177	115	10	56	499		7	37.04	125	172	128	15	76
454		7	37.60	132	178	120	9	58	500		8	30.56	125	172	123	14	70
455		8	38.87	133	180	121	9	55	501	56	1	35.46	114	146	99	13	56
456		9	44.00	133	180	127	10	58	502		2	26.20	114	146	100	13	55
457		10	44.50	133	180	106	9	53	503		3	38.56	114	146	104	12	56
458		11	40.06	133	180	103	9	50	504		4	42.06	114	146	101	11	52
459	48	1	37.42	114	151	101	13	72	505		5	38.54	114	146	99	13	58
460		2	41.00	114	151	110	16	86	506		6	44.38	119	150	100	13	50
461		3	39.16	114	151	124	15	92	507		7	45.40	119	150	104	13	56
462		4	41.38	114	151	97	16	82	508	57	1	41.70	112	166	116	14	58
463		5	36.70	114	151	119	11	76	509		2	51.02	112	163	125	14	68
464		6	38.94	114	151	105	13	60	510		3	50.40	112	166	103	13	58
465		7	43.88	111	150	98	16	82	511		4	51.06	112	165	128	14	62
466		8	42.08	111	150	113	15	92	512		5	38.68	112	163	102	14	66
467		9	45.05	111	150	120	14	74	513		6	54.48	112	163	110	13	62
468		10	40.86	111	150	107	11	68	514		7	48.18	112	163	117	13	53
469		11	50.94	111	150	101	13	72	515		8	44.60	112	163	110	14	62
470		12	33.78	111	150	110	13	68	516		9	45.48	112	163	109	13	60
471		13	45.12	111	150	96	14	78	517		10	51.48	111	162	114	17	76
472		14	45.05	111	150	115	15	78	518		11	63.18	111	162	107	13	72
473	49	1	46.90	114	165	112	15	82	519		12	50.44	111	162	103	14	76
474		2	50.98	114	156	116	14	80	520		13	52.90	111	160	108	15	80
475	50	1	51.42	123	169	130	15	72	521		14	45.36	112	160	116	15	86
476		2	53.20	123	169	108	12	50	522		15	41.54	112	160	121	15	80
477		3	49.30	123	169	103	11	50	523	58	1	45.04	120	179	129	14	81
478		4	43.98	123	169	124	14	66	524	59	1	53.98	124	179	100	11	68
479	51	1	49.92	113	153	110	14	70	525		2	53.54	124	179	111	13	72
480		2	46.98	113	153	112	16	100	526		3	44.10	124	158	115	13	77
481	52	1	40.24	114	153	99	11	60	527		4	45.62	124	158	118	13	79
482		2	33.72	114	153	106	11	57	528		5	44.96	124	158	109	13	70
483		3	39.08	114	154	95	14	82	529		6	48.72	124	158	103	13	72
484		4	35.20	114	154	97	13	72	530		7	47.18	124	173	100	12	78
485		5	41.60	114	153	95	11	62	531		8	49.00	124	173	104	13	66
486		6	38.36	114	163	105	14	100	532		9	45.46	124	173	106	13	68
487		7	36.52	114	164	110	11	45	533		10	37.52	121	173	110	13	66
488	53	1	48.44	110	154	110	13	72	534		11	42.02	120	173	103	13	68
489		2	51.50	110	154	119	16	82	535	60	1	46.08	125	162	109	11	58
490		3	42.54	110	154	108	13	70	536		2	56.56	125	162	103	11	55
491		4	45.14	110	154	125	18	86	537		3	40.36	126	162	115	13	66
492	54	1	53.66	124	171	109	16	87	538	61	1	47.24	121	164	105	11	68
493	55	1	44.36	126	173	103	20	110	539		2	38.70	121	164	105	12	72
494		2	33.72	128	171	130	13	50	540		3	37.74	121	164	105	13	88
495		3	31.90	128	171	132	15	70	541		4	37.72	121	164	110	13	66

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
496		4	34.40	125	172	123	15	66	542		5	35.80	121	164	121	13	62
543		6	44.92	121	164	107	12	63	589	67	1	59.84	116	159	121	15	71
544	62	1	42.98	125	173	127	16	93	590		2	42.28	114	153	116	13	86
545	63	1	28.46	128	174	118	14	81	591	68	1	39.40	116	164	103	12	62
546		2	43.40	128	163	120	13	51	592		2	30.66	116	164	100	13	68
547		3	42.32	128	162	100	18	90	593		3	28.80	116	161	105	14	77
548		4	45.64	128	167	110	16	60	594		4	38.64	121	165	96	15	68
549		5	47.18	128	167	118	15	54	595		5	45.64	121	166	101	16	76
550		6	52.48	128	167	130	15	62	596		6	44.72	121	164	90	14	70
551		7	42.16	128	167	103	13	53	597		7	40.36	125	163	96	13	70
552		8	50.12	128	167	100	12	54	598		8	37.12	125	164	91	13	72
553		9	45.92	128	167	121	13	63	599		9	44.78	125	164	100	14	76
554		10	43.44	128	167	116	13	72	600		10	45.14	125	163	101	14	76
555		11	46.34	128	167	120	14	78	601		11	40.56	125	164	110	14	78
556		12	45.10	128	167	130	14	96	602		12	45.56	125	165	98	13	72
557		13	37.36	128	167	123	14	76	603		13	30.58	125	165	92	14	72
558	64	1	49.14	118	147	117	11	86	604		14	34.46	125	164	102	14	70
559		2	44.56	118	153	103	13	88	605		15	40.20	125	164	106	15	80
560	65	1	41.66	114	163	91	16	100	606		16	50.42	125	163	91	13	67
561		2	43.96	114	163	97	15	74	607		17	35.82	125	165	97	14	70
562		3	45.74	114	163	106	16	82	608		18	43.30	125	165	100	14	70
563		4	38.34	114	163	120	17	100	609		19	41.70	125	165	98	14	70
564		5	37.64	114	166	100	17	110	610		20	40.02	125	165	112	14	69
565		6	36.30	114	166	93	15	78	611		21	48.06	125	166	93	13	78
566		7	49.74	112	150	100	16	100	612		22	46.38	125	165	97	13	76
567		8	48.06	112	152	96	17	90	613		23	39.98	129	165	94	13	72
568		9	46.46	112	151	95	16	83	614		24	43.10	129	166	102	16	78
569		10	45.28	112	150	103	16	80	615		25	49.22	128	165	105	15	77
570		11	39.92	112	150	93	14	76	616		26	47.84	128	165	109	15	84
571		12	38.92	112	150	91	15	80	617		27	48.80	128	165	91	13	68
572		13	49.26	112	150	110	16	76	618		28	38.84	128	165	98	14	72
573		14	45.56	112	150	97	15	74	619		29	42.12	126	166	100	14	70
574	66	1	49.70	117	154	130	14	78	620		30	50.75	126	166	96	13	66
575		2	40.36	115	147	110	12	76	621		31	40.14	126	166	101	15	76
576		3	45.94	115	147	109	15	78	622		32	37.20	126	166	96	13	68
577		4	47.00	115	147	130	14	70	623		33	47.76	126	166	110	13	68
578		5	52.90	115	147	118	14	68	624		34	38.26	126	166	102	14	70
579		6	42.90	115	147	124	14	72	625		35	48.58	126	165	115	13	76
580		7	47.86	115	147	108	13	65	626		36	49.34	126	165	98	13	68
581		8	43.74	115	149	115	14	72	627		37	49.38	126	165	91	13	70
582		9	45.92	115	147	129	15	76	628		38	39.92	125	165	100	14	70
583		10	47.06	115	147	126	15	78	629		39	36.74	125	167	96	13	68
584		11	43.98	115	150	130	15	110	630		40	36.44	125	168	94	17	106
585		12	41.16	115	147	123	14	68	631		41	35.04	125	168	93	13	68
586		13	43.22	115	159	110	13	62	632		42	35.96	125	168	100	15	79

Table 44. Phenotypic evaluation of 'bread wheat/synthetic hexaploid' F_7 derivatives produced for bread wheat improvement using exotic germ plasm during 2008–09 crop cycle (SH = synthetic hexaploid parent line, GW = 1,000-kernel weight (g), DH = day-to-heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), and GS = grains/spike).

Line	Combination	SH	TKW	DH	DM	PH	SL	GS	Line	Combination	SH	TKW	DH	DM	PH	SL	GS
587		14	46.60	115	158	128	13	62	633		43	34.22	125	167	112	13	70
588		15	51.02	115	159	135	14	68	634		44	41.92	112	163	100	12	40
635		45	50.74	112	157	94	12	52	676		86	38.18	118	167	102	15	54
636		46	43.88	112	163	97	13	68	677		87	44.84	118	166	97	14	76
637		47	32.52	118	165	103	13	68	678		88	49.54	118	165	103	13	72
638		48	35.92	118	165	91	12	56	679		89	47.46	118	163	106	14	74
639		49	36.72	118	166	95	13	70	680		90	45.90	114	164	98	13	68
640		50	34.20	118	165	98	13	70	681		91	49.56	114	165	110	14	74
641		51	44.38	118	165	100	15	76	682		92	45.20	114	166	97	14	73
642		52	38.04	118	165	103	13	62	683		93	43.88	114	166	95	13	68
643		53	47.76	118	165	101	13	68	684		94	40.58	114	166	103	13	70
644		54	45.58	118	163	99	13	71	685		95	36.68	114	166	99	13	72
645		55	49.38	118	165	100	14	72	686		96	42.34	114	165	106	14	69
646		56	44.98	118	163	98	13	70	687		97	44.16	114	165	108	15	78
647		57	32.82	118	165	106	15	71	688		98	42.50	114	165	103	13	68
648		58	30.32	118	165	99	13	72	689		99	38.06	114	165	104	14	70
649		59	31.40	118	165	105	16	80	690		100	42.46	114	164	108	15	78
650		60	44.84	118	165	94	13	70									
651		61	43.42	118	163	99	13	72									
652		62	40.82	118	162	93	13	69									
653		63	41.82	118	165	106	14	70									
654		64	40.84	120	165	104	13	68									
655		65	42.24	120	165	103	13	72									
656		66	44.20	120	163	97	13	72									
657		67	51.50	117	165	94	13	73									
658		68	39.32	17	165	104	13	70									
659		69	45.80	117	164	91	13	76									
660		70	40.50	119	165	103	14	80									
661		71	42.10	119	165	98	13	71									
662		72	41.40	119	165	101	14	74									
663		73	43.00	119	163	100	15	86									
664		74	50.96	119	163	96	13	72									
665		75	54.96	119	165	101	14	72									
666		76	38.88	119	162	99	13	76									
667		77	35.36	119	163	98	14	78									
668		78	30.18	117	165	105	12	50									
669		79	34.32	117	165	95	14	72									
670		80	45.96	117	165	103	15	78									
671		81	49.72	117	165	100	14	76									
672		82	45.84	118	167	94	14	71									
673		83	49.60	118	167	103	15	74									
674		84	49.64	118	167	106	17	92									
675		85	42.66	118	167	98	13	52									

based derivatives in Kenya, the hot spot site, and the eight lines identified provide stimulus to use these in breeding after we ascertain their resistance to the local race and test more elite germ plasms that are emerging. Even on the international front, synthetics from other alien resources have been incorporated in programs for addressing Ug99 resistance.

Breeding with synthetics requires some aspects to reconcile. First, the tough threshing character of the SH lines, which is a dominant trait and so inherited. Second, the presence of hybrid necrosis that causes F_1 seedlings to die prematurely due to the presence of the recessive *ne1* and *ne2* necrotic genes. Selection pressure in F_2 was for free-threshing types, whereas the necrotic combinations were automatically eliminated when F_1s were advanced; these were few.

The phenotypic attributes of the 68 combinations offer an enormous range of useful agronomic characteristics. For days-to-heading, the earliest was 110 days for combinations 41 and 53, 111 days for 48 and 57, and 112 days for 38, 65, and 68. The 1,000-kernel weight was 65 g in combination 1, 59.06 g for 46, 55.82 g for 14, 53.98 g for 59, and 53.52 g for 4; a major yield-enhancing component useful in wheat breeding. A spike length of 20 cm was in entry 55; 19 cm in 22; 18 cm for 3 and 35; 17 cm for 21, 65, and 68; and 16 cm for entry 18. Grains/spike were 110 in combinations 22, 23, 24, 28, 30, 55, 65, and 66; combinations 35 and 68 had 106; combinations 3, 14, 51, and 52 had 100; and several entries had grain numbers between 80 and 98, which also is advantageous for exploiting.

Deploying cultivars in irrigated and rain-fed locations of each of the four national provinces from the F_7 selections made is possible. For example, the eight Ug99 resistant entries (combinations 3, 4, 9, 20, 26, 27, 50, and 62) can be targeted for Baluchistan, Sindh, and lower Punjab where stem rust is prevalent and migration of Ug99 more imminent.

For the rain-fed areas of the country, 25 combinations (from 32 to 56) are ideal candidates. These have stripe rust resistance with a drought tolerant parental structure. The germ plasm is suitable for use in upper Punjab. The remaining combinations are suited for the NWFP. When choosing lines for deployment, high yield is coupled with priority constraints for the specific province; some are met here, some need to be further addressed, and the advanced are further to be studied over the next few generations.

The D-genome encoded storage protein subunits are very important because they strongly influence bread-making quality in wheat. The 690 advanced lines derived from 68 different cross combinations were subjected to SDS–PAGE to identify HMW-glutenin subunits in the D-genome. In the final analysis, sister lines derived from the same cross and having same subunit composition were not included. In the total of 68 advanced lines, 1Dx5+1Dy10 was predominant, found in 34 lines, followed by 1Dx2+1Dy12 in 22 advanced lines. Some novel HMW-glutening subunits were found. Among these novel subunits, 1Dx1.5+1Dy10 was found in six, 1Dx1.5+1Dy12 in three, 1Dx2.1+1Dy12 in four, and 1Dx2+1Dy10 and 1Dx3+1Dy12 in three advanced lines. Some rare subunits, such as 1Dx2+1DyT2, 1Dx3+1Dy10, 1Dx4+1Dy10, and 1Dx5+1Dy12, also were observed once in these advanced lines.

In this study the pre-dominant 1Dx5+1Dy10 is a superior subunit imparting better quality characteristics. Some better quality characteristics encoded by novel subunits are also very well documented. Conclusively these synthetic derivatives possess rich allelic diversity for HMW-GS which the conventional germplasm lacks due to the presence of only two subunits (1Dx5+1Dy10 and 1Dx2+1Dy12). So, more options become available to the wheat breeders if utilizing synthetic hexaploids in recombination breeding.

Phenotypic and molecular characterization of candidate wheat cultivars and their evaluation to key biotic stresses.

Alvina Gul Kazi, Awais Rasheed, Farrukh Bashir, and Abdul Mujeeb-Kazi.

Six candidate wheat genotypes derived from synthetic hexaploids are the subject for varietal release. Morphological observations (Table 45, p. 175) and their resistance to key biotic stresses, including leaf, stem, and stripe rust (Table 46, p. 176), were made.

The grain color of all these lines was amber, red, or their combination. Kazi-1 showed the maximum 1,000-kernel weight (55.70 g) followed by Kazi-2 (46.23 g). An important yield determinant, wheat grains having a 1,000-kernel weight greater than 55 g are categorized as extra large. Kazi-6 took the minimum number of days to mature (154), fol-

Table 45. Pedigree and phenotypic data of six candidate lines for varietal release (TKW = 1,000-kernel weight and DPM = days to physiological maturity).

Line	Pedigree	Grain color	TKW (g)	DPM	Plant height (cm)	Spike length (cm)	Awn color
Kazi-1	Not available	Amber	55.70	163	118	14.66	Light Brown
Kazi-2	QT8343/PASTOR*2/OPATA	Amber	46.23	170	102.3	12.66	Light Brown
Kazi-3	TURACO/5/CHIR3/4/SIREN//ALTAR84/ *Ae. tauschii* (205)/3/3*BUC/6/CNO	Red	44.11	171	108.6	13.66	Light Brown
Kazi-4	TURACO/5/CHIR3/4/SIREN//ALTAR84/ *Ae. tauschii* (205)/3/3*BUC/6/FCT	Amber-red	43.45	170	102.3	12.66	Light Brown
Kazi-5	MAYOOR//TKSN1081/*Ae. tauschii* (222)/3/CNO	Amber-red	41.45	160	123	13.3	Light Brown
Kazi-6	TURACO/5/CHIR3/4/SIREN//ALTAR84/ *Ae. tauschii* (205)/3/3*BUC/6/BCN	Red	40.80	154	119.6	10.6	Light Brown

lowed by Kazi-5 (160 days). Kazi-2 and Kazi-4 have the same minimum plant height (102.3 cm). Kazi-1 exhibited the maximum spike length (14.66 cm) followed by Kazi-3 (13.66 cm). All lines have light brown awns.

All genotypes were resistant to stripe rust at the adult-plant stage. Kazi-1–Kazi-5 were immune to stripe rust whereas Kazi-6 showed a trace stripe rust and Kazi-6 showed a terminal response of 5R. Similarly, stem rust resistance in these genotypes was evaluated at seedling stage under glass house conditions. The inoculum used to screen these genotypes were collected from two different locations (Sindh and Bahawalpur). Both inoculum were used separately for seedling tests (Table 46). All the lines tested with Sindh inoculum were resistant except Kazi-3, which showed an intermediate response and also gave the same response when tested with the inoculum from Bahawalpur. Kazi-5 exhibited an intermediate response to stem rust with Sindh inoculum but was immune when tested with inoculum from Bahawalpur. Heterogeneity in stem rust response also was observed in Kazi-1 for both inoculum types. We concluded that the stem rust inoculum from both location is diverse and has different virulence pattern. All genotypes had intermediate resistance to leaf rust at the seedling stage except for Kazi-4 and Kazi-6, which were immune. Kazi-1, Kazi-2, and Kazi-3 are

Table 46. Disease resistance data of six candidate lines for varietal release.

Line	Stripe rust (adult)	Stem rust (seedling) Matli, Sindh	Stem rust (seedling) Bahawalpur	Leaf rust (seedling)	Powdery mildew (seedling)	Spot blotch (seedling)
Kazi-1	0	1	4	4	R	4
Kazi-2	0	1	;	4	R	2
Kazi-3	0	12	23	34	R	2
Kazi-4	0	0	;	0	S	5
Kazi-5	TR	3	;	4	S	4
Kazi-6	5R	0	0	0	S	4

resistant powdery mildew, but the others are susceptible. However, powder mildew is not a big problem in most areas and susceptible cultivars can be deployed to Punjab and Sindh. For spot blotch, Kazi-2 and Kazi-4 were found to be resistant and the others showed a moderate reaction.

These six cultivars, along with eight Pakistani commercial wheat cultivars, also were evaluated for their molecular diversity using 264 SSR markers (Roder et al. 1998). The other elite Pakistani cultivars included Inqilab-91, Pak-81, Watan, Rohtas-90, Pasban-90, TJ-83, Bakhtawer-92, and Pirsabak-85. Kazi-6 grouped in a separate subcluster with Pak-81 and Inqilab-91 (Fig. 39). On the

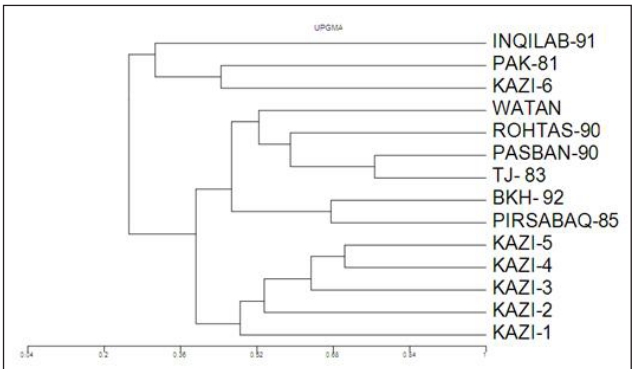

Fig. 39. Genetic diversity evaluation of the six candidate lines along with eight commercial cultivars of Pakistan using SSR markers.

other hand, Kazi 1–Kazi-5 were in a separate subcluster in which no current Pakistani cultivar was grouped; showinbg the unique genetic composition of Kazi-1–Kazi-5. Kazi-1 and Kazi-2 showed the maximum genetic diversity among all six candidate lines. Conclusively deploying these cultivars due to their molecular diversity from the existing commercial cultivars will be beneficial and enhance field diversity that will be difficult for the dynamic biotic stresses to cope with.

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Genetic discrimination for some quality attributes in genotypes with T1BL·1RS.

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High yield potential, better adaptability, and resistance to several biotic components are the advantages of the T1BL·1RS translocation in wheat. Cultivars carrying the T1BL·1RS translocation, such as Seri-82, Kavkaz, Neuzucht, and Lorvin10 and their derivatives, were highly involved in crossing programs from early 1970s to 1990s. Earlier reports suggested a negative effect of T1BL·1RS on dough and bread-making properties (Pena et al. 1990). Later, Mujeeb-Kazi et al. (1995) suggested that the adverse bread-making quality is not an exclusive function of T1BL·1RS. So, identifying genotypes with promising quality characteristics and carrying T1BL·1RS is of breeder's interest. In this study, 36 genotypes carrying the T1BL·1RS translocation were studied for some physio-chemical characteristics contributing to end-use quality.

The maximum variability was found for the gluten index (46.75%) followed by falling number (25.06%). The most consistent character was moisture content, which had a co-efficient of variability of 3.69%. Falling number ranged from 330.5 sec to 941.50 sec with an average of 466.30 sec. Eighteen of the 36 genotypes were found significantly different from mean at a CD 0.05. The standard deviation forfalling number was very high, and it also exhibited a higher co-efficient of variation (25.06%). Falling number is an indirect measure of α-amylase activity, and grains with a value greater than 400 sec have very low or no α-amylase activity. Protein content ranged from 9.03–14.97% with an average of 11.93%. Eighteen cultivars performed significantly different from the mean, and 15 had protein percentage greater than the overall mean. The co-efficient of variation for protein content was 12.53%. T1B·1R-510 showed the maximum protein content, whereas T1B·1R-500 had the minimum water content. Grain texture is the most important trait that determines hardness or softness of wheat. Hardness scores ranged from 27.33–59.67 with an average of 45.35. Replications were nonsignificant, whereas the genotypes were statistically significant. For co-efficient of variation for this trait, four genotypes were significantly different from mean and the others were not significant at a $CD_{0.05}$. Grain hardness is a key determinant for the classification of wheat and end-product quality (Campbell et al. 1999). Grain hardness primarily influences rheological properties of dough. The most important physical difference between the endosperm of hard and soft wheats lies in the adhesion between the starch granules and the surrounding protein matrix (Simmonds et al. 1973). All 36 wheat genotypes fell into the soft wheat category according to the NIR hardness scale. Moisture content ranged from 9.23–10.48% with an average of 9.78%. The co-efficient of variation for this trait was 3.69%, indicating lower variability among genotypes for this trait compared to others. Moisture content is greatly influenced by variation in the processing of grain and the method of grinding as well as variation in climatic conditions and temperature during harvest.

Thousand-kernel weight ranged from 22.40–50.00 g with an average of 35.69 g. The co-efficient of variability (6.02%) was lower for this trait (Table 47, p. 177). Fourteen genotypes were significantly different from the mean at $CD_{0.05}$. This trait is a function of grain size and density. Wheat kernels can be classified according to grain weight; 15–25 g (very small), 26–35 g (small), 36–45 g (medium), 46–55 g (large), and over 55 g (very large). Most of the genotypes are in the medium graincategory according to this scale. The ash content of these genotypes ranged from 1.45–1.85% with an average of 1.65%. All the genotypes were significantly different from the mean at $CD_{0.05}$. Ash content is the inorganic material left after flour is burned and is an important determinant of extraction rate and influences flour color and quality. Zahoor (2003) reported an ash content of 0.30–0.53% in Pakistani wheat cultivars. The higher ash content found in these genotypes indicates the presence of a higher proportion of bran than endosperm flour.

Wet gluten was observed maximum in T1B·1R-488 (36.38%) and minimum in T1B·1R-492 (18.67%). The average wet gluten was 24.53%. Five genotypes performed significantly different from mean at CD0.05. Wet gluten has a strong effect on dough rheology and baking performance. Wet forms are more quickly incorporated into low-protein

Table 47. Some quality attributes in genotypes with T1BL·1RS. Means significantly different from mean at a CD = 0.05.

Genotype	Falling number	Protein (%)	Hardness score	Moisture (%)	1,000-kernel weight	Ash (%)	Wet gluten (%)	Gluten index
T1B·1R-469	330.50	10.30	34.00	9.60	39.40	1.65	21.44	58.70
T1B·1R-470	343.67	10.97	36.00	9.73	41.20	1.78	20.97	40.51
T1B·1R-471	427.33	11.35	49.50	9.65	33.80	1.74	23.12	29.17
T1B·1R-472	461.00	11.53	51.00	10.10	30.40	1.60	22.09	11.05
T1B·1R-474	538.50	14.13	46.00	9.83	31.40	1.83	35.71	36.54
T1B·1R-475	510.00	12.93	46.67	9.60	29.83	1.66	27.02	82.13
T1B·1R-476	427.50	11.93	41.33	9.47	29.68	1.66	22.00	64.00
T1B·1R-478	336.00	12.80	43.67	9.57	33.00	1.80	25.20	58.45
T1B·1R-479	434.00	12.97	45.00	9.43	27.40	1.70	26.34	67.00
T1B·1R-480	419.50	12.40	27.33	9.83	33.00	1.52	23.45	92.75
T1B·1R-481	422.00	13.90	42.33	9.50	22.40	1.69	27.33	83.00
T1B·1R-482	462.00	12.23	42.33	9.67	32.50	1.68	26.97	22.52
T1B·1R-483	464.50	12.93	55.00	9.40	30.80	1.65	25.61	8.48
T1B·1R-485	455.00	12.27	53.00	10.13	31.20	1.56	26.84	12.44
T1B·1R-486	501.00	11.43	49.67	10.47	33.20	1.51	26.65	12.70
T1B·1R-487	477.50	12.33	52.50	9.63	36.80	1.60	28.93	16.27
T1B·1R-488	450.00	13.73	53.00	9.63	37.40	1.69	36.38	27.20
T1B·1R-489	405.50	12.50	48.00	9.43	30.00	1.83	26.33	59.81
T1B·1R-490	377.33	11.37	48.00	9.41	33.40	1.60	23.79	46.10
T1B·1R-491	397.50	11.43	42.67	9.23	29.80	1.66	19.75	61.00
T1B·1R-492	441.50	10.27	38.67	10.17	31.80	1.63	18.67	73.00
T1B·1R-493	323.33	11.37	48.00	9.38	34.80	1.54	21.29	66.00
T1B·1R-494	421.00	10.00	47.33	9.59	32.50	1.54	21.85	81.18
T1B·1R-496	501.50	11.17	47.33	9.54	36.60	1.61	23.02	45.44
T1B·1R-497	449.50	10.03	47.33	9.53	36.00	1.62	19.47	85.00
T1B·1R-498	437.00	10.87	48.00	10.10	38.80	1.61	20.45	83.21
T1B·1R-500	538.00	9.03	45.67	10.18	33.80	1.51	21.40	82.00
T1B·1R-501	403.50	9.57	26.00	9.70	33.20	1.68	22.34	88.22
T1B·1R-502	398.00	10.43	31.67	9.47	35.00	1.45	20.13	36.88
T1B·1R-503	403.50	10.20	46.00	9.50	39.40	1.55	20.30	83.05
T1B·1R-508	458.50	11.70	55.67	10.48	48.60	1.61	28.56	86.00
T1B·1R-509	691.00	13.93	57.67	10.33	43.00	1.57	27.31	78.50
T1B·1R-510	556.50	14.97	59.00	10.14	48.20	1.78	23.45	54.76
T1B·1R-511	941.50	13.77	56.00	10.07	46.60	1.77	22.78	65.34
T1B·1R-512	724.00	14.87	59.67	10.05	50.00	1.85	27.76	43.23
T1B·1R-514	458.00	11.90	46.67	10.61	49.60	1.64	28.54	45.00
Mean	466.30	11.93	46.32	9.78	35.68	1.65	24.53	55.18
Standard deviation	116.87	1.50	8.10	0.36	6.58	0.10	4.10	25.80
CV(%)	25.06	12.53	17.48	3.69	18.44	6.02	16.69	46.75

flour than dry form (Czuchajowska and Paszczynska, 1996) and also affects dough strength, gas retention and controlled expansion, structural enhancement, water absorption and retention, and natural flavor (Grausgruber et al. 2000).

Conclusively, T1B·1R-512 showed over all better quality characteristics with a falling number of 724 sec, indicating no α-amylase activity. Protein content is 14.87%, 1,000-kernel weight is 50 g, and wet gluten is 27.76%, which make it distinct in this group of genotypes. The reported negative effects of T1BL·1RS translocations on wheat quality also can be avoided by the introgression of superior HMW-glutenin subunits at *Glu-B1* (7+8) and *Glu-D1* (5+10).

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Pasting properties of wheat flours of eight hard white spring wheat cultivars.

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Starch is the main fraction of wheat. One of the main functions of starch is to set the pasting properties of wheat flour. Other factors, including protein, particle size distribution, α-amylase, starch damage, sugar, and salt, have a minor to significant impact on pasting properties of wheat flour (Nagao 1995; Wei 2002; Mousia et al. 2004). The pasting properties of wheat flour from eight hard white spring wheat (HWSW) cultivars grown in two locations in Pakistan were studied (Table 48, p. 179). The pasting profile of wheat cultivars was evaluated in terms of pasting temperature, peak viscosity, time to reach peak viscosity, hot-paste viscosity, breakdown viscosity, setback viscosity, and cold-paste viscosity using a Brabender Microviscoamylography (Model 803201, Brabender, Germany).

The pasting temperature of wheat cultivars ranged from 56.8–62.8°C and 56.5–58.4°C at Nawabshah and Tandojam, respectively. Imdad, Mehran, Abadgar, Moomal, and SKD-1 showed significant variation in pasting temperature with location. Thus, providing credence to the notion that a change in growing conditions can significantly affect the architecture of wheat kernel, which subsequently modifies the physico-chemical properties of wheat flour from the corresponding wheat cultivars.

Peak viscosity is a very important parameter that governs the thickening property of wheat flour. Viscosity is highest when there is a maximum number of swollen intact starch granules present in the wheat flour slurry (Thomas and Atwell 1999). Peak viscosity was found to vary significantly with location and ranged between 1,029–1,296 BU and 875–1,230 BU for HWSW cultivars at Nawabshah and Tandojam, respectively. The extent of variation with location ranged between 18–174 BU. The lowest and highest variation were in Anmol and Mehran, respectively. Sowing conditions could affect peak viscosity; researchers have found increased peak viscosity under late-sown conditions (Singh et al. 2010).

The time to reach peak viscosity is basically the measure of gelatinization of starch granules. Variation in location significantly effected time to reach peak viscosity of all HWSW cultivars except Anmol. The time to reach peak viscosity ranged between 14:30–16:30 min at Nawabshah and 13:10–16:20 min at Tandojam. SKD-1 at Tandojam took the least time to reach peak viscosity whereas Anmol took the longest.

Breakdown viscosity also measures the extent of fragility of starch granules (Thayumanavan and Kumari 1998). Higher breakdown values reflect less ability of starch granules to withstand high shear conditions often encountered in food processes such as blending, homogenization, and extrusion. Lower breakdown values indicate a high shear

resistance of starch granules. Breakdown viscosity of the flours ranged between 395–695 BU, with the lowest and highest values in Imdad at Tandojam and TJ-83 at Nawabshah, respectively. Change in location significantly effected the breakdown viscosity of the wheat cultivars; the minimum in Mehran and the maximum variations in Abadgar. Breakdown is low in flours with a high protein content (Singh et al. 2010) and higher amylose content (Miuria et al. 2002; Blazek and Copeland 2008). Singh et al, (2010) also found an increase in breakdown under rain-fed conditions.

Table 48. Pasting properties of wheat flours of eight hard white spring wheat cultivars at two locations in Pakistan, Nawabshah (NS) and Tandojam (TJ). Different superscript letters within the same column are significantly different at a $p < 0.05$.

Location	TD-1	Imdad	Mehran	Abadgar	Moomal	Anmol	SKD-1	TJ-83
Pasting temperature								
NS	57.3[a]	58.3[a]	56.8[a]	62.8[a]	57.0[a]	57.2[a]	58.5[a]	58.6[a]
TJ	57.1[a]	56.6[b]	58.3[b]	57.0[b]	56.5[b]	57.4[a]	60.4[b]	58.4[a]
Peak wiscosity								
NS	1,108[a]	1,174[a]	1,049[a]	1,065[a]	1,029[a]	1,212[a]	1,145[a]	1,296[a]
TJ	999[b]	1,033[b]	875[b]	1,202[b]	992[b]	1,230[b]	1,074[b]	1,208[b]
Time to reach peak wiscosity								
NS	16:30[a]	15:40[a]	16:00[a]	14:55[a]	15:15[a]	16:20[a]	14:30[a]	15:00[a]
TJ	14:00[b]	16:10[b]	14:35[b]	15:10[b]	16:00[b]	16:35[a]	13:10[b]	16:20[b]
Breadown								
NS	479[a]	578[a]	623[a]	403[a]	606[a]	542[a]	597[a]	695[a]
TJ	528[b]	395[b]	597[b]	640[b]	396[b]	569[b]	523[b]	592[b]
Hot-paste viscosity								
NS	629[a]	594[a]	424[a]	662[a]	423[a]	682[a]	548[a]	601[a]
TJ	471[b]	638[b]	277[b]	561[b]	597[b]	660[a]	550[a]	606[a]
Setback								
NS	378[a]	613[a]	516[a]	585[a]	563[a]	561[a]	523[a]	501[a]
TJ	540[b]	669[b]	467[b]	557[b]	579[a]	566[a]	472[b]	515[a]
Cold-paste viscosity								
NS	1,146[a]	1,166[a]	934[a]	1,214[a]	981[a]	1,221[a]	998[a]	1,048[a]
TJ	962[b]	1,213[b]	796[b]	1,089[b]	1,115[b]	1,153[b]	853[b]	1,056[a]

The hot-paste viscosity of TD-1, Imdad, Mehran, Abadgar, and Moomal varied significantly with location. The cultivars at Nawabshah ranged between 423–682 BU and those at Tandojam 277–660 BU. The variation in hot-paste viscosity in the cultivars ranged between 2–174 BU.

Cold-paste viscosity measured at 50°C varied with the change of location and the extent of variation ranged between 8–184 BU. Mehran at Tandojam and Abadgar at Nawabshah showed lowest and highest CPV values, respectively. Setback viscosity is the measure of retrogradation tendency of starch granules (Karim et al. 2000). When a gelatinized starch slurry is cooled, the leached out amylose chains reassociate with each other. Therefore, higher setback values reflect increased retrogradation tendency of starch granules. TD-1, Imdad, Mehran, Abadgar, and SKD-1 showed significant differences in setback viscosity with location. Compared to other HWSW cultivars, TD-1 at Nawabshah showed a very low setback value of 378 BU, whereas Imdad at Tandojam showed highest setback value of 669. Peak viscosity for the cultivars was found to be positively correlated with cold-paste viscosity with a Pearson correlation coefficient of 0.660 at $p < 0.01$. Cold-paste viscosity was found to be positively correlated with hot-paste viscosity (0.857) and time to reach peak viscosity (0.626) with Pearson coefficients $p < 0.01$.

The pasting properties of wheat flour were related to cultivar as well as growing location. Furthermore, other cultivars, including approved and those in the pipeline, shall be exploited for their pasting profiles.

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Arabinoxylan levels in hard wehat of various origin.

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A total of 39 hard wheat samples representing seven origins (Australia, Argentina, Brazil, Canada, France, Pakistan, and the Russian Federation) and two classes (white and red) were analyzed for their total arabinoxylan (AXt) and water-extractable arabinoxylan (WeAX) content.

The mean, minimum, and maximum values for AXt and WeAX of wheat of various origin are given in Table 49. AXt and WeAX were 45.6–84.2 mg/g and 5.2–12.4 mg/g in meal and 11.1–24.1 mg/g and 2.7–8.7 mg/g in flour, respectively. The highest and lowest values were found in Pakistani wheat. However, the highest mean values for AXt and WeAX in meal and flour were found in the wheats from Argentina. These values were significantly different from those of Pakistani wheats. On the other hand, Pakistani wheat was not statistically different from Australian wheat in their AX levels. For WeAX, the lowest meal value was in Australian and French wheats. The flours of Pakistani and Australian wheats contained the lowest amount of WeAX. The variation observed in the AX content of these wheats is due to their different genetic background and market classes. Hong et al. 1989; Anderson et al. 1992; Saulnier et al. 1995; Lempereur et al. 1997 all reported that AX content varies with genotype and environment. Furthermore, we analyzed the relationship of AX content with other quality parameters and found no clear relationship. Li et al. (2009) also found no significant relationship of AX with test weight, protein, or hardness. However, some obvious relationships were found between the AXt and WeAX. AXt was positively related with WeAX in meal (r = 0.919**) and flour (r = 0.949**). In flour, AXt and WeAX was directly related with their amount in meal. Highly significant relationships were found between AXt in meal and flour (r = 0.892**), and WeAX in meal was significantly related with that in flour (r = 0.872**).

Table 49. Minimum, maximum and mean[1] values for total arabinoxylan (AXt) and water-extractable arabinoxylan (WeAX) content of wheat of different origin.

	Arabinoxylan contents (mg/g)			
	Meal		Flour	
Origin	AXt	WeAX	AXt	WeAX
Australia				
Min	51	6.3	12.2	3.6
Max	63	8.2	17.2	6.5
Mean	55[a]	7.2[ad]	15.1[a]	5.3[a]
Argentina				
Min	67.2	8.7	18.0	7.2
Max	77.3	10.4	21.1	8.0
Mean	72.4[bc]	9.5[ab]	19.6[b]	7.6[b]
Brazil				
Min	65.4	8.5	17.7	6.7
Max	76	10.0	20.1	7.7
Mean	70.7[ab]	9.2[bc]	18.9[bc]	7.2[bc]
Canada				
Min	55	6.9	15.0	5.5
Max	63	8.1	17.4	6.5
Mean	58.5[ab]	7.4[bc]	16.4[ac]	6.0[ab]
France				
Min	51	6.1	12.5	3.7
Max	66	8.7	17.7	6.6
Mean	59.5[ab]	7.2[c]	15.7[a]	5.6[ac]
Pakistan				
Min	45.6	5.2	11.1	2.7
Max	84.2	12.4	24.1	8.7
Mean	59.9[a]	7.9[d]	15.2[ac]	5.3[a]
Russia				
Min	67	8.9	17.9	6.8
Max	75	10.0	20.7	7.8
Mean	70.7[c]	9.3[ab]	18.8[b]	7.3[b]

Saulnier et al. (1995) evaluated the usefulness of wheat as poultry feed with a major emphasis on AX content in 22 wheat cultivars grown at different locations in France. They found that cultivars with a high natural variation (CV 8%) in total AX content ranging from 5.53–7.79% with the mean value of 6.63%. In our study, the AX content of French wheat ranged from 51–66 mg/g (5.1-6.6%) with the mean value of 59.5 mg/g (5.95%). These varied results were obtained due to different samples. In another study by Lempereur et al. (1997), the AX content ranged from 4.07–6.02% in durum wheat cultivars grown in France under different agronomic conditions. The value of AX in durum wheat is similar to that of bread wheat (Medcalf & Gilles 1968). All wheats except those from the Russian Federation were not found statistically different from the French wheat in their AXt level (meal). Furthermore, the AXt and WeAX content of French wheat (meal and flour) were found to be significantly different from that of Russian wheat but not significantly different from Canadian wheat. Canadian wheat samples ranged from 55–63 mg/g (5.5–6.3%) with the mean value of 58.2 mg/g (5.82%). Wang et al. (2006) reported almost the same range (5.45–7.32%) for AX content in six commercially grown samples of common hard spring wheats. In addition to French wheat, Canadian wheat was found to be not significantly different from Brazilian wheat in AX level. Specifically, the WeAX content in the flour of Canadian wheat was not statistically different from that of all wheat samples in the study.

In this study, a total of 39 hard spring wheats were analyzed; 24 were white and 15 were red. The AX content of the white wheats varied widely (Table 50). However, the mean AX content of the red wheats was greater than that of the white wheats. We have not found consistent differences in AX content of white wheats and red wheats (Table 50).

Table 50. Levels of arabinoxylan in red and white wheats of different origin.

	Meal				Flour			
	Total arabinoxylan content		Water-extractable arabinoxylan content		Total arabinoxylan content		Water-extractable arabinoxylan content	
Type	Red	White	Red	White	Red	White	Red	White
Minimum	51.0	45.6	6.1	5.2	12.5	11.1	3.7	2.7
Maximum	77.3	84.2	10.4	12.4	21.1	24.1	8.0	8.7
Mean	68.0	59.2	8.8	7.8	18.1	15.3	6.9	5.3

The development of high quality wheat depends on a thorough understanding of the influential factors and parameters. No doubt, AXs have a significant impact on the quality of the end-product. Because they are mainly concentrated in outer layer, AX was greater in the meal than in the flour. AX varied with the growing location irrespective of wheat class (red or white). Wheat of different origin with a known AX content can be better utilized for its desired end-product. Information about AX level will be useful for a country like Pakistan that imports wheat from diversified origins.

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High-molecular-weight glutenin subunit variation in B-genome amphiploids (2n=6x=AABBBB).

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Sixteen B-genome amphiploids (2n=6x=42; AABBBB) were analyzed for their HMW -glutenin subunit diversity using SDS-PAGE. Three durum and 13 *Ae. speltoides* accessions were utilized to develop these amphiploids. All the durum parents had null subunit encoded by the allele *Glu-A1c* at the *Glu-A1* locus. Three different subunit pairs, 7+8, 17+18, and 13+16, were found at the *Glu-B1* locus in the amphiploids (Table 51). The locus contributed by the Ae. *speltoides* was designated as *Glu-B^{s}1*. The allelic classification at this locus followed international recommendations (McIntosh et al. 1998, 2007), although the genes were designated with Roman numerals to avoid possible ambiguities for inclusion in Wheat Gene Catalogue. The name of each allele was sequentially based on frequency among accessions.

Table 51. Allelic variation at the *Glu-1* loci in B-genome amphiploids (2n=6x=42; AAAABB) derived from *Aegilops speltoides*.

Line	Pedigree	*Glu-A1*	*Glu-B1*	*Glu-B^{s}1*
B1	CETA/*Ae. speltoides* (127)	Null	13+16	*Glu-B^{s}1-IV*
B2	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (133)	Null	7+8	*Glu-B^{s}1-V*
B3	ARLIN_1/*Ae. speltoides* (134)	Null	17+18	*Glu-B^{s}1-I*
B4	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (135)	Null	7+8	*Glu-B^{s}1-VI*
B5	CETA/*Ae. speltoides* (139)	Null	13+16	*Glu-B^{s}1-VII*
B6	ARLIN_1/*Ae. speltoides* (126)	Null	17+18	*Glu-B^{s}1-VIII*
B7	ARLIN_1/*Ae. speltoides* (128)	Null	17+18	*Glu-B^{s}1-IX*
B8	ARLIN_1/*Ae. speltoides* (130)	Null	17+18	*Glu-B^{s}1-X*
B9	ARLIN_1/*Ae. speltoides* (131)	Null	17+18	*Glu-B^{s}1-XI*
B10	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (143)	Null	7+8	*Glu-B^{s}1-XII*
B11	ARLIN_1/*Ae. speltoides* (144)	Null	17+18	*Glu-B^{s}1-XIII*
B12	ARLIN_1/*Ae. speltoides* (147)	Null	17+18	*Glu-B^{s}1-II*
B13	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (147)	Null	7+8	*Glu-B^{s}1-II*
B14	ARLIN_1/*Ae. speltoides* (156)	Null	17+18	*Glu-B^{s}1-III*
B15	CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. speltoides* (156)	Null	7+8	*Glu-B^{s}1-III*
B16	ARLIN_1/*Ae. speltoides* (131)	Null	17+18	*Glu-B^{s}1-XIV*

A very rich diversity was contributed by *Ae. speltoides*. All accessions used to develope these amphiploids had a unique allele at *Glu-B^{s}1* except for *Ae. speltoides* lines 134 and 139. Lines B13 and B15 encoded only x-type subunits, whereas all the remaining accessions encoded both x- and y-type subunits at the *Glu-B^{s}1* locus. A total of 14 different subunits were observed in these 16 amphiploids. Lines B14 and B15 and B12 and B13 had same durum and *Ae. speltoides* parents, therefore they did not show any heterogeneity between one another. Previously, Fernández-Calvín (1990) identified HMW-glutenin subunits in *Ae. searsii* and *Ae. speltoides* and concluded that these subunits moved within the range of B-genome in hexaploid wheat. However, *Ae. speltoides* is the only species that could explain the variability for HMW-subunits previously described for the B genome of wheat, and therefore, cannot be excluded as a possible donor of this genome. These genetic resources can be a good source for using the allelic variation in *Ae. speltoides* in common hexaploid wheat through standard breeding methodologies.

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Bread quality of hard white spring wheat cultivars grown at two locations.

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The bread-making performance of flours from eight Pakistani hard white spring wheat (HWSW) cultivars grown at two locations were evaluated for their quality attributes including loaf height (LH), loaf volume (LV), specific loaf volume (SLV), and sensory and textural properties (Table 52).

Table 52. Loaf height, loaf volume, specific loaf volume, and crumb firmness of breads prepared from hard white spring wheat cultivars grown at Nawabshah (NS) and Tandojam (TJ), in Pakistan.

Cultivar	Loaf height (cm)		Loaf volume (cm^3)		Specific loaf volume (cm^3/g)		Crumb firmness (g)	
	NS	TJ	NS	TJ	NS	TJ	NS	TJ
TD-1	8.4	7.0	709.8	591.5	5.1	4.2	829.90	946.83
Imdad	7.6	8.0	642.2	676.0	4.6	4.8	865.64	850.10
Mehran	8.1	9.5	684.5	802.8	4.9	5.7	837.27	802.70
Abadgar	7.1	10.0	600.0	845.0	4.3	6.0	909.30	750.40
Moomal	6.1	7.8	515.5	659.1	3.7	4.7	964.91	858.40
Anmol	7.1	7.8	600.0	659.1	4.3	4.7	925.60	869.13
SKD-1	5.8	7.9	490.1	667.6	3.5	4.8	990.69	852.30
TJ-83	6.3	8.4	532.4	709.8	3.8	5.1	940.41	835.80

Breads varied in their LH, LV, and SLV with the change of genotype and location. Many workers have found the significant effects of genotype and environment on bread-making quality in wheat (Johansson et al. 1999; Anjum and Walker 2000; Mladenov et al. 2001; Yong et al. 2004; Finlay et al. 2007). The cultivars ranged from 5.8–8.4 cm (LH), 490.1–709.8 cm^3 (LV), and 3.5–5.1 cm^3/g (SLV) when grown at Nawabshah, and, they ranged from 7.0–10.0 cm (LH), 591.5 to 845.0 cm^3 (LV), and 4.2 to 6.0 cm^3/g (SLV) when grown at Tandojam. All the cultivars, except TD-1, performed better at Tandojam than at Nswabshah for LH, LV, and SLV. The highest and lowest values for LH, LV, and SLV were by Abadgar (at Tandojam) and SKD-1 (at Nawabshah), respectively.

Quality assessment of bread by sensory evaluation is a subjective evaluation based on personal judgment. The results are, therefore, not absolute and reflect consumer preference. Several workers suggest that baking scores be made in addition to loaf volume (Bhatt and Derera 1975; Mladenov et al. 2001). Similar to physical properties, the sensory characteristics of breads varied with cultivar and location. The results were inline with previous studies (Mladenov et al. 2001). All the cultivars had scores greater than 70 out of 100 at both locations (Table 53). Bread from TD-1 (at Nawabshah) was superior with respect to sensory attributes. Marginal differences were observed between the dough scores of different cultivars. One reason would be the optimum addition of water as assessed by Farinograph. The dough scores of cultivars grown at Nawabshah and Tandojam ranged from 23 to 25 and 24 to 25, respectively.

Table 53. Dough and bread quality scores of Pakistani wheat cultivars grown at Nawabshah (NS) and Tandojam (TJ), in Pakistan.

Cultivar	Dough score (27)		External score (18)		Internal score (55)		Total score (100)	
	NS	TJ	NS	TJ	NS	TJ	NS	TJ
TD-1	25	25	18	11	48	43	91	79
Imdad	23	25	17	16	46	45	86	86
Mehran	24	24	18	18	48	48	90	90
Abadgar	25	24	15	18	44	45	84	87
Moomal	25	24	9	11	40	43	74	78
Anmol	24	25	15	17	35	46	74	88
SKD-1	24	24	11	15	39	41	74	80
TJ-83	25	25	14	18	38	46	76	89

Breads were analyzed for external quality including external symmetry, break and shred, crust character, and color. All cultivars had external scores in between 15 and 18 out of 18 except Moomal, SKD-1, and TD-1. Moomal had the lowest external score (9) when grown at Nawabshah and was nearly similar at Tandojam with a score of 11. Cultivars SKD-1 and TD-1 scored an 11 at both locations, however, they performed better with the change of location as SKD-1 scored a 15 at Nawabshah and TD-1 scored an 18 at Tandojam.

Internal scores were given on the basis of internal grain, texture, crumb body, crumb color, taste/aroma, and mouth feel. At Nawabshah, the cultivars ranged from 35 to 48, and the lowest internal score was given to the bread from Anmol due to its inferior internal grain, texture, and crumb body. This cultivar's internal quality was found in a narrow range (41–48) at Tandojam. Mehran had the highest score (48) at both locations. All the cultivars had nearly same taste, aroma, and mouth feel.

The crumb firmness varied with cultivar and growing location (Table 52, p. 183). Crumb firmness of breads was 829.90–990.69 g at Nawabshah and 750.40–946.83g at Tandojam. All cultivars except TD-1 produced firmer breads when grown at Nawabshah. Cultivars having the highest and lowest SLV, e.g., Abadgar (at Tandojam) and SKD-1 (at Nawabshah), respectively, also have the lowest and highest crumb firmness, which agrees with previous studies by Axford et al. (1968), Maleki et al. (1980), and Courtin et al. (2001).

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Marker-assisted selection for stripe rust resistance genes and allelic variation at the Glu-1 locus in synthetic-derived, advanced lines.

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SDS-PAGE analysis was utilized to study HMW-GS composition in 95 advanced synthetic derivatives, five local cultivars (Inqilab-91, Seher, Bhakkar, TD-1, and Fareed), a durum wheat, and SH-854 (Table 54, pp. 185-186). These advanced synthetic derivatives were partitioned into 27 different HMW-GS combinations (Table 55, p. 186-187). At the *Glu-A1* locus, the composition of alleles was only contributed by x-type subunits, 1Ax1, 1Ax2*, and null, which are controlled by alleles *Glu-A1a*, *Glu-A1b*, and *Glu-A1c*, respectively. Of the advanced synthetic derivatives, the null allele was the most frequent (63, 61.76%), followed by 1Ax1 (20, 19.60%), and 1Ax2* (19, 18.62%). The predominant null allele at this locus was reported previously by several workers. A higher proportion of the null allele has been reported in synthetic hexaploids (Pena et al. 1995) and in the world collection of wheat cultivars (Payne and Lawrence 1983) and justifies the predominance of null in these advanced synthetic derivatives. The subunit composition 'null 17 + 18 and 5 + 10' was the most frequent, found in 15 advanced lines (Kazi-09, Kazi-24, Kazi-32, Kazi-33, Kazi-53, Kazi-55, Kazi-58, Kazi-60, Kazi-61, Kazi-63, Kazi-65, Kazi-69, Kazi-71, Kazi-102, and Kazi-108). Another frequent subunit composition was 'null 7 + 8 and 5 + 10' was found in nine entries (Seher, Bhakkar, Kazi-17, Kazi-43, Kazi-49, Kazi-50, Kazi-51, Kazi-52, and Kazi-92). Apart from the null allele, 39 (38.23%) of the 102 advanced lines had either 1Ax1 or 1Ax2*, which impart better quality to wheat flour and are associated with higher extensibility and better dough strength (Branlard and Dardevet 1985). Several other subunits with different unique compositions also were found in these advanced synthetic derivatives. The subunits null and 2* also were found in large number of entries. The majority

Table 54. Pedigrees of advanced lines used to assay stripe rust resistance genes and allelic variation at the *Glu-1* locus.

Entry #	Name	Pedigree
1	INQILAB	WL 711/CROW`S'
2	SEHER	CHILL/2* STAR/4/BOW//BUC/PVN/3/2* VEE#10
3	BHAKKAR	P20102/PIMA/SKA/3/TTR`S'/BOW`S'
4	TD-1	MAI'S' X NORTENO65 X H68
5	FAREED	PT'S'/3/TOB/LFN//BB/4/BB/HD-832-5//ON/5/G-V/ALD'S'//HPO
6	SH	D67.2/P66.270//AE.SQUARROSA (634)
7	DURUM	ROK/KML
8	KAZI-9	SERI.1B*2/3/KAUZ*2/BOW/KAUZ/4/PBW343*2/KUKUNA
9	KAZI-10	WHEAR/TUKURU//WHEAR
10	KAZI-11	WHEAR/KUKUNA/3/CBO.1/3*BATAVIA//2*WBLLI
11	KAZI-12	TURACO/5/CHIR3/4/SI-REN/ALTAR84/*Ae. tauschii* (205)/3/3*BUC/6/CNO
12	KAZI-13	CHAPIO/INQALAB 91 x RABI//GS/CRA
13	KAZI-14	CHAPIO/INQALAB 91 x RABI//GS/CRA
14	KAZI-15	TURACO/5/CHIR3/4/SI-REN/ALTAR84/*Ae. tauschii* (205)/3/3*BUC/6/BCN
15	KAZI-16	TURACO/5/CHIR3/4/SI-REN/ALTAR84/*Ae. tauschii* (205)/3/3*BUC/6/CNO
16	KAZI-17	TURACO/5/CHIR3/4/SI-REN/ALTAR84/*Ae. tauschii* (205)/3/3*BUC/6/FCT
17	KAZI-18	TURACO/5/CHIR3/4/SI-REN/ALTAR84/*Ae. tauschii* (205)/3/3*BUC/6/FCT
18	KAZI-19	SABUF/3/BCN/CETA/*Ae. tauschii*/4/BCN
19	KAZI-20	SABUF/3/BCN/CETA/*Ae. tauschii*/4/CNO
20	KAZI-21	SABUF/3/BCN/CETA/*Ae. tauschii*/4/FCT
21	KAZI-22	MAYOOR//TKSN1081/*Ae. tauschii*/3/OPA
22	KAZI-23	MAYOOR//TKSN1081/*Ae. tauschii*/3/CNO
23	KAZI-24	MAYOOR//TKSN1081/*Ae. tauschii*/3/FCT
24	KAZI-25	MAYOOR//TKSN1081/*Ae. tauschii*/3/FCT
25	KAZI-26	YS/PASTOR
26	KAZI-27	12*2
27	KAZI-28	KARIEGA/SAAR
28	KAZI-29	KARIEGA/SAAR

Table 54. Pedigrees of advanced lines used to assay stripe rust resistance genes and allelic variation at the *Glu-1* locus.

Entry #	Name	Pedigree
29	KAZI-30	KARIEGA/SAAR
30	KAZI-31	KARIEGA/SAAR
31	KAZI-32	KARIEGA/SAAR
32	KAZI-33	KARIEGA/SAAR
33	KAZI-34	KARIEGA/SAAR
34	KAZI-35	KARIEGA/SAAR
35	KAZI-36	KARIEGA/SAAR
36	KAZI-37	KARIEGA/SAAR
37	KAZI-38	KARIEGA/SAAR
38	KAZI-39	KARIEGA/SAAR
39	KAZI-40	KARIEGA/SAAR
40	KAZI-41	KARIEGA/SAAR
41	KAZI-42	KARIEGA/SAAR
42	KAZI-43	KARIEGA/SAAR
43	KAZI-44	KARIEGA/SAAR
44	KAZI-45	KARIEGA/SAAR
45	KAZI-46	KARIEGA/SAAR
46	KAZI-47	KARIEGA/SAAR
47	KAZI-48	KARIEGA/SAAR
48	KAZI-49	KARIEGA/SAAR
49	KAZI-50	KARIEGA/SAAR
50	KAZI-51	KARIEGA/SAAR
51	KAZI-52	KARIEGA/SAAR
52	KAZI-53	KARIEGA/SAAR
53	KAZI-54	KARIEGA/SAAR
54	KAZI-55	KARIEGA/SAAR
55	KAZI-56	KARIEGA/SAAR
56	KAZI-57	KARIEGA/SAAR
57	KAZI-58	KARIEGA/SAAR
58	KAZI-59	KARIEGA/SAAR
59	KAZI-60	KARIEGA/SAAR
60	KAZI-61	KARIEGA/SAAR
61	KAZI-62	KARIEGA/SAAR
62	KAZI-63	KARIEGA/SAAR
63	KAZI-64	KARIEGA/SAAR
64	KAZI-65	KARIEGA/SAAR
65	KAZI-66	KARIEGA/SAAR
66	KAZI-67	KARIEGA/SAAR
67	KAZI-68	KARIEGA/SAAR
68	KAZI-69	KARIEGA/SAAR
69	KAZI-70	KARIEGA/SAAR
70	KAZI-71	KARIEGA/SAAR
71	KAZI-72	KARIEGA/SAAR
72	KAZI-73	KARIEGA/SAAR
73	KAZI-74	FILIN/KARIEGA
74	KAZI-75	FILIN/KARIEGA
75	KAZI-76	FILIN/KARIEGA
76	KAZI-77	FILIN/KARIEGA
77	KAZI-78	FILIN/KARIEGA
78	KAZI-79	FILIN/KARIEGA

Table 54. Pedigrees of advanced lines used to assay stripe rust resistance genes and allelic variation at the *Glu-1* locus.

Entry #	Name	Pedigree
79	KAZI-80	FILIN/KARIEGA
80	KAZI-81	FILIN/KARIEGA
81	KAZI-82	FILIN/KARIEGA
82	KAZI-83	FILIN/SAAR
83	KAZI-84	FILIN/SAAR
84	KAZI-85	FILIN/SAAR
85	KAZI-86	FILIN/SAAR
86	KAZI-87	FILIN/SAAR
87	KAZI-88	FILIN/SAAR
88	KAZI-89	PFAU/WEAVER*2/3/WEAVER/ ESDA//BORL95
89	KAZI-90	BL 1496/MILAN/3/CROC_1/*Ae. tauschii* (205)//…
90	KAZI-91	MILAN/S87230//BABAX
91	KAZI-92	PSN/BOW//SERI/3/MILAN/4/AT-TILA
92	KAZI-93	CROC_1/*Ae. tauschii* (205)// KAUZ/3/BJY/COC//PRL/BOW
93	KAZI-94	KRICHAUFF/2*PASTOR
94	KAZI-95	OASIS/SKUAZ//4*BCN/3/WBLL1
95	KAZI-96	BABAX/3/PRL/SARA//TSI/ VEE#5/4/WBLL1
96	KAZI-97	JNRB.5/PIFED
97	KAZI-98	CROC_1/*Ae. tauschii* (205)// BORL95/3/KENNEDY
98	KAZI-99	D67.2/P66.270//*Ae. tauschii* (320)/3/…
99	KAZI-100	QT6581/4/PASTOR//SITE/MO/3/ CHEN/…
100	KAZI-101	BL 1496/MILAN/3/CROC_1/ *Ae. tauschii* (205)//…
101	KAZI-102	KAUZ//ALTAR 84/AOS/3/MILAN/ KAUZ/4/HUITES
102	KAZI-103	CAR//KAL/BB/NAC/4/VEE/ PJN//2*TUI/5/MILAN
103	KAZI-104	INQALAB91*2/TUKURU
104	KAZI-105	FRET2/TUKURU//FRET2
105	KAZI-106	TUKURU//BAV92/RAYON
106	KAZI-107	SANSU/CHIBA
107	KAZI-108	YACO//ALTAR 84/*Ae. tauschii* (191)/3/…
108	KAZI-109	SCA/A*Ae. tauschii* (409)//PAS-TOR/3/PASTOR
109	KAZI-110	KS940935.7.1.2/2*PASTOR
110	KAZI-111	LOCAL CHECK **CHECK**
111	KAZI-112	CROC_1/*Ae. tauschii* (205)// BORL95/3/FILIN/4/…
112	KAZI-113	SLVS/3/CROC_1/*Ae. tauschii* (224)//OPATA

Table 55. High-molecular-weight glutenin subunit composition and quality score of 102 synthetic-derived, advanced lines.

Subunit combination	Number of entries	Quality score	Entry name
1, 6+8, 5+10	1	10	SH-854
1, 17+18, 2+12	1	8	Kazi-45
1, 7+8, 5+10	2	10	Kazi-54, Kazi-109
1, 17+18, 5+10	3	10	Kazi-86, Kazi-88, Kazi-91
1, 13+16, 5+10	8	10	Kazi-72, Kazi-73, Kazi-74, Kazi-75, Kazi-76, Kazi-77, Kazi-78, Kazi-79
1, 7, 5+10	4	9	Kazi-94, Kazi-98, Kazi-100, Kazi-103
1, 7+9, 2+12	1	8	Kazi-97
2*, 6+9, 5+10	1	10	Kazi-80
2*, 6+8, 5+10	1	10	Kazi-70
2*, 13+16, 2+10	1	8	Kazi-62
2*, 13+16, 5+10	1	10	Kazi-44
2*, 7+8, 5+10	2	10	TD-1, Kazi-23
2*, 17+18, 5+10	8	10	Inqilab-91, Kazi-31, Kazi-37, Kazi-39, Kazi-40, Kazi-67, Kazi-68, Kazi-56
2*, 7+8, 2+12	5	8	Kazi-34, Kazi-36, Kazi-38, Kazi-41, Kazi-110
Null, 7+8, 5+10	9	8	Seher, Bhakkar, Kazi-17, Kazi-43, Kazi-49, Kazi-50, Kazi-51, Kazi-52, Kazi-92
Null, 13+16, 5+10	6	8	Kazi-16, Kazi-18, Kazi-19, Kazi-27, Kazi-59, Kazi-96
Null, 6+8, 2+12	1	6	Kazi-22
Null, 13+16, 2+12	2	6	Kazi-20, Kazi-81

Table 55. High-molecular-weight glutenin subunit composition and quality score of 102 synthetic-derived, advanced lines.

Subunit combination	Number of entries	Quality score	Entry name
Null, 17+18, 5+10	15	8	Kazi-09, Kazi-24, Kazi-32, Kazi-33, Kazi-53, Kazi-55, Kazi-58, Kazi-60, Kazi-61, Kazi-63, Kazi-65, Kazi-69, Kazi-71, Kazi-102, Kazi-108
Null, 7+8, 2+12	6	6	Kazi-21, Kazi-25, Kazi-26, Kazi-83, Kazi-107, Kazi-112
Null, 13+16	1	4	Durum
Null, 17+18, 2+12	8	6	Kazi-29, Kazi-30, Kazi-42, Kazi-46, Kazi-47, Kazi-105, Kazi-106, Kazi-111
Null, 7+9, 5+10	2	8	Kazi-15, Kazi-82
Null, 6+8, 5+10	4	8	Kazi-28, Kazi-57, Kazi-64, Kazi-99
Null, 13+16, 2+10	1	6	Kazi-48
Null, 7, 5+10	5	7	Kazi-66, Kazi-84, Kazi-85, Kazi-95, Kazi-104
Null, 7+9, 2+12	3	6	Fareed-06, Kazi-93, Kazi-101

of entries possessed either subunit 17+18 or 5+10. Subunit 17+18 was found in 35 (34.31%) of the 102 entries, subunit 7+8 in 24 (22.54%), 13+16 in 20 (19.60), 7 in nine (8.82%), 6+8 in seven (6.86%), and 6+9 in one (0.98%). All these subunits are controlled by allele *Glu-D1*. *S*ubunit 5+10 was found in 73 (71.56%) of the 102 entries, 2+12 in 27 (26.47%), and 2+10 in two (1.96%), all of these are controlled by allele *Glu-B1*.

The variation in the HMW-glutenin subunits of wheat are known to be correlated with bread making quality. Payne et al. (1987) were able to determine the overall quality of a cultivar in terms of HMW-glutenin subunits by adding together the score of individual subunits. For most entries, the quality score was 8 or greater. Twenty-five entries (Inqilab-91, Kazi-31, Kazi-37, Kazi-39, Kazi-40, Kazi-67, Kazi-68, Kazi-56, SH-854, Kazi-54, Kazi-109, Kazi-86, Kazi-88, Kazi-91, Kazi-72, Kazi-73, Kazi-74, Kazi-75, Kazi-76, Kazi-77, Kazi-78, Kazi-79, Kazi-80, TD-1, Kazi-23, Kazi-44, and Kazi-70) scored 10, four entries (Kazi-94, Kazi-98, Kazi-100, Kazi-103) scored 9, and the remaining 44 scored 8 according to Payne et al. (1987).

Marker-assisted selection for effective stripe rust resistance genes. Marker assisted selection for stripe rust resistance genes *Yr15*, *YrSp*, and *YrTp-1* were carried out on these advanced lines. The SSR marker GWM155-1A, linked to stripe rust resistance gene *YrSp* (Yan-Ling et al. 2003), was used to detect a 147-bp fragment in the 102 entries. Only two entries, Kazi-84 and Kazi-85, had *YrSp*.

The SSR marker GWM413-1B, which is linked to stripe rust resistance gene *Yr15* (Peng et al. 2000), was used to detect a 96-bp fragment in the germ plasm. Five of the entries, Kazi-44, Kazi-77, Kazi-78, Kazi-84, and Kazi-85, had *Yr15*.

The SSR marker WMC477-2B, which is linked to stripe rust resistance gene *YrTp-1* (Yin et al. 2006) was used to detect a 167-bp fragment in the 102 entries. Six entries had gene *YrTp-1*; Kazi-09, Kazi-17, Kazi-28, Kazi-44, Kazi-84, and Kazi-85. Some of 102 entries possessed more than one gene of stripe rust resistance (Table 56). Kazi-84 and Kazi-85 have all of three stripe rust resistance genes, *Yr15*, *YrSp*, and *YrTp-1*, and Kazi-44 has *Yr15* and *YrTp-1*.

Table 56. Marker-assisted selection for effective yellow rust resistance genes *Yr15*, *YrSp*, and *YrTp-1* (+ = present and – = absent).

Entry	Marker		
	GWM155-3A$_{147bp}$ (*YrSp*)	**GWM413-1B$_{96bp}$ (*Yr15*)**	**WMC477-2B$_{167bp}$ (*YrTp-1*)**
Kazi-9	–	–	+
Kazi-17	–	–	+
Kazi-28	–	–	+
Kazi-44	–	+	+
Kazi-77	–	+	–
Kazi-78	–	+	–
Kazi-84	+	+	+
Kazi-85	+	+	+

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Grain quality characteristics of synthetic derived genotypes advanced by doubled haploidy.

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The end-use quality and utilization of wheat is highly dependent on the traits such as kernel texture, protein content, ash content, wet-gluten content, and α-amylase activity. To capture the diversity in synthetic hexaploids for grain quality parameters, 35 synthetic-derived, advanced lines were screened for essential quality characteristics. A significant genotype effect was shown for all the characters studied (Table 57, p. 189).

The falling number of these genotypes ranged from 266.67–788.00 sec with an average of 416.97. Replications were not significant but genotypes were significant at $P_{0.05}$. Five genotypes were found significant at $CD_{0.05.}$ Falling number is an important determinant of α-amylase activity and also an indicator of sprout damage and flour set up ability. Mailhott and Patton (1988) reported that all types of bread flour should have falling number values of 200–300 sec. Wheat flour with a falling number value higher than 400 sec has very low or no α-amylase activity. In our study, 16 genotypes had a falling number greater than 400 sec. DH-4 showed the lowest value, 266.67 sec, and DH-13 the maximum.

Protein content was the maximum in DH-12 (16.03%) and the minimum in DH-34 (9.70%). All genotypes were significantly different at $CD_{0.05}$ except DH-3, DH-13, DH-17, DH-18, DH-25, and DH-32. Mean protein content was 12.78% with a CV = 10.05%, indicating better variability among genotypes for this character. Broad-sense heritability was 0.71, which indicated a lesser role of the environment in the transfer of this trait. Protein content in Pakistani wheat cultivars was 10.32–15.42% (Ahmad et al. 2001); Finney and Bolte (1985) recorded protein in the range of 9.0–14.6% in different wheat cultivars. The strong negative association between protein content and grain yield makes breeding for both traits difficult. However, identifying lines with high yield and high protein is of prime importance, and advanced lines with promising grain yield can be an important sources of higher protein content.

Grain texture is the most important trait that determines the hardness or softness of wheat. Hardness scores were 30.00–53.67, with an average of 45.10. Replications were not significant but genotypes were statistically significant. Twenty-nine genotypes were significantly different from mean, whereas the others were not significant at $CD_{0.05.}$ Grain hardness is the key determinant for the classification of wheat and end product quality (Campbell et al. 1999). Grain hardness primarily influences the rheological properties of dough. The most important physical difference between the endosperm of hard and soft wheat lies in the adhesion between the starch granules and the surrounding protein matrix (Simmonds et al. 1973). All 35 genotypes fall into the soft wheat category according to the NIR hardness scale. Some authors also reported that kernel size exerts an effect on grain hardness, however they differ in their opinion about the extent of the effect. Williams et al. (1987) emphasized that kernel size exerts a small effect, whereas Pomeranz et al. (1988) reported a direct effect of kernel size on grain hardness.

Moisture content was 9.22–11.33% with an average of 10.25%. The co-efficient of variation for this trait was 6.20%, indicating lower variability among genotypes compared to other traits. Moisture content is greatly influenced by variation in the processing of the grains and the method of grinding as well as variation in the climatic conditions and temperature during harvest.

Table 57. Quality characteristics of 35 synthetic-derived, advanced lines (lines with an * are significantly different from mean at CD 0.05).

Genotype	Falling number	Protein (%)	Hardness score	Moisture (%)	1,000-kernel weight (g)	Ash (%)	Wet gluten (%)	Gluten index
DH-1	427.00	14.67*	46.67	9.50	29.80*	1.78	33.62	49.80
DH-2	316.50	13.53*	47.00	9.37*	39.80	1.63	26.74	76.10
DH-3	490.00	12.77	39.00*	9.53	37.60	1.55	29.36	48.50
DH-4	266.67*	12.80	49.00*	9.42*	43.00*	1.72	26.10	61.00
DH-5	393.00	14.73*	45.33	9.41*	38.20*	1.83	25.60	55.00
DH-6	387.00	12.23*	34.00*	9.57	32.00*	2.00*	28.10	36.00
DH-7	467.50	13.40*	41.33*	9.57	36.80	1.74	34.26	64.92
DH-8	528.00	15.40*	51.67*	9.65	35.40*	1.78	27.70	44.50*
DH-9	339.00	12.47*	51.00*	9.22*	42.20*	1.69	27.05	10.89*
DH-10	296.00	11.67*	48.67*	9.78	22.90*	1.90	30.19	37.55
DH-11	343.67	12.00*	42.33*	9.57	44.20	1.70	28.20	13.96*
DH-12	389.50	16.03*	48.00*	9.70	38.60	1.72	37.75*	46.50
DH-13	788.00*	12.70	47.33*	9.40*	33.40	1.65	28.03	40.50
DH-14	375.00	12.37*	42.33*	9.83	27.20*	1.78	26.89	37.00
DH-15	368.50	12.00*	50.33*	10.73	40.80	1.88	25.49	37.00
DH-16	465.00	13.27*	47.33*	10.96	37.80	1.59	25.38	92.50*
DH-17	456.50	12.60	37.00*	10.82	32.40	1.77	17.05*	91.00*
DH-18	526.50	12.67	30.00*	10.53	31.60*	1.60*	31.85	62.00
DH-19	477.00	12.50*	37.33*	10.80	32.20	1.81	28.76	37.35
DH-20	531.00	12.07*	34.33*	10.62	32.60	1.88	28.97	33.2*
DH-21	537.50	12.43*	47.33*	11.33*	28.80*	1.71	24.06	80.50
DH-22	442.50	12.03*	35.33*	10.79	32.80	1.70	22.83	32.00*
DH-23	636.50*	13.33*	48.67*	11.20*	26.40*	1.82	25.68	47.00
DH-24	388.50	14.00*	52.67*	10.62	48.00*	1.59	32.67	46.50
DH-25	241.00*	12.87	53.67*	10.63	40.00	1.70	27.08	29.50*
DH-26	262.00*	14.17*	51.33*	10.62	27.80*	1.90	26.72	66.00
DH-27	478.50	11.70*	46.33	10.74	33.80	1.75	28.45	83.00*
DH-28	495.00	11.17*	47.33*	10.47	38.00	1.70	19.61	96.00*
DH-29	365.00	12.57*	36.00*	10.62	42.80*	1.89	26.93	71.50
DH-30	299.50	10.80*	48.33*	10.92	38.20	1.79	18.94	93.00
DH-31	283.00	11.67*	47.00	10.63	49.00*	1.94	20.38	70.50
DH-32	328.00	12.77	47.00	10.70	34.80	1.70	22.24	90.00*
DH-33	464.50	11.93*	50.67*	10.39	40.00	1.61	22.09	83.00
DH-34	396.00	9.70*	48.33*	11.03	48.40*	1.52*	19.27	52.00
DH-35	345.00	14.47*	48.33*	10.12	34.80	1.66	30.57	90.50
Mean	416.97	12.78	45.10	10.25	36.07	1.75	26.65	56.99
Standard deviation	113.09	1.28	6.09	0.64	6.45	0.11	4.77	24.29
CV(%)	27.12	10.05	13.49	6.20	17.88	6.29	17.90	42.62
Heritability	0.53	0.71	0.62	0.85	0.92	0.65	0.77	0.63

Thousand-kernel weight ranged from 22.90 (DH-10) to 48.40 g (DH-34) with an average of 36.07 g. The co-efficient of variability (17.88%) was sufficient for this trait among genotypes. Sixteen of the advanced lines were significantly different from the mean at $CD_{0.05.}$ Both replication and genotypic effects were significant at 0.05. This trait is a function of grain size and density. Wheat kernels can be classified according to grain weight 15–25 g (very small), 26–35 g (small), 36–45 g (medium), 46–55 g (large), and > 55 g (very large). According to this scale, most of the genotypes are medium grained. Zanetti et al. (2001) reported a 1,000-kernel weight of 42.4–48.7 g in 128 wheat cultivars and Anjum et al. (2002) reported grain weight of 31.43–37.28 g in Pakistani wheat cultivars.

The ash content of these genotypes ranged from 1.52% (DH-34) to 2.0% (DH-6) with an average of 1.75%. All the genotypes were significantly different from the mean at $CD_{0.05}$. Ash content is the inorganic material left after flour is burned, is an important determinant of the extraction rate, and influences flour color and quality. Zahoor (2003) reported the ash contents of 0.30–0.53% in Pakistani wheat cultivars. The higher ash content found in these genotypes indicates the presence of a higher bran proportion than of endosperm flour.

Maximum wet gluten was observed DH-12 (37.75%) and the minimum in DH-17 (17.05%); the average was 26.65%. Both replication and genotype were significantly different P = 0.05. Wet gluten has a strong effect on dough rheology and baking performance. Wet forms are more quickly incorporated into low protein flour than dry form (Czuchajowska and Paszczynska 1996) and also effects dough strength, gas retention and controlled expansion, structural enhancement, water absorption and retention, and natural flavor (Grausgruber et al. 2000).

Previously, these advanced lines were found promising for better yield and drought tolerance in Pakistan (unpublished data). Most of these have good characteristics for useful quality traits and offer variability for these traits. A detailed analysis of advanced lines carrying higher protein content and higher thousand gain weight is required in order to exploit these genotypes further via a a recombination-breeding program.

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Unique high-molecular-weight glutenin subunits in synthetic hexaploids to bridge the gap at the Glu-D1 locus.

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Break-making quality in wheat is largely controlled by high-molecular-weight glutenin subunits (HMW-GS). The D-genome encoded subunits have the most influence but have limited variability. New subunits found in the D-genome synthetic hexaploids can be deployed for break-making quality improvement but require proper identification and characterization for different quality parameters. We identified the HMW-GS in 33 synthetic hexaploids using SDS-PAGE (Tables 58 and 59).

Table 58. Allelic frequencies of HMW-GS at *Glu-1* loci in 33 synthetic hexaploids accessions.

Locus	Subunit	Allele	Number of accessions	Proportion	Frequency
Glu-A1	1	a	4	0.1379	13.79
	2*	b	2	0.0690	6.90
	null	c	23	0.7931	79.31
Glu-B1	6+8	d	2	0.0690	6.90
	7+8	b	6	0.2069	20.69
	7+9	c	3	0.1034	10.34
	17+18	i	13	0.4483	44.83
	13+16	f	5	0.1724	17.24
Glu-D1	5+10	d	10	0.3103	31.03
	1.5+10	ah	2	0.0690	6.90
	1.5+12	aj	2	0.0690	6.90
	2+12	a	8	0.2759	27.59
	2.1+12	n	3	0.1034	10.34
	1.5+ T2	ag	1	0.0345	3.45
	2+ T2	x	3	0.1050	6.90

At the *Glu-A1* locus, the x-type subunits 1, 2*, and null, which encode *Glu-A1a, Glu-A1b*, and *Glu-A1c* respectively, were observed. The subunits null and 1 were not very frequent. The null subunit, which does not code for any protein, was the most frequent and was found in 23 (79.31%) accessions. The remaining accessions were found to possess subunit 1, found in four (13.79%), and 2* in two (6.90%) genotypes at the *Glu-A1* locus.

Five different co-dominant alleles are at the *Glu-B1* locus, *Glu-B1b, Glu-B1c, Glu-B1d, Glu-B1f, and Glu-B1i* controlling the subunits 7+8, 7+9, 6+8, 13+16, and 17+18, respectively. In these subunits, four are x- and four are y-type. The *Glu-B1d* allele controlling the subunit 6+8 was less frequent (6.90%) among all the subunits at this locus. and the most frequent was 17+18 at *Glu-B1*, which appeared in 13 (44.83%) accessions. Other subunits were 7+8, present in six (20.69%), 13+16 in five (17.24%), and 7+9 in three (10.34%) genotypes.

Table 59. Allelic composition and frequency in 33 synthetic hexaploid accessions.

Subunit composition	Allelic combination	Number of accessions	Accession
Null, 17+18, 2+T2	c, i, x	1	E-1
Null, 7+8, 2+12	c, b, a	2	E-2, E-24
Null, 7+8, 2.1+12	c, b, n	3	E-3, E-27, E-28
Null, 7+8, 1.5+T2	c, b, ag	1	E-4
Null, 6+8, 1.5+12	c, d, aj	2	E-5, E-9
1, 17+18, 5+10	a, i, d	2	E-7, E-17
Null, 17+18, 1.5+10.5	c, i, ah	2	E-8, E-22
l, 13+16, 5+10	a, f, d	1	E-10
Null, 17+18, 2+12	c, i, a	2	E-11, E-29
Null, 17+18, 5+10	c, i, d	4	E-12, E-14, E-23, E-16, E-30
2*, 17+18, 5+10	b, i, d	1	E-15
1, 17+18, 2+12	a, i, a	1	E-17
2*, 13+16, 5+10	b, f, d	1	E-19
Null, 7+9, 2+12	c, c, a	3	E-20, E-21,E-30
1, 13+16, 2+12	a, f, a	1	E-25
Null, 13+16, 2+T2	c, f, x	1	E-26, E-13

Valuable genetic variability was found at the *Glu-D1* locus in these synthetics. The the allelic variation of HMW-GS strongly influence the variability in bread-making quality and the D-genome strongly influences bread-making quality

(William et al. 1993; Pfluger et al. 2001). At *Glu-D1,* nine different co-dominant alleles, *Glu-D1a, Glu-D1ah, Glu-D1ag, Glu-D1aj ,Glu-D1d, Glu-D1f*, *Glu-D1i*, *Glu-D1n,* and *Glu-D1x* controlling subunits 5+10, 2+12, 2.1+12, 1.5+10, 1.5+12, 1.5+T2, and 2+T2, were found. The *Glu-D1d* allele controlling subunit 5+10 is the most important and superior bread-making quality subunit and was found most frequently (31.03%). Li et al. (2009) reported the superiority of this allele among all the other alleles at the *Glu-1* locus. Luo et al. (2001) reported the association of subunit 5+10 with sedimentation volume and longer pelshenke time. They also reported that the presence of 5+10 subunit in a genotype results in greater whole-meal flour protein. Payne et al. (1981) established that subunit 5+10 has a superior quality effect over 2+12 and all other alleles at *Glu-D1*. Eight genotypes (27.59%) had 2+12, encoded by *Glu-D1a*. The unique subunits 1.5+T2 and 2+ T2 also were observed at this locus. Other important subunits at *Glu-D1* were 1.5+12, found in two (6.90%), and 2.1+12 in three (10.34%) accessions. Subunit 1.5+10 was present in two of the 33 synthetics, and this subunit has better overall quality characteristics than genotypes having other subunits (Pena et al. 1995).

Eighteen different HMW-GS compositions were observed in the synthetic hexaploid wheats (Table 59, p. 191). Four (13.79%) genotypes had the combination null, 17+18, 5+10. Other frequent subunit compositions were null, 7+9, 2+12 and null, 7+8, 2.1+12 recorded in 3 (10.34%) accessions. Several other sub-units with different unique combinations like T2 were also found in this group of accessions. Four synthetics showed the presence of rare allele T2 at *Glu-D1* locus with either of subunit 1.5 or 2. The quality effects of genotypes with T2 subunit were not determined because these are rare subunits and their quality effects are yet to be determined. Superior bread making quality characteristics in a genotypes are accredited by presence of either of subunit 1 or 2* at *Glu-A*1 along with subunits 7+8, 17+18 or 13+16 at *Glu-B1*. Seven of these synthetics had one of these combinations. From these results, it is concluded that synthetics have good potential towards the bread making quality and their utilization in breeding programmes can become a first choice to the breeder emphasizing on wheat breeding for high grain quality.

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QTL-based phenotyping of a molecular mapping population for salinity tolerance in wheat.

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In developed countries, around 90% of the wheat area is rain-fed. In developing countries, wheat is mainly cultivated in irrigated areas, especially by large producers such as India and China. Irrigated land is believed to be most productive but, unfortunately, it faces a great production constraint in salinity. Currently, about 20% of the 275 x 10^6 ha of irrigated land globally is salt affected. The most important and the productive part of Pakistan, the Indus Plain, is effected by salinity of varying degrees. In Pakistan, about 5.30 x 10^6 ha of land are salt-affected. Therefore, nationally and internationally, salinity represents a great threat to our food production and limits it in many farming systems including the arid and semi-arid regions.

To be able to effectively utilize saline land and water resources, we can either improve the soil, breed for salt tolerance to enable them to grow under harsher conditions, or develop new crops that have high productivity in a highly

saline environment. Knowing the complex physiology and genetics of salt tolerance for crop development poses a difficult task for plant breeders. So far, little progress has been made. This slow progress can be accredited to different factors, such as the genetic, physiological, and biochemical basis for salt tolerance, which are not well understood due to polygenic inheritance in plants such as wheat; an incomplete knowledge of the effects of salinity on plants; and unproductive selection methods. The success of a breeding program can be enhanced by knowledge of these areas. Some basics for improving salt tolerance can be the availability of suitable genetic variability in the cultivated species or their wild relatives, methods of selection and screening large numbers of genotypes for salt tolerance, and a suitable breeding methodology.

Salinity affects the most important and productive land of Pakistan as well as of the world. Salt-tolerant cultivars will play a great role in achieving future production goals. To develop salt tolerance in existing or new crops, the diversity in germ plasm becomes important. Genetic variation for salt tolerance has been reported in many crop species, including wheat, and the potential exists for improvements using conventional and novel breeding techniques. Our objectives were to exploit genetic diversity for salt tolerance in 100 F_1-based, doubled haploids developed from the parental lines Prinia and 2407, develop plant population in hydroponic culture at 75 mMol NaCl and perform phenotyping for salinity tolerance using different physiological tests and assessing agronomical data, and identify good, agronomic, salt-tolerant lines on the basis of this phenotyping that could be used in wheat breeding and improvement programs.

The germ plasm consisted of 75 doubled-haploid (DH) lines and three check cultivars Kharchia and Shorawaki (salt tolerant), and PBW-343 (sensitive). This plant material was screened for salt tolerance under hydroponic conditions using K^+:Na^+ analytical parameters complimented by other test indicators such as relative growth rate, chlorophyll content, K^+/Na^+ ratio, and ion flux (Table 60, pp. 193-195; Table 61, p. 195-196, and Table 62, p. 197-198).

Table 60. Mean values of shoot/root length,and relative growth rates of 93 doubled haploid lines and check cultivars Kharchia, Shorawaki, and PBW-343 (The relative growth rate is gram per gram of dry weight of the sample per day).

Line	Shoot length (cm)	Root length (cm)	Shoot dry weight		Natural log shoot dry weight 1st and 2nd harvests	Relative growth rate (g/g/d)
			1st harvest (g)	2nd harvest (g)		
DH1	21.3	3.0	0.0240	0.249	0.223	0.022
DH4	25.4	4.9	0.0290	0.283	0.216	0.022
DH6	16.9	4.8	0.0117	0.108	0.431	0.043
DH7	18.3	4.2	0.0155	0.170	0.056	0.006
DH9	26.2	8.0	0.0153	0.207	0.217	0.022
DH10	24.4	8.0	0.0133	0.146	0.127	0.013
DH11	16.0	2.9	0.0160	0.189	0.172	0.017
DH12	21.9	3.3	0.0289	0.167	0.190	0.019
DH13	22.6	5.8	0.0250	0.175	0.005	0.001
DH14	13.5	4.8	0.0160	0.229	0.177	0.018
DH15	18.7	5.0	0.0170	0.185	0.378	0.038
DH16	17.7	3.3	0.0160	0.159	0.118	0.012
DH17	17.6	3.6	0.0204	0.296	0.163	0.016
DH18	27.6	3.6	0.0262	0.347	0.168	0.017
DH19	31.6	9.0	0.0246	0.301	0.165	0.016
DH20	32.0	6.4	0.0267	0.285	0.079	0.008
DH21	36.7	12.2	0.0250	0.378	0.247	0.025
DH22	21.3	4.5	0.0301	0.385	0.159	0.016
DH23	25.4	3.7	0.0208	0.212	0.360	0.036
DH24	24.5	4.5	0.0312	0.216	0.114	0.011
DH25	22.3	6.9	0.0190	0.253	0.010	0.001
DH26	27.3	4.9	0.0206	0.246	0.075	0.007
DH27	25.7	5.3	0.0221	0.291	0.302	0.030

Table 60. Mean values of shoot/root length,and relative growth rates of 93 doubled haploid lines and check cultivars Kharchia, Shorawaki, and PBW-343 (The relative growth rate is gram per gram of dry weight of the sample per day).

Line	Shoot length (cm)	Root length (cm)	Shoot dry weight		Natural log shoot dry weight 1st and 2nd harvests	Relative growth rate (g/g/d)
			1st harvest (g)	2nd harvest (g)		
DH28	27.8	6.6	0.0202	0.202	0.359	0.036
DH29	34.2	4.6	0.0340	0.317	0.137	0.014
DH30	27.0	5.5	0.0385	0.318	0.172	0.017
DH32	27.5	3.8	0.0317	0.249	0.119	0.012
DH33	20.1	4.9	0.0180	0.164	0.269	0.027
DH34	20.9	4.5	0.0324	0.277	0.133	0.013
DH35	30.3	6.9	0.0360	0.200	0.079	0.008
DH36	24.0	4.8	0.0200	0.394	0.668	0.067
DH39	24.3	3.4	0.019	0.030	0.470	0.047
DH40	22.9	4.3	0.018	0.028	0.442	0.044
DH41	22.7	6.8	0.028	0.036	0.243	0.024
DH42	30.5	4.8	0.024	0.034	0.357	0.036
DH43	25.2	4.9	0.016	0.032	0.681	0.068
DH44	20.9	4.5	0.019	0.022	0.126	0.013
DH45	26.0	7.8	0.018	0.028	0.474	0.047
DH46	25.1	4.4	0.020	0.024	0.167	0.017
DH47	28.0	4.7	0.016	0.023	0.386	0.039
DH48	24.4	3.8	0.020	0.032	0.470	0.047
DH49	16.8	3.5	0.014	0.021	0.442	0.044
DH51	26.2	4.6	0.058	0.074	0.250	0.025
DH52	17.8	5.3	0.027	0.042	0.420	0.042
DH53	21.5	5.6	0.045	0.060	0.288	0.029
DH57	16.4	5.7	0.016	0.017	0.036	0.004
DH59	17.2	5.7	0.013	0.019	0.411	0.041
DH60	25.4	3.4	0.018	0.029	0.471	0.047
DH61	29.8	5.8	0.015	0.024	0.470	0.047
DH62	27.5	4.8	0.013	0.018	0.349	0.035
DH63	23.4	6.3	0.018	0.020	0.110	0.011
DH64	11.7	3.5	0.016	0.030	0.624	0.062
DH65	24.3	4.7	0.015	0.028	0.619	0.062
DH66	23.4	4.1	0.019	0.027	0.362	0.036
DH67	23.3	6.3	0.013	0.026	0.660	0.066
DH68	17.0	5.8	0.011	0.020	0.625	0.062
DH69	16.9	7.2	0.018	0.024	0.278	0.028
DH70	31.1	4.8	0.024	0.037	0.423	0.042
DH72	27.3	5.6	0.022	0.040	0.590	0.059
DH73	26.6	7.3	0.013	0.024	0.653	0.065
DH76	20.1	5.4	0.008	0.010	0.281	0.028
DH77	25.8	10.3	0.022	0.040	0.593	0.059
DH78	22.9	4.0	0.030	0.043	0.334	0.033
DH79	24.7	5.7	0.030	0.038	0.102	0.010
DH81	22.3	5.2	0.030	0.032	0.028	0.003
DH82	26.7	7.5	0.040	0.052	0.215	0.021
DH83	19.9	4.9	0.020	0.026	0.198	0.020
DH84	25.0	4.4	0.020	0.027	0.271	0.027
DH85	22.6	4.7	0.030	0.041	0.381	0.038

Table 60. Mean values of shoot/root length,and relative growth rates of 93 doubled haploid lines and check cultivars Kharchia, Shorawaki, and PBW-343 (The relative growth rate is gram per gram of dry weight of the sample per day).

Line	Shoot length (cm)	Root length (cm)	Shoot dry weight		Natural log shoot dry weight 1st and 2nd harvests	Relative growth rate (g/g/d)
			1st harvest (g)	2nd harvest (g)		
DH87	22.90	3.20	0.030	0.040	0.165	0.016
DH89	21.10	3.80	0.030	0.039	0.253	0.025
DH90	14.50	4.90	0.010	0.022	0.394	0.039
DH91	21.60	6.20	0.030	0.033	0.121	0.012
DH92	16.80	7.30	0.020	0.024	0.121	0.012
DH93	23.50	5.10	0.030	0.034	0.148	0.015
Kharchia	21.00	3.00	0.030	0.035	0.230	0.023
PBW-343	14.90	5.20	0.010	0.016	0.099	0.010
Shorawaki	18.50	5.60	0.020	0.034	0.506	0.051

Table 61. Mean values of leaf fresh/dry weight and chlorophyll content of 93 doubled haploid lines and the check cultivars Kharchia, Shorawaki and PBW-343.

Line	Leaf fresh weight (g)	Leaf dry weight		Chlorophyll absorbance (at 666 nm)	Chlorophyll content (mg/mg)
		g	mg		
DH1	0.0750	0.0054	5.4000	1.1940	0.0118
DH4	0.0633	0.0051	5.1000	1.0180	0.0107
DH6	0.0640	0.0056	5.6000	1.0160	0.0097
DH7	0.0410	0.0041	4.1000	0.4747	0.0061
DH9	0.0793	0.0005	0.5100	0.9300	0.0974
DH10	0.0118	0.0020	2.0000	0.5040	0.0133
DH11	0.0357	0.0028	2.8000	0.3623	0.0068
DH12	0.0911	0.0052	5.1583	0.0500	0.0004
DH13	0.3332	0.0189	18.8588	0.5220	0.0015
DH14	0.0773	0.0054	5.4000	1.1370	0.0113
DH15	0.0540	0.0043	4.3000	0.6680	0.0083
DH16	0.0410	0.0035	3.5000	0.6820	0.0104
DH17	0.1010	0.0082	8.2000	1.8760	0.0123
DH18	0.0443	0.0023	2.3000	0.5280	0.0122
DH19	0.0363	0.0016	1.6000	0.3610	0.0118
DH20	0.0490	0.0028	2.8000	0.5200	0.0098
DH21	0.0413	0.0052	5.2000	0.5240	0.0053
DH22	0.1127	0.0064	6.3775	1,4298	0.0120
DH23	0.1126	0.0044	4.4000	1.0650	0.0129
DH24	0.0879	0.0050	4.9764	0.4870	0.0052
DH25	0.0763	0.0062	6.2000	0.5440	0.0046
DH26	0.0840	0.0045	4.5000	1.0860	0.0129
DH27	0.0890	0.0050	5.0378	1.1295	0.0120
DH28	0.0091	0.0005	0.5151	0.8500	0.0880
DH29	0.1196	0.0068	6.7722	1.5183	0.0120
DH30	0.1154	0.0065	6.5311	1.4643	0.0120
DH32	0.1258	0.0071	7.1214	1.5966	0.0120
DH33	0.1630	0.0092	9.2237	2.0680	0.0120
DH34	0.0790	0.0045	4.4719	1.0026	0.0120
DH35	0.2089	0.0118	11.8248	2.6511	0.0121
DH36	0.0444	0.0049	4.9000	0.6020	0.0065
DH39	0.0926	0.0041	4.1000	0.9370	0.0122

Table 61. Mean values of leaf fresh/dry weight and chlorophyll content of 93 doubled haploid lines and the check cultivars Kharchia, Shorawaki and PBW-343.

Line	Leaf fresh weight (g)	Leaf dry weight		Chlorophyll absorbance (at 666 nm)	Chlorophyll content (mg/mg)
		g	mg		
DH40	0.0690	0.0033	3.3000	0.6970	0.0112
DH41	0.0540	0.0031	3.1000	0.7920	0.0136
DH42	0.0483	0.0050	5.000	0.5070	0.0054
DH43	0.0636	0.0038	3.8000	0.7780	0.0109
DH44	0.1093	0.0040	4.0000	0.9030	0.0120
DH45	0.0166	0.0021	2.1000	0.6420	0.0162
DH46	0.0383	0.0023	2.3000	0.3760	0.0086
DH47	0.1140	0.0062	6.2000	1.0350	0.0089
DH48	0.0396	0.0012	1.2000	0.5030	0.0222
DH49	0.0061	0.0003	0.3453	0.0774	0.0105
DH51	0.1941	0.0110	10.9852	2.4629	0.0121
DH52	0.0076	0.0004	0.4302	0.0964	0.0108
DH53	0.0090	0.0005	0.5094	0.1142	0.0110
DH57	0.0041	0.0002	0.2321	0.0520	0.0098
DH59	0.0075	0.0004	0.4245	0.0952	0.0108
DH60	0.0055	0.0003	0.3113	0.0698	0.0104
DH61	0.0048	0.0003	0.2717	0.6000	0.1172
DH62	0.0093	0.0005	0.5264	0.8201	0.0831
DH63	0.0065	0.0004	0.3679	0.1450	0.0198
DH64	0.0713	0.0040	4.0368	0.0850	0.0010
DH65	0.0068	0.0004	0.3849	0.8300	0.1150
DH66	0.0041	0.0002	0.2321	0.2110	0.0467
DH67	0.0065	0.0004	0.3679	0.0730	0.0092
DH68	0.0052	0.0003	0.2943	0.0810	0.0130
DH69	0.0040	0.0002	0.2264	0.1270	0.0279
DH70	0.0109	0.0006	0.6169	0.6870	0.0592
DH72	0.0098	0.0006	0.5547	0.6030	0.0577
DH73	0.0081	0.0005	0.4585	0.5330	0.0616
DH76	0.3091	0.0175	17.4974	3.9229	0.0121
DH77	0.0221	0.0013	1.2535	0.9110	0.0388
DH78	0.0875	0.0050	4.9543	1.1108	0.0120
DH79	0.0763	0.0043	4.3158	0.9676	0.0120
DH81	0.1870	0.0106	10.5825	0.7000	0.0035
DH82	0.0175	0.0010	0.9890	0.2217	0.0116
DH83	0.1996	0.0113	11.2949	2.5323	0.0121
DH84	0.1924	0.0109	10.8878	0.5001	0.0024
DH85	0.0329	0.0019	1.8614	0.4173	0.0118
DH87	0.0340	0.0019	1.9238	0.4313	0.0118
DH89	0.0891	0.0050	5.0456	1.1312	0.0120
DH90	0.2130	0.0121	12.0543	2.7026	0.0121
DH91	0.0566	0.0032	3.2036	0.7183	0.0119
DH92	0.1034	0.0059	5.8551	1.3127	0.0120
DH93	0.2430	0.0138	13.7513	0.7390	0.0029
Kharchia	0.0577	0.0027	2.7000	3.0900	0.0616
PBW-343	0.0321	0.0028	2.8000	0.8910	0.0170
Shorawaki	0.0532	0.0026	2.6000	3.0100	0.0623

Table 62. Mean values for sodium ion flux, potassium ion flux, and potassium:sodium ratios after 5 and 15 days of salinization in doubled haploid lines and the check cultivars Kharchia and Shorawaki. (J_s = net ion transport rate from roots to shoots in moles/gram/day).

Line	K^+:Na^+		Sodium (J_s) (mol/g/d)	Potassium (J_s) (mol/g/d)
	5 days	15 days		
DH1	1.35	1.70	18.57	63.64
DH4	0.97	0.89	39.35	28.57
DH6	2.77	2.75	9.31	24.51
DH7	0.73	0.69	9.58	0.53
DH9	1.69	1.84	1.36	25.50
DH10	1.87	1.87	1.23	4.53
DH11	1.20	1.22	29.26	36.49
DH12	1.44	1.46	16.28	27.18
DH13	1.76	1.81	53.55	104.54
DH14	1.43	1.55	8.69	31.21
DH15	1.55	1.63	3.31	13.33
DH16	1.72	1.72	9.03	15.98
DH17	0.65	0.50	19.47	0.91
DH18	1.44	1.33	73.22	81.92
DH19	0.94	0.92	29.21	22.45
DH20	0.78	0.72	50.28	9.94
DH21	0.96	0.86	68.18	31.05
DH22	1.66	1.67	37.79	69.42
DH23	0.59	0.60	76.95	47.03
DH24	0.51	0.56	25.51	21.14
DH25	0.99	0.59	274.32	40.46
DH26	0.92	0.84	120.70	51.95
DH27	1.67	1.69	10.13	21.46
DH28	0.89	0.87	38.20	29.09
DH29	0.82	0.83	23.97	21.08
DH30	1.45	1.58	3.29	15.76
DH32	1.81	1.72	9.45	11.88
DH33	0.79	0.64	140.41	42.78
DH34	0.51	0.55	19.73	16.13
DH35	0.85	0.83	43.70	35.04
DH36	2.66	2.77	1.48	10.25
DH39	0.91	0.91	44.08	40.49
DH40	1.00	0.87	71.10	16.02
DH41	1.67	1.75	6.64	15.62
DH42	1.64	1.80	5.98	36.23
DH43	0.97	0.91	86.13	59.58
DH44	1.39	1.40	74.09	107.09
DH45	0.88	0.85	114.05	77.54
DH46	0.67	0.61	47.71	7.00
DH47	0.72	0.69	137.85	85.14
DH48	1.79	1.80	4.13	11.56
DH49	0.86	0.79	19.02	2.70
DH51	1.65	1.70	9.46	17.56
DH52	1.84	2.02	4.43	13.77
DH53	1.71	1.88	4.70	15.79

The relative growth rate (gram per gram of dry weight of the sample per day = g/g/d) of the shoots were calculated according to the following formula where WS_1 and WS_2 are shoot weights at harvest time t_1 and t_2 and In is the natural log:

$RGR\ (g/g/d) = In\ WS_2 – InWS_1 / t_2 – t_1$

Chlorophyll content was calculated according to the following formula:
Chlorophyll (mg/mg dry weight of sample) = (chlorophyll absorbance – 0.01) x 5 / 92.6474 x dry weight of sample

The ion fluxes for sodium and potassium were calculated according to the following formula:

$J_s = OS_2–OS_1/t_2\text{-}t_1 x InWR_2–InWR_1/WR_2–WR_1$

Relative growth rate (g/g/d). The relative growth rate (RGR) reflects the growth potential under the stress conditions imposed over plants and the overall growth and development and total biomass production by the plants during the period of stress (Table 60, pp. 194-196). The tolerant check lines showed RGR values of 0.0230 g/g/d (Kharchia) and 0.0506 g/g/d (Shorawaki). The sensitive line PBW-343 had an RGR value of 0.00099 g/g/d. The RGR values for the DHs ranged from minimum of 0.0005 g/g/d (DH-13) to the maximum of 0.0681 g/g/d (DH-43). A few lines showed RGR values more than the tolerant checks, DH-72 (0.0590 g/g/d), DH-77 (0.0593 g/g/d), DH-65 (0.0619 g/g/d), DH-64 (0.0624 g/g/d), DH-68 (0.0625 g/g/d), DH-73 (0.0653 g/g/d), DH-67 (0.0660 g/g/d), and DH-36 (0.0668 g/g/d). These lines possess good potential to grow and develop under salt stress.

The mean data for shoot length also shows a good positive correlation for the relative growth rates of plants. Thirty-ong DH lines had an RGR value between those of both tolerant check cultivars ranging from 0.0470 g/g/d (DH-45) to 0.0243 g/g/d (DH-41), which is promising growth potential under stress. The remaining 35 DH lines had RGR values less than both the tolerant checks, from 0.0223 g/g/d (DH-1) to 0.0005 g/g/d (DH-13), indicating poor growth under salt stress.

Relative growth rates were calculated on the shoot dry weight basis, because it also effects the ion accumulation in the shoot and, hence, the K^+:Na^+ ratio. We observed

Table 62. Mean values for sodium ion flux, potassium ion flux, and potassium:sodium ratios after 5 and 15 days of salinization in doubled haploid lines and the check cultivars Kharchia and Shorawaki. (J_s = net ion transport rate from roots to shoots in moles/gram/day).

Line	K^+:Na^+		Sodium (J_s) (mol/g/d)	Potassium (J_s) (mol/g/d)
	5 days	15 days		
DH57	0.66	0.52	102.89	28.71
DH59	0.89	0.66	100.91	36.50
DH60	1.90	2.06	11.46	50.30
DH61	0.73	0.71	21.46	9.13
DH62	0.72	0.70	12.72	0.94
DH63	0.35	0.38	70.54	30.22
DH64	1.27	1.33	4.28	11.65
DH65	2.52	2.77	1.76	21.11
DH66	0.78	0.78	47.92	35.80
DH67	1.57	1.54	47.01	68.87
DH68	0.81	0.81	66.41	54.00
DH69	0.89	0.81	18.80	6.59
DH70	2.26	2.54	7.11	31.84
DH72	2.63	2.56	14.91	34.02
DH73	3.32	3.47	5.21	28.26
DH76	1.97	1.99	39.60	84.08
DH77	0.77	0.70	14.79	3.04
DH78	1.74	1.65	15.008	16.22
DH79	0.77	0.70	21.236	10.75
DH81	0.92	0.83	32.759	21.43
DH82	0.55	0.54	8.221	2.90
DH83	1.50	1.56	16.945	30.40
DH84	1.74	1.86	14.504	39.31
DH85	1.53	1.58	0.902	5.68
DH87	0.82	0.71	24.920	6.05
DH89	0.97	0.76	49.326	15.86
DH90	1.97	2.12	15.849	57.62
DH91	0.50	0.51	13.522	7.82
DH92	1.65	1.68	10.586	20.15
DH93	1.80	1.89	16.269	38.24
Kharchia	3.29	3.82	1.757	17.65
PBW-343	0.67	0.60	156.593	73.74

that the relative growth rate showed a positive correlation (Pearson's correlation coefficient, r = 0.3588) with the K^+:Na^+ ratio taken 15 days after salinization. The DH lines having high RGR values also showed higher K^+:Na^+ ratio and vice versa, for instance, DH-36, with a higher RGR value of 0.0668 g/g/d, also had a higher K^+:Na^+ ratio (2.768) and DH-25, with a lower RGR value of 0.0010 g/g/d, also showed a lower K^+:Na^+ ratio (0.587).

Chlorophyll content (mg/mg). Chlorophyll carries out photosynthesis in plants and so directly effects growth and development. A decrease in chlorophyll content results in a reduction of photosynthesis under salt stress. We observed that lines that could not survive under salt stress also had a lower chlorophyll content, in contrast with salt-tolerant lines, which showed a greater chlorophyll content in their leaves. A decrease in chlorophyll content means a decrease in photosynthesis, which will affect the overall growth and survival of plants. Therefore, chlorophyll content can be used as an indicator of salt tolerance. The check cultivars, Kharchia, Shorawaki, and PBW-343, had a chlorophyll content of 0.0616 (mg/mg), 0.0623 (mg/mg), and 0.0170 (mg/mg), respectively. Five lines had a chlorophyll content greater than the tolerant checks. The maximum chlorophyll content was in DH-61, 0.1172 mg/mg. The chlorophyll content showed a positive correlation (r = 0.3409) with the relative growth rate, which suggests that a greater chlorophyll content contributes to more biomass production and the overall growth and development of the plant makes them tolerant to salt stress. However, the correlation between the chlorophyll content and Na^+ flux was negative (r = –0.189); favoring the fact that more uptake and accumulation of Na^+ in the shoot results in more chlorophyll damage and reduction.

K^+:Na^+ descrimination. Sodium ion exclusion and a greater accumulation of K^+ is one of the adaptations to salt stress that results in enhanced performance under stress conditions. Increased Na^+ exclusion improves salt tolerance and grain yield in wheat. Several sources of enhanced Na^+ exclusion and higher salt tolerance have been identified within the Triticeae. Bread wheat is, in general, a better Na^+ excluder and shows higher K^+:Na^+ ratio. The K^+:Na^+ ratios for all DH lines and checks were calculated after 5 and 15 days of salinization (Table 62, pp. 197-198). The maximum K^+:Na^+ ratio after 15 days of salinization was in Kharchia (3.823), followed by Shorawaki (3.560). The K^+:Na^+ ratio for PBW-343 (sensitive check) was 0.600. The K^+/Na^+ ratios for the DH lines ranged from 3.469 to 0.380. The maximum K^+:Na^+ ratio was in DH-73 (3.469).

The correlation between relative growth rate and K^+:Na^+ ratio also was positive. A positive correlation means that plants having good potential to grow under salt stress have better ability to exclude Na^+, which ultimately results in development of tolerance against salt stress. The D genome contributes to lower rates of Na^+ accumulation and a higher

K^+:Na^+ ratio in the leaves, in both diploid *Ae. tauschii* (DD) and hexaploid (AABBDD) wheat. This trait of high K^+:Na^+ ratio could be used to increase salt tolerance of current wheat culitvars, which is supported by this study.

Ion fluxes (J_s, Mol/g/d). The ability of plants to uptake sodium and potassium ion also affects their tolerance to salt. The net ion uptake (ion flux) for potassium is higher in salt-tolerant cultivars, whereas ion flux for sodium is higher in salt-sensitive cultivars. Th e ion flux for potassium in the DH lines ranged from a high of 107.091 mol/g/d in DH-44, which was higher than the tolerant check Shorawaki (95.872 mol/g/d), to a low of 0.532 mol/g/d in DH-7.

The correlation between K^+ flux and K^+:Na^+ ratio also was found to be positive (r = 0.147), suggesting that the lines having a greater ability to discriminate potassium and sodium ions also have a greater ability to uptake and accumulate potassium and exclude sodium ions. This potassium/sodium ion discrimination is the most important character used to determine the salt tolerance of genotypes.

Generally, the tolerant genotypes showed fluxes of K^+ and less of Na^+. Variation in the uptake of K^+ and Na^+ has already been reported in wheat genotypes. Enhanced leaf K^+:Na^+ ratios and a greater flux of K^+ and less of Na^+ can be used to develop an effective screening procedure that can be more fruitful while breeding for salt tolerance.

Conclusion. The relative growth rate values for DN lines ranged from 0.0005 g/g/d to 0.0681 g/g/d/. Chlorophyll content was between 0.0004 mg/mg and 0.1172 mg/mg, whereas the K^+:Na^+ ratios observed were from a minimum of 0.380 to a maximum of 3.469. Ion flux for K^+ in the DH lines ranged from a high of 107.091 mol/g/d to a low of 0.532 mol/g/d. The DH lines that showed good performance for both agronomic and physiological parameters were DH-36, DH-65, DH-72, DH-73, and DH-76.

These results will become more authenticated after genotyping this germ plasm. Furthermore, the entries of agronomic promise serve as a useful source of salinity tolerance for different wheat breeding programs aimed at developing salt-tolerant wheat cultivars.

Cytological and molecular characterization of elite Pakistani wheat germ plasm for the T1BL·1RS chromosome translocation.

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Food security is an important issue prevailing throughout the world; which is lacking in one-third of the population. According to production estimates for the year 2025, a world population increase to 8.5×10^9 will require a doubling in food supplies. Food security could be achieved by developing and applying improved agricultural technologies. Our objectives were to cytologically characterize the elite Pakistani wheat cultivars and germ plasm of the National Uniform Wheat Yield Trials for the T1BL·1RS translocation using conventional somatic cytology and C-banding technique, screen the germ plasm for T1BL·1RS through molecular diagnostics using SSR markers, and validate the characterized germ plasm through biochemical analysis using glucose phosphate isomerase (GPI) and low-molecular-weight glutenin subunits (LMW-GS).

Germ plasm. The experimental material comprised of two sets of germ plasm. The first group comprised of the 40 elite Pakistani wheat cultivars (Table 63, pp. 200-201). The second group comprised of all entries of the National Uniform Wheat Yield Trials (NUWYT) of two crop cycles, 2008–09 and 2009–10, for both rain-fed and irrigated categories. The total number of entries of NUWYT (rainfed and irrigated) was 62 as first crop cycle comprised of 30 entries (Table 64, pp. 201-203) and second crop cycle comprised of 32 entries (Table 65, pp. 204). These wheat lines/entries were analyzed for the presence of the T1BL·1RS translocation. This study was conducted in the research laboratory of the Wheat Wide Crosses and Cytogenetics Programme in National Agriculture Research Centre, Islamabad, during 2009–10.

Results and discussion. Elite Pakistani wheat germ plasm was characterized for the T1BL·1RS translocation using the cytological, molecular, and biochemical techniques. The 40 selected and approved wheat cultivars and the National Uniform Wheat Yield Trial entries for 2008–09 and 2009–10 crop cycles, i.e., were analyzed using a conventional somatic cytological technique, C-banding, and SSR markers, and then validated by using a biochemical marker, GPI.

Table 63. A list of Pakistani wheat cultivars characterized for the T1BL·1RS translocation by cytology (the presence of two satellites (6B,6B) shows the presence of translocation and four satelllites (6B,6B,1B,1B) shows its absence), C–banding, SSR marker, and glucose phosphate isomerase (GPI) analyses (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Cultivar	Parentage	Cytological validation (number of satellites)	C–banding diagonistics	Molecular diagonistics	GPI validation
Lasani-2008	LUAN/Kohistan-97	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Punjnad-88	K4500.2/BJY	6B,6B	1RS +ve	1RS +ve	1RS +ve
Miraj-2008	Sparrow/Inia//V.7394/ WL711/13/BAU'S'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Kiran-95		6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Farid-2006	PT'S'/3/TOB/LFN/BB/4/ BB/HD-832-5//ON/5/G-V/ ALD'S'//HPO	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Bhittai	VEE/TRAP//Soghat-90	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
AS-2002	KHP/D31708// CM74A370/3/Ciano79/4/ RL6043/*4NAC	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Faislabad-2008	PBW65/2*Pastor	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Khirman		6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Pirsabak-05	Munia/CHTO//Amsel	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Momal-2002	BUC'S'/4/TZPP/IRN46	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Zarghoon-79	CC/Inia/3/TOB/CTFN// BB/4/7C	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Saleem-2000	Cham-6//Kite/PGO	6B,6B	1RS +ve	1RS +ve	1RS +ve
Marvi-2000	CMH-77A917/PKV 1600//RL6010/6*SKA	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Shafaq-2006	V 81094(LU 26/HD 21790/ 2* Inqalab 91)	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Chakwal-50	Attila/3/HUI/CARC// CHEN/CHTO/4/Attila	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Sehar-2006	CHILL/2* Star/4/BOW// BUC/PVN/3/2*VEE#10	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
TD-1	MAI'S' X NORTENO65 X H68	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Imdad-2005		6B,6B	1RS +ve	1RS +ve	1RS +ve
Pak-81	KVZ//BUHO//KAL/BB	6B,6B	1RS +ve	1RS +ve	1RS +ve
Shalimar-88	PB81/HD2182/PB81	6B,6B	1RS +ve	1RS +ve	1RS +ve
Pavon	VCM//CNO/7C/3/KAL/ BB	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Auqab-2000	Crow's'/NAC//BOW'S'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Tatara	JUP/ALD'S'//KLT'S	6B,6B	1RS +ve	1RS +ve	1RS +ve
Sarsabz	M20/79	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Chakwal-97	BUC'S'/FCT'S'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Margalla-99	Opata/BOW'S'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Inqalab-91	WL 711/Crow's'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Wafaq-2001	Opata/Rayon//Kauz	6B,6B	1RS +ve	1RS +ve	1RS +ve
Blue Silver	1154-388/AN/3/YT54/ N10B//LR64	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Tandojam-83	TZPP/PL/7C	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
GA-2002	DWL 5023/S N B// SNB	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Pirsabak-85	KVZ/BUHO/KAL/BB	6B,6B	1RS +ve	1RS +ve	1RS +ve

Table 63. A list of Pakistani wheat cultivars characterized for the T1BL·1RS translocation by cytology (the presence of two satellites (6B,6B) shows the presence of translocation and four satelllites (6B,6B,1B,1B) shows its absence), C–banding, SSR marker, and glucose phosphate isomerase (GPI) analyses (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Cultivar	Parentage	Cytological validation (number of satellites)	C–banding diagonistics	Molecular diagonistics	GPI validation
Chakwal-86	Fln/ACS/ANA	6B,6B	1RS +ve	1RS +ve	1RS +ve
LU-26	Blue Silver/Khushal	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Pasban-90	Inia F 66/A.Distchum// Inia66/3/GEN	6B,6B	1RS +ve	1RS +ve	1RS +ve
Bhakkar-2002	P20102/PIMA/ SKA/3/TTR'S'/ BOW'S',Pb.23826-D-1a-1a-1t-1t-0t	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
Rohtas-90	Inia F 66/A.Distchum// Inia66/3/GEN	6B,6B	1RS +ve	1RS +ve	1RS +ve
Fakhr-e-Sarhad	PFAU'S'/Seri//BOW'S'	6B,6B	1RS +ve	1RS +ve	1RS +ve
Zardana	CNO S/8156 TOB 66 CNO6-PVN	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve

Table 64. Wheat genotypes in National Uniform Wheat Yield Trails (Rainfed, 1-11, and Irrigated, 12-30), 2008–09, characterized for the T1BL·1RS translocation by cytology (the presence of two satellites (6B,6B) shows the presence of translocation and four satelllites (6B,6B,1B,1B) shows its absence), C–banding, SSR marker, and glucose phosphate isomerase (GPI) analyses (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Cultivar	Parentage	Cytological validation (number of satellites)	C–banding diagonistics	Molecular diagonistics	GPI validation
NR-358	PFAU/Weaver*2//Kiritati CGSS01B00076T-099Y-099M-099B-75Y-0B-01D	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
PR-98	CMH84.3379/ CMH78.578//Milan CMSS93Y006285-7Y-010Y-010M-010Y-10M-0Y-3KBY-0KBY	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NR-360	PFAU/Seri.1B// AMAD/3/Waxwing CGSS02Y00153S-099M-099Y-099M-46Y-0B-01D	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
SN-151	Kambara-1 CGSS9500016F-099Y-099B-099Y-099B-15Y-0B-0SY	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
04FJS35	PASTOR// HXL7573/2*BAU CMSS97M00306S-0P-95Y-90M-010Y	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
AZRC-2008-1	Tracha's//CMH76-252/ Pvn's ICW93-0065-6AP-0L-3AP-0L-1AP-0AP	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve

Table 64. Wheat genotypes in National Uniform Wheat Yield Trails (Rainfed, 1-11, and Irrigated, 12-30), 2008–09, characterized for the T1BL·1RS translocation by cytology (the presence of two satellites (6B,6B) shows the presence of translocation and four satelllites (6B,6B,1B,1B) shows its absence), C–banding, SSR marker, and glucose phosphate isomerase (GPI) analyses (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Cultivar	Parentage	Cytological validation (number of satellites)	C–banding diagonistics	Molecular diagonistics	GPI validation
PR-99	Hamam-4/Star"S"/Liz 0F-0K-2F-0K	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
KT-4	Altar84/ *Ae.squarrosa*219//SER CMBW91Y00892S-8Y-11KBY-2KBY-010M-9Y-3M-0Y-0SY	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
V-05003	Karvan2/4/Burgus/ Sort12-13//Kal/BB/3/ Pak81	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NRL-0320	FRET 2 CGSS96Y00146T-099B-099Y-099B-16Y-0B-0SY	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
5C011	Skauz/BAV92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
DN-62	SW89.5181/Kauz CMSS93B00824S-24Y-010M-010Y-010M-9Y-0M-0HTY	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
V-04178	Shalimar88/90A-204// MH97	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
SM-07018	Shalimar-88/Atilla// MH97	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
22-03	Snb(s')//Kea(s')/Snb(s')	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
B-07/Bkhtwr	LFN/1158.57//Prl/3/ Hahn/4/Kauz CMBW 89Y1044-0t0PM-8Y-010M-020B-0NPL-0T0Y	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
V-05082	Chenab2000/ Inqal-ab-91	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
PR-90	CNDO/R143//Ente/ Mexi-213/ CMSS93Bo1824M-040Y-73Y-010M-010Y-010M-10Y-0M	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
ZAS70	Inqalab 91*2/Tukuru CGSS99B00015F-099Y-099M-099Y-099M-31Y-0B	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
33010	KT/Bage//Fnu/3/Chak-wal-86 BR.4457-1B-5B-3B-0B	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve

Table 64. Wheat genotypes in National Uniform Wheat Yield Trails (Rainfed, 1-11, and Irrigated, 12-30), 2008–09, characterized for the T1BL·1RS translocation by cytology (the presence of two satellites (6B,6B) shows the presence of translocation and four satelllites (6B,6B,1B,1B) shows its absence), C–banding, SSR marker, and glucose phosphate isomerase (GPI) analyses (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Cultivar	Parentage	Cytological validation (number of satellites)	C–banding diagonistics	Molecular diagonistics	GPI validation
AUP-4008	Gen*2//Buc/ Flk/3/Buchin CMSS96M03098S-12M-010SY-010M-010SY-3M-0Y	6B,6B	1RS +ve	1RS +ve	1RS +ve
NIA-8/7	SHA4/Weaver// Skauz*2/SRMA	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
V-05066	Amsel/Attila// Inqal-ab-91/Pew'S'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
CT-03457	Attila*2/Yaco CGSS96B00134F-099B-028Y-099M-4Y-0B	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
66284	Inqalab-91/CB-271	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
SD-4085/3	Sarsabz/Sunco*2	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NR-356	Oasis/ Skauz//4*BC/3/2*Pastor CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-01D	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
9268	7012/PBW-222	6B,6B	1RS +ve	1RS +ve	1RS +ve
V-05BT006	Maya/Mon'S//Hork/ Fsd85 Iotech-0R4-1R1-2R7-3RK-0R	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
V-04022	Inqalab-91/3/Crow/ Nac//Bow'S'	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve

Conventional somatic cytology. Wheat cultivars show secondary constrictions on chromosomes 1B, 6B, and 5D when analyzed by conventional somatic cytological techniques. The 5D chromosome is resolved rather inconsistently. Generally, the secondary constriction of 1RS does not get resolved in T1BL·1RS wheat cultivars. The detection of only two satellited chromosomes in the somatic cells gives a quick, initial indication of the presence of 1RS in T1BL·1RS. The satellites on the short arm of chromosomes 1B and 6B were frequently observed, however, the chromosome 5D satellite appeared infrequently. The satellites of chromosome 5D were visible only in the good preparations. The translocated lines showed only two satellites on the short arm of 6B chromosome, whereas lines lackiing T1BL·1RS had six satellites, a pair of satellites on short arm of each of 1B, 6B, and 5D chromosomes (Fig. 40).

The difference observed between chromosomes 1B and 6B was that the short arm of the chromosome 1B was shorter than the short arm of chromosome 6B. There was a significant difference between the length of the long and the short arm of chromosome 1B whereas chromosome 6B had nearly equal short and long arms.

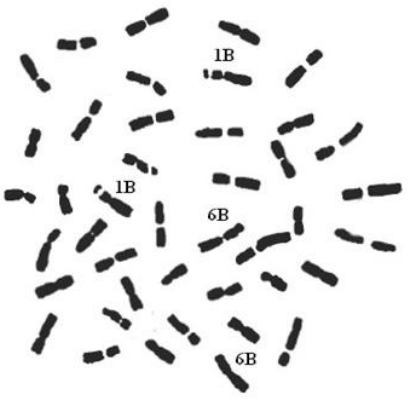

Fig. 40. Representative cell of wheat containing 42 chromosomes showing satellites on 1B and 6B chromosomes.

Table 65. Wheat genotypes in National Uniform Wheat Yield Trails (rain-fed, 1-12 and irrigated, 13-32), 2009–10, characterized for the T1BL·1RS translocation by cytology (the presence of two satellites (6B,6B) shows the presence of translocation and four satelllites (6B,6B,1B,1B) shows its absence), C–banding, SSR marker, and glucose phosphate isomerase (GPI) analyses (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Line/cultivar	Cytological validation (number of satellites)	C–banding diagonistics	Molecular diagonis-tics	GPI validation
NUWYT-1	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-2	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-3	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-4	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-5	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-6	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-7	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-8	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-9	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-10	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-11	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-12	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-13	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-14	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-15	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-16	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-17	6B,6B	1RS +ve	1RS +ve	1RS +ve
NUWYT-18	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-19	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-20	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-21	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-22	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-23	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-24	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-25	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-26	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-27	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-28	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-29	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-30	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-31	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve
NUWYT-32	6B,6B,1B,1B	1RS –ve	1RS –ve	1RS –ve

Somatic cells of the germ plasm lines were analyzed, chromosome were counted, and satellites observed at metaphase. Each germ plasm entry had a normal euploid status with 42 chromosomes. Twelve of the 40 wheat cultivars had only 6B satellites and the remaining 28 had four satellites, chromosomes 1B and 6B, and in rare cases 5D also was observed. The cultivars with translocation 6B satellites included Punjnad-88, Chakwal-86, Saleem-2000, Imdad-2005, Pak-81, Shalimar-88, Tatara, Wafaq-2001, Pirsabak-85, Pasban-90, Rohtas-90, and Fakhr-e-Sarhad.

Two of the 30 NUWYT entries for the 2008–09 crop cycle had only 6B satellites, and the remaining 28 entries had four satellites for chromosomes 1B and 6B. Only 6.66% of the NUWYT entries for this crop cycle possessed the T1BL·1RS translocation. This trial had no translocated entry present in the rain-fed category, both were in the irrigated group. For the 2009–10 crop cycle, ten of the 32 NUWYT entries exhibited only 6B satellites, and the remaining 22 entries had four satellites for chromosomes 1B and 6B. For the 2009–10 crop cycle, 31.25% of the NUWYT entries had the T1BL·1RS translocation, an increase.

C-banding technique. Unlike wheat, heterochromatin is present at the terminal ends of rye chromosomes making it possible to identify 1RS Robertsonian translocations, 1R substitutions, or 1R additions in wheat. The C-banding for a particular chromosome is believed to be the constant for that chromosome. The wheat and rye karyotypes were produced by this technique, and these karyotypes are helpful in the identification of rye chromosomes in the wheat background. The B genome of wheat is the most heterochromatic, followed by A genome, which is slightly more heterochromatic than the D genome. The D genome is the least heterochromatic in terms of the total heterochromatin per genome in wheat. Chromosomes 4A, 1B, 2B, 5B, and 6B are the most heterochromatic chromosomes. When analyzed by C-banding, the T1BL·1RS chromosome contained prominent banding sites on the long arm terminal end, at the centromeric region, and terminal and subterminal sites on the short arm, with a fainter interstitial band on the long arm. Banding patterns observed were very clear in good preparations.

Prominent bands on the terminal end of the long arm, and centromeric, terminal, and subterminal bands on the short arm were shown in 12 of the 40 wheat cultivars, and these cultivars were classified as translocated. Quite clear banding patterns were observed in the good preparations. Cultivars with the translocation included Punjnad-88, Chakwal-86, Saleem-2000, Imdad-2005, Pak-81, Shalimar-88, Tatara, Wafaq-2001, Pirsabak-85, Pasban-90, Rohtas-90, and Fakhr-e-Sarhad.

Two of the 30 NUWYT entries of the 2008–09 crop cycle showed prominent bands on terminal end of long arm, and centromeric, terminal, and subterminal bands on the short arm, and remaining 28 entries showed bands specific for arm 1BS. Only 6.66% of the NUWYT entries for this crop cycle possessed T1BL·1RS. This trial had no T1BL·1RS entry present in the rain-fed category, both translocation lines were present in the irrigated set. For the 2009–10 crop cycle, ten of 32 NUWYT entries showed prominent bands on terminal end of long arm, the centromeric, terminal, and the subterminal band on the short arm, and remaining 22 entries showed bands specific for arm 1BS, indicating that 31.25% of the NUWYT entries for this crop cycle possessed the translocation.

Cytological techniques provide a powerful tool for the identification of the T1BL·1RS translocation in germ plasm. The conventional somatic cytological technique used proved to be an efficient means for characterizing the germ plasm with T1BL·1RS through the identification of the satellites present on short arm of the chromosome 6B. Secondary constrictions present on the chromosomes 1B, 6B, and 5D are very helpful for the characterization of germ plasm carrying translocations. Rye chromatin also can be characterized using C-banding. First established as a technique applicable to animal chromosomes, chromosome banding is now an established procedure for the characterization of rye chromatin in plants. To apply chromosome banding and in situ hybridization, the base essentials include ideal chromosome contractions and a high number of mitotic metaphase spreads.

Molecular characterization. Many scientists use molecular diagnostics to identify the T1BL·1RS translocation. Molecular markers, including SSRs or microsatellites, have been used efficiently for the identification of this translocation. When rye-specific SSR primers are used to identify T1BL·1RS, they generate diagnostic bands that help identify translocation genotypes. The 1RS-specific RYE-NOR marker was used for the molecular evaluation of the Pakistani wheat cultivars and the entries of the two NUWYT trials.

Amplification and polymorphism generated by RYE-NOR. The RYE-NOR is specific to the short arm of rye and amplifies bands of 300 bp, 400 bp, 700 bp, and 800 bp in the T1BL·1RS genotypes; it generated no amplification in the nontranslocation genotypes. Wheat cultivars that were amplified by the marker included Punjnad-88, Chakwal-86, Saleem-2000, Imdad-2005, Pak-81, Shalimar-88, Tatara, Wafaq-2001, Pirsabak-85, Pasban-90, Rohtas-90, and Fakhr-e-Sarhad. The maximum number of bands observed was three and the minimum was two.

Of the 30 NUWYT entries observed for the 2008–09 crop cycle, only two were amplified by the marker The remaining 28 entries were not amplified by this marker, thus, only 6.66% of the NUWYT entries for this crop cycle possessed T1BL·1RS. This trial had no entry with the translocation present in the rain-fed category, both translocation lines were present in the irrigated set. For the 2009–10 crop cycle, ten of the 32 NUWYT entries observed were amplified by the marker, the remaining 22 entries were not, thus, 31.25% of the NUWYT entries for this crop cycle possessed T1BL·1RS.

Biochemical validation with glucose phosphate isomerase analysis. Biochemical diagnostics using GPI allelic variation and LMW-GS allelic variation were used for further validate results obtained by using cytological and molecular techniques. The rye proteins specific to 1R had unique characteristics compared to each another and to wheat proteins, which makes it possible to characterize 1RS in wheat-rye translocation lines. The short arms of chromosome 1R, 1A,

1B, and 1D have GPI loci and at least two enzyme subunits are controlled by each GPI locus. The appearance of unique, rye GPI bands makes possible the identification of rye in a wheat background.

Twelve of the 40 wheat cultivars observed showed the unique 1RS GPI bands, indicating the T1BL·1RS translocation. These bands were distinguishable from those of 1BS of the normal wheat. Cultivars with the T1BL·1RS translocation included Punjnad-88, Chakwal-86, Saleem-2000, Imdad-2005, Wafaq-01, Shalimar-88, Tatara, Pak-81, Pirsabak-85, Pasban-90, Rohtas-90, and Fakhr-e-Sarhad.

Of the 30 NUWYT entries for the 2008–09 crop cycle, only two had unique 1RS GPI bands and the remaining 28 entries showed diagnostic bands for arm 1BS; only 6.66% of the NUWYT entries for this crop cycle possessed T1BL·1RS. The genotypes specified for the rain-fed category had no translocation and only two genotypes for irrigated areas had translocation. For the 2009–10 crop cycle, ten of the 32 NUWYT entries had unique 1RS GPI bands; the remaining 22 entries showed bands specific for 1BS, 31.25% of the NUWYT entries.

Low-molecular-weight glutenin subunit analysis. The LMW-GS comprise of an important class of glutenins. Approximately 40% of the total wheat gluten fraction is represented by LMW-GS. The LMW-GS are encoded by the *Glu-A3, Glu-B*3, and *Glu-D3* loci on the short arm of chromosomes 1D, 1B, and 1D, respectively. Thus, analyzing the LMW-GS is an efficient means to identify the T1BL·1RS translocation. *Glu-B3j*, a low-molecular-weight subunit encoded by rye chromatin is the indicator of the T1BL·1RS translocation.

Sixteen wheat cultivars were validated using LMW-GS analysis. Among these 16, seven had the T1BL·1RS translocation and the remaining nine lacked it (Table 66). Cultivars with the T1BL·1RS translocation expressed subunit *Glu-B3j*. Cultivars found to have T1BL·1RS included Punjnad-88, Pak-81, Shalimar-88, Tatara, Pirsabak-85, Pasban-90, Rohtas-90, and Fakhr-e-Sarhad; Blue Silver, Sarsabz, Bhakkar-2002, Margalla-99, Auqab-2000, Inqalab-91, Lasani-2008, Shafaq-2006, and Miraj-2008 lacked *Glu-B3j*.

Table 66. Low-molecular-weight glutenin subunit (LMW-GS) validation for the T1BR·1RS translocation in Pakistani wheat cultivars (1RS +ve indicates presence of heterochromatin bands of rye, 1RS –ve shows absence).

Cultivar	LMW–GS validation
Punjnad-88	1RS +ve
Pak-81	1RS +ve
Shalimar-88	1RS +ve
Lasani-2008	1RS –ve
Shafaq-2006	1RS –ve
Inqalab-91	1RS –ve
Fakhr-e-Sarhad	1RS+ve
Blue Silver	1RS –ve
Pasban-90	1RS +ve
Sarsabz	1RS –ve
Bhakkar-2002	1RS –ve
Pirsabak-85	1RS +ve
Rohtas-90	1RS +ve
Miraj-2008	1RS –ve
Margalla-99	1RS –ve
Auqab-2000	1RS –ve

This study generated valuable information about Pakistani wheat cultivars and the entries of NUWYT for two crop cycles. These results showed that the percent of entries with the T1BL·1RS translocation increased from 6.66% in the 2008–09 trial to 31.25% in 2009–10. This increase is desirable because many advantages are associated with this translocation. The T1BL·1RS lines tend to have greater above-ground biomass, 1,000-kernel weight, test weight, higher grain yield, and spike fertility.

Along with high yield, stability, and adaptability, the T1BL·1RS lines also may possess resistance to *Septoria tritici* blotch and moderate aluminium toxicity tolerance. In addition, resistance to several important pathogens, such as leaf, strip, and stem rusts and downy mildew has been associated with chromosome arm 1RS. Grains of T1BL·1RS lines are rich in trace minerals. A positive effect of T1BL·1RS on the concentration of iron and zinc in the grain of the CIMMYT wheat germ plasm also has been reported. The T1BL·1RS translocation lines have a high harvest index and water-use efficiency under drought conditions than their non-T1BL·1RS counterparts. The T1BL·1RS wheat–rye translocation also is useful for improving the adaptability of wheat to zinc deficient and acidic soils. However, some quality concerns exist about T1BL·1RS germ plasm. The advantages are making the T1BL·1RS lines desirable to be used in the breeding programs worldwide, and future strategies to exploit these sources to get more benefit from this sort of novel germ plasm should be encouraged.

QTL analysis of a wheat double haploid mapping population for salinity tolerance.

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Through the combined use of DNA marker technology and advanced statistical methods, chromosome regions that contain the genes that determine quantitative traits (QTL) can be identified. Gene cloning technologies that originally targeted major genes are increasingly including those genes responsible for quantitative, multigenic traits. Identifying genes behind these QTL is a big challenge. However, now that a few plant QTL have been cloned and accurately tagged, they might be accurately positioned within 2 cM or less on the genome. We see circumstances when map-based cloning using only original mapping data would be a realistic option that avoids time-consuming and expensive fine mapping. Keeping this in view, our study was designed to find DNA markers linked to salinity tolerance traits in common wheat using the QTL mapping technique to map QTL for salt tolerance traits in a wheat mapping population, use in vitro screening for salt tolerance monitoring physiological parameters through hydroponic tests, and study the phenotype to identify entries with good morphological characters.

Materials and methods. The plant material consisted of 61 double haploids (DH) derived from the cross of 'Croc/Stylet'. Croc is salinity resistant and Stylet is salinity susceptible. Seeds of these lines were collected from the Wheat Wide Crosses, Islamabad. A hydroponic experiment was conducted at two salinity levels, at 0 mM NaCl, which served as a control experiment under nonsaline conditions, and at 75 mM NaCl, under saline conditions to evaluate the performance of the mapping population and parents.

Screening of parents for physiological characteristics. The mean values for both parents revealed a large amount of variation for these traits at 0 mM. The K^+:Na^+ ratio was higher in Croc (2.5) than Stylet (0.1). Chlorophyll a content was higher in Croc than Stylet. Croc showed a significantly higher value in different physiological traits than Stylet. A significant difference in total chlorophyll was noted between Croc (5.3 mg/g) and Stylet (52 mg/g). The same pattern was observed for sugar content, which was higher in Croc (3.01 mg/g) than Stylet (0.12 mg/g). Thus, Croc showed better results than Stylet (Table 67). There was a significant difference in both parents at 75 mM. The K^+:Na^+ ratio was higher in Croc (1.25) than Stylet (0.07). Chlorophyll content was higher in Croc (Table 67). A significant increase in sugar content under saline conditions was observed in Croc (4.15 mg/g) compared to Stylet (1.25 mg/g). The data revealed that Croc showed better performance under 75 mM salt stress than Stylet.

Table 67. Physiological characterization of a 'Croc/Stylet' mapping population and the parents at two salinity levels.

Parameter	Salt concentration (mM)	Mean (±SD)		Mapping population				h^2
				Minimum value	Maximum value	Skewness	Kuertosis	
K^+:Na^+	0	2.50	0.10	0.11	2.32	–0.24	–1.17	0.82
	75	1.25	0.07	0.07	1.23	0.14	–0.44	0.54
Chlorophyll a	0	4.02	0.43	0.43	3.87	0.11	–0.25	0.44
	75	2.80	0.10	0.10	2.72	0.12	–1.10	0.72
Chlorophyll b	0	2.20	0.07	0.08	2.00	0.75	0.26	0.56
	75	1.50	0.06	0.06	1.42	0.87	0.25	0.73
Total chlorophyll	0	5.30	0.52	0.52	5.16	0.19	–0.56	0.48
	75	4.23	0.18	0.19	4.05	0.26	–0.95	0.73
Sugar	0	3.01	0.12	0.13	2.92	–0.14	-1.08	0.80
	75	4.15	1.25	1.27	4.15	–0.01	-0.11	0.84

Screening of the parent lines for morphological characteristics. Significant variability was observed in both parents at control (0 mM) conditions. Both parents differed significantly from each other for all the parameters studied (Table 68, p. 208). The shoot length of Croc was 37.3 cm, whereas that of Stylet was 18 cm. Root length was greater in Croc (21.50 cm) than Stylet (5.44 cm). The shoot dry weight of Croc was 0.7 g and Stylet was 0.16 g. Root dry weight of Croc was 0.060 g, whereas of Stylet was 0.006 g.

At saline conditions (75 mM NaCl), Croc performed better than Stylet (Table 68). The means of the different morphological parameters showed significant differences in both parents. The shoot length of Croc was 33cm and that of Stylet 14 cm. The difference in root length also was large; Croc was 21.2 cm and Stylet was 3.00 cm. Fresh shoot weight was significantly different in both parents; Croc had a weight of 0.52 g and Stylet had 0.07 g. Shoot dry weight also was significantly higher in Croc (0.06 g) than in Stylet (0.01 g). The root dry weight of Croc was 0.280 g, whereas that of Stylet was 0.004 g.

Table 68. Morphological characterization of a 'Croc/Stylet' mapping population and the parents at two salinity levels.

Parameter	Salt concentration (mM)	Croc_1	Stylet	Mapping population				h^2
		Mean±SD		Minimum value	Maximum value	Skewness	Kuertosis	
Shoot length (cm)	0	37.4	18.0	19.0	36.3	–0.38	1.45	0.68
	75	33.0	14.0	14.0	32.0	–0.81	2.51	0.67
Root length (cm)	0	21.5	5.440	5.44	20.6	0.39	–0.31	0.59
	75	21.2	3.000	3.02	20.5	1.35	2.74	0.76
Shoot fresh weight (g)	0	0.70	0.16	0.16	0.60	–0.11	-0.73	0.58
	75	0.52	0.07	0.08	0.51	0.18	-0.74	0.75
Shoot dry weight (g)	0	0.12	0.03	0.03	0.12	1.85	5.05	0.14
	75	0.06	0.01	0.01	0.06	0.48	–0.26	–0.12
Root dry weight (g)	0	0.06	0.006	0.006	0.054	2.44	9.05	0.42
	75	0.28	0.004	0.004	0.023	0.44	1.09	0.46

Screening of the mapping population for physiological characteristics. The mean, maximum, and minimum values revealed that variation exists among the members of mapping population (Table 68). No transgressive segregation at the lower and upper limits of any trait was observed. The graphical representation of these traits also revealed that, in most of the cases, the data distribution is normal and there is no need to standardize the data set.

K^+:Na^+ ratio. The K+:Na+ ratio ranged from 0.11 to 2.32 in the population at the control conditions. The skewness of the potassium sodium ratio was –0.24 and kurtosis was –1.17. The negative value for skewness indicated that most of the lines had a value less than the average. At 75 mM salt, the K^+:Na^+ ratio was 0.07–1.23, which is less than the control. The skewness of K^+:Na^+ ratio at saline conditions was positive (0.14) being greater than its mean value. The heritability under control condition (0 mM) was 0.82 and at salt stress conditions (75 mM) was 0.54, which is less than the control condition and, thus, could not be made a criteria of selection for salinity tolerance.

Chlorophyll a. Chlorophyll a was higher in 0 mM salt (3.87 mg/g) and reduced in saline conditions (2.72 mg/g). Under the control conditions chlorophyll was 0.43–3.87 mg/g and 0.10–2.72 mg/g at saline conditions (75 mM NaCl). The skewness of chlorophyll a in the population is 0.12 in saline (75 mM NaCl) and 0.11 in nonsaline (0 mM) conditions. In both cases, the positive value for skewness showed that the performance of most of the lines was equal or greater than the mean value. Kuertosis in the population in saline conditions was –1.1 and in nonsaline conditions was –0.25. The estimate pf heritability of chlorophyll a under control conditions was 0.44 and 0.72 under salt stress.

Chlorophyll b. Chlorophyll b content was higher under control conditions (0.08–2.00 mg/g) and reduced in saline conditions (0.06–1.42 mg/g). The skewness of chlorophyll b in the population was 0.87 in saline and 0.75 in nonsaline conditions. Skewness was positive in both saline and nonsaline conditions. Kurtosis in the population under saline conditions was 0.26 and 0.25 in nonsaline. Heritability for chlorophyll b under control conditions was 0.56 and 0.73 under salt stress.

Total chlorophyll. The total chlorophyll also decreased due to salinity stress, ranging from 0.52 mg/g to 5.16 mg/g under the control conditions and 0.19 mg/g to 4.05 mg/g uder saline conditions. The skewness in the population was 0.26 in saline and 0.19 in control conditions. The population showed a higher skewness value for total chlorophyll at saline conditions (0.26) than at control conditions (0.19). A positive value for skewness showed that they were equal or greater than the mean value. Kurtosis in the population under saline conditions was –0.95 and in nonsaline conditions was –0.56. Heritability for total chlorophyll was 0.48 and 0.73 under control and salt stress, respectively.

Sugar content. Sugar content increased in stressed conditions; the range of sugar was 0.13–2.92 mg/g at the control conditions and 1.27–4.15 mg/g in saline. A significant increase in sugar content was observed in saline conditions; increasing from 2.92 mg/g in he control and 4.15 mg/g in saline. Skewness in population was –0.01 in saline and –0.14 in nonsaline conditions. Sugar showed a negative value for skewness indicating less than the mean value. Skewness is much less in saline conditions than in the control conditions. Kurtosis in the population under saline conditions was –0.11 and –1.08 in nonsaline conditions was. Heritability for sugar contents in the control was 0.80 and 0.84 under salt stress conditions.

Screening of the mapping population for morphological characters. Sufficient variability was observed in the 61 lines for the morphological characters studied.

Shoot length. The shoot length ranged from 14.0–32.0 cm in the population under saline conditions, which is within the limits of the parental means (14.0–33.0 cm). Under control conditions, shoot length ranged from 19.0–36.3 cm; a decrease under salinity. The skewness of shoot length was –0.81 under saline and –0.38 under control conditions, a negative move from the mean values. Kuertosis was –2.51 at saline and 1.45 at control conditions. Heritability for shoot length was 0.68 under control and 0.67 under salt stress condition.

Root length. Root length was higher in the control (5.44–20.50 cm), which was within the limit of the parental mean (5.44–21.50 cm) and reduced under saline conditions (3.02–20.50 cm). Under saline conditions the parental mean for root length was 3.00–21.20 cm. The skewness of root length in the population is 1.35 in saline and 0.39 in nonsaline conditions. A positive value for the skewness showed that these values were equal or greater than the mean value. Kurtosis in saline conditions was 2.74 and –0.31 in nonsaline conditions. The negative value showed that these values were less than the mean value. Under control conditions, heritability for root length was 0.59 and 0.76 under salt stress.

Shoot fresh weight. Fresh weight of the shoots was higher in control conditions (0.16–0.60 g) and reduced in saline (0.08–0.51 g). The parental mean values for shoot fresh weight was 0.70 g under control conditions and 0.52 g under saline. The skewness of shoot fresh weight in the population was 0.18 under saline and –0.11 under nonsaline conditions. The skewness for shoot fresh weight under saline condition was higher with a positive value and smaller in controlled conditions with value negative from the mean. The kurtosis in saline conditions was –0.74 and in nonsaline conditions was –0.73. Heritability for shoot fresh weight under control conditions was 0.58 and under salt stress was 0.76.

Shoot dry weight. The dry weight of the shoot also decreased due to salinity stress ranging from 0.03–0.12g under control conditions, within the limit of their parental mean values (0.03–0.12g). On the other hand, under saline condition, it ranged from 0.01–0.06 g, exactly within the parental mean value (0.01–0.06 g). Skewness in the population was 0.48 under saline and 1.85 under control conditions, showing a positive shift from the mean value. Kurtosis under saline conditions was 5.05 and under nonsaline conditions was –0.26. Heritibility for shoot dry weight was 0.14 under control and –0.12 under salt stress conditions.

Root dry weight. The root dry weight decreased under stress conditions. A significant decrease under saline condition was observed. At control conditions root dry weight was 0.006–0.054g with the parent mean 0.006–0.060 g. The root dry weight ranged from 0.004 to 0.023 g under salt stress, which is within the parental mean values (0.004–0.028 g). Skewness in the population was 0.44 under saline and 2.44 under nonsaline conditions and higher under control conditions (2.44) than under saline condition (0.44). Kurtosis under saline conditions was 9.05 and 1.09 under nonsaline. Heritability for root dry weight was 0.42 under control and 0.46 under salt stress conditions.

Correlation between different physiological parameters at 0 mM. Correlation ranged from 0.98 to –0.42 among the different physiological and morphological parameters. The maximum correlation was observed between chlorophyll a and total chlorophyll, and the minimum correlation was observed between the sugars and K^+:Na^+. The correlation matrix showed positive correlation between most of the physiological parameters at a 0 mM salinity level. There are fewer negative correlations, between chlorophyll a and sugar (–0.26), chlorophyll b and sugar (–0.36), total chlorophyll and sugar (–0.31), sugar and K^+:Na^+ (–0.42), sugar and shoot length (–0.12), sugar and root length (–0.12), sugar and shoot fresh weight (–0.23), chlorophyll a and shoot dry weight (–0.088), chlorophyll b and shoot dry weight (–0.14), total chlorophyll and shoot dry weight (–0.11), and K^+:Na^+ and shoot dry weight (–0.1). Positive correlations were observed among rest of the characteristics.

Correlation between pifferent physiological parameters at 75 mM. The correlation among the different physiological and morphological parameters ranged from 0.98 to –0.31. The maximum correlation was observed between chlorophyll a and total chlorophyll, and the minimum correlation was observed between the sugar and root length. Correlation matrix showed a positive correlation between most of the physiological parameters at 75 mM salinity. Fewer negative correlations were observed between different parameters; chlorophyll a and sugar (–0.21), chlorophyll b and sugar (–0.26), total chlorophyll and sugar (–0.23), sugar and shoot length (–0.13), sugar and root length (–0.31), K^+:Na^+ and root length (–0.14), sugar and shoot fresh weight (–0.29), chlorophyll a and shoot dry weight (–0.18), chlorophyll b and shoot dry weight (–0.28), total chlorophyll and shoot dry weight (–0.22), sugar and shoot dry weight (–0.14), chlorophyll a and root dry weight (–0.35), chlorophyll b and root dry weight (–0.37), total chlorophyll and shoot dry weight (–0.37), and sugar and shoot dry weight (–0.02).

Genotyping. ***Formation of linkage groups.*** The data were subjected to Mapmaker/EXP version 3.0 to construct genetic linkage maps with a LOD threshold of 2.0 and maximum distance of 50 cM between adjacent markers. Centimorgan (cM) values were calculated from recombination frequencies based on the Kosambi mapping function. The LOD score is defined as the base-10 logarithm of the ratio of the maximum likelihood values assuming linkage versus no linkage. Nine linkage groups were formed for the chromosomes 1A, 6A, 7B, 1D, 2D, 4D, 5D, 6D, and 7D (Fig. 41). The 2D chromosome was divided into two linkage groups 2D.1 and 2D.2 due to the greater recombination fraction among the adjacent markers.

QTL analysis. QTL mapping analyses for the traits tested were performed using the composite interval mapping method implemented by the software package Q Gene V. 4.1. A log- likelihood (LOD) score threshold of 2.0 was used to identify regions containing putative loci associated with traits under study. Three data pools for each trait were prepared and subjected to QTL analysis. A third data pool for the difference at both salinity levels was used to identify any additional QTL controlling the difference of these traits. The total LOD score and variance explained (R^2) in each trait were determined in a multiple-QTL model that included all of the significant QTL. Results for the different traits follow.

Chlorophyll a content. Total of two QTL for Chlorophyll a were identified on chromosomes 6A and 7D (Table 69). A QTL on 6A was identified to control chlorophyll a under 0 mM conditions and 7A controls the trait at 75 mM salt-stress conditions. These QTL on 6A and 7D were linked with their respective markers and explained 17.6% (6A) and 17.0% (7D) of the variation (R^2) chlorophyll a. The additive effect of 6A and 7D were 0.407 and –0.329, respectively (Table 69).

Table 69. QTL for various traits using composite interval mapping in Richard's Salinity Mapping Population.

Trait		QTL location	Closest marker	LOD score	R^2	Additive effect
Chlorophyll a	0 mM	7D	BARC 57	2.560	17.6%	0.407
	75 mM	6A	BARC 169	2.470	17.0%	–0.329
Chlorophyll b	0 mM	6A	BARC 169	2.290	15.9%	–0.188
	0 mM	7D	BARC 53	2.160	15.0%	0.205
	75 mM	6A	BARC 169	2.670	18.3%	–0.168
Total chlorophyll	0 mM	7D	BARC 53	2.170	15.2%	0.550
	75 mM	6A	BARC 169	2.710	18.5%	–0.528
Sugar	0 mM	1D	*Xgdm19*	2.060	14.4%	1.252
	75 mM	1D	*Xgdm19*	2.840	19.3%	1.361
	75 mM	5D	*X292.5D*	2.820	19.2%	–30.03
K^+:Na^+ ratio	75 mM	2D2	BARC159	2.210	15.4%	–1.021
Shoot length	75 mM	1A	BARC 62	4.675	29.7%	2.094
	75 mM	2D2	*X320.D*	4.041	26.3%	13.154
Shoot fresh weight	75 mM	6D	*Xgdm14*	2.490	17.2%	–0.529
	Difference	4D	*Xgdm61*	2.590	17.8%	–0.070
Shoot dry weight	Difference	1A	BARC 62	2.890	19.6%	-0.01

Chlorophyll b content. Three QTL for Chlorophyll b were identified on chromosomes 6A and 7D under 0 mM conditions and one on chromosome 6A under salt stress condition (Table 69, p. 210). These QTL are exactly linked with their respective markers and explained 15.9% (6A), 15.0% (7D), and 18.3% (6A, 75 mM) of the variation for chlorophyll b. The additive effects of 6A were –0.188 (6A), 0.205 (7B), and –0.168 (6A, 75 mM).

Total chlorophyll content. Two QTL for total chlorophyll were identified on chromosomes 7D and 6A (Table 69, p. 210). These QTL are exactly linked with respective markers and explained 15.2% (7A) and 18.5% (6A) of the variation for total chlorophyll. The additive effects of 6A and 7D were 0.550 and –0.528, respectively.

Sugar content. Three QTL for sugar were identified on chromosome 1D under 0 mM conditions and two were identified on chromosomes 1D and 5D under salt-stress conditions (Table 69, p. 210). The QTL on chromosome 1D at both salinity levels were exactly linked with their respective marker and explained 14.4% and 19.3% of the variation. The additive effects of the 1D QTL were 1.252 and 1.361. A third QTL is found on 5D chromosome. The position of the QTL was 226.0 cM on the genetic map of chromosome 5D. This QTL explained 19.2% of the variation for sugar and the additive effect of 5D was –30.03.

K^+:Na^+ ratio. One QTL is found on chromosome 2D2 for K^+:Na^+ ratio (Table 69, p. 210). The position of the QTL was 422.0 cM on genetic map of chromosome 2D2. This QTL explained 15.4% of the variation for the K^+:Na^+ ratio and the additive effect of 2D was –1.021.

Shoot length. One QTL is found on 1D chromosome for shoot length (Table 69, p. 210). The position of the QTL was 34.0 cM on the genetic map of chromosome 1D. This QTL explained 13.9 % of the variation for shoot length. The additive effect of 1D was –4.029.

Shoot fresh weight. Two QTL for shoot fresh weights were identified on chromosomes 6D and 4D (Table 69, p. 210). The position of the QTL was 332.0 cM on genetic map of chromosome 6D and 2.0 cM on the genetic map of chromosome 4D. These QTL explained 17.2% (6D) and 17.8% (4D) of the variation for shoot fresh weight. The additive effect of 6D and 4D were –0.529 and –0.07, respectively.

Shoot dry weight. One QTL is found on 1A chromosome for shoot dry weight (Table 69, p. 210). The position of QTL was 152.0 cM on genetic map of chromosome 1A. This QTL explained 19.6% of the variation shoot dry weight. The additive effect of 1A was –0.01.

Characterization of the mapping population for morphological and physiological traits. A wheat DH population subjected to salt stress of 75mM NaCl indicated highly significant differences among the population for all the morpho-physiological traits studied. However, the differences in the parents for the physiological parameters studied were more prominent than morphological traits. Croc has a 25 times higher K^+:Na^+ ratio than Stylet under control conditions, whereas it has 18 times greater K^+:Na^+ ratio than Stylet at 75 mM salt stress. These results revealed that Croc is more tolerant than Stylet. Under salt-stress conditions, there is a decrease in the K^+:Na^+ ratio. The salinity tolerance in wheat is associated with the accumulation of K^+ and exclusion of Na^+ under saline conditions. These results indicated that parents slightly decrease K^+ accumulation under salinity stress. We observed a similar percent decrease in the K^+:Na^+ ratio. In Richard's population, genotype HW775*C22 showed the highest K^+:Na^+ ratio and HW775*A13 the lowest.

Sodium competes with K^+ for uptake through a common transport system and does this effectively because the Na^+ concentration in saline environments is usually considerably greater than that of K^+. The sensitivity of some crops to salinity is due to the inability to keep Na^+ and Cl^- out of transpiration streams. Plants limiting the uptake of toxic ions or maintaining normal nutrient ion contents could show greater tolerance, which also was the case with our study. Uptake mechanisms that discriminate similar ions, such as Na^+ and K^+, can provide a useful selection criteria for salt tolerance in wheat and breeding for efficient nutrient uptake. All the wheat genotypes studied showed a decreasing trend in K^+ content due to salinity stress. The decrease in K^+ was due to the presence of excessive Na^+ in the growth medium because high external Na^+ content is known to have an antagonistic effect on K^+ uptake in plants. Salt tolerance is reported to be associated with K^+ content because of its involvement in osmotic regulation and competition with Na^+. Regulation of K^+ uptake, prevention of Na^+ entry, and efflux of Na^+ from cell are commonly used by plants to maintain desirable K^+:Na^+ ratio in the cytosol.

The chlorophyll content of leaves generally decreases under salt stress. The oldest leaves start to develop chlorosis and fall with prolonged period of salt stress. In this study, the chlorophyll a content of the leaves decreased due to salt stress. In both parents, the percent reduction varied from 76.6 % in Stylet and to 30.3 %Croc. Stylet was more sensitive towards salt stress shown by a greater decrease in chlorophyll a content in the leaves under salt stress. Croc had less of a decrease in chlorophyll a content of the leaves (30.3%) than that of Stylet, showing tolerant behavior under salt stress. The mapping population also had a decreased chlorophyll a content within the range of the parental reduction. Genotype HW775*C16 showed high chlorophyll a content and genotype HW775*A51 showed a low content in the mapping population. The chlorophyll b content in leaves of Croc decreased about 32% and in Stylet about 14.2%. The population also had a decreased chlorophyll b content. In the population, genotype HW775*C29 showed a higher content of chlorophyll b and genotype HW775*C16 had a lower content.

Similarly, total chlorophyll also decreased in the parents as well as in the population. In Croc, the total chlorophyll reduction was 20.2 % and the reduction was 65.3% in Stylet. These results revealed that Stylet was more sensitive to salt stress because of a more pronounced decrease in chlorophyll. In the population, genotype HW775*C27 showed a higher content of chlorophyll b and genotype HW775*B7 had a lower content. The reduction in chlorophyll content is to be expected under stress; being membrane bound, its stability is dependent on membrane stability, which under saline condition seldom remains intact.

During salt stress, an increase in sugar concentration has been reported in many species. In this study, the sugar content in the leaves of Croc increased 27.5% under salt stress whereas Stylet increased 90.4% to overcome salinity stress. Similar behavior was observed in the population with with genotype HW775*B19 under salt stress showing less of an increase in sugar content, exhibiting tolerance, and genotype HW775*C35 showing an increase in sugar content under salt stress.

Shoot length also decreased due to salt stress. The percent reduction in shoot length in Croc was 11.7% and 22.2% in Stylet, twice the reduction in shoot length. Stylet was sensitive for salt tolerance and the population also showed a reduction in shoot length under salt stress conditions. Genotype HW775*C36 had the highest shoot length and genotype HW775*A35 the smallest.

Root length decreased in Croc by 1.4% and in Stylet by 44.8%. A similar range of reduction was observed in the population. Genotype HW775*C35 in the population had the longest root length and with HW775*C32 the shortest under salt stress. Shoot fresh weight decreased 25.7% in Croc and 57% in Stylet. These results indicate that Croc, the tolerant parent, produced a smaller reduction in shoot fresh weight than Stylet. The population also showed a similar range of reduction in shoot fresh weight where HW775*C35 showed less reduction in shoot fresh weight and genotype HW775*C34 showed greater reduction under salt stress.

Shoot dry weight and root dry weight also decreased under salinity stress. Shoot dry weight decreased 50.0% and 53.0% of root dry weight in Croc, whereas the reductions in Stylet were 66.6% of shoot dry weight and 33.3 % of root dry weight under salt stress conditions. Genotype HW775*B6 had less of a reduction in shoot dry weight and genotype HW775*B17 in root dry weight showing tolerant behavior in these traits. Because salinity stress results in a clear stunting of plants, it also results in a considerable decrease in fresh and dry weights of leaves, stems, and roots. The frequency distributions for a majority of the traits were normal and variation for most of the morphological traits studied was more prominent in the population than among the parents.

Linkage map construction. The genetic map depicted that the D genome had three to eight times the number of markers compared to the A and B genomes (Fig. 41, p. 213). The chromosome length of the A and B genomes also was less than that of the D genome.

Salt tolerance is located on D genome of bread wheat. Experiments on hexaploid bread wheat and its ancestors confirmed that *Ae. tauschii* and *T. aestivum* had high K^+:Na^+ ratios, whereas *T. turdigum* subsp. *dicoccoides* and *Ae. speltoides* had low ratios. These studies demonstrated that the D genome contains a trait for enhanced K^+:Na^+ discrimination, which is located on chromosome 4D. In our study, QTL located for K^+:Na^+ ratio were found on chromosome 2D, possibly because our map is not highly dense and the QTL is a false positive. As far as the total map length is concerned, Richards map spanned 2,195.1 cM with a average distance of 2 cM between two markers.

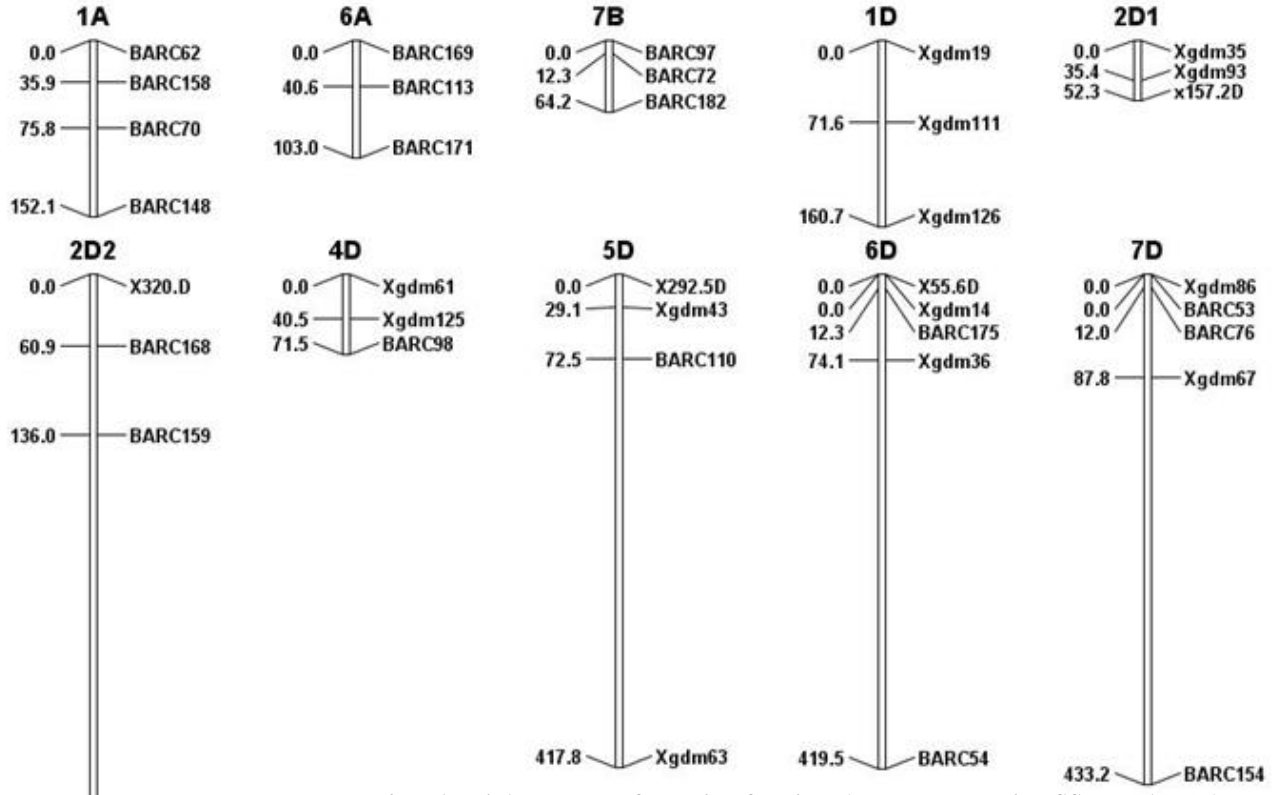

Fig. 41. Linkage group formation for nine chromosomes using SSR markers showing polymorphism in parents (DNA marker names are given on the right and centimorgan distances are on the left).

QTL mapping. The advent of molecular markers has revolutionized the genetic analysis of complex traits, and reports on the location of QTL for yield in many cereal crops are commonplace. However, QTL analysis in bread wheat has been hampered in part by its large genome size, estimated to be around 14,500 Mbp/1C, with the large majority of this DNA being repetitive sequences. Thus, many markers are required to cover the whole genome adequately. In addition, because of the relatively recent origin of the species, hexaploid wheat also suffers from relatively low levels of polymorphism. In consequence, detailed genetic maps of the whole genome are much more difficult to achieve than for most other crop species.

We observed QTL for shoot dry weight and shoot length located on chromosome 1A. Regions of QTL for total chlorophyll and chlorophyll b are located on 6A. QTL influencing chlorophyll content have been well identified in rice but none were found on chromosome B. QTL for sugar were detected on two chromosomes, one on chromosome 1D and a second on chromosome 5D. Chromosome 2D contains a region for K^+:Na^+ ratio and shoot length. The K^+:Na^+ ratio and shoot length decrease with salt stress. Shoot fresh weight has QTL on chromosomes 4D and 6D. A total of six QTL associated with shoot fresh weight were detected on chromosomes 1, 3, 5, 6, 7, and 12. Chromosomes 7D has QTL for total chlorophyll and chlorophyll a.

We could conclude that in this population, seven markers were mapped on the A genome, three markers in the B genome, and 24 markers in the D genome of the wheat. Although there was significant variation in the population for most of morpho-physiological traits studied, QTL individually explained up to 50% of the variation present in this population for most of the traits. Further improvement by the addition of more markers is needed in this genetic map to have a more extensive coverage of the genome, which could be helpful in finding QTL with major effects for salt tolerance in wheat.

Evaluation of high temperature tolerance of bread wheat germ plasm.

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To achieve self-sufficiency and sustainable productivity in wheat is of prime importance in the context of food security. The major limiting factors in wheat production are associated with several abiotic and biotic stresses. This problem could be resolved by the development of heat-tolerant wheat genotypes through conventional breeding by incorporating physiological characteristics such as membrane thermostability, and a higher proline accumulating ability. To assure success in this strategy, the coördinated efforts of a plant physiologist, molecular biologist, and crop breeder is imperative. Because high temperature stress is the second most limiting factor hampering wheat productivity in Pakistan, an in vitro and in vivo study was undertaken to screen wheat genotypes for heat tolerance based on physiological parameters at the seedling and pre-anthesis growth stages, evaluate wheat genotypes for phenological characteristics under control and heat stress, and identify heat-shock proteins expressed during heat stress. The effects of heat stress on growth, physiology, and yield were assayed in 24 wheat genotypes differing in heat tolerance. The heat stress was imposed at the seedling (15 days after sowing) and pre-anthesis (80 datys after sowing) stages. Heat stress during seedling stage was imposed by placing the seedlings in an incubator for 6 h at 25–30°C for ten days and at pre-anthesis by placing pots in a glasshouse for 3 h at 45°C for ten days.

Effect of heat stress on proline content (*µ*g/g fresh weight) of leaves in different wheat genotypes. ***Seedling stage.*** The analysis of variance revealed a significant difference among the different wheat genotypes for proline content at $P < 0.05$. In the control treatment, high proline content was observed in genotype 5 followed by 3 and 19; the minimum proline content was observed in genotype 7 (Table 70). Due to heat stress treatment at the seedling stage, a high proline content was observed in genotype 7 followed by 10 and 11 and the minimum in 24 (Table 70). Compared to the control, the highest proline content was observed in genotype 7 (84%) followed by 14 (81%), 15 (75%), and 13 (74%), and lowest was observed in genotype 3. The proline content in genotype 14 was similar to that for genotype 7. However, the magnitude of increase in proline content was relatively higher in genotype 7 than in genotype 14 compared to the control.

Table 70. Interaction between genotypes and treatment for proline content (*µ*g/g fresh weight) at the seedling stage. A heat stress at 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) = 440.6).

Line	Control		Heat stress	
1	1,058.77	BCDEFGHIJ	1,288.93	ABCDEFG
2	524.78	KLMN	1,077.18	BCDEFGHIJ
3	1,224.49	ABCDEFGH	1,224.49	ABCDEFGH
4	874.63	EFGHIJKLM	1,160.04	BCDEFGHI
5	1,307.35	ABCDEF	1,537.51	ABC
6	736.53	HIJKLMN	1,528.31	ABC
7	290.7	MN	1,904.94	AB
8	377.47	MN	1,362.59	ABCDE
9	644.47	IJKLMN	1,509.89	ABC
10	626.05	JKLMN	1,555.93	AB
11	681.29	IJKLMN	1,694.03	A
12	405.09	MN	1,546.72	AB
13	359.06	MN	1,408.62	ABCD
14	294.61	N	1,537.51	ABC
15	377.47	MN	1,537.51	ABC
16	1,051.37	BCDEFGHIJ	1,236.40	ABCDEFGH
17	1,100.18	BCDEFGHIJ	1,369.00	ABCDE
18	1,021.00	CDEFGHIJK	1,424.23	ABCD
19	1,155.40	BCDEFGHI	1,496.03	ABC
20	970.33	DEFGHIJKL	1,543.00	ABC
21	835.90	FGHIJKLM	1,310.03	ABCDEF
22	1,107.50	BCDEFGHIJ	1,441.70	ABCD
23	773.33	GHIJKLMN	1,489.57	ABCD
24	595.60	JKLMN	777.00	GHIJKLMN

Pre-anthesis stage. At pre-anthesis, statistically significant differences were observed among the wheat genotypes. The analysis of variance revealed significant differences among different wheat genotypes for proline content at $P < 0.05$. Under control conditions, high proline content was observed in genotype 8 followed by 10 and 11, and the least content was in 24 (Table 71, p. 215). Heat stress imposed at pre-anthesis stage increased proline content in wheat genotypes. A high proline content under heat stress was found in genotype 9, followed by 4 and 8, whereas genotype 16 showed the least proline content at pre-anthesis stage (Table 71, p. 215). Compared to the control, the highest proline content was observed in genotype 7 (90%) and genotype 16 the least. The percentage increase in proline content was greater at the preanthesis growth stage than that at the seedling stage.

Effect of heat stress on total soluble protein content (*µ*g/g) of leaves in different wheat genotypes. ***Seedling stage.*** The results showed that the interaction between treatments and genotypes was significant for protein content at $P < 0.05$.

Heat stress at the seedling stage significantly increased protein content in different wheat genotypes. The highest protein content under normal condition was observed in genotype 1 followed by 4 and 5, and the lowest protein content was observed in genotype 21 (Table 72). Nevertheless, high protein content under heat stress treatment at seedling stage was observed in genotype 7 followed by 8 and 15 and the minimum was observed in genotype 1 (Table 72). Compared to the control, the highest protein content was recorded in genotype 7 (24%) followed by 19, 15, 21, and 8. The ;owest protein content was found in genotype 1. The protein content in genotype 19 was near that of 7, conversely, the magnitude of increase in protein content was relatively higher in genotype 7 than 19 compared to the control.

Pre-anthesis stage.

At pre-anthesis, a statistically significant difference was observed among wheat genotypes. The analysis of variance revealed significant difference among different wheat genotypes for protein content at $P < 0.05$. Genotype 13 showed high protein content under control conditions followed by 15 and 16; the minimum under control conditions was in genotype 18 (Table 73, p. 216). Under heat stress treatment, high protein accumulation was observed in genotype 7 followed by 15 and 8 and a minimum in genoytpe 10. Compared to the control, the highest protein content was observed in genotype 7 (73%) and the least observed in genotype 10. The protein content in genotype 14 was similar to that of genotype 7. However, the extent of the increase in protein content was relatively higher in 7 than in 14 compared to the control. The results indicated that the percent increase in soluble protein content of leaves was greater at pre-anthesis stage in wheat genotypes than that at the seedling stage.

Table 72. Interaction between genotypes and treatment for protein contents (μg /g) at the seedling stage. A heat stress at 25–30ºC was imposed at 15 days after sowing for 10 days. LSD (0.05) = 117.7.

Line	Control		Heat stress	
1	1,367.83	A	351.10	AB
2	1,169.93	FGHIJKLMN	1,253.60	ABCDEFGHIJ
3	1,320.27	ABCDE	1,301.77	ABCDEF
4.	1,356.67	A	1,278.57	ABCDEFGHJI
5	1,342.93	ABC	1,290.00	ABCDEFGH
6	1,250.93	ABCDEFGHIJK	1,288.57	ABCDEFGH
7	1,059.87	MNO	1,403.07	IJKL
8	1,167.57	FGHIJKLMN	1,369.00	A
9	1,191.67	DEFGHIJKLM	1,296.77	ABCDEF
10	1,149.97	HIJKLMNO	1,290.63	ABCDEFG
11	1,203.70	CDEFGHIJKL	1,327.30	ABCD
12	1,197.23	DEFGHIJKL	1,311.17	ABCDE
13	1,203.40	CDEFGHIJKL	1,305.00	ABCDEF
14	1,151.13	GHIJKLMNO	1,338.47	ABC
15	1,140.00	IJKLMNNO	1,355.23	A
16	1,079.73	LMNO	1,180.80	EFGHIJKLM
17	1,053.06	MNO	1,168.74	FGHIJKLMN
18	1,111.80	KLMNO	1,192.27	DEFGHIJKLM
19	1,033.06	NO	1,349.37	AB
20	1,129.67	JKLMNO	1,188.16	DEFGHIJKLM
21	1,015.46	O	1,194.89	DEFGHIJKL
22	1,183.18	EFGHIJKLM	1,195.17	DEFGHIJKL
23	1,077.12	LMNO	1,209.57	CDEFGHIJKL
24	1,133.23	JKLMNO	1,212.20	BCDEFGHIJKL

Table 71. Interaction between genotypes and treatment for proline content (μg/g fresh weight) at pre-anthesis. A heat stress at 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 1,291).

Line	Control		Heat stress	
1	785.73	HIJKL	2,114.73	EFGHI
2	767.80	HIJKL	1,793.40	EFGHIJ
3	416.10	JKL	255.90	KL
4	677.07	HIJKL	5,164.90	C
5	1,171.50	FGHIJKL	2,132.20	EFGHI
6	1,332.60	FGHIJKL	1,565.07	EFGHIJKL
7	444.28	JKL	4,290.37	C
8	2554.33	EF	4,595.90	C
9	888.87	GHIJKL	8,877.00	A
10	2,345.80	EFG	1,740.00	EFGHIJK
11	1,994.10	EFGHI	4,072.03	CD
12	1,637.37	EFGHIJKL	6,921.50	B
13	1,708.73	EFGHIJKL	2,139.60	EFGH
14	1,761.63	EFGHIJK	1,329.40	FGHIJKL
15	1,752.90	EFGHIJK	1,040.27	FGHIJKL
16	1,604.23	EFGHIJKL	189.60	L
17	492.37	FGHIJKL	350.73	JKL
18	31.97	HIJKL	1658.07	EFGHIJKL
19	349.37	JKL	1,065.17	FGHIJKL
20	374.20	JKL	194.23	L
21	933.97	GHIJKL	1201.40	FGHIJKL
22	453.37	JKL	1,876.30	EFGHIJ
23	1,136.03	FGHIJKL	847.90	GHIJKL
24	376.97	JKL	596.53	IJKL

Effect of heat stress on superoxide dismutase activity (units/g fresh weight) in different wheat genotypes. ***Seedling stage.*** Superoxide dismutase activity (SOD) was measured in wheat genotypes at the seedling stage (Table 74, p. 216). The analysis of variance revealed significant differences among the different wheat genotypes for SOD activity at the seedling stage at a $P < 0.05$. The highest SOD activity under control conditions was observed in genotype 24 followed by 18 and 20; the minimum in genotype 12. Under heat stress, the maximum SOD activity was observed in genotype 24 and the minimum in geno-

Table 73. Interaction between genotypes and treatment for protein contents (μg/g) at pre-anthesis. A heat stress at 40-45ºC was imposed at 80 days after sowing for 10 days. LSD (0.05) = 99.95.

Line	Control		Heat stress	
1	165.40	CDEFG	203.73	BCDEF
2	137.53	EFG	212.00	BCDEF
3	189.23	BCDEF	139.46	DEFG
4	190.97	BCDEF	234.60	BCDEF
5	164.10	CDEFG	209.07	BCDEF
6	139.73	DEFG	258.10	BCD
7	130.30	FG	476.55	A
8	168.97	CDEFG	304.17	B
9	158.40	CDEFG	214.63	BCDEF
10	163.83	CDEFG	21.70	H
11	147.93	DEFG	52.80	GH
12	153.97	DEFG	431.03	A
13	212.87	BCDEF	244.60	BCDE
14	129.43	EFGH	439.27	A
15	201.37	BCDEF	412.27	A
16	202.27	BCDEF	143.00	DEFG
17	173.53	CDEF	241.33	BCDE
18	118.30	FGH	185.87	BCDEF
19	194.50	BCDEF	200.23	BCDEF
20	173.97	CDEF	153.57	DEFG
21	164.70	CDEFG	177.63	CDEF
22	154.57	DEFG	165.00	CDEFG
23	170.57	CDEFG	182.30	CDEF
24	142.40	DEFG	203.73	BCDEF

Table 74. Interaction between genotypes and treatment for superoxide dismutase activity (units/g fresh weight) at the seedling stage. A heat stress of 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) =1.942).

Line	Control		Heat stress	
1	1.30	JKL	3.80	CDEFGHI
2	2.90	CDEFGHI	3.76	CDEFGHI
3	2.28	CDEFGHIJK	4.06	CDEFG
4	1.63	IJKL	4.34	CDE
5	2.46	EFGHIJKL	3.75	CDEFGHI
6	1.85	GHIJKL	4.11	CDEFG
7	2.55	DEFGHIJKL	4.91	C
8	1.97	FGHIJKL	3.86	CDEFGHI
9	0.81	L	3.39	CDEFGHIJ
10	1.25	JKL	4.47	CDE
11	0.83	L	3.49	CDEFGHI
12	0.99	KL	3.49	CDEFGHIJ
13	2.73	CDEFGHIJKL	4.15	CDEFG
14	1.41	JKL	4.82	CD
15	2.46	EFGHIJKL	4.50	CDE
16	3.86	CDEFGHI	7.91	B
17	1.00	KL	4.68	CDE
18	4.84	CD	8.15	B
19	1.72	HIJKL	2.72	CDEFGHIJKL
20	4.20	CDEF	2.74	CDEFGHIJKL
21	3.85	CDEFGHI	4.44	CDE
22	3.98	CDEFGH	5.00	C
23	3.53	CDEFGHIJ	7.08	B
24	9.00	B	14.08	A

type 19. The highest SOD activity was observed in genotype 17 (79%) followed by 11, 9, and 10, whereas the least SOD activity was observed in genotype 20, compared to the control. The SOD activity in genotype 11 was close to that of 17, however, the magnitude of increase was relatively higher in genotype 17 than in 11.

Pre-anthesis stage. Nonsignificant differences were present among different wheat genotypes for SOD activity at $P > 0.05$. Under control conditions, the maximum SOD activity was shown by genotype 9 followed by 5 and 21 and the minimum by genotype 17 (Table 75, p. 217). Under heat stress treatment, high SOD activity was observed in genotype 7 followed by 8 and 21 (Table 75, p. 217). Compared to the control, the highest SOD activity was observed in genotype 17 followed by 11, 16, and 14 with the least SOD activity observed in genotype 5. Genotype 17 showed a 79% increase in SOD activity under heat stress imposed at pre-anthesis compared to the control.

Effect of heat stress on peroxidase (POD) activity (μmol/g fresh weight) in different wheat genotypes. ***Seedling stage.*** The analysis of variance revealed significant difference among different wheat genotypes for POD activity at $P < 0.05$. The highest POD activity under control condition was observed in genotype 1 followed by 17 and 23. The least POD activity under control condition was observed in genotype 9. Under heat stress, the maximum POD activity was recorded in genotype 21 followed by 11 and 22 and minimum in genotype 9 (Table 76, p. 217). The highest POD activity was observed in genotype 11 (36%) and the least activity in genotype 1 compared to the control. The POD activity in genotype 15 was similar to that of genotype 11, however, the degree of increase was relatively higher in 11 than in 15 compared to the control.

Pre-anthesis stage. At pre-anthesis, statistically significant differences were recorded among wheat genotypes. The analysis of variance revealed significant difference among different wheat genotypes for POD activity at $P < 0.05$. The maximum POD activity under control conditions was recorded in genotype 17 followed by 16 and 19 and the minimum

Table 75. Interaction between genotypes and treatment for superoxide dismutase activity (units/g fresh weight) at pre-anthesis stage. A heat stress of 40–45ºC was imposed at 80 days after sowing for 10 days (LSD (0.05) = 18.66).

Line	Control		Heat stress	
1	12.33	CDEFGH	25.16	ABCDEFGH
2	10.80	CDEFGH	26.28	ABCDEFGH
3	10.67	CDEFGH	24.44	ABCDEFGH
4	11.27	CDEFGH	23.36	ABCDEFGH
5	16.60	ABCDEFGH	21.07	ABCDEFGH
6	14.87	ABCDEFGH	26.74	ABCDEFGH
7	12.63	BCDEFGH	35.33	A
8	13.93	ABCDEFGH	34.79	AB
9	20.33	ABCDEFGH	23.93	ABCDEFGH
10	7.77	FGH	23.54	FGH
11	6.40	GH	26.67	ABCDEFGH
12	8.20	EFGH	25.07	ABCDEFGH
13	11.17	CDEFGH	27.36	ABCDEFGH
14	8.50	DEFGH	30.03	ABCDE
15	9.73	CDEFGH	29.45	ABCDEF
16	6.03	H	21.93	ABCDEFGH
17	5.23	H	25.08	ABCDEFGH
18	12.23	CDEFGH	23.73	ABCDEFGH
19	10.67	CDEFGH	24.13	ABCDEFGH
20	8.37	DEFGH	20.47	ABCDEFGH
21	16.20	ABCDEFGH	30.97	ABC
22	14.97	ABCDEFGH	28.37	ABCDEFG
23	11.63	CDEFGH	28.80	ABCDEF
24	15.40	ABCDEFGH	30.53	ABCD

Table 76. Interaction between genotypes and treatment for peroxidase activity (μmol/g fresh weight) at the seedling stage. A heat stress of 25–30ºC was imposed at 15 days after sowing for 10 days (LSD (0.05) = 0.2838).

Line	Control		Heat stress	
1	1.21	A	0.57	DEF
2	0.76	BCDEF	0.86	BCDE
3	0.77	BCDEF	0.84	BCDEF
4	0.84	BCDEF	0.76	BCDEF
5	0.71	BCDEF	0.70	BCDEF
6	0.66	BCDEF	0.79	BCDEF
7	0.72	BCDEF	0.85	BCDEF
8	0.69	BCDEF	0.55	EF
9	0.52	F	0.64	BCDEF
10	0.55	EF	0.80	BCDEF
11	0.58	CDEF	0.91	BC
12	0.70	BCDEF	0.60	CDEF
13	0.57	DEF	0.72	BCDEF
14	0.68	BCDEF	0.83	BCDEF
15	0.55	EF	0.84	BCDEF
16	0.87	BCDE	0.61	BCDEF
17	0.89	BCD	0.83	BCDEF
18	0.76	BCDEF	0.85	BCDEF
19	0.84	BCDEF	0.74	BCDEF
20	0.82	BCDEF	0.65	BCDEF
21	0.67	BCDEF	0.94	AB
22	0.81	BCDEF	0.89	BCD
23	0.88	BCDE	0.82	BCDEF
24	0.71	BCDEF	0.74	BCDEF

in genotype 22. Under heat stress, the highest activity was observed in genotype 23 followed by 18 and 11 and the minimum in genotype 2 (Table 77, p. 218). The highest POD activity was in genotype 23 (65%) followed by 1, 22, and 8; the least activity was in genotype 17 compared to the control, indicating that the percentage increase in POD activity was greater at pre-anthesis than at the seedling stage.

Effect of heat stress on chlorophyll a content (mg/g) in different wheat genotypes. ***Seedling stage***.
Heat stress has remarkable effect on chlorophyll *a* content. The analysis of variance revealed significant differences among the different wheat genotypes for chlorophyll a content at $P < 0.05$. The maximum chlorophyll a degradation under control conditions was observed in genotype 9 followed by 2 and 11. Genotype 19 showed minimum degradation under control conditions. However, under heat stress, the maximum degradation was recorded in genotype 17 followed by 24 and the minimum degradation was observed in genotypes 20 and 21 (Table 78, p. 218). Chlorophyll a content decreased at the seedling stage in all genotypes. Genotype 18 showed an 86% decrease in chlorophyll a content followed by 8, 13, and 21, compared to the control, and the minimum decrease was in genotypes 17 and 7, compared to the control.

Pre-anthesis stage. At pre-anthesis, statistically significant differences were found among wheat genotypes. The greatest decrease in chlorophyll a content under control conditions was observed in genotype 1 and the minimum in genotype 8, whereas under heat stress, maximum degradation was in genotype 7 followed by 6 and 5, and the minimum in genotypes 9 and 23 (Table 79, p. 218). When the heat-stress treatment was compared with the control, the largest decrease in chlorophyll a content at pre-anthesis was in genotype 22 (67%) and the minimum was observed in genotypes 2, 3, 7, 8, 13, 14, 15, 17, 18, 19, 20, 21, 23, 24, which all are statistically similar. Our data show that the percentage decrease in chlorophyll a content was greater at seedling stage than at pre-anthesis.

Table 77. Interaction between genotypes and treatment for peroxidase activity (μ mol/g fresh weight) at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 0.6349).

Line	Control		Heat stress	
1	0.52	HI	1.23	DEFGHI
2	0.52	HI	0.73	EFGHI
3	0.82	DEFGHI	0.72	EFGHI
4	0.59	EFGHI	1.14	DEFGHI
5	0.90	DEFGHI	1.26	DEFGH
6	0.84	DEFGHI	1.12	DEFGHI
7	0.80	DEFGHI	0.97	DEFGHI
8	0.58	FGHI	1.31	DEFG
9	0.87	DEFGHI	0.84	DEFGHI
10	1.03	DEFGHI	1.20	DEFGHI
11	0.84	DEFGHI	1.34	DE
12	0.58	FGHI	1.21	DEFGHI
13	0.94	DEFGHI	1.26	DEFGH
14	0.68	EFGHI	1.27	DEFGH
15	0.56	GHI	1.26	DEFGH
16	2.92	AB	1.11	DEFGHI
17	3.38	A	1.19	DEFGHI
18	1.20	DEFGHI	1.50	D
19	2.29	BC	1.18	DEFGHI
20	0.52	HI	1.11	DEFGHI
21	0.87	DEFGHI	1.32	DEF
22	0.48	I	1.12	DEFGHI
23	0.77	DEFGHI	2.21	C
24	0.61	EFGHI	0.95	DEFGHI

Table 78. Interaction between genotypes and treatment for chlorophyll a content (mg/g) at the seedling stage. A heat stress of 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) = 0.2051).

Line	Control		Heat stress	
1	0.66	AB	0.22	FGHIJ
2	0.76	A	0.22	FGHIJ
3	0.63	ABC	0.18	GHIJ
4	0.72	A	0.18	GHIJ
5	0.60	ABCD	0.19	GHIJ
6	0.63	ABC	0.19	GHIJ
7	0.42	CDEFG	0.27	FGHIJ
8	0.44	BCDEF	0.10	IJ
9	0.77	A	0.23	FGHIJ
10	0.67	AB	0.21	FGHIJ
11	0.73	A	0.24	FGHIJ
12	0.65	ABC	0.25	FGHIJ
13	0.69	A	0.17	HIJ
14	0.37	DEFGH	0.20	FGHIJ
15	0.56	ABCDE	0.20	FGHIJ
16	0.64	ABC	0.25	FGHIJ
17	0.38	DEFGH	0.31	FGHI
18	0.42	CDEFG	0.06	J
19	0.24	FGHIJ	0.10	IJ
20	0.31	FGHI	0.09	IJ
21	0.35	EFGH	0.09	IJ
22	0.37	DEFGH	0.20	FGHIJ
23	0.62	ABC	0.16	HIJ
24	0.59	ABCD	0.30	FGHIJ

Effect of heat stress on chlorophyll b content (mg/g) in different wheat genotypes. ***Seedling stage.*** The analysis of variance revealed nonsignificant differences among different wheat genotypes for chlorophyll b content at $P > 0.05$. The greatest decrease in chlorophyll b content under control conditions was in genotype 17 and the minimum in genotype 2. Under heat stress at the seedling stage, the maximum effect was observed in genotype 21 and the lowest in genotype 2 (Table 80, p. 219). All genotypes showed a decrease in chlorophyll b content. The greatest decrease was in genotype 1 (65%) and the least in genotype 7, compared to the control.

Pre-anthesis stage. The chlorophyll b content at pre-anthesis analysis of variance revealed nonsignificant differences among different wheat genotypes at $P > 0.05$. Under controled conditions, the maximum decrease in chlorophyll b was observed in genotypes 7, 12, 15, and 17, and under heat stress the maximum decrease was in genotype 7 and the minimum (Table 81, p. 220). Compared to the control, the maximum decrease in chlorophyll b content was in genotype 12 (50%) followed by 17 and 24; all the remaining genotypes showed a minimum decrease at pre-anthesis, indicating that the percent decrease was greater at the seedling stage.

The effect of heat stress on fresh shoot weight (g). Heat stress imposed a decrease fresh shoot weight at the seedling stage. Under controled conditions, the maximum fresh shoot weight was in genotype 16 and the minimum in genotype 18. Under heat-stress conditions, the maximum shoot weight was observed in genotype 4 and the minimum in genotype 18 (Table 82, p. 220). The wheat genotypes did not significantly differ with respect to fresh root weight. When heat stress was compared with the control treatment, a maximum (75%) reduction was observed in genotype 20 and a minimum reduction was observed in genotype 7 followed by 17 and 24.

Effect of heat stress on fresh shoot length (cm). An analysis of variance revealed that the interaction between genotypes and treatment was significant for fresh shoot length. Under control conditions, the maximum fresh shoot length was in genotype 5 followed by 15 and 23. Under heat stress, the maximum length was observed in genotype 7 followed

Table 79. Interaction between genotypes and treatment for chlorophyll a content (mg/g) at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 0.01034).

Line	Control		Heat stress	
1	0.04	A	0.03	AB
2	0.03	AB	0.03	AB
3	0.03	AB	0.03	AB
4	0.04	A	0.03	AB
5	0.04	A	0.02	BC
6	0.04	A	0.03	AB
7	0.04	A	0.04	A
8	0.02	BC	0.02	BC
9	0.02	BC	0.01	C
10	0.04	A	0.02	BC
11	0.04	A	0.02	BC
12	0.03	AB	0.02	BC
13	0.03	AB	0.03	AB
14	0.04	AB	0.04	A
15	0.04	AB	0.04	A
16	0.03	AB	0.02	BC
17	0.04	A	0.04	A
18	0.04	AB	0.04	A
19	0.04	AB	0.04	A
20	0.04	AB	0.04	A
21	0.03	AB	0.03	AB
22	0.03	AB	0.03	AB
23	0.03	AB	0.01	C
24	0.03	AB	0.03	AB

Table 80. Interaction between genotypes and treatment for chlorophyll b content (mg/g) at the seedling stage. A heat stress of 25–30ºC was imposed 15 das after sowing for 10 days (LSD (0.05) = 0.09406).

Line	Control		Heat stress	
1	0.26	ABCD	0.09	IJKL
2	0.24	ABCDEF	0.10	HIJKL
3	0.77	ABC	0.84	JKL
4	0.84	ABC	0.76	IJKL
5	0.71	ABCD	0.70	JKL
6	0.66	ABCD	0.79	IJKL
7	0.58	ABCDE	0.91	GHIJKL
8	0.69	ABCDEFGHI	0.55	L
9	0.52	A	0.64	HIJKL
10	0.55	ABCDEF	0.80	IJKL
11	0.72	ABCDE	0.85	JKL
12	0.70	ABCDE	0.60	HIJKL
13	0.57	ABC	0.72	IJKL
14	0.68	ABCD	0.83	HIJKL
15	0.55	ABC	0.84	HIJKL
16	0.87	ABCDEF	0.61	FGHIJKL
17	0.89	CDEFGHIJK	0.83	FGHIJKL
18	0.76	ABCDEF	0.85	L
19	0.84	DEFGHIJKL	0.74	KL
20	0.82	BCDEFGHIJ	0.65	KL
21	0.67	BCDEFGHIJ	0.94	JKL
22	0.81	ABCDEFGH	0.89	GHIJKL
23	0.88	ABCDEFG	0.82	DEFGHIJKL
24	0.71	AB	0.74	EFGHIJKL

by 4 and 10 and the minimum in genotype 18 (Table 83, p. 221). When heat stress was compared with the control, the maximum (41%) reduction for fresh shoot length was shown by genotypes 20 and the minimum in genotype 21 followed by 7 and 17. These genotypes show tolerance to heat stress, which will be confirmed by comparing the yield of genotypes.

Effect of heat stress on fresh root weight (g). Statistical analysis of the data showed that at the seedling stage, interaction among the various wheat genotypes and treatments was significant for fresh root weight. The maximum root weight under control conditions was recorded in genotype 19 followed by 20 and 4 and the minimum was in genotype 2. Under heat stress, the maximum fresh root weight was observed in genotype 22, followed by 23 and 7 and the minimum in genotype 2 (Table 84, p. 221). Heat stress imposed at seedling stage caused a reduction in root weight. Compared to the control, the maximum (82%) reduction was in genotype 19 and the minimum in genotypes 7 and 17.

Effect of heat stress on fresh root length (cm). The analysis of variance shows that interaction among genotypes and treatment at seedling stage for root length was not significant. The maximum root length in control conditions was observed in genotype 4 followed by 21 and 11 and the minimum in genotype 18. Under heat stress, genotype 11 had the maximum root length followed by genotypes 8 and 4 (Table 85, p. 222). Similar to fresh root weight, root length decreased due to heat stress imposed at the seedling stage in the different wheat genotypes. However, when heat-stress genotypes are compared with the control, the maximum reduction of root length observed was in genotype 14 and the minimum effect of heat stress on root length was observed in genotypes 13, 18, and 1.

Effect of heat stress on plant height (cm). The interaction between treatment and genotypes for plant height was highly significant at $P < 0.05$. Maximum plant height under controled conditions was observed in genotype 8, followed by 23 and 5 and the minimum was recorded in genotype 17. With a heat-stress treatment, the maximum plant height

Table 81. Interaction between genotypes and treatment for chlorophyll b content at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 0.006607).

Line	Control		Heat stress	
1	0.01	B	0.01	B
2	0.01	B	0.01	B
3	0.01	B	0.01	B
4	0.01	B	0.01	B
5	0.01	B	0.01	B
6	0.01	B	0.01	B
7	0.02	A	0.02	A
8	0.01	B	0.01	B
9	0.01	B	0.01	B
10	0.01	B	0.01	B
11	0.01	B	0.01	B
12	0.02	A	0.01	B
13	0.01	B	0.01	B
14	0.01	B	0.01	B
15	0.02	A	0.01	B
16	0.01	B	0.01	B
17	0.02	A	0.01	B
18	0.01	B	0.01	B
19	0.01	B	0.01	B
20	0.01	B	0.01	B
21	0.01	B	0.01	B
22	0.01	B	0.01	B
23	0.01	B	0.01	B
24	0.01	B	0.01	B

Table 82. Interaction between genotypes and treatments for fresh shoot weight (g). A heat stress of 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) =20.53).

Line	Control		Heat stress	
1	0.3480	B	0.3087	B
2	0.2907	B	0.1880	B
3	0.3043	B	0.2070	B
4	0.5570	B	0.4583	B
5	0.3317	B	0.2143	B
6	0.4377	B	0.2433	B
7	0.3437	B	0.3253	B
8	0.2970	B	0.2247	B
9	0.3127	B	0.2817	B
10	0.3400	B	0.2897	B
11	0.5083	B	0.4067	B
12	0.4073	B	0.3080	B
13	0.4290	B	0.2597	B
14	0.2060	B	0.1480	B
15	0.4220	B	0.2553	B
16	0.7447	B	0.2140	B
17	0.3293	B	0.3057	B
18	0.1753	B	0.0506	B
19	0.2431	B	0.0867	B
20	0.2459	B	0.0603	B
21	0.2700	B	0.1940	B
22	0.3806	B	0.1700	B
23	0.3316	B	0.2567	B
24	0.3212	B	0.2970	B

was observed in genotype 8 followed by 12 and 19 and the minimum was in genotype 3 (Table 86, p. 222). Heat stress imposed at pre-anthesis caused a significant decrease in plant height. The maximum effect of heat stress on plant height was observed in genotypes 21, 20, and 11 compared to the control. In genotype 21, heat stress imposition caused a reduction of 24% in plant height, followed by genotypes 20 and 10, and the minimum effect was observed in genotypes 17, 7, 12, 19, and 24 compared to the control. In genotype 17, no effect of heat stress on plant height compared to the control was observed, and genotypes 7 (1%) and 12 (2%) had a slight decrease compared to control. We concluded that heat stress imposed at pre-anthesis has minimum effect on plant height.

Effect of heat stress on spike length (cm). An analysis of variance revealed that the wheat genotypes significantly differed with respect to spike length at $P < 0.05$. Under normal conditions, the maximum spike length was observed in genotype 10 and the minimum in genotype 16. With a heat treatment, the maximum length observed was in genotype 7 followed by 17 and the minimum in genotype 23 (Table 87, p. 223). Heat stress significantly decreases the spike length in the different wheat genotypes. Maximum reduction in spike length was shown in genotype 21 (49%) compared to the control, and the minimum effect of heat stress was observed in genotypes 2, 4, 12, 19, 17, and 7 compared to the control. In these genotypes, heat stress effects ranged from 0 to 3%, indicating that heat stress imposed at pre-anthesis influences spike length.

Effect of heat stress on the number of spikelets/spike. Wheat genotypes were significantly different for number of spikelets/spike at $P < 0.05$. The maximum number of spikelets/spike under control conditions was in genotypes 1 and 3 followed by 2 and 4, the minimum number was in genotype 16. Genotype 1 produced the maximum number of spikelets/spike under heat stress, followed by genotypes 3 and 5, and the minimum number observed in genotype 21 (Table 88, p. 223). When compared with the control, the maximum reduction in the number of spikelets/spike was in genotype 22 (23%) and the minimum by genotype 7 followed by genotypes 17, 19, and 12, indicating that heat stress imposed at pre-anthesis causes a reduction in the number of spikelets/spike.

Table 83. Interaction between genotypes and treatment for fresh shoot length (cm) at the seedling stage. A heat stress of 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) = 6.746).

Line	Control		Heat stress	
1	28.6	ABCD	25.9	ABCDEF
2	28.8	ABCD	22.3	CDEFGHI
3	29.8	ABC	26.2	ABCDEF
4	29.5	ABC	28.4	ABCD
5	31.8	A	24.6	ABCDEFGH
6	27.9	ABCD	25.9	ABCDEF
7	30.0	ABC	28.8	ABCD
8	30.4	AB	23.7	BCDEFGHI
9	29.6	ABC	26.4	ABCDEF
10	28.5	ABCD	27.5	ABCD
11	21.3	DEFGHI	13.9	JK
12	27.6	ABCD	23.9	ABCDEFGH
13	30.7	AB	26.2	ABCDEF
14	24.6	ABCDEFGH	22.2	BCDEFGHI
15	30.5	AB	19.3	EFGHIJK
16	24.3	ABCDEFGH	16.7	HIJK
17	25.5	ABCDEF	25.2	ABCDEFG
18	18.6	FGHIJK	12.0	K
19	22.8	BCDEFGHI	17.3	GIJK
20	26.9	ABCDE	15.9	IJK
21	21.0	DEFGHIJ	21.0	DEFGHIJ
22	28.4	ABCD	17.1	HJK
23	30.4	AB	23.8	BCDEFGHI
24	28.1	ABCD	22.9	BCDEFGHI

Table 84. Interaction between genotypes and treatment for fresh root weight (g) at the seedling stage. A heat stress of 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) = 0.1722).

Line	Control		Heat stress	
1	0.1503	ABCDE	0.0663	DE
2	0.0510	DE	0.0443	E
3	0.0580	DE	0.0473	E
4	0.3107	AB	0.0750	DE
5	0.1777	ABCDE	0.0487	DE
6	0.0843	DE	0.0607	DE
7	0.1460	ABCDE	0.1402	ABCDE
8	0.1370	ABCDE	0.1030	CDE
9	0.1677	ABCDE	0.0953	CDE
10	0.1790	ABCDE	0.0810	DE
11	0.2533	ABCD	0.1250	BCDE
12	0.2103	ABCDE	0.1040	CDE
13	0.2523	ABCD	0.0903	CDE
14	0.2917	ABC	0.1257	BCDE
15	0.2003	ABCDE	0.1293	BCDE
16	0.0853	DE	0.0623	DE
17	0.0964	CDE	0.0897	CDE
18	0.0967	CDE	0.0431	E
19	0.3402	A	0.0620	DE
20	0.2920	ABC	0.0577	DE
21	0.1373	ABCDE	0.1007	CDE
22	0.0913	CDE	0.1428	ABCDE
23	0.1735	ABCDE	0.1420	ABCDE
24	0.1540	ABCDE	0.1213	BCDE

Effect of heat stress on the number of grains/spike. Heat significantly decreases the number of grains/spike. The analysis of variance revealed that wheat genotypes were not significantly different with respect to the number of seeds/spike at $P > 0.05$. Under controled conditions, the maximum number of grains/spike was in genotype 2 and the minimum in genotype 14. Under heat stress, the maximum number of grains/spike was observed in genotype 3 and minimum in genotype 14 (Table 89, p. 224). A minimum effect of heat stress on number of grains/spike was observed in genotypes 7, 12, 17, and 24, compared to the control, indicating that heat stress imposed at pre-anthesis reduces the number of grains/spike.

We concluded that heat stress imposed at pre-anthesis stage causes a decrease in yield by reducing the number of grains/spike.

Effect of heat stress on the number of florets/spike. The analysis of variance showed a significant interaction for the number of florets/spike between genotypes and treatments. The maximum number of florets/spike under control conditions was observed in genotype 1, followed by genotypes 2 and 4, and the minimum in genotype 19. The maximum number of number of florets/spike under hgeat stress was recorded in genotype 1, followed by genotypes 3 and 4, and the minimum number in genotype 11 (Table 90. p. 224). Heat stress at pre anthesis significantly decreases the number of florets/spike compared to the control treatment. The maximum reduction for number of florets/spike was in genotype 21 (34%) and the minimum in genotype 1, followed by 7, 17, and 19. These results indicate that a heat stress imposed at pre-anthesis reduces the number of florets/spike.

Effect of heat stress on biomass/plant. Heat stress imposed at pre-anthesis decreases plant biomass, and the interaction among the wheat genotypes and treatments for biomass/plant was highly significant. We observed that heat stress imposed at pre-anthesis growth stage significantly decreases biomass per plant at $P < 0.05$. Under the control conditions, the maximum biomass/plant was recorded in genotype 6 and minimum in genotype 18, under heat stress, the maximum

Table 85. Interaction between genotypes and treatment for fresh root length (cm) at the seedling stage. A heat stress of 25–30ºC was imposed 15 days after sowing for 10 days (LSD (0.05) = 3.891).

Line	Control		Heat stress	
1	5.1	BCD	5.1	BCD
2	6.8	ABCDE	4.6	BCD
3	7.4	ABCDE	4.5	BCDE
4	10.7	A	6.5	ABCDE
5	6.3	ABCDE	4.6	BCDE
6	6.1	ABCDE	4.7	BCDE
7	6.0	BCDE	3.8	DE
8	7.7	ABCDE	6.6	ABCDE
9	7.0	ABCDE	5.5	BCDE
10	6.2	ABCDE	5.3	BCDE
11	8.6	ABC	8.1	ABCD
12	7.2	ABCDE	5.9	BCDE
13	6.0	BCDE	6.0	BCDE
14	7.9	ABCDE	4.8	BCDE
15	4.2	CDE	3.3	E
16	4.8	BCDE	3.7	DE
17	6.3	ABCDE	4.2	CDE
18	3.6	DE	3.6	DE
19	5.0	BCDE	4.7	BCDE
20	5.5	BCDE	5.0	BCDE
21	9.0	AB	5.8	BCDE
22	6.5	ABCDE	4.4	BCDE
23	6.9	ABCDE	5.7	BCDE
24	7.3	ABCDE	5.2	BCDE

Table 86. Interaction between genotypes and treatment for plant height (cm) at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 10.93).

Line	Control		Heat stress	
1	60.3	BCDEFGHIJK	54.0	EFGHIJKL
2	55.3	DEFGHIJKL	51.0	IJKL
3	59.0	CEFGHIJKL	48.0	KL
4	63.0	BCDEFGHI	60.3	BCDEFGHIJK
5	68.6	ABC	58.3	BCDEFGHIJKL
6	66.6	ABCDE	59.3	BCDEFGHIJKL
7	66.0	ABCDEFG	65.3	ABCDEFG
8	76.3	A	68.0	ABCD
9	53.0	GHIJKL	48.3	KL
10	66.0	ABCDEFG	52.0	HIJKL
11	66.3	ABCDEF	51.6	HIJKL
12	64.6	ABCDEFGH	63.6	ABCDEFGHI
13	59.3	CDEFGHIJKL	53.3	FGHIJKL
14	51.0	IJKL	49.6	JKL
15	58.0	DEFGHIJKL	49.3	JKL
16	63.3	BCDEFGHI	55.0	DEFGHIJKL
17	46.6	L	46.6	L
18	60.0	BCDEFGHIJK	52.0	HIJKL
19	65.8	ABCDEFG	62.3	BCDEFGHIJ
20	62.0	BCDEFGHIJ	48.0	KL
21	68.0	ABCD	52.0	HIJKL
22	63.3	BCDEFGHI	54.6	EFGHIJKL
23	71.0	AB	60.5	BCDEFGHIJK
24	60.6	BCDEFGHIJK	57.0	CDEFGHIJKL

was in genotype 8 and the minimum in genotype 18 (Table 91, p. 224). The maximum decrease in biomass/plant was found in genotype 18 (48%) and the minimum was observed in genotypes 7, 17, 12, and 24, compared to the control.

Effect of heat stress on 100-kernel weight. Heat stress imposed at pre-anthesis stage significantly decreases 100-kernel weight at $P < 0.05$. Under controled conditions, the maximum 100-kernel weight was observed in genotype 2 and the minimum in genotype 22. Under heat stress, the maximum 100-kernel weight was recorded in genotype 17 and the minimum in genotype 18 (Table 92, p. 225). Heat stress significantly decreased 100-kernel weight in the different wheat genotypes. Genotype 18 showed the maximum reduction (36%) due to high temperature imposed at pre-anthesis and genotypes 7, 12, 17, and 19 the minimum compared to the control. These results indicate that a heat stress imposed at pre-anthesis causes reduction in crop yield.

Identification of heat-shock proteins. ***Effect of heat-stress treatment on the change in the protein banding patterns of various wheat genotypes.*** Changes in the protein patterns were observed in wheat grown under control and heat-stressed conditions at the seedling stage of the wheat genotypes (Table 93, p. 225). Proteins extracted from the leaves were separated by SDS–PAGE. The appearance or disappearance of proteins was identified visually in control and heat stressed plants. The position of the proteins bands against those of known molecular weight markers were carefully measured with a ruler. The soluble protein from the leaves revealed the presence of 55-kDa polypeptides in both control and heat-stress treatments of all the ten genotypes except the genotype 8 control, and a 43-kDa band appeared in ten genotypes in both control and heat-stressed plants. A 72-kDa band appears under heat stress in nine genotypes, but the same polypeptide band was present in genotype 10 in both control and heat-stressed plants (Table 93, p. 225). However, a new protein of 35 kDa appeared in genotype 7 only.

Table 87. Interaction between genotypes and treatment for spike length (cm) at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 2.083).

Line	Control		Heat stress	
1	10.6	ABCDE	9.3	BCDEFGH
2	9.6	ABCDEFG	9.6	ABCDEFG
3	11.0	ABCD	8.3	EFGH
4	10.0	ABCDEF	10.0	ABCDEF
5	10.0	ABCDEF	9.3	BCDEFGH
6	10.6	ABCDE	9.3	BCDEFGH
7	11.6	ABC	11.3	ABCDE
8	10.6	ABCDE	10.3	ABCDE
9	9.0	CDEFGH	8.6	DEFGH
10	12.0	A	9.3	BCDEFGH
11	10.6	ABCDE	9.0	CDEFGH
12	9.6	ABCDEFG	9.6	ABCDEFG
13	11.0	ABCD	8.6	DEFGH
14	9.6	ABCDEFG	8.6	DEFGH
15	9.3	BCDEFGH	9.0	CDEFGH
16	8.3	EFGH	7.6	FGH
17	11.0	AB	10.8	ABCDEF
18	9.6	ABCDEFG	9.3	BCDEFGH
19	9.3	BCDEFGH	9.3	BCDEFGH
20	9.6	ABCDEFG	8.3	EFGH
21	10.3	ABCDE	5.3	I
22	9.3	BCDEFGH	7.3	GHI
23	9.3	BCDEFGH	7.0	HI
24	10.6	ABCDE	9.3	BCDEFGH

Table 88. Interaction between genotypes and treatment for number of spikelets/spike at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 3.439).

Line	Control		Heat stress	
1	22.3	A	21.6	AB
2	21.6	AB	20.3	AB
3	22.3	A	21.0	AB
4	21.3	AB	20.3	AB
5	21.0	AB	20.3	AB
6	21.6	AB	21.0	AB
7	20.3	AB	20.3	AB
8	19.6	ABC	17.6	BCDE
9	19.6	ABC	17.6	BCDE
10	21.0	AB	19.0	ABCD
11	20.3	AB	14.3	EF
12	19.6	ABC	19.0	ABCD
13	19.6	ABC	18.3	ABCDE
14	19.6	ABC	17.6	BCDE
15	20.3	AB	19.6	ABC
16	17.6	BCDE	15.6	CDEF
17	18.3	ABCDE	18.3	ABCDE
18	18.3	ABCDE	17.6	BCDE
19	17.6	BCDE	17.6	BCDE
20	21.0	AB	19.0	ABCD
21	19.6	ABC	13.0	F
22	19.6	ABC	15.0	DEF
23	18.3	ABCDE	14.3	EF
24	19.0	ABCD	15.6	CDEF

In all ten genotypes 11–20, SDS-PAGE analysis of the soluble protein from leaves revealed that polypeptides of 26 kDa, 43 kDa, and 55 kDa appeared during both control and heat-stress conditions. Similarly, a protein band of 55 kDa also appeared during both control and heat stress in the four wheat genotypes 21–24, whereas band of 72 kDa appeared in genotypes 21 and 22 under both control and heat stress plants. A new 20-kDa protein appeared in genotype 17 and a new 25-kDa protein band appeared in genotype 24 under heat stress treatment at the seedling stage.

Genetic diversity in wheat genotpes using SSR markers. A set of 50 simple sequence repeat (SSR) primers was used to detect genetic diversity at DNA level in the 24 wheat genotypes. Using the discrimination among genotypes based on these SSR markers, a dendrogram was prepared using Nei and Lei co-efficient. In order to elucidate genetic diversity at each locus, the polymorphic information content (PIC) value was calculated (Table 94, p. 226). The highest PIC value was 0.87 exhibited by D genome, whereas the lowest PIC value of 0 was shown by the A and D genomes.

A total of 179 alleles were detected in the 24 wheat genotypes using 50 pairs of primers that produced clearly polymorphic fragments. The maximum number of alleles (10) were amplified by primer WMC-42 and the minimum (1) by WMC-15, WMC-17, WMC-22, WMC-23, and WMC-26. Most of the SSR loci in the wheat genotypes contained dinucleotide repeats, with a much smaller fraction containing trinucleotide repeats. The CA repeat was the most common type.

The mean PIC values among the genomes were 0.38 (A), 0.51 (B), and 0.40 (D). The highest PIC values were 0.87 (WMC-42) on chromosome 7D, 0.84 (WMC-31) on 1B, and 0.83 (WMC-45) on 3A. In general, the variance of the PIC mean values was similar among the A, B, and D genomes with B > D > A.

Table 89. Interaction between genotypes and treatments for number of grains/spike at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 19.59).

Line	Control		Heat stress	
1	44.0	ABCD	18.0	GHIJKL
2	53.6	A	40.6	ABCDEFGH
3	49.6	AB	45.6	ABC
4	51.6	A	39.6	ABCDEFGH
5	34.0	ABCDEFGHI	32.0	ABCDEFGHIJ
6	49.3	AB	45.3	ABC
7	48.2	ABCDEFG	47.2	ABCDE
8	38.0	ABCDEFGHI	21.3	DEFGHIJKL
9	36.0	ABCDEFGHI	32.0	ABCDEFGHIJ
10	41.6	ABCDEF	25.6	CDEFGHIJK
11	20.3	EFGHIJKL	20.3	EFGHIJKL
12	41.3	ABCDEFG	40.3	ABCDEF
13	34.0	ABCDEFGHI	17.6	HIJKL
14	2.0	L	1.6	L
15	44.0	ABCD	33.0	ABCDEFGHI
16	9.0	JKL	5.0	KL
17	38.0	ABCDEFGHI	37.0	ABCDEFGH
18	42.0	ABCDE	23.6	CDEFGHIJKL
19	32.6	ABCDEFGHI	26.6	BCDEFGHIJK
20	39.0	ABCDEFGH	18.3	FGHIJKL
21	25.3	CDEFGHIJK	18.6	FGHIJKL
22	23.3	CDEFGHIJKL	15.3	IJKL
23	23.0	CDEFGHIJKL	17.6	HIJKL
24	34.3	ABCDEFGHI	33.0	ABCDEFGHI

Table 90. Interaction between genotypes and treatments for the number of florets/spike at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 10.30).

Line	Control		Heat stress	
1	67.0	A	65.0	AB
2	65.0	AB	61.0	AB
3	67.0	A	63.0	AB
4	63.0	AB	61.0	AB
5	63.0	AB	61.0	AB
6	65.0	AB	63.0	AB
7	61.0	AB	61.0	AB
8.	59.0	ABC	53.0	BCDE
9	59.0	ABC	53.0	BCDE
10	63.0	AB	57.0	ABCD
11	61.0	AB	43.0	EF
12	59.0	ABC	57.0	ABCD
13	59.0	ABC	55.0	ABCDE
14	59.0	ABC	53.0	BCDE
15	61.0	AB	59.0	ABC
16	53.0	BCDE	47.0	CDEF
17	55.0	ABCDE	55.0	ABCDE
18	55.0	ABCDE	53.0	BCDE
19	53.0	BCDE	53.0	BCDE
20	63.0	AB	57.0	ABCD
21	59.0	ABC	39.0	F
22	59.0	ABC	45.0	DEF
23	55.0	ABCDE	46.3	DEF
24	57.0	ABCD	47.0	CDEF

Table 91. Interaction between genotypes and treatments for biomass/plant at pre-anthesis. A heat stress at 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 0.7514).

Line	Control		Heat stress		Line	Control		Heat stress	
1	4.4	BCDEFG	4.0	DEFGHI	13	4.9	ABC	3.5	HIJKL
2	4.3	CDEFGH	3.2	IJKLM	14	4.8	ABCD	3.6	GHIJKL
3	3.2	IJKLM	2.5	MN	15	4.3	CDEFGH	3.6	GHIJKL
4	3.9	EFGHIJ	3.5	HIJKL	16	3.9	EFGHIJ	3.0	KLM
5	3.8	EFGHIJK	3.6	HIJKL	17	4.7	ABCDE	4.5	BCDEF
6	5.2	AB	4.4	BCDEFG	18	4.0	DEFGHI	2.1	N
7	3.8	EFGHI	3.6	HIJKL	19	3.1	JKLM	2.9	LM
8	5.4	A	4.6	ABCDEF	20	4.3	CDEFGH	3.6	GHIJKL
9	4.6	ABCDEF	4.3	CDEFGH	21	5.0	ABC	4.3	CDEFGH
10	3.6	GHIJKL	3.2	IJKLM	22	3.9	EFGHIJ	3.4	IJKL
11	4.7	ABCDE	3.4	IJKL	23	3.8	FGHIJK	3.4	IJKL
12	4.6	ABCDEF	4.4	BCDEFG	24	3.8	FGHIJK	3.6	GHIJKL

Conclusion. On the basis of yield, physiological, and molecular attributes, wheat genotypes 7 and 17 were tolerant to high temperature. Genotypes 7 and 17 exhibited better osmoregulation by accumulation of compatible solutes, such as prolines and induced heat-shock proteins. High-temperature stress triggered an antioxidant defense mechanism in these two cultivars that helped them survive under heat stress. An urgent need is to fully explore the genetic diversity among the present wheat germ plasm in field under heat stress. The information generated in this investigation will be helpful for the plant breeders when including these traits in a breeding program for

Table 92. Interaction between genotypes and treatments for 100-kernel weight at pre-anthesis. A heat stress of 40–45ºC was imposed 80 days after sowing for 10 days (LSD (0.05) = 0.4384).

Line	Control		Heat stress		Line	Control		Heat stress	
1	3.693	ABCD	2.432	JKL	13	3.307	BCDEF	3.140	DEFGH
2	3.913	A	2.643	HIJKL	14	3.680	ABCD	2.757	GHIJKL
3	3.640	ABCD	2.467	JKL	15	3.617	ABCD	2.947	EFGHIJ
4	3.850	AB	2.650	HIJKL	16	3.127	DEFGH	2.870	FGHIJK
5	3.140	DEFGH	2.667	HIJKL	17	3.600	ABCDE	3.500	ABCDE
6	3.293	CDEFG	2.183	L	18	3.427	ABCDE	2.121	L
7	3.497	ABCDE	3.383	ABCDE	19	3.440	ABCDE	3.402	ABCDE
8	3.413	ABCDE	3.070	EFGH	20	3.407	ABCDE	2.780	GHIJK
9	3.150	DEFGH	2.463	JKL	21	3.150	DEFGH	2.397	KL
10	3.317	BCDEF	2.413	JKL	22	3.090	DEFGH	2.377	KL
11	3.777	ABC	2.543	IJKL	23	3.640	ABCD	2.790	GHIJK
12	3.227	DEFG	3.100	DEFGH	24	3.163	DEFG	3.005	EFGHI

Table 93. Distribution pattern of protein bands in wheat genotypes under control and heat stress conditions at the seedling stage (+ = band present, – = band absent).

	Marker	Genotype									
	(kDa)	1	2	3	4	5	6	7	8	9	10
Control	130	–	–	–	–	–	–	–	–	–	–
	95	–	–	–	–	–	–	–	–	–	–
	72	–	–	–	–	–	–	–	–	–	+
	55	+	+	+	+	+	+	+	–	+	+
	43	+	+	+	+	+	+	+	+	+	+
	34	–	–	–	–	–	–	–	–	–	–
	Marker	Genotype									
	(kDa)	1	2	3	4	5	6	7	8	9	10
Heat stress	130	–	–	–	–	–	–	–	–	–	–
	95	–	–	–	–	–	–	–	–	–	–
	72	+	+	+	+	+	+	+	+	+	+
	55	+	+	+	+	+	+	+	+	+	+
	43	+	+	+	+	+	+	+	+	+	+
	34	–	–	–	–	–	–	–	–	–	–
	Marker	Genotype									
	(kDa)	11	12	13	14	15	16	17	18	19	20
Control	72	–	–	–	–	–	–	–	–	–	–
	55	+	+	+	+	+	+	+	+	+	+
	43	+	+	+	+	+	+	+	+	+	+
	34	–	–	–	–	–	–	–	–	–	–
	26	+	+	+	+	+	+	+	+	+	+
	17	–	–	–	–	–	–	–	–	–	–
	Marker	Genotype									
	(kDa)	11	12	13	14	15	16	17	18	19	20
Heat stress	72	–	–	–	–	–	–	–	–	–	–
	55	+	+	+	+	+	+	+	+	+	+
	43	+	+	+	+	+	+	+	+	+	+
	34	–	–	–	–	–	–	–	–	–	–
	26	+	+	+	+	+	+	+	+	+	+
	17	–	–	–	–	–	–	–	–	–	–

	Marker	Genotype			
	(kDa)	21	22	23	24
Control	95	–	–	–	–
	72	+	+	–	–
	55	+	+	+	+
	43	–	–	–	–
	34	–	–	–	–
	26	–	–	–	–
	17	–	–	–	–
	Marker	Genotype			
	(kDa)	21	22	23	24
Heat stress	95	–	–	–	–
	72	+	+	–	–
	55	+	+	+	+
	43	–	–	–	–
	34	–	–	–	–
	26	–	–	–	–
	17	–	–	–	–

the development of heat-tolerant wheat cultivars. Genotypes 7 and 17 should be grown in the warmer areas to obtain economic yield.

Table 94. Genetic diversity among the A, B, and D genomes. The number of alleles and polymorphic information content (PIC) detected in 24 wheat genotypes are presented.

Genome	Line	Primer	Locus designation	Alleles amplified	PIC value
A	1	WMC-9	*Xwmc*9-1A	5	0.68
	2	WMC-11	*Xwmc* 11-3A	4	0.62
	3	WMC-13	*Xwmc* 13-7A	2	0.19
	4	WMC-15	*Xwmc* 15-4A	1	0.00
	5	WMC-17	*Xwmc* 17-7A	1	0.00
	6	WMC-21	*Xwmc* 21-6A	3	0.40
	7	WMC-24	*Xwmc* 24-1A	6	0.72
	8	WMC-29	*Xwmc* 29-7A	3	0.26
	9	WMC-30	*Xwmc* 30-5A	2	0.04
	10	WMC-33	*Xwmc* 33-6A	2	0.08
	11	WMC-39	*Xwmc* 39-1A	4	0.62
	12	WMC-40	*Xwmc* 40-4A	3	0.62
	13	WMC-45	*Xwmc* 45-3A	7	0.83
B	1	WMC-1	*Xwmc* 1-3B	3	0.32
	2	WMC-3	*Xwmc*3-4B	5	0.37
	3	WMC-5	*Xwmc* 5-5B	3	0.16
	4	WMC-7	*Xwmc* 7-3B	3	0.43
	5	WMC-10	*Xwmc* 10-7B	6	0.73
	6	WMC-16	*Xwmc* 16-4B	2	0.50
	7	WMC-19	*Xwmc* 19-6B	3	0.40
	8	WMC-20	*Xwmc* 20-7B	4	0.53
	9	WMC-27	*Xwmc* 27-2B	5	0.73
	10	WMC-28	*Xwmc* 28-5B	4	0.61
	11	WMC-31	*Xwmc* 31-1B	8	0.84
	12	WMC-35	*Xwmc* 35-2B	5	0.74
	13	WMC-37	*Xwmc* 37-7B	3	0.65
	14	WMC-44	*Xwm44*-1B	4	0.73
	15	WMC-46	*Xwmc* 46-2B	3	0.59
	16	WMC-53	*Xwmc* 53-4B	3	0.16
	17	WMC-54	*Xwmc* 54-3B	3	0.58
	18	WMC-55	*Xwmc55* -1B	2	0.5
	19	WMC56	*Xwmc56*-1B	2	0.16
	20	WMC-57	*Xwmc* 57-1B	2	0.48
D	1	WMC-4	*Xwmc* 4-3D	2	0.09
	2	WMC-6	*Xwmc* 6-5D	3	0.16
	3	WMC-8	*Xwmc* 8-4D	6	0.76
	4	WMC-14	*Xwmc* 14-7D	5	0.68
	5	WMC-18	*Xwmc* 18-2D	3	0.45
	6	WMC-22	*Xwmc* 22-5D	1	0.00
	7	WMC-23	*Xwmc* 23-6D	1	0.00
	8	WMC-25	*Xwmc*25- 2D	5	0.75
	9	WMC-26	*Xwmc* 26-1D	5	0.00
	10	WMC-32	*Xwmc* 32-5D	4	0.60
	11	WMC-34	*Xwmc*34- 6D	2	0.05
	12	WMC-38	*Xwmc* 38-7D	6	0.74
	13	WMC-41	*Xwmc* 41-2D	5	0.56
	14	WMC-42	*Xwmc* 42-7D	10	0.87
	15	WMC-43	*Xwmc* 43-3D	3	0.63
	16	WMC-58	*Xwmc* 58-7D	2	0.18

Salinity tolerance potential of some durum cultivars and their derived D-genome synthetic hexaploid wheats.

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Among the agricultural crops, wheat is an extremely important source of food for human beings. Wheat originated about 10,000 years ago in the Fertile Crescent, one of the most diversified region in the world, comprising a wide array of habitats. Bread wheat originated about 8,000 years ago by hybridization of a tetraploid *T. turgidum* species with diploid donor of D genome, *Ae. tauschii*. The A and B genomes were most likely provided by *T. tugidum* itself, presumably formed from the wild diploid *T. urartu* (A genome) and the donor of B genome *Ae. speltoides*.

Bread wheat is moderately tolerant to the stress and durum wheat is more susceptible. One reason for this is absence of trait for enhanced K^+:Na^+ discrimination in durum wheat, which is carried on long arm of chromosome 4D in bread wheat and is also present in D-genome ancestors of wheat. The D genome of *Ae. tauschii* is homologous to the D genome of bread wheat. For wheat improvement, one route is therefore via bridge crosses that utilize synthetic hexaploids (SH), which are produced by crossing *T. turgidum* (2n=4x=28, AABB) with *Ae. tauschii* (2n=2x=14, DD). *T. turgidum* is generally used as a female parent. The result of the cross is an F_1 hybrid with 21 chromosomes (ABD), which are doubled with a colchicine treatment to produce 42 chromosomes SH (AABBDD) wheats. The hexaploid formation also could be spontaneous.

Over 1,000 new SH wheats have been produced from more than 600 *Ae. tauschii* accessions at CIMMYT, Mexico. The SHs are agronomically poor, difficult to thresh, generally tall, low yielding, and frequently have poor quality. However, they do carry useful and new variation for a range of economically important characters. Potentially, new genetic variation among primary synthetics also have been found for tolerance to drought and salinity. These primary synthetics have been crossed to adapted wheat and agronomically improved materials have been developed with superior yield performance compared to check cultivars under stress.

Salinity is a world-wide problem for many crops, including wheat, and it reduces yield. The yield reduction is due to disturbed metabolic processes. Despite reasonable work done in this regard, the mechanism of salinity tolerance is still not yet fully explored and abundance of genetic diversity remains elusive.

Table 95. Pedigrees of wheat synthetic hexaploid (SH) lines.

SH #	Pedigree
4	CETA/*Ae. tauschii* (540)
5	D67.2/P66.270//*Ae. tauschii* (213)
6	GARZA/BOY//*Ae. tauschii* (268)
10	D67.2/P66.270//*Ae. tauschii* (308)
11	CETA /*Ae. tauschii* (1016)
12	D67.2/P66.270//*Ae. tauschii* (221)
13	DVERD_2/*Ae. tauschii* (1027)
14	68.111/RGB-U//WARD/3/*Ae. tauschii* (329)
15	GARZA/BOY//*Ae. tauschii* (467)
16	DVERD_2/*Ae. tauschii* (221)
17	DVERD_2/*Ae. tauschii* (214)
20	CETA/*Ae. tauschii* (327)
21	D67.2/P66.270//*Ae. tauschii*
28	CPI/GEDIZ/3/GOO//JO6/CRA/4/*Ae. tauschii* (215)
30	ALTAR 84/*Ae. tauschii* (333)
32	GAN/*Ae. tauschii* (182)
35	CETA /*Ae. tauschii* (661)
36	DVERD_2/*Ae. tauschii* (402)
37	CETA /*Ae. tauschii* (174)
38	CETA /*Ae. tauschii* (1024)
39	CROC_1/*Ae. tauschii* (886)
40	CROC_1/*Ae. tauschii* (444)
41	CROC_1/*Ae. tauschii* (518)
42	CETA /*Ae. tauschii* (256)
43	6.111/RGB-U//WARD/3/*Ae. tauschii* (325)
44	DOY 1/*Ae. tauschii* (188)
46	DVERD_2/*Ae. tauschii* (1022)
48	GAN/*Ae. tauschii* (236)
52	ALTAR 84/*Ae. tauschii* (332)
53	GAN/*Ae. tauschii* (180)
54	DOY 1/*Ae. tauschii* (255)
58	D67.2/P66.270//*Ae. tauschii* (217)
60	CROC_1/*Ae. tauschii* (170)
61	DVERD_2/*Ae. tauschii* (1031)
62	CROC_1/*Ae. tauschii* (213)
63	ALTAR 84/*Ae. tauschii* (304)
66	ALTAR 84/*Ae. tauschii* (507)
68	GAN/*Ae. tauschii* (163)
72	GAN/*Ae. tauschii* (201)
76	GAN/*Ae. tauschii* (285)
77	DOY 1/*Ae. tauschii* (333)
78	ALTAR 84/*Ae. tauschii* (219)
79	CPI/GEDIZ/3/GOO//JO6/CRA/4/*Ae. tauschii* (208)
80	DOY 1/*Ae. tauschii* (1030)
81	DOY 1/*Ae. tauschii* (515)
82	CPI/GEDIZ/3/GOO//JO6/CRA/4/*Ae. tauschii* (637)
83	ALTAR 84/*Ae. tauschii* (502)
84	DOY 1/*Ae. tauschii* (517)
85	CROC_1/*Ae. tauschii* (224)
86	GAN/*Ae. tauschii* (890)
87	DOY 1/*Ae. tauschii* (458)
88	DVERD_2/*Ae. tauschii* (1029)
89	ALTAR 84/*Ae. tauschii* (211)
90	CROC_1/*Ae. tauschii* (879)

Screening for salt stress has been done at germination and at the adult-plant stage, because tolerance varies at both stages. Keeping in view the economic characteristics of wheat, we plan the following research work to screen for salinity tolerant lines: explore the salinity tolerance potential of some durum cultivars and their derived D-genome SHs and evaluate the performance of different *Ae. tauschii* accessions in similar durum backgrounds for which ten groups are to be studied.

Germ plasm. From the set of SH lines, germ plasm was selected for estimating the salt-tolerance potential where the study structure was classed in to same durum with diverse *Ae. tauschii* accessions. Ten such groups were utilized with 54 entries (Table 95, p. 227). Seed of the 54 lines was provided by Laboratory of Wheat Wide Crosses and Cytogenetics, NARC, Islamabad. Two salt-tolerant, bread wheat checks, Shorawaki and Kharchia 65, and one salt-susceptible durum cultivar, PDW 34, also were evaluated for their morphological and physiological attributes.

A hydroponic experiment was conducted at control (0 mM NaCl) and stress (75 mM NaCl) conditions to evaluate the performance of the SHs. All 54 lines were subjected to chlorophyll analysis, sugar analysis, shoot length, root length, shoot fresh weight, shoot dry weight, root fresh weight, and root dry weight at control and stress levels. The K^+:Na^+ discrimination was observed at 75 mM NaCl. The ten best lines were selected at 75 mM on the basis of their K^+:Na^+ discrimination, shoot dry weight, chlorophyll, sugar content, and fresh and dry weight. These ten lines were then further analysed for SOD, protein, proline, shoot dry weight, and K^+:Na^+ at 100 $molm^{-3.}$

An analysis of variance was made of total chlorophyll content, sugar content, and K^+:Na^+ ratio of the 54 wheat synthetic lines along with the two check cultivars, Shorawaki and PDW34, grown under control and stress conditions (Table 96). The stress treatment had significant ($P \leq 0.05$) adverse effects on total chlorophyll content and sugar content increases significantly. The genotypes also differed significantly from each other for both parameters, but the 'treatment × genotype' interactions were not significant for these parameters. There was a significant difference in the genotypes for K^+:Na^+ ratio.

Table 96. Analysis of variance summaries (mean squares) for total chlorophyll content (mg\g), sugar content (mg\g), and K^+:Na^+ ratio of 54 synthetic wheat lines grown at two salinity levels, 0 mM and 75 mM NaCl (* = significant at the 0.05 level; NS = not significant).

Source of variation	df	Total chlorophyll (mg/g)	df	Sugar content (mg/g)	df	K^+:Na^+ discrimination
Treatment	1	7.264*	1	4.82*		
Genotype	55	1.047*	55	0.64*	55	4.75*
Treatment × Genotype	55	0.066 NS	55	0.12 NS		
Error	449	0.082	222	0.14	220	0.27

Results of the basic, descriptive statistics applied on the 54 synthetic wheat lines at both control (0 mM) and stress levels (75 mM NaCl) indicate that there is a significant difference in morphological, physiological, and biochemical attributes of genotypes at both conditions. The mean value of total chlorophyll content of the 54 SH lines under control conditions was 1.111 mg/g (0.208–2.698 mg/g), whereas the mean value the stress level was 0.884 mg/g. The total chlorophyll decrease in saline conditions ranging from 0.111 to 1.889 mg/g. The skewness value was 0.486 under control (0 mM) and 0.292 under stress (75 mM NaCl) conditions. Heritability for total chlorophyll was 0.72 under control and 0.81 under stress conditions (Table 97).

Table 97. Evaluation of 54 synthetic wheat lines for physiological traits under saline and nonsaline conditions.

Parameter	Salt concentration	Mean	S.D	Minimum	Maximum	Skewness	h^2
Total chlorophyll (mg/g)	0 mM	1.111	0.338	0.208	2.698	0.486	0.72
	75 mM	0.884	0.326	0.111	1.889	0.292	0.81
Sugar (mg/g)	0 mM	0.776	0.373	0.137	2.207	1.078	0.64
	75 mM	0.996	0.478	0.069	3.203	0.986	0.57
K^+:Na^+	75 mM	1.338	0.962	0.234	5.652	1.736	0.93

A significant decrease in chlorophyll content in saline conditions is observed, decreasing from 2.698 mg/g to 1.889 mg/g. Genotypes showed a higher skewness value for total chlorophyll at the control conditions (0.486) than at saline conditions (0.292). A positive skewness value showed that the performance of most of the genotypes for this trait was equal to or greater than the mean value. Heritiability for total chlorophyll was greater in stress condition (0.81) than in control condition (0.72) (Table 97, p. 228).

The mean performance of the 54 SH lines for sugar content at the control conditions was 0.776 mg/g, and the range was 0.137 mg/g to 2.207 mg/g. The skewness value in nonsaline conditions was 1.078. Heritability for sugar content at control conditions was 0.641. Sugar content increased under stressed conditions. The mean value of sugar content was 0.996 mg/g (0.069–3.203 mg/g) under saline conditions. Skewness in the genotypes was 0.986 and heritability was 0.577 in saline conditions (Table 97, p. 228).

Sugar content increases significantly in saline conditions; from 0.137 mg/g under control and 3.203 mg/g under saline conditions. A positive skewness value is indicative of the fact that it is equal to or greater than the mean value. The skewness is less in saline conditions than in the control.

The mean value of K^+:Na^+ ratio at stressed condition was 1.33. The K^+:Na^+ ratio ranged from 0.23 to 5.65 in genotypes under stress conditions. The skewness of the K^+:Na^+ ratio was 1.73 and kurtosis was 3.44. The positive value of skewness indicated that most of the lines had a value equal to or greater than the average. The heritability under salt stress conditions was 0.93, which indicates that it can be used as a criteria for selection for salinity tolerance (Table 97, p. 228).

The mean data for total chlorophyll content, sugar content, and K^+:Na^+ discrimination of the 54 wheat synthetic lines and the salt-tolerant and salt-susceptible checks gives a clear picture that salt stress caused a significant reduction in total chlorophyll content in the SHs (Table 98). The highest total chlorophyll content was found in SH-16 (1.42 mg/g), followed by SH-20 (1.28 mg/g). Shorawaki had a total chlorophyll content of 2.75 mg/g. The lowest value for total chlorophyll content was in SH-39 (0.44 mg/g) and SH-41 (0.50 mg/g); all other synthetic lines had intermediate performance.

Sugar content increased under salt stress (Table 98). The maximum sugar

Table 98. Means of total chlorophyll content, sugar content, and K^+:Na^+ ratio of 54 synthetic wheat lines grown at two salinity levels, 0 mM NaCl and 75 mM NaCl.

	Chlorophyll (mg/g)		Sugar (mg/g)		K^+:Na^+
Genotype	0 mM	75 mM	0 mM	75 mM	75 mM
SH-4	1.11±0.13	1.08±0.03	1.14±0.36	1.27±0.23	1.00±0.16
SH-5	0.88±0.15	0.65±0.12	0.70±0.12	0.73±0.03	0.64±0.04
SH-6	0.77±0.20	0.61±0.06	1.20±0.33	1.28±0.41	0.59±0.06
SH-10	1.42±0.26	0.86±0.08	0.97±0.21	1.12±0.15	0.59±0.06
SH-11	0.96±0.21	0.63±0.04	1.21±0.50	1.27±0.07	0.95±0.07
SH-12	1.09±0.15	0.93±0.04	0.78±0.06	0.90±0.04	0.78±0.25
SH-13	1.32±0.07	0.74±0.15	0.33±0.03	1.67±0.39	0.37±0.07
SH-14	0.96±0.11	0.81±0.21	0.65±0.07	0.81±0.09	0.51±0.09
SH-15	1.15±0.21	1.02±0.12	0.84±0.23	0.94±0.13	0.49±0.04
SH-16	1.55±0.18	1.42±0.09	1.17±0.27	1.34±0.19	3.83±0.37
SH-17	1.04±0.03	0.96±0.17	0.68±0.12	1.41±0.40	0.94±0.12
SH-20	1.35±0.08	1.28±0.22	1.15±0.31	1.67±0.78	0.59±0.07
SH-21	1.26±0.08	1.11±0.17	0.87±0.10	0.91±0.05	0.61±0.04
SH-28	0.94±0.14	0.83±0.16	0.97±0.20	1.06±0.34	0.68±0.07
SH-30	1.37±0.10	0.80±0.12	1.04±0.14	1.12±0.13	0.91±0.07
SH-32	1.15±0.04	0.66±0.04	1.09±0.12	1.12±0.09	0.64±0.06
SH-35	1.46±0.10	1.22±0.16	1.20±0.23	1.30±0.15	0.62±0.07
SH-36	1.40±0.07	1.19±0.24	1.00±0.06	1.10±0.04	0.71±0.11
SH-37	1.51±0.29	1.24±0.10	0.88±0.18	1.14±0.05	0.62±0.07
SH-38	1.40±0.19	0.73±0.32	0.52±0.05	0.80±0.11	0.48±0.04
SH-39	0.63±0.04	0.44±0.04	0.39±0.10	0.41±0.03	2.03±0.22
SH-40	0.63±0.05	0.511±0.04	0.83±0.09	1.04±0.07	2.53±0.18
SH-41	0.78±0.03	0.50±0.18	0.62±0.18	0.85±0.45	2.51±0.28
SH-42	0.85±0.07	0.62±0.02	0.89±0.08	1.07±0.11	3.01±0.15
SH-43	0.85±0.09	0.67±0.05	0.95±0.13	1.22±0.10	3.00±0.43
SH-44	1.10±0.11	0.52±0.02	0.82±0.08	1.20±0.11	1.32±0.16
SH-46	0.86±0.10	0.58±0.03	0.47±0.03	1.51±0.23	2.26±0.24
SH-48	0.87±0.06	0.61±0.07	0.33±0.05	0.64±0.02	1.77±0.20
SH-52	1.03±0.04	0.57±0.07	0.39±0.13	0.50±0.25	1.88±0.46
SH-53	1.17±0.16	1.10±0.20	0.96±0.10	1.10±0.10	2.00±0.14
SH-54	1.16±0.16	1.02±0.06	0.50±0.09	0.69±0.04	1.53±0.10
SH-58	1.20±0.07	0.94±0.11	0.75±0.19	0.83±0.26	1.40±0.09
SH-60	0.96±0.09	0.84±0.07	0.72±0.08	0.88±0.13	1.73±0.17
SH-61	1.15±0.04	0.99±0.08	0.50±0.08	1.06±0.33	1.15±0.21
SH-62	0.94±0.08	0.76±0.07	0.94±0.26	1.07±0.06	1.03±0.08
SH-63	1.21±0.07	0.84±0.19	0.95±0.18	1.01±0.40	1.11±0.10
SH-66	1.15±0.07	0.93±0.07	0.63±0.05	1.55±0.22	1.10±0.12
SH-68	1.40±0.08	0.84±0.11	0.68±0.08	0.71±0.05	0.85±0.09
SH-72	1.06±0.05	0.92±0.09	0.54±0.06	0.56±0.17	0.74±0.08
SH-76	0.93±0.06	0.76±0.03	0.80±0.07	0.98±0.66	1.46±0.66
SH-77	1.07±0.13	0.68±0.07	0.39±0.06	0.59±0.25	0.83±0.16
SH-78	1.23±0.09	1.20±0.08	0.81±0.17	1.20±0.24	3.04±0.33
SH-79	1.22±0.09	1.03±0.10	0.78±0.19	1.14±0.49	1.26±0.19
SH-80	1.29±0.11	1.07±0.10	0.50±0.08	0.54±0.14	1.12±0.14
SH-81	1.29±0.05	1.03±0.08	0.30±0.04	0.48±0.11	1.49±0.20
SH-82	1.24±0.19	1.15±0.15	0.72±0.24	1.09±0.10	2.14±0.26
SH-83	1.20±0.08	0.90±0.05	0.25±0.03	0.42±0.07	0.94±0.07
SH-84	1.09±0.12	0.96±0.07	1.04±0.39	1.22±0.26	1.00±0.15
SH-85	1.34±0.35	1.16±0.10	1.16±0.23	1.24±0.15	3.49±0.29
SH-86	1.15±0.06	0.72±0.18	0.34±0.06	0.38±0.11	1.35±0.08
SH-87	0.89±0.25	0.79±0.12	0.97±0.19	1.39±0.35	0.83±0.12
SH-88	1.09±0.04	1.04±0.14	0.76±0.07	0.86±0.04	0.67±0.07
SH-89	0.98±0.04	0.80±0.08	0.91±0.30	0.91±0.03	0.83±0.18
SH-90	1.04±0.05	0.98±0.11	0.94±0.27	1.53±0.20	1.12±0.20
Shorawaki	0.94±0.24	2.75±0.37	1.47±0.18	1.52±0.10	4.96±0.65
PDW 34	1.10±0.23	0.32±0.06	1.47±0.12	2.93±0.25	0.84±0.17

content was observed in PDW 34 (2.93 mg/g), followed by SH-20 (1.67 mg/g), Shorawaki (1.52 mg\g), and SH-16 (1.34 mg/g). Minimum sugar contents were found in SH-86 (0.38 mg\g), SH-72 (0.56 mg\g), and SH-68 (0.71 mg\g). The rest of the genotypes accumulated sugar between these maximum and minimum values.

The highest K^+:Na^+ ratio was recorded in Shorawaki (4.96), followed by SH-16 (3.83) and SH-85 (3.49), and the lowest was in SH-13 (0.32), SH-38 (0.47), and SH-15 (0.48) (Table 98, p. 229).

The analysis of variance in for shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight of the 54 SH lines and two check genotypes grown under control and stress conditions indicates that the treatment (stress) had a significant ($P \leq 0.05$) adverse effect on all these parameters except for root dry weight, where the treatment was non-significant (Table 99). A significant difference between the genotypes was observed for all these traits, whereas the 'treatment x genotype' interactions were not significant for shoot length, root length, and root fresh weight.

Table 99. Analysis of variance summaries (mean squares) of shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight of 54 synthetic wheat lines grown at two salinity levels, 0 mM NaCl and 75 mM NaCl (* = significant at the 0.05 level; NS = not significant).

Source of variation	df	Shoot length (cm)	Root length (cm)	Shoot fresh weight (g)	Root fresh weight (g)	Shoot dry weight (g)	Root dry weight (g)
Treatment	1	614.4*	128.16*	0.469*	0.0373*	0.0021*	2.1804 NS
Genotype	55	87.13*	23.3*	0.059*	0.0112*	0.0021*	3.1837*
Treatment × Genotype	55	15.04 NS	4.31 NS	0.0069*	0.0015 NS	1.5581*	1.626*
Error	449	11.99	4.33	0.0043	0.0011	6.2192	6.1744

A significant difference for all the observed morphological attributes under control and stress conditions was observed for the 54 SHs (Table 100). The mean value for shoot length under the control condition was 28.8 cm (18–42 cm) and under the stress condition was 26.9 cm (17–40 cm). The skewness of shoot length was –0.120 under the control condition, negative from the mean values in the control condition, but was 0.139 at the stress condition. Heritability for shoot length was 0.726 in control and 0.890 under salt stress. Shoot length decreased under the stress condition.

Table 100. Evaluation of 54 synthetic wheat lines for morphological traits at saline (75 mM NaCl) and nonsaline (0 mM NaCl) conditions.

Parameter	Salt concentration	Mean	S.D	Minimum	Maximum	Skewness	h^2
Shoot length (cm)	0 mM	28.8	4.38	18	42	–0.120	0.72
	75 mM	26.9	3.80	17	40	0.139	0.73
Shoot fresh weight (g)	0 mM	0.329	0.10	0.12	0.59	0.095	0.86
	75 mM	0.273	0.08	0.08	0.50	0.164	0.87
Root fresh weight (g)	0 mM	0.085	0.048	0.010	0.298	1.043	0.79
	75 mM	0.071	0.035	0.006	0.179	0.427	0.91
Shoot dry weight (g)	0 mM	0.034	0.010	0.010	0.088	0.925	0.78
	75 mM	0.032	0.009	0.010	0.082	1.092	0.77
Root dry weight (g)	0 mM	0.008	0.003	0.001	0.023	1.188	0.68
	75 mM	0.008	0.002	0.002	0.019	1.113	0.82

The mean value of shoot fresh weight in the nonsaline condition was 0.32g and 0.27g in the saline condition. The range of shoot fresh weight was 0.120–0.596 g under the control condition and 0.083–0.500g at the stress level. The skewness of shoot fresh weight in the genotypes in the control condition was 0.095 and 0.164 at the stress condition. Heritability at controls was 0.86 and 0.87 under saline conditions (Table 100).

Shoot fresh weight was higher in the control condition (0.12–0.596g) and reduced in saline (0.083–0.500 g), indicating that salinity stress reduces shoot fresh weight. Positive skewness values at both levels show that the majority of genotypes performed equal to or greater than the mean value for this parameter (Table 100, p. 230).

The mean value for root fresh weight at the control condition was 0.085 g (0.01–0.29 g) and the skewness value was 1.043. At saline stress levels, the mean value was 0.071 g (0.006–0.179 g) and the skewness was 0.427. Heritability for root fresh weight was 0.79 at control and 0.91 at saline conditions. Salt stress has a negative effect on root fresh weight, decreasing in the stress condition. Skewness was positive from mean value under both control and stress conditions (Table 100, p. 230).

The mean value for shoot dry weight under control condition was 0.034 g and 0.032 g under stress condition. Shoot dry weight ranged from 0.010 g to 0.088 g at the control level and 0.012 g to 0.082 g in genotypes under saline conditions. Skewness in the genotypes was 0.925 and 1.092 in control and stress conditions, respectively. Heritability for shoot dry weight was 0.78 under control and 0.77 under salt stress conditions. Shoot dry weight decreases under stress condition. The positive skewness value at both levels shows that the performance of most of the genotypes for this trait was equal to or greater than the mean value (Table 100, p. 230).

The mean value of root dry weight under control and stress condition was 0.008 (0.001–0.023 g) under the nonsaline condition and 0.002–0.010 g under saline condition. Skewness in the genotypes was 1.18 and 1.11 at 0 mM and 75 mM NaCl, respectively. Heritability for root dry weight was 0.68 under control and 0.82 under stress conditions (Table 100, p. 230).

Mean data for morphological traits fo the 54 SH lines was determined (Table 101, p. 232-233). Shoot length decreased under salt stress. The greatest shoot length was found in Shorawaki (40.2 cm), followed by SH-38 (33.4 cm) and SH-20 (31.6 cm), whereas the lowest was in SH-40 (22.4 cm), SH-78 (23.2 cm), and SH-90 (24.1 cm).

Root length increased under salt stress (Table 101, p. 232). The maximum root length was recorded in SH-6 (9.2 cm), followed by SH-16 (9.1 cm) and SH-15 (8.8 cm) and was lowest in SH-30 (3.0 cm), SH-5 (3.7 cm) and SH-17 (4.0 cm). Shoot fresh weight also decreased under salt stress. The greatest shoot fresh weight was observed in Shorawaki (0.47 g), followed by SH-16 (0.42 g) and SH-12 (0.41 g), and SH-52 (0.13 g) and SH-46 (0.14 g) had the lowest weight. Root fresh weight was the maximum in SH-16 (0.13 g), SH-14 (0.12 g), and SH-15 (0.11 g) and the minimum in SH-41 (0.013 g), SH-53 (0.016 g), and SH-41 (0.018 g). Root fresh weight of Shorawaki was 0.11 g and that of PDW34 was 0.06 g. Shoot dry weight and root dry weight decreased under salt stress. The highest shoot dry weight was in SH-16 (0.060 g), followed by SH-6 (0.042 g) and SH-21 (0.041 g), and the lowest in SH-58 (0.020 g), SH-46 (0.022 g), and SH-88 (0.028 g). The greatest root dry weight was found in Shorawaki (0.012 g) and SH-39 (0.011 g) and the lowest in SH-53 (0.004 g), SH-32 (0.005 g), and SH-21 (0.006 g). The dry weight of the shoots of Shorawaki was 0.011 g and of PDW 34 was 0.025 g and of the roots were 0.011 g (Shorawaki) and 0.006 (PDW 34) respectively. All other synthetic lines were intermediate between the two check lines.

Based on the overall performance of the 54 synthetic wheat lines, SH-16, SH-82, and SH-78 performed better with respect to morphological, physiological, and biochemical attributes and were found to be tolerant at 75 mM NaCl stress. On the other hand, SH-13, SH-10, and SH-77 showed poor performance with respect to biomass production and physiological and biochemical traits and were susceptible at 75mM NaCl stress.

A reduction in chlorophyll content is to be expected under stress. Being membrane bound, chlorophyll content is dependent on membrane stability, which under saline conditions seldom remains intact. Salinity stress is well known to cause significant reduction in leaf chlorophyll concentration. Reduction in chlorophyll content is probably due to the inhibitory effect of the accumulated ions of various salts on the biosynthesis of different chlorophyll fractions. In tolerant wheat lines, there was less reduction in total chlorophyll content compare to the susceptible DH lines. The highest chlorophyll content and them minimum reduction (1.55–1.42 mg/g) under salt stress was found in SH-16.

The accumulation of solutes, especially proline, glycine-betaine, and sugar, is a common observation under stress conditions. During salt stress, an increase in sugar concentration has been reported in many species, possibly due to inhibitory effects of salinity stress on the translocation of assimilates. The increased content of sucrose with salinity (but to a lesser extent in tolerant wheat cultivars) is probably due to starch hydrolysis by enhanced activity of α-amylase under salinity. Sugar may contribute to salt-stress tolerance either by serving as osmotica or as respiratory substrate. High sugar under salt stress prevents plants from oxidative damage and maintains structure of different proteins and

Table 101. Means of shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight of 54 synthetic wheat lines grown at two salinity levels, 0 mM NaCl and 75 mM NaCl.

	Shoot length (cm)		Root length (cm)		Shoof fresh weight (g)		Root fresh weight (g)	
Genotype	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM
SH-4	29.3±0.56	26±1.45	6±1.04	7.74±0.77	0.49±0.02	0.32±0.05	0.15±0.017	0.13±0.022
SH-5	26.64±0.83	26.08±0.90	3.68±0.61	3.78±0.41	0.38±0.01	0.30±0.02	0.090. ±01	0.07±0.006
SH-6	32±0.74	27±1.05	8±1.36	9±2.27	0.50±0.02	0.32±0.05	0.14±0.01	0.12±0.016
SH-10	24.4±2.17	21±2.18	7±2.80	9±2.80	0.22±0.03	0.17±0.03	0.15±0.03	0.13±0.016
SH-11	30.42±0.88	27±1.60	6±1.93	8.18±1.78	0.42±0.041	0.36±0.05	0.09±0.009	0.08±0.004
SH-12	30.04±0.25	30±0.34	6±0.53	7.82±0.95	0.45±0.02	0.41±0.02	0.10±0.01	0.08±0.004
SH-13	27.5±1.36	26±0.729	5±1.27	9±0.49	0.43±0.02	0.29±0.03	0.12±0.01	0.09±0.01
SH-14	29.44±1.05	28±1.43	6±0.85	7.74±0.74	0.419±0.017	0.35±0.04	0.18±0.02	0.12±0.01
SH-15	32±2.10	27±1.38	6±0.14	8.8±0.79	0.421±0.053	0.31±0.05	0.19±0.03	0.11±0.01
SH-16	28±1.30	27±1.57	7±1.05	9.1±1.28	0.50±0.027	0.42±0.03	0.15±0.013	0.13±0.006
SH-17	33±1.12	31±3.20	5±0.33	4±0.67	0.39±0.04	0.27±0.03	0.06±0.01	0.060.008
SH-20	34±1.64	311±.41	5±0.48	4±0.85	0.35±0.03	0.30±0.02	0.07±0.02	006±0.003
SH-21	32±0.93	31±0.41	5±1.22	5±1.16	0.34±0.006	0.32±0.02	0.08±0.006	0.07±0.01
SH-28	30±0.54	29±0.22	5±0.37	6±0.32	0.25±0.03	0.39±0.02	0.084±0.016	0.07±0.002
SH-30	31±0.27	30±0.51	3±0.20	3±0.17	0.32±0.02	0.26±0.02	0.06±0.001	0.05±0.004
SH-32	29±1.69	29±0.84	3±0.40	7±0.23	0.279±0.04	0.21±0.01	0.06±0.008	0.05±0.003
SH-35	29±1.49	28±0.81	5±0.22	5±0.38	0.30±0.03	0.24±0.02	0.08±0.01	0.06±0.01
SH-36	30±1.75	25±2.0	4±0.0	7±1.05	0.34±0.01	0.16±0.011	0.10±0.002	0.04±0.01
SH-37	31±1.47	30±0.31	4±0.33	6±0.70	0.30±0.04	0.24±0.05	0.05±0.01	0.05±0.01
SH-38	34±2.63	33±1.78	6.9±1.005	8±0.66	0.37±0.05	0.30±0.01	0.06±0.01	0.04±0.01
SH-39	29±1.84	24±0.45	6±0.94	8±0.66	0.19±0.03	0.16±0.01	0.05±0.03	0.03±0.01
SH-40	23±1.29	22±0.70	6±1.58	9±1.11	0.24±0.01	0.22±0.02	0.03±0.01	0.036±0.005
SH-41	31±2.12	24±1.72	5±0.73	9±1.06	0.24±0.04	0.18±0.03	0.02±0.005	0.01±0.002
SH-42	31±1.47	30±0.59	6±0.75	7±1.77	0.23±0.02	0.19±0.01	0.03±0.01	0.02±0.003
SH-43	30±2.62	23±1.48	6±1.05	7±0.88	0.26±0.01	0.23±0.01	0.05±0.002	0.04±0.01
SH-44	27±1.67	26±1.52	6±0.47	8±0.99	0.18±0.005	0.15±0.01	0.05±0.002	0.04±0.01
SH-46	29±2.0	25±0.83	3±0.33	6±0.61	0.18±0.004	0.13±0.01	0.04±0.002	0.02±0.004
SH-48	27±3.12	27±1.90	7±1.86	8±1.82	0.19±0.03	0.17±0.03	0.07±0.005	0.06±0.02
SH-52	28±0.58	28±1.73	6±0.64	6±0.98	0.14±0.01	0.13±0.01	0.02±0.002	0.02±0.004
SH-53	27±1.37	26±0.20	5±0.8	7±0.44	0.20±0.003	0.18±0.03	0.01±0.001	0.01±0.002
SH-54	33±2.80	26±2.38	6±0.61	8±1.17	0.45±0.05	0.28±0.02	0.13±0.02	0.09±0.01
SH-58	27±1.70	23±0.37	4±0.65	6±0.58	0.28±0.03	0.20±0.01	0.11±0.01	0.09±0.01
SH-60	31±1.10	28±1.49	5±0.76	8±0.51	0.35±0.05	0.31±0.03	0.09±0.03	0.09±0.002
SH-61	32±0.83	29±1.74	6±0.72	7±0.92	0.37±0.03	0.33±0.01	0.08±0.01	0.07±0.005
SH-62	29±1.69	25±1.42	6±1.07	7±0.87	0.33±0.03	0.27±0.05	0.10±0.01	0.08±0.01
SH-63	32±2.43	25±1.06	5±0.75	6±0.54	0.41±0.04	0.28±0.01	0.10±0.02	0.09±0.01
SH-66	25±2.23	25±3.55	6±1.62	5±1.12	0.31±0.05	0.24±0.05	0.09±0.01	0.08±0.002
SH-68	28±1.96	28±1.91	5±0.59	6±0.36	0.34±0.01	0.34±0.04	0.12±0.02	0.08±0.02
SH-72	27±1.46	27±0.99	5±0.41	6±0.48	0.30±0.03	0.29±0.01	0.07±0.01	0.06±0.002
SH-76	29±2.63	27±2.99	5±0.82	6±0.42	0.32±0.06	0.23±0.04	0.09±0.005	0.08±0.01
SH-77	28±2.30	25±0.10	4±0.60	7±0.85	0.35±0.07	0.21±0.01	0.10±0.02	0.07±0.004
SH-78	23±2.84	23±1.03	5±1.0	6±0.78	0.30±0.03	0.28±0.01	0.10±0.021	0.06±0.01
SH-79	28±1.12	26±1.21	5±0.32	5±0.82	0.34±0.03	0.25±0.02	0.16±0.02	0.10±0.01
SH-80	25±2.80	24±0.42	5±0.83	5±1.10	0.37±0.024	0.31±0.01	0.13±0.06	0.10±0.02
SH-81	26±1.11	25±1.53	4±0.76	5±0.85	0.34±0.02	0.28±0.03	0.08±0.02	0.07±0.002
SH-82	29±0.73	271.03	5±0.42	5±0.67	0.39±0.002	0.37±0.02	0.095±0.005	0.08±0.01
SH-83	26±1.40	26±1.27	6±1.27	8±1.91	0.41±0.03	0.40±0.02	0.07±0.02	0.09±0.02
SH-84	26±0.49	25±0.58	6±0.41	6±0.86	0.33±0.05	0.30±0.03	0.08±0.01	0.07±0.01
SH-85	26±0.92	25±0.28	4±0.49	4±1.25	0.40±0.02	0.32±0.05	0.08±0.01	0.07±0.003
SH-86	25±0.80	24±0.30	6±0.83	6±0.72	0.34±0.01	0.30±0.02	0.10±0.01	0.09±0.003
SH-87	32.16±2.11	28.2±1.47	5±0.34	7.52±1.26	0.37±0.05	0.29±0.03	0.05±0.004	0.04±0.01
SH-88	30.90±1.95	27.38±3.16	5.36±0.71	3.44±0.45	0.31±0.03	0.26±0.03	0.08±0.01	0.05±0.01
SH-89	31.5±0.85	31±0.42	7±1.25	6.9±0.59	0.36±0.01	0.35±0.01	0.06±0.01	0.13±0.016
SH-90	24±2.78	24±2.74	6±1.17	6±0.99	0.29±0.05	0.28±0.05	0.043±0.012	0.08±0.014
Shorawaki	420.99	400.41	130.50	140.48	0.550.01	0.470.03	0.130.004	0.110.003

Table 101. Means of shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight of 54 synthetic wheat lines grown at two salinity levels, 0 mM NaCl and 75 mM NaCl.

	Shoot dry weight (g)		Root dry weight (g)	
Genotype	0 mM	75 mM	0 mM	75 mM
SH-4	0.042±0.001	0.04±0.005	0.009±0.001	0.008±0.001
SH-5	0.04±0.003	0.036±0.003	0.008±0.001	0.007±0.001
SH-6	0.05±0.003	0.04±0.003	0.01±0.0003	0.008±0.001
SH-10	0.036±0.005	0.028±0.005	0.01±0.002	0.007±0.002
SH-11	0.04±0.004	0.04±0.006	0.01±0.001	0.01±0.001
SH-12	0.04±0.002	0.03±0.004	0.01±0.001	0.01±0.001
SH-13	0.043±0.003	0.029±0.004	0.01±0.001	0.007±0.001
SH-14	0.04±0.002	0.03±0.005	0.01±0.001	0.009±0.001
SH-15	0.04±0.007	0.03±0.004	0.009±0.002	0.007±0.001
SH-16	0.065±0.009	0.060±.007	0.006±0.001	0.008±0.001
SH-17	0.04±0.004	0.03±0.005	0.01±0.001	0.008±0.0011
SH-20	0.04±0.004	0.03±0.004	0.006±0.001	0.005±0.001
SH-21	0.05±0.003	0.03±0.003	0.01±0.001	0.006±0.001
SH-28	0.031±0.003	0.030±0.0002	0.006±0.001	0.005±0.0003
SH-30	0.032±0.001	0.03±0.004	0.01±0.01	0.006±0.0005
SH-32	0.034±0.005	0.028±0.002	0.005±0.001	0.005±0.0002
SH-35	0.032±0.002	0.03±0.004	0.008±0.001	0.007±0.001
SH-36	0.04±0.001	0.02±0.003	0.01±0.001	0.01±0.0003
SH-37	0.036±0.001	0.03±0.004	0.007±0.001	0.007±0.001
SH-38	0.042±0.003	0.04±0.001	0.005±0.001	0.007±0.001
SH-39	0.031±0.002	0.026±0.002	0.01±0.003	0.011±0.001
SH-40	0.042±0.002	0.036±0.004	0.01±0.002	0.01±0.001
SH-41	0.03±0.005	0.025±0.003	0.01±0.001	0.006±0.0
SH-42	0.04±0.003	0.035±0.002	0.01±0.002	0.01±0.001
SH-43	0.030±0.004	0.03±0.001	0.01±0.0004	0.009±0.001
SH-44	0.03±0.002	0.03±0.003	0.01±0.0002	0.009±0.001
SH-46	0.025±0.002	0.022±0.003	0.008±0.001	0.0006±0.0005
SH-48	0.03±0.005	0.029±0.003	0.007±0.002	0.01±0.001
SH-52	0.03±0.003	0.026±0.004	0.008±0.001	0.01±0.001
SH-53	0.031±0.002	0.029±0.005	0.005±0.0004	0.004±0.001
SH-54	0.05±0.004	0.03±0.003	0.01±0.001	0.01±0.001
SH-58	0.024±0.002	0.02±0.001	0.01±0.001	0.01±0.001
SH-60	0.033±0.004	0.032±0.003	0.01±0.002	0.01±0.001
SH-61	0.04±0.003	0.037±0.002	0.01±0.001	0.008±0.001
SH-62	0.033±0.002	0.03±0.005	0.01±0.001	0.009±0.001
SH-63	0.04±0.004	0.03±0.001	0.01±0.002	0.009±0.001
SH-66	0.03±0.005	0.027±0.006	0.01±0.002	0.008±0.001
SH-68	0.034±0.002	0.03±0.003	0.01±0.002	0.009±0.001
SH-72	0.03±0.002	0.03±0.002	0.01±0.001	0.007±0.001
SH-76	0.03±0.007	0.026±0.003	0.01±0.001	0.009±0.002
SH-77	0.034±0.006	0.028±0.002	0.006±0.001	0.006±0.001
SH-78	0.032±0.001	0.03±0.005	0.008±0.001	0.007±0.001
SH-79	0.03±0.003	0.025±0.002	0.01±0.003	0.008±0.001
SH-80	0.031±0.002	0.03±0.001	0.01±0.005	0.01±0.002
SH-81	0.03±0.004	0.03±0.01	0.01±0.001	0.008±0.001
SH-82	0.04±0.002	0.04±0.003	0.009±0.003	0.007±0.001
SH-83	0.03±0.003	0.029±0.0003	0.007±0.001	0.007±0.0003
SH-84	0.03±0.006	0.03±0.001	0.01±0.001	0.008±0.001
SH-85	0.04±0.001	0.04±0.01	0.01±0.002	0.008±0.001
SH-86	0.042±0.001	0.039±0.004	0.01±0.001	0.009±0.0004
SH-87	0.033±0.004	0.03±0.003	0.01±0.001	±0.0080.0003
SH-88	0.03±0.003	0.028±0.003	0.01±0.002	0.008±0.001
SH-89	0.036±0.005	0.03±0.0001	0.009±0.0004	0.009±0.001
SH-90	0.028±0.006	0.030±0.005	0.006±0.0003	0.006±0.0007
Shorawaki	0.16±0.006	0.11±0.005	0.014±0.001	0.011±0.001
PDW 34	0.034±0.002	0.025±0.002	0.02±0.001	0.006±0.001

membranes. Our results show the accumulation of sugar content under salt stress in SH-13 (0.33–1.67mg/g) increased.

K^+:Na^+ discrimination in SHs has been determined by different scientists at different salinity levels. We screened the genotypes at 75 mM NaCl. Line SH-16 was found to have highest K^+:Na^+ ratio, and lowest was in SH-13. Although the salt-tolerant check Shorawaki was higher than SH-16.

The salinity tolerance in wheat is associated with the accumulation of K^+ and exclusion of Na^+ under saline conditions. Sodium competes with K^+ for uptake through common transport system and does this effectively since the Na^+ concentration in saline environment is usually considerably greater than that of K^+. The sensitivity of some crops to salinity is due to the inability to keep Na^+ and Cl^- out of transpiration streams. Plants limiting the uptake of toxic ions or maintaining normal nutrient ion contents could show greater tolerance, which was the case with our study. Uptake mechanisms that discriminate similar ions, such as Na^+ and K^+, could be useful selection criteria for salt tolerance in wheat and breeding for efficient nutrient uptake. All the genotypes showed a decreasing trend in K^+ content due to salinity stress. The decrease in K^+ was due to the presence of excessive Na^+ in the growth medium, because high external Na^+ content is known to have an antagonistic effect on K^+ uptake in plant. Salt tolerance is associated with K^+ content, because of its involvement in osmotic regulation and competition with Na^+. Regulation of K^+ uptake and prevention of Na+ entry and efflux of Na^+ from cell are the strategies commonly used by plants to maintain desirable K^+:Na^+ ratio in the cytosol.

Plants irrigated with saline water show great depression in dry weight. Such a reduction is due to inadequacy of nutrients present in growing media or due to decrease in water entry rate into plants. Because root pressure is reduced under saline conditions causing a decrease in water flow, less water is available for normal growth and development. The decrease in shoot fresh weight may be due to low uptake of water by plants as well as toxicity of Na^+ and Cl^- because of their high concentration in the nutrient solution. A similar trend was noted in the fresh and dry root weights and also in dry shoot weights in the lines under saline conditions by other scientists. We also observed a decrease in

shoot and root fresh and dry weight under salinity stress. Shoot fresh weight was reduced the least in SH-16, SH-78, and SH-82 under salt stress and a smaller decrease in root fresh weight in SH-16 and SH-82 showed their tolerant behavior under salt stress. Shoot fresh weight was reduced significantly in SH-13. Smaller reductions in the shoot and root dry weights of the tolerant genotypes compared to the susceptible genotypes were observed**.**

Physiological and morphological evaluation of ten selected lines at 75 mM NaCl. The ten best lines (SH-4, SH-16, SH-40, SH-42, SH-43, SH-44, SH-53, SH-78, SH-82, and SH-85) were selected at 75mM on the basis of their K^+:Na^+ discrimination, cholorophyll content, sugar content, and root and shoot fresh and dry weights. For these ten lines, SOD, protein, proline, shoot dry weight and K^+/Na^+ were further evaluated at 100 mM NaCl.

Physiological parameters under salt stress. A high K^+:Na^+ value indicates a high level of salt tolerance, because it shows that plant have greater ability to exclude Na^+ and accumulate K^+ at high NaCl concentrations. To accumulate more K^+ compared to Na^+ under saline conditions is a character that determines salinity tolerance of plant at the seedling stage.

In the ten selected lines at 75 mM NaCl, the highest K^+:Na^+ was observed in SH-16 (3.83), followed by SH-85 (3.49), SH-78 (3.04), and SH-42 (3.01) and the lowest was found in SH-4 (1.0). The salt-tolerant genotype Shorawaki had a K^+:Na^+ ratio of 4.96 and the salt-susceptible PDW 34 was 0.84 (Table 102). The highest chlorophyll content was found in SH-16 (1.42 mg/g), followed by SH-78 (1.20 mg/g), SH-85 (1.16 mg/g), and SH-82 (1.15 mg/g), and the lowest was observed in SH-43 (0.62 mg/g). The salt-tolerant genotype Shorawaki had a 2.75 mg/g chlorophyll content and in the salt-susceptible genotype PDW 34, it was reduced to 0.32 mg/g. Sugar content did not increase much compared to that at the control level, but in the salt-sensitive genotype PDW 34, sugar content was increased from 1.47 mg/g under control condition to 2.93 mg/g under stress conditions.

Table 102. Means of physiological parameters of ten selected wheat lines at control and stress level (75 mM NaCl).

	Chlorophyll content (mg/g)		Sugar (mg/g)		K^+:Na^+ discrimination
Genotype	0 mM	75 mM	0 mM	75 mM	75mM
SH-4	1.11	1.08	1.14	1.27	1.00
SH-16	1.55	1.42	1.17	1.34	3.83
SH-40	0.63	0.51	0.83	1.04	2.53
SH-42	0.85	0.62	0.89	1.07	3.01
SH-43	0.85	0.67	0.95	1.22	3.00
SH-44	1.10	0.52	0.82	1.20	1.32
SH-53	1.17	1.10	0.96	1.10	2.00
SH-78	1.23	1.20	0.81	1.20	3.04
SH-82	1.24	1.15	0.72	1.09	2.14
SH-85	1.34	1.16	1.16	1.24	3.49
Shorawaki	2.94	2.75	1.47	1.52	4.96
Pbw343	1.10	0.32	1.47	2.93	0.84

Morphological parameters under salt stress. The ten lines also performed well regarding their agronomical parameters and showed less reduction in biomass as compared to the controls. At 75 mM in ten tolerant lines, the maximum shoot length was observed in SH-42 (30 cm). Shoot length was 40 cm in Shorawaki and 26 cm in PDW 34 under salt stress (Table 103, p. 235).

The highest shoot fresh weight in the selected lines at 75 $molm^{-3}$ was found in SH-16 (0.42 g), followed by SH-82 (0.37 g) and SH-4 (0.32 g). In the salt-tolerant check Shorawaki, shoot fresh weight was 0.47 g, whereas in PDW 34, shoot fresh weight decreased from 0.39 (control) to 0.25 (stress). SH-4 and SH-16 (0.13 g) performed well with respect to root fresh weight, whereas in Shorawaki, root fresh weight was 0.11 g and in PDW 34 0.06 g (Table 103, p. 235).

Genotypes with high K^+:Na^+ value have a high shoot dry weight, indicating that this trait is associated with performance of plant under stress. The highest shoot dry weight was found in SH-16 (0.06 g) among the ten lines under saline conditions. The shoot dry weight of Shorawaki was 0.11 g and that of PDW 34 was 0.025 g at this stress level. Among the selected lines, the highest root dry weight was observed in SH-40 and SH-42 (0.01 g) (Table 103, p. 235).

Screening for salt tolerance at 100 mM NaCl stress. The ten best lines identified at 75 mM and the salt-tolerant check Kharchia 65 were subjected to proline, protein, and superoxide dismutase (SOD) analysis at 100 mM NaCl stress to further fine tune the identification of tolerant lines for future use. The shoot dry weight and K^+:Na^+ also also recorded to check salt tolerance at 100 mM (Table 104, p. 235).

Table 103. Mean values of morphological parameters of ten selected wheat lines at control and stress level (75 mM NaCl)

Genotype	Shoot length (cm)		Root length (cm)		Shoot fresh weight (g)		Root fresh weight (g)		Shoot dry weight (g)		Root dry weight (g)	
	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM
SH-4	29	26	6.0	7.7	0.49	0.32	0.15	0.13	0.042	0.040	0.009	0.008
SH-16	28	27	7.0	9.1	0.50	0.42	0.15	0.13	0.070	0.060	0.006	0.008
SH-40	23	22	6.3	9.0	0.24	0.22	0.03	0.03	0.042	0.040	0.010	0.010
SH-42	31	30	6.4	7.0	0.23	0.19	0.03	0.02	0.040	0.035	0.010	0.010
SH-43	30	23	6.2	7.0	0.26	0.23	0.05	0.04	0.030	0.030	0.010	0.009
SH-44	27	26	6.0	8.0	0.18	0.15	0.05	0.04	0.030	0.030	0.010	0.009
SH-53	27	26	5.0	7.0	0.20	0.18	0.01	0.01	0.031	0.030	0.005	0.004
SH-78	23	23	5.0	6.0	0.30	0.28	0.10	0.06	0.032	0.030	0.008	0.007
SH-82	29	27	5.0	7.0	0.39	0.37	0.10	0.08	0.040	0.040	0.009	0.007
SH-85	26	25	4.0	6.0	0.40	0.32	0.08	0.07	0.040	0.040	0.010	0.009
Shorawaki	42	40	13.0	14.0	0.55	0.47	0.13	0.11	0.160	0.110	0.014	0.011
PDW34	35	26	6.0	9.0	0.39	0.25	0.11	0.06	0.034	0.025	0.020	0.006

Among the selected lines at 100 mM salt stress, the SOD value ranged from 25.8 μg/mL to 74.3μg/mL. SH-42 (74.3 units/g) was found to have highest SOD content, and the lowest was observed in SH-85 (25.8 units/g). The check Kharchia 65 had 51.2 units/g SOD content (Table 104).

Table 104. Mean evaluation superoxide dismutase (SOD), protein, proline, shoot dry weight, and K^+:Na^+ of ten selected wheat synthetic lines at 100mM NaCl stress.

Genotype	SOD (units/g)	Protein (μg/g)	Proline (μg/mL)	Shoot dry weight (g)	K^+:Na^+ discrimination
SH-4	49.9	1,291.4	338.8	0.023	0.850
SH-16	66.0	1,291.8	328.8	0.040	2.310
SH-40	71.7	1,224.6	257.4	0.030	2.050
SH-42	74.3	1,141.7	259.1	0.024	1.251
SH-43	53.5	1,181.8	195.9	0.033	2.540
SH-44	64.2	1,206.4	300.6	0.024	0.870
SH-53	30.1	1,163.9	134.5	0.025	0.941
SH-78	50.8	1,134.8	209.2	0.036	2.650
SH-82	46.6	1,259.1	554.7	0.028	1.140
SH-85	25.8	1,206.7	368.6	0.032	2.740
Kharchia 65	51.2	1,256.7	702.5	0.072	3.450

The highest protein content accumulated in SH-16 (1,291.8 μg/g) and the lowest was observed in SH-78 (1,134.8 μg/g). Kharchia 65 showed a protein content of 1,256.7 μg/g at 100mM NaCl stress (Table 104).

Synthetic SH-53 showed the lowest proline content of 134.5 μg/mL and the highest value of 554.7 μg/mL was found in SH-82. Kharchia 65 accumulated proline content of 702.4 μg/mL at 100 mM saline condition (Table 104).

The highest shoot dry weight among ten SHs was in SH-16 (0.040 g) and the lowest in SH-4 (0.023 g). Kharchia 65 was found to have a 0.072 g shoot dry weight at 100 mM stress.

The K^+:Na^+ ratio ranged from 0.85 (SH-4) to 2.74 (SH-85) and the check Kharchia 65 was 3.450 (Table 104).

Conclusion. In addition to achieving quantity and quality, wheat improvement programs focus on two major problems, biotic and abiotic production constraints. In Pakistan, rusts are the key biotic constraint to production and the abiotic factors of drought, salinity, and heat play significant roles. For each objective to be achieved, the appropriate genetic diversity is essential to have in a cultivar to give a useful product. Focusing on salinity, which is an abiotic constraint mainly in irrigated agriculture, the available wheat cultivars do not have an abundance of diversity. Limited conventional cultivars are available, and these have been underexploited and poorly characterized for their molecular profiles. However, new diversity around parental genomes (particularly *Ae. tauschii*) has become available and is a potent re-

source for wheat improvement. Resistance against many of the biotic and abiotic factors has been incorporated from *Ae. tauschii* to synthetic wheats. We focused on screening for salinity tolerant lines on the basis of morphological characters and physiological/biochemical attributes.

Based on overall performance of 54 synthetic wheat lines, SH-16, SH-82, and SH-78 performed better with respect to morphological, physiological, and biochemical attributes and were found to be tolerant at 75 mM NaCl stress. Lines SH-13, SH-10, and SH-77 had poor performance with respect to biomass production and physiological and biochemical traits and were susceptible at 75 mM NaCl stress.

The highest chlorophyll content was found in SH-16 and also the minimum (1.55–1.42 mg/g) reduction of chlorophyll under salt stress. Among the genotypes screened at 75 mM NaCl, SH-16 was found to have the highest K^+:Na^+ ratio; the lowest was observed in SH-13. Tolerant lines also performed better with respect to their morphological traits.

We found that synthetic wheat lines provide a good source of tolerance to salinity and are morphologically and physiologically good with a high level of genetic diversity, which is a prerequisite of any crop improvement program. We conclude that these SHs are a valuable source for genetic improvement of wheat for salinity tolerancefor plant breeders to use in breeding for saline soils.

Phenological and molecular characterization of the International Triticeae Mapping Initiative Wheat Population for salinity tolerance.

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Salinity is a worldwide problem causing reduction in growth and yield of many crops including wheat. In Pakistan, rusts are is the key biotic constraint to production and in the abiotic category, drought, salinity, and heat play a significant role. The feasible way to address this problem is development of wheat cultivars that can thrive and give reasonable yield, when grown in such problem soils. To achieve this, existence of appropriate amount of genetic variability and physiological and biochemical mechanisms of salinity tolerance are prerequisite. New diversity around the parental genomes (particularly D-genome diploid) has become available and is a potent resource for wheat improvement. Resistance against many of the biotic and abiotic factors has been incorporated from this diploid wheat progenitor to synthetic wheats. This study focused on determining genetic diversity of some salinity tolerant germ plasm for its utilization in crop improvement programs.

The germ plasm selected for this study has been characterized as the International Triticeae Mapping Initiative (ITMI) population produced in the USA using two wheat parents from CIMMYT, Mexico; Opata and a D-genome synthetic hexaploid wheat. The F_1s derived from the cross between the above two parents have been advanced by single seed descent (SSD) up to F_6 and have 149 recombinant inbred lines. The whole ITMI population was subjected to chlorophyll analysis, sugar, shoot fresh weight, root fresh weight, and their biomass were taken at 0 and 75mM stress, K^+:Na^+ discrimination was taken only at 75 mM salt stress, and the top ten tolerant lines were subjected to SOD, protein, and proline analyses at 100 mM salt stress.

Table 105. Analysis of variance summaries (mean squares) of total chlorophyll content (mg/g), sugar content (mg/g), and K^+:Na^+ ratio of 97 wheat lines grown at two salinity levels, 0 mM NaCl and 75 mM NaCl (* = significant).

Source of variation	Degrees of freedom	Total chlorophyll (mg/g)	Degrees of freedom	Sugar content (mg/g)	Degrees of freedom	K^+:Na^+
Treatment	1	22.39*	1	8.646*		
Variety	96	1.416*	96	1.979*	96	0.850*
Treatment x Variety	96	0.200*	96	0.185		
Error	777	0.397	386	0.355	388	0.124

The analyses of variance of total chlorophyll content, sugar content, and K^+:Na^+ ratio of 97 RILs grown under control and stress conditions are presented (Table 105) shows that stress (treatment) has significant ($P \leq 0.05$) adverse effect on total chlorophyll content while sugar content increase significantly ($P \leq 0.05$) under stress (75 mM) conditions.

Lines also differed significantly from each other but the 'variety x treatment' interactions were not significant in both the above parameters. There was significant ($P \leq 0.05$) difference in varieties for K^+:Na^+ ratio.

The total chlorophyll decreased due to salinity stress, ranging from 0.09 mg/g to 4.02 mg/g in the control and 0.09–3.75 mg/g at saline conditions. The population had a higher skewness value for total chlorophyll in saline conditions (1.46) than at control conditions (1.45). A positive value of the skewness showed that these values were equal or greater than the mean value. Heritability for total chlorophyll was 0.80 and 0.82 at control and salt conditions, respectively (Table 106).

Sugar content increased in stressed conditions; the range was 0.17–4.11 mg/g in the control and 0.16–7.39

Table 106. Physiological and morphological characterization of the ITMI mapping population at 0 mM and 75 mM NaCl (Shoot fresh weight = SFW, shoot dry weight = SDW, root fresh weight = RFW, and root dry weight = RDW)..

	Mean	Standard deviation	Minimum value	Maximum value	Skewness	Kurtosis	Heritibility
0 mM NaCl							
Cholophyll content	1.12	0.60	0.09	3.75	1.45	2.95	0.80
Shoot length (cm)	23.3	4.56	12.8	36.5	0.14	-0.35	0.83
Root length (cm)	4.38	2.05	1.00	14.5	1.04	1.64	0.78
Shoot fresh weight (g)	0.21	0.10	0.09	0.79	1.57	3.08	0.89
Root fresh weight (g)	0.07	0.06	0.01	0.67	3.52	23.6	0.33
Shoot dry weight (g)	0.02	0.009	0.01	0.06	1.19	1.88	0.27
Root dry weight (g)	0.008	0.004	0.01	0.02	0.57	-0.38	0.82
SDW/RDW	3.61	2.78	0.83	29	3.58	19.9	0.73
RDW/SDW	0.38	0.19	0.03	1.2	1.14	2.07	0.82
Sugar (mg/g)	1.03	0.67	0.17	4.11	1.97	4.55	0.80
75 mM NaCl							
Cholophyll	0.91	0.55	0.09	4.02	1.46	3.65	0.82
K	3.37	1.30	0.87	7.41	0.43	0.01	0.86
Na	5.57	2.95	0.63	15.7	0.96	0.66	0.93
K^+:Na^+	0.77	0.56	0.15	6.00	3.58	22.5	0.84
Shoot length (cm)	21.2	4.42	10.2	34.0	0.29	0.06	0.84
Root length (cm)	3.72	1.84	1.0	12.9	1.36	2.47	0.79
Shoot fresh weight (g)	0.19	0.07	0.1	0.50	1.29	2.09	0.88
Root fresh weight (g)	0.05	0.04	0.01	0.26	1.70	3.41	-0.25
Shoot dry weight (g)	0.02	0.008	0.01	0.06	1.74	5.23	0.20
Root dry weight (g)	0.007	0.004	0.001	0.01	0.70	–0.20	0.27
SDW/RDW	3.84	3.54	0.5	25.7	2.99	11.12	0.74
RDW/SDW	0.41	0.28	0.04	2.00	1.87	5.44	0.83
Sugar (mg/g)	1.27	0.85	0.16	7.39	2.35	9.60	0.70

mg/g in salt strell, a significant increase of from 4.11 mg/g in the control. Skewness in the population was 2.35 in saline and 1.97 in nonsaline conditions. Sugar showed a positive value of skewness and was much less in saline conditions. Heritability for sugar content in the control was 0.80, whereas in salt conditions was 0.70 (Table 106). The K^+:Na^+ ratio ranged from 0.15–6.00 with a skewness value of 3.58.

Total chlorophyll content, sugar content, and K^+:Na^+ discrimination were measured for the 97 RILs (Table 107, pp. 238-239). The data gives a clear picture that salt stress caused significant reductions in total chlorophyll content in the RILs. The greatest total chlorophyll content was found in ITMI-6 (2.01 mg/g), followed by ITMI-97 (1.93 mg/g) and ITMI-29 (1.92 mg/g). The lowest value of total chlorophyll content was in ITMI-14 (0.14 mg/g), ITMI-96 (0.19 mg/g), and ITMI-75 (0.48 mg/g).

Sugar content increased under salt stress. The maximum sugar content was observed in ITMI-34 (3.27 mg/g), followed by ITMI-3 (3.11 mg/g) and ITMI-12 (2.83 mg/g), and the minimum was in ITMI-77 (0.43 mg/g), ITMI-4 (0.48 mg/g), and ITMI-61 (0.49 mg/g).

K^+:Na^+ increased under salt stress. The maximum K^+:Na^+ was observed in ITMI-24 (2.69), followed by ITMI-23 (2.60) and ITMI-20 (1.77) and the minimum was found in ITMI-73 (0.27), ITMI-84 (0.28 mg/g), and ITMI-81 (0.31).

The analysis of variance (Table 108, p. 239) for shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight indicate that the treatment (stress) had a significant ($P \leq 0.05$) adverse effect on all these parameters. A significant ($P \leq 0.05$) difference was found between varieties for all these traits and the 'treatment x variety' interaction was not significant for shoot length and root length and significant ($P \leq 0.05$) for the remaining parameters.

The shoot length ranged from 10.2 –34.0 cm in populations under saline conditions, whereas in the control conditions, it was 12.8–36.5 cm, a decrease under salinity. The skewness of the shoot length was 0.29 at saline and 0.14 at control conditions, positive from the mean values. Heritability was 0.83 at control and 0.84 at salt stress conditions (Table 109, pp. 240-241).

Morphological traits also decreased under salt stress. Shoot length decreased under salt stress. RILs ITMI-32 (28.7 cm), ITMI-86 (28.1 cm), and ITMI-17 (26 cm) had the highest shoot length and the lowest was in ITMI-81 (12.7 cm), ITMI-60 (12.8 cm), and ITMI-79 (13.7 cm). Root length increased under salt stress (Table 109, pp. 242-243). The maximum root length was recorded in ITMI-3 (9.4 cm), followed by ITMI-8 (7.6 cm) and ITMI-7 (7.5 cm) and the minimum was found in ITMI-122 (1.3 cm), ITMI-144 (1.2 cm) and ITMI-95 (1.1 cm).

Table 107. Mean values for chlorophyll, sugar, and K^+:Na^+ discrimination 97 lines of ITMI population

	Chlorophyll (mg/g)		Sugar (mg/g)		K^+:Na^+
Genotype	0 mM	75 mM	0 mM	75 mM	75 mM
ITMI-6	2.10	2.01	0.58	0.60	1.35
ITMI-8	2.11	1.47	0.37	1.85	1.23
ITMI-12	1.27	1.31	2.74	2.98	0.65
ITMI-13	1.00	0.95	0.93	1.45	0.65
ITMI-3	1.20	0.99	3.10	3.12	1.61
ITMI-4	1.50	0.31	0.48	0.49	0.69
ITMI-7	1.30	0.53	1.30	1.40	0.79
ITMI-11	1.00	0.71	1.29	1.50	1.00
ITMI-17	1.50	1.10	0.98	1.21	0.73
ITMI-18	1.50	1.50	1.09	1.82	0.53
ITMI-21	1.54	1.10	1.32	1.40	1.03
ITMI-25	1.46	1.13	0.86	0.93	0.78
ITMI-27	1.30	1.13	0.94	1.16	0.83
ITMI-28	1.50	1.13	0.90	0.97	0.64
ITMI-32	1.50	1.47	1.84	2.41	0.64
ITMI-36	1.50	1.45	0.67	0.76	0.94
ITMI-39	0.87	0.84	1.12	1.45	0.35
ITMI-40	1.50	1.36	0.80	0.87	0.72
ITMI-41	2.00	1.36	0.51	0.71	1.28
ITMI-44	0.70	0.73	0.50	0.51	1.77
ITMI-45	1.30	1.54	0.84	0.80	1.01
ITMI-46	1.70	1.00	0.93	1.45	0.57
ITMI-50	1.20	1.07	1.12	1.69	2.60
ITMI-52	1.20	1.20	0.94	0.97	2.69
ITMI-66	0.72	0.49	1.07	1.14	0.60
ITMI-67	0.70	0.39	0.46	0.55	0.59
ITMI-72	0.50	0.57	0.84	1.23	0.93
ITMI-75	0.52	0.45	0.66	1.06	1.37
ITMI-77	0.69	0.63	0.60	0.26	1.04
ITMI-78	1.98	1.84	0.71	0.75	0.72
ITMI-82	3.06	1.62	0.72	0.74	0.76
ITMI-84	2.38	0.75	1.14	1.22	0.28
ITMI-85	1.66	0.56	0.79	0.91	0.34
ITMI-86	0.98	0.95	0.53	1.10	0.56
ITMI-88	1.32	1.20	0.98	1.11	0.41
ITMI-91	0.91	0.63	1.28	1.39	0.33
ITMI-92	1.30	0.75	0.86	1.61	0.38
ITMI-94	1.48	1.90	0.96	0.99	0.54
ITMI-96	1.24	1.09	0.62	0.64	0.71
ITMI-97	2.11	1.93	0.93	1.08	0.48
ITMI-98	1.49	0.56	0.80	1.01	0.45
ITMI-99	0.77	0.72	1.00	1.20	0.46
ITMI-101	0.68	0.60	0.74	0.86	0.36
ITMI-79	1.05	0.85	1.22	0.93	1.02
ITMI-81	0.78	0.55	0.47	0.63	0.72
ITMI-116	0.70	0.59	1.22	1.24	0.64
ITMI-85	0.78	0.67	0.45	0.53	1.49
ITMI-14	0.35	0.14	0.48	3.03	0.37
ITMI-16	0.84	0.25	0.28	0.97	0.39
ITMI-47	0.74	0.33	0.32	0.85	0.36
ITMI-49	0.74	0.19	2.11	2.31	0.42
ITMI-54	0.78	0.29	0.97	1.14	0.33
ITMI-57	0.71	0.33	0.97	0.99	0.54
ITMI-58	0.71	0.27	0.95	0.97	0.36
ITMI-59	0.89	0.29	0.85	1.03	0.35
ITMI-60	0.83	0.42	1.46	1.63	0.53

Shoot fresh weight also decreased under salt stress. The largest shoot fresh weight was observed in ITMI-66 (0.32 g), followed by ITMI-11 (0.30 g) and ITMI-3 (0.28 g). ITMI-96 (0.12 g), ITMI-50 (0.14 g) and ITMI-29 (0.15 g) had the lowest shoot fresh weight values. Shoot fresh weight was higher in the control condition (0.09–0.70 g) and reduced in saline (0.1–0.5 g). The skewness of shoot fresh weight in the RIL population was 1.29 in saline and 1.57 in nonsaline conditions. Skewness at saline conditions was higher than the mean with a positive value and smaller in the controlled condition. Heritability for shoot fresh weight in the control was 0.89 and 0.88 at salt stress (Table 109, pp. 240-241).

Root fresh weight was the maximum in ITMI-67 (0.14 g), ITMI-28 (0.13 g), and ITMI-14 (0.08 g) and the minimum in ITMI-80 (0.02 g) and ITMI-20 (0.01 g). Shoot dry weight and root dry weight also decreased under stress.

Root fresh weight was higher in the control (0.01–0.67 g) and reduced in saline conditions (0.01–0.26 g). The skewness of root fresh weight in the RIL population was 1.70 in saline and 3.52 in nonsaline conditions. The skewness for shoot fresh weight in saline conditions was low with a positive value and higher in the control. Heritability for shoot fresh weight in the control was 0.33 and at salt stress was –0.25 (Table 109, pp. 240-241).

The largest root dry weight was found in ITMI-52 (0.02 g) and ITMI-77 (0.011 g) and lowest in ITMI-95 (0.002 g) and ITMI-34 (0.003 g). All other RILs had intermediate values for each attribute. Root dry weight decreased significantly in stressed conditions. In the controlled condition, root dry weight was 0.004–0.014 g and 0.004–0.001 g in stress conditions. Skewness in population was 0.70 in saline and 0.57 in non-saline conditions. The skewness value was higher in saline conditions (0.70) than in the control (0.57). Heritability was 0.82

Table 107. Mean values for chlorophyll, sugar, and K^+:Na^+ discrimination 97 lines of ITMI population

Genotype	Chlorophyll (mg/g)		Sugar (mg/g)		K^+:Na^+
	0 mM	75 mM	0 mM	75 mM	75 mM
ITMI-62	0.57	0.52	0.77	0.87	0.41
ITMI-70	0.71	0.69	0.63	0.86	0.33
ITMI-73	0.84	0.82	1.99	2.06	0.27
ITMI-74	0.87	0.87	1.14	1.24	0.42
ITMI-81	0.78	0.76	2.15	2.39	0.31
ITMI-87	1.21	0.94	1.22	1.29	0.43
ITMI-15	1.14	1.06	2.16	2.20	0.53
ITMI-103	1.10	1.06	0.63	0.80	0.39
ITMI-95	1.03	0.96	1.02	1.54	0.35
ITMI-31	1.35	1.24	0.79	1.44	0.52
ITMI-35	0.94	0.89	0.47	1.02	0.47
ITMI-9	0.87	0.84	0.61	0.68	0.63
ITMI-20	0.93	0.86	0.53	0.61	0.69
ITMI-110	1.10	1.02	0.72	0.92	1.00
ITMI-105	1.48	1.18	0.66	0.97	0.38
ITMI-26	1.33	1.25	0.89	0.92	0.57
ITMI-24	0.88	0.65	0.54	0.57	0.73
ITMI-55	1.00	0.87	0.86	1.50	0.74
ITMI-61	0.89	0.94	0.48	0.49	0.46
ITMI-63	1.29	0.66	0.59	0.70	0.39
ITMI-68	1.57	0.83	0.58	0.59	1.02
ITMI-90	1.11	0.87	0.73	0.78	0.57
ITMI-93	1.76	0.87	0.77	0.78	0.69
ITMI-33	1.02	0.67	0.58	0.62	0.79
ITMI-1	1.32	0.73	1.13	1.17	0.57
ITMI-89	1.15	1.05	1.64	1.67	0.81
ITMI-34	1.52	1.25	2.92	3.61	0.82
ITMI-144	1.49	0.50	1.49	2.08	0.77
ITMI-104	2.07	0.56	1.83	2.12	0.86
ITMI-2	1.34	0.62	0.80	0.83	1.18
ITMI-121	1.16	0.83	0.99	1.04	0.80
ITMI-55	1.48	0.90	0.71	1.37	1.37
ITMI-51	2.33	0.62	1.68	1.97	1.35
ITMI-122	1.11	1.35	1.69	1.96	1.11
ITMI-56	0.99	1.03	0.87	1.42	1.49
ITMI-69	1.53	1.38	0.8	0.92	0.91
ITMI-29	1.97	1.92	1.09	1.71	0.7
ITMI-19	1.85	1.10	1.95	2.06	1.37
ITMI-76	1.96	0.82	2.00	2.25	1.51
ITMI-26	1.23	1.17	1.88	2.23	1.13

Table 108. Analysis of variance summaries (mean squares) of shoot length (cm), root length (cm), shoot fresh weight (g), root fresh weight (g), shoot dry weight (g), and root dry weight (g) of the 97 RILs fo the ITMI mapping population grown at two salinity levels, 0 mM and 75 mM NaCl (* = significant).

Source of variation	Degrees of freedom	Shoot length (g)	Root length (g)	Shoot fresh weight (g)	Root fresh weight (g)	Shoot dry weight (g)	Root dry weight (g)
Treatment	1	1,006.63*	108.022*	0.192*	0.061*	0.002*	1.614*
Variety	96	107.91*	16.9071*	0.043*	0.016*	2.593*	6.307*
Treatment x Variety	96	7.44	1.929	0.007*	0.004*	1.803*	4.4869*
Error	777	10.78	2.416	0.003	0.001	4.297	1.039

Table 109. Mean values for the 97 RILs of the ITMI population for shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight.

	Shoot length (cm)		Root length (cm)		Shoot fresh weight (g)		Root fresh weight (g)		Shoot dry weight (g)		Root dry weight (g)	
Genotype	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM
ITMI-6	24.6	22.9	3.7	4.2	0.28	0.25	0.11	0.07	0.025	0.01	0.09	0.01
ITMI-8	26.1	22.7	5.8	7.6	0.25	0.21	0.11	0.06	0.020	0.01	0.01	0.01
ITMI-12	30.0	25.5	5.7	6.4	0.30	0.20	0.04	0.03	0.03	0.02	0.01	0.01
ITMI-13	28.1	26.7	4.6	4.7	0.26	0.24	0.04	0.03	0.02	0.01	0.004	0.01
ITMI-3	29.9	28.0	5.9	9.4	0.50	0.41	0.11	0.07	0.04	0.03	0.01	0.009
ITMI-4	27.8	25.1	3.7	4.7	0.32	0.23	0.06	0.07	0.02	0.01	0.007	0.003
ITMI-7	28.5	26.1	3.2	7.5	0.41	0.28	0.10	0.09	0.04	0.03	0.01	0.005
ITMI-11	25.5	24.4	5.9	6.5	0.40	0.30	0.11	0.06	0.03	0.02	0.01	0.01
ITMI-17	29.0	26.6	5.6	6.0	0.27	0.26	0.11	0.09	0.03	0.02	0.01	0.008
ITMI-18	29.0	26.6	5.4	6.0	0.33	0.27	0.10	0.09	0.03	0.02	0.01	0.005
ITMI-21	24.0	23.4	5.2	5.0	0.29	0.25	0.11	0.10	0.02	0.01	0.01	0.01
ITMI-25	27.0	24.2	7.0	7.0	0.39	0.30	0.15	0.13	0.04	0.02	0.01	0.01
ITMI-27	29.0	25.7	3.7	4.0	0.33	0.25	0.18	0.09	0.03	0.01	0.01	0.01
ITMI-28	25.8	21.8	5.2	5.2	0.43	0.30	0.18	0.13	0.02	0.01	0.01	0.01
ITMI-32	30.0	28.7	4.6	6.0	0.34	0.28	0.18	0.16	0.02	0.01	0.01	0.008
ITMI-36	24.0	20.8	6.0	6.0	0.37	0.26	0.19	0.12	0.02	0.01	0.01	0.01
ITMI-39	25.9	25.8	5.4	6.0	0.28	0.18	0.11	0.04	0.02	0.01	0.008	0.01
ITMI-40	27.9	25.6	4.7	5.1	0.34	0.19	0.17	0.04	0.03	0.02	0.01	0.004
ITMI-41	22.5	21.5	5.3	5.8	0.18	0.15	0.13	0.02	0.03	0.02	0.008	0.001
ITMI-44	25.2	22.9	4.0	4.2	0.21	0.17	0.03	0.01	0.03	0.02	0.01	0.01
ITMI-45	24.6	23.0	3.0	3.4	0.18	0.12	0.02	0.02	0.03	0.01	0.01	0.02
ITMI-46	27.2	18.6	5.2	4.8	0.20	0.23	0.02	0.01	0.03	0.01	0.009	0.02
ITMI-50	19.8	18.4	4.3	4.4	0.18	0.14	0.02	0.01	0.02	0.01	0.01	0.004
ITMI-52	24.7	17.0	4.3	4.4	0.17	0.22	0.04	0.03	0.03	0.02	0.02	0.02
ITMI-66	20.2	19.0	6.3	6.6	0.53	0.32	0.19	0.09	0.03	0.01	0.01	0.004
ITMI-67	26.8	25.1	4.3	6.0	0.25	0.27	0.20	0.14	0.02	0.01	0.01	0.01
ITMI-72	26.2	24.4	4.3	4.7	0.23	0.18	0.18	0.08	0.02	0.01	0.01	0.01
ITMI-75	22.0	21.0	2.8	3.8	0.18	0.15	0.09	0.06	0.02	0.01	0.006	0.01
ITMI-77	22.8	19.0	4.6	5.2	0.17	0.15	0.11	0.05	0.02	0.02	0.02	0.01
ITMI-78	28.7	26.5	3.6	4.0	0.29	0.25	0.02	0.01	0.03	0.02	0.02	0.01
ITMI-80	24.6	23.6	2.6	3.6	0.20	0.16	0.02	0.01	0.03	0.02	0.01	0.01
ITMI-82	24.3	22.2	4.6	4.6	0.16	0.17	0.02	0.01	0.02	0.02	0.01	0.004
ITMI-84	25.5	22.9	5.2	5.6	0.19	0.14	0.02	0.01	0.02	0.02	0.01	0.01
ITMI-85	26.1	26.0	3.3	3.9	0.26	0.19	0.03	0.01	0.03	0.01	0.01	0.005
ITMI-86	28.4	28.1	4.4	4.8	0.28	0.23	0.03	0.02	0.03	0.02	0.01	0.01
ITMI-88	24.3	20.0	4.5	5.3	0.23	0.17	0.04	0.03	0.03	0.02	0.01	0.01
ITMI-91	22.7	20.2	5.3	5.9	0.20	0.14	0.04	0.03	0.02	0.01	0.01	0.01
ITMI-92	19.1	17.6	2.8	3.1	0.14	0.13	0.01	0.02	0.021	0.01	0.004	0.01
ITMI-94	23.7	22.1	3.0	3.6	0.20	0.19	0.04	0.03	0.02	0.02	0.01	0.005
ITMI-96	20.0	19.5	3.2	2.5	0.12	0.12	0.02	0.01	0.01	0.02	0.01	0.005
ITMI-97	20.7	19.9	2.7	4.3	0.20	0.14	0.04	0.02	0.02	0.03	0.01	0.004
ITMI-98	27.2	26.5	2.5	4.8	0.20	0.15	0.02	0.03	0.02	0.02	0.01	0.01
ITMI-99	26.6	24.0	5.1	5.4	0.17	0.17	0.03	0.02	0.03	0.02	0.01	0.005
ITMI-101	22.3	22.2	2.4	2.6	0.16	0.13	0.02	0.01	0.01	0.02	0.01	0.01
ITMI-79	16.2	13.7	2.3	2.8	0.14	0.22	0.06	0.04	0.02	0.02	0.01	0.01
ITMI-81	13.7	12.7	3.02	3.9	0.16	0.11	0.04	0.03	0.02	0.02	0.01	0.01
ITMI-116	16.5	14.9	2.0	2.7	0.16	0.16	0.03	0.02	0.01	0.02	0.004	0.01
ITMI-85	16.6	16.4	3.3	3.6	0.17	0.14	0.04	0.03	0.02	0.03	0.01	0.01
ITMI-14	21.4	18.8	4.8	4.3	0.16	0.14	0.03	0.02	0.03	0.01	0.01	0.01
ITMI-16	20.9	19.7	4.5	5.0	0.13	0.12	0.04	0.03	0.02	0.02	0.01	0.01
ITMI-47	23.0	18.4	4.5	4.3	0.14	0.12	0.04	0.02	0.03	0.02	0.01	0.01
ITMI-49	21.4	19.2	5.0	5.5	0.15	0.12	0.10	0.09	0.02	0.01	0.01	0.01

Table 109. Mean values for the 97 RILs of the ITMI population for shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, and root dry weight.

	Shoot length (cm)		Root length (cm)		Shoot fresh weight (g)		Root fresh weight (g)		Shoot dry weight (g)		Root dry weight (g)	
Genotype	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM	0 mM	75 mM
ITMI-54	21.1	20.5	2.0	2.4	0.14	0.11	0.02	0.01	0.02	0.02	0.01	0.01
ITMI-57	25.5	23.8	2.9	3.4	0.12	0.20	0.05	0.04	0.03	0.02	0.01	0.01
ITMI-58	24.1	19.9	2.2	2.7	0.14	0.14	0.03	0.02	0.02	0.02	0.01	0.01
ITMI-59	19.3	18.9	2.1	3.1	0.15	0.13	0.02	0.01	0.01	0.03	0.01	0.01
ITMI-60	18.3	12.8	3.6	4.6	0.15	0.15	0.04	0.03	0.02	0.02	0.01	0.01
ITMI-62	22.1	18.1	4.2	5.2	0.16	0.17	0.07	0.05	0.03	0.02	0.01	0.01
ITMI-70	23.4	21.1	4.0	5.1	0.22	0.16	0.06	0.05	0.02	0.02	0.01	0.01
ITMI-73	21.1	20.3	3.8	4.0	0.16	0.13	0.04	0.03	0.01	0.03	0.004	0.01
ITMI-74	21.8	21.3	2.9	3.9	0.15	0.22	0.05	0.04	0.01	0.03	0.005	0.01
ITMI-81	21.5	20.5	3.6	4.4	0.13	0.13	0.08	0.06	0.01	0.02	0.01	0.01
ITMI-87	24.3	23.1	4.6	6.2	0.22	0.23	0.06	0.04	0.05	0.01	0.01	0.01
ITMI-15	19.8	18.0	3.0	3.1	0.32	0.29	0.11	0.08	0.05	0.03	0.02	0.01
ITMI-103	19.9	18.7	2.6	2.9	0.15	0.15	0.04	0.02	0.01	0.01	0.005	0.01
ITMI-95	18.2	15.1	1.2	1.4	0.15	0.18	0.03	0.01	0.03	0.02	0.01	0.002
ITMI-31	23.6	21.1	3.1	5.2	0.24	0.22	0.07	0.06	0.02	0.04	0.01	0.01
ITMI-35	22.8	20.8	2.8	3.8	0.29	0.25	0.10	0.08	0.02	0.02	0.01	0.01
ITMI-9	22.4	21.4	3.6	4.0	0.18	0.28	0.05	0.04	0.02	0.02	0.01	0.02
ITMI-20	21.2	19.3	3.7	4.1	0.15	0.12	0.05	0.04	0.02	0.02	0.004	0.01
ITMI-110	20.2	18.0	1.3	4.2	0.17	0.15	0.04	0.03	0.02	0.02	0.01	0.05
ITMI-105	19.3	15.8	2.7	4.1	0.14	0.19	0.07	0.03	0.02	0.03	0.005	0.01
ITMI-26	20.0	18.7	2.8	3.2	0.16	0.15	0.06	0.05	0.02	0.01	0.01	0.01
ITMI-24	20.9	19.8	2.8	3.2	0.17	0.13	0.06	0.05	0.01	0.02	0.007	0.01
ITMI-55	23.6	21.8	4.1	4.0	0.23	0.20	0.06	0.04	0.02	0.02	0.005	0.01
ITMI-61	23.7	22	3.9	4.4	0.21	0.24	0.08	0.07	0.02	0.02	0.005	0.01
ITMI-63	19.8	18.8	3.1	3.7	0.19	0.16	0.06	0.04	0.02	0.01	0.006	0.01
ITMI-68	25.2	23.6	3.3	3.8	0.23	0.22	0.07	0.06	0.04	0.04	0.005	0.01
ITMI-90	22.5	21.7	2.8	4.3	0.21	0.12	0.10	0.04	0.02	0.01	0.01	0.005
ITMI-93	23.0	22.2	2.8	6.1	0.23	0.22	0.06	0.05	0.02	0.02	0.08	0.01
ITMI-33	20.4	19.4	4.2	5.5	0.13	0.21	0.17	0.03	0.02	0.02	0.01	0.01
ITMI-1	24.0	23.0	2.0	3.4	0.14	0.13	0.05	0.06	0.02	0.03	0.01	0.01
ITMI-89	20.4	17.6	2.9	2.8	0.14	0.14	0.05	0.03	0.02	0.01	0.01	0.01
ITMI-34	21.8	17.4	2.7	2.3	0.16	0.12	0.07	0.04	0.02	0.02	0.01	0.003
ITMI-144	19.0	18.2	1.5	1.2	0.13	0.13	0.04	0.02	0.02	0.01	0.005	0.004
ITMI-104	26.6	23.6	2.3	4.9	0.13	0.17	0.02	0.02	0.02	0.02	0.01	0.004
ITMI-2	19.7	18.7	2.4	2.9	0.21	0.15	0.07	0.05	0.01	0.02	0.003	0.01
ITMI-121	23.5	20.2	2.5	3.6	0.24	0.15	0.07	0.04	0.02	0.02	0.004	0.01
ITMI-55	23.0	20.1	3.8	4.5	0.16	0.15	0.02	0.01	0.03	0.02	0.01	0.004
ITMI-51	18.8	17.3	1.6	3.3	0.13	0.12	0.03	0.02	0.02	0.01	0.005	0.004
ITMI-122	23.3	22.2	2.2	1.3	0.22	0.16	0.05	0.08	0.02	0.02	0.01	0.01
ITMI-56	27.9	19.4	3.0	3.2	0.17	0.14	0.06	0.09	0.02	0.01	0.01	0.01
ITMI-69	26.9	22.8	2.1	2.3	0.31	0.29	0.12	0.10	0.02	0.02	0.01	0.01
ITMI-29	21.2	21.5	2.3	2.7	0.24	0.28	0.07	0.06	0.02	0.02	0.01	0.01
ITMI-19	20.2	19.8	1.7	2.9	0.16	0.24	0.07	0.06	0.02	0.01	0.01	0.005
ITMI-76	22.6	22.4	5.2	4.1	0.23	0.19	0.06	0.05	0.02	0.02	0.01	0.01
ITMI-26	25.2	25.7	2.0	2.4	0.19	0.17	0.06	0.08	0.02	0.02	0.01	0.01

in control and 0.27 at salt stress condition (Table 109, pp. 240-241).

Of the 97 RILs, ITMI-3, ITMI-17, and ITMI-32 performed better with respect to morphological, physiological, and biochemical attributes. Lines ITMI-85, ITMI-90, and ITMI-66 did not perform with good results with respect to biomass production, morphological, physiological, and biochemical attributes, thus, they were not salt tolerant.

Total chlorophyll also decreased in the population. Line ITMI-6 has the highest chlorophyll content and ITMI-3 the lowest. The reduction in chlorophyll content is to be expected under stress. Being membrane bound, chlorophyll stability dependends on membrane stability, which under saline condition seldom remains intact. In this study, the minimum reduction in chlorophyll content was observed in ITMI-3, ITMI-32, and ITMI-17 and, because of this positive response, these lines are tolerant.

The ITMI population was subjected to salt stress of 75mM NaCl and highly significant differences among the RILs were found for all the morpho-physiological traits studied. At salt stress conditions, the K^+:Na^+ ratio decreases. Salinity tolerance in wheat is associated with the accumulation of K^+ and exclusion of Na^+ under saline conditions. In our study, a similar percent decrease in the K^+:Na^+ ratio was found. Genotype ITMI-1 has the highest K^+:Na^+ ratio and ITMI-21 has the lowest.

During salt stress, an increase in sugar concentration has been reported in many species. Sugar might contribute to salt stress tolerance either by serving as osmotic or as respiratory substrate. High sugar under salt stress prevents plants from oxidative damage and maintains the structure of different proteins and membranes. Similar behavior was observed in tje population with an increase of sugar content in ITMI-17 and ITMI-32, thus showing their tolerant behavior, whereas ITMI-3 showed less sugar content under salt stress.

Table 110. Mean values for plant height, spike length, number of grains/spike, number of spikelets/spike, and 1,000–kernel weight for 97 RILs of the ITMI mapping population (not pubescent (–) or pubescent (+)).

Entry (ITMI–)	Pubes-cence	Plant height (cm)	Spike length (cm)	Grains/ spike	Spikelets/ spike	1,000-kernel weight (g)
1	–	110.0	11.2	26	20	34.2
2	–	97.0	11.9	32	22	28.7
3	+	103.9	12.0	54	18	35.5
4	+	103.9	11.3	32	21	35.4
6	–	102.8	11.2	43	18	29.9
7	+	99.4	9.8	21	17	27.7
8	+	86.9	10.1	22	19	20.1
9	+	90.9	10.4	26	18	30.9
11	+	93.1	10.6	45	17	30.5
12	–	115.1	11.35	42	17	36.7
13	+	89.6	10.0	37	18	36.9
14	+	97.6	10.1	26	19	32.6
16	–	86.9	8.1	29	17	29.5
17	–	84.5	8.0	52	17	34.9
18	–	97.0	10.5	50	16	37.0
19	+	97.5	10.3	48	18	35.9
20	+	97.0	9.86	27	17	36.0
21	+	104.0	9.75	38	19	35.9
22	+	101.8	9.8	50	21	41.0
24	+	103.7	10.0	26	18	40.8
25	+	104.9	10.9	27	19	44.6
26	+	98.0	9.3	26	16	39.7
27	+	96.8	10.1	34	17	35.8
28	–	75.0	9.1	43	17	33.9
29	+	77.6	9.6	47	19	37.0
31	+	97.5	12.9	38	22	40.0
32	–	92.3	11.1	42	23	42.3
33	+	88.1	10.1	45	23	36.8
34	+	93.4	9.9	19	23	37.4
35	+	95.1	10.7	34	18	36.5
36	+	86.6	10.5	27	18	35.3
39	–	77.3	10.3	36	18	44.6
40	–	94.3	9.3	45	18	40.5
41	–	89.6	10.8	52	18	33.2
44	+	84.5	10.6	50	20	33.3
45	–	78.0	10.1	49	17	30.6
46	+	116.1	9.6	39	17	43.0
47	+	113.7	9.7	20	18	41.6
49	+	85.3	9.4	29	18	32.7
50	+	81.9	8.3	43	17	34.9
51	+	94.0	10.6	43	17	31.4
52	–	92.3	9.3	52	16	43.6
53	+	93.1	9.6	50	17	43.2
54	+	90.0	8.3	26	18	29.6
55	+	81.4	9.1	25	18	39.3

Salinity reduced the dry weight of roots and shoots by 52.5% and 60.6%, respectively, for plant grown on sand soil compared with those grown in clay soil. On the other hand, the dry weight of roots and shoots decreased by about 24% and 21%, respectively, due to salinity compared with the control treatment. ITMI-3 and ITMI-32 showed the least dry biomass and, on this basis, were considered tolerant. Salinity inhibits the growth of many plants.

Shoot fresh weight and root fresh weight are generally retarded with elevated salinity in wheat. ITMI-3, ITMI-17 and ITMI-32 showed a minimal reduction in their fresh biomass. Increasing the concentration of NaCl significantly reduces plant growth. This reduction in root and shoot fresh weight is due to less uptake of essential nutrients.

in vitro studies indicate that ITMI-77, ITMI-8, ITMI-6, ITMI-50, ITMI-51. ITMI-117, ITMI-21, ITMI-75, ITMI-44, and ITMI-3 performed well, especially with reference to K^+:Na^+ discrimination.

Phenotypic evaluation. Morphological characters of selected ITMI lines were assessed phenotypically (Table 110, pp. 242-243).

Plant height (cm). Moderate plant height is good for a crop because it makes the mechanical operations easy and also reduces the chances of loss from lodging. The value for plant height ranged from 55.1 cm to 116.1 cm. Maximum height was observed ITMI-46 and the minimum was in ITMI-120.

Pubescence. Data for pubescence were taken using hand lens by observing hairs on the base of spikes, i.e., the peduncle. Pubescence was scored as absent (–) or present (+). Most lines were pubescent (+).

Table 110. Mean values for plant height, spike length, number of grains/spike, number of spikelets/spike, and 1,000–kernel weight for 97 RILs of the ITMI mapping population (not pubescent (–) or pubescent (+)).

Entry (ITMI–)	Pubes-cence	Plant height (cm)	Spike length (cm)	Grains/ spike	Spikelets/ spike	1,000-kernel weight (g)
56	+	94.8	11.0	27	18	41.7
57	–	107.9	11.4	29	18	41.6
58	–	110.1	11.6	30	19	39.9
59	+	104.4	13.8	35	20	38.8
60	+	101.0	13.1	32	20	42.4
61	+	97.0	9.0	22	16	41.1
62	+	90.4	7.8	29	17	32.5
63	+	91.4	9.3	28	17	41.9
66	+	95.4	10.4	27	15	42.6
67	+	103.8	11.8	18	21	48.8
68	+	98.6	12.1	46	21	49.1
69	+	98.8	11.5	33	20	47.3
70	+	99.4	12.1	36	18	44.8
72	+	87.3	10.5	32	17	38.1
73	+	108.6	9.6	19	17	38.5
74	+	99.4	11.4	40	18	39.0
75	+	103.6	11.1	42	17	47.5
76	+	94.3	8.3	39	17	45.4
77	–	107.9	8.8	36	15	38.8
78	+	97.9	10.2	29	20	39.5
79	+	93.3	11.5	35	19	36.9
80	–	96.5	11.5	44	20	40.9
81	+	91.5	11.3	51	19	48.3
82	+	93.2	10.4	50	20	37.5
83	+	85.8	8.3	52	20	33.8
84	–	80.0	9.0	38	18	34.2
85	+	82.7	11.4	33	21	35.3
86	+	82.4	10.9	27	18	40.2
87	+	88.6	7.4	47	17	35.7
88	+	103.5	11.8	32	18	40.3
89	+	83.0	7.0	28	18	39.3
90	+	83.6	8.4	44	17	42.4
91	+	70.9	8.4	46	20	31.5
92	–	97.4	12.4	36	19	37.1
93	–	96.7	11.9	39	18	40.4
94	+	65.2	8.2	45	18	29.3
95	+	70.6	12.4	32	18	22.5
96	+	68.6	10.5	36	14	23.3
97	+	66.3	8.8	27	14	33.2
98	+	85.1	10.5	20	23	34.1
99	+	86.4	11.0	34	21	35.9
101	+	85.3	8.4	50	19	36.8
103	+	90.8	8.3	29	19	38.7
104	+	93.1	11.1	26	19	34.0
105	–	92.0	10.8	38	20	31.9
110	+	87.8	11.0	30	19	32.0
117	–	80.7	10.3	29	23	38.6
120	+	55.1	10.7	32	20	40.6
121	+	64.0	10.1	44	20	35.6
122	+	85.3	12.9	39	19	38.3
144	–	85.5	11.5	30	21	36.6

Spike length. Spike length was measured in centimeters and ranged from 7.0 cm to 13.8 cm. Lines ITMI-17, ITMI-62, and ITMI-87 had the shortest and ITMI-59 (13.8 cm) had the longest spikes.

Number of grains/spike. The data for number of grains/spike ranged from 15 to 54. Line ITMI-3 had the maximum number and line ITMI-18 the least; this was a great range of variation.

Number of spikelets/spike. The number of spikelets/spike in ITMI RIL population ranged from 15 to 23. Genotypes with long spikes had a greater number. Lines ITMI-32, ITMI-33, ITMI-98, and ITMI-117 had the maximum number.

1,000-kernel weight. Grain weight is major component of seed yield. For each entry, 1,000-kernel weight was calculated, and it ranged from 20.1 to 49.1 g. Line ITMI-68 was very good and useful in wheat breeding. The above mentioned genotypes are suggested as agronomically good with high yield potential. This morphological analysis showed that there is maximum diversity among the ITMI population.

Physiological characterization of ten selected lines. The top ten lines, ITMI-77, ITMI-8, ITMI-6, ITMI-50, ITMI-51, ITMI-117, ITMI-21, ITMI-75, ITMI-44, and ITMI-3, were selected on the basis of their performance on K^+:Na^+ discrimination levels (Table 111, p. 246). The maximum shoot length was in ITMI-3 (25.06 cm) and the minimum was in ITMI-117 (14.94 cm). The greatest root length was found in ITMI-3 (5.9 cm), followed by ITMI-8, ITMI-50, and ITMI-6. The largest shoot fresh weight was 0.28 g in ITMI-3 and lowest, at 0.12 g, was found in ITMI-50 and ITMI-51.

Root fresh weight under salt stresss among the top 10 lines was found highest in ITMI-6 (0.07 g) and 0.01 g at control conditions, indicating that root fresh weight decreased at high salinity levels (Table 111). Chlorophyll content ranged from 2.01 to 0.42. The highest amount of chlorophyll was found in ITMI-6 (2.01) and the lowest in ITMI-33 (0.42). Sugar content increased at 75 mM NaCl in the top 10 tolerant lines, ranging from 0.51 to 3.72. The lowest sugar content was detected in ITMI-44 and the highest in ITMI-3, followed by ITMI-51, ITMI-8, ITMI-50, ITMI-21, and ITMI-117. Among top ten lines, the K+/Na+ ratio ranged from 2.69 to 1.03. The highest range of K^+:Na^+ was found to be 2.69 (ITMI-51) followed by ITMI-50, ITMI-44, and ITMI-75.

Table 111. Mean evaluation of morphological parameters of top 10 tolerant RILs in the ITMI Mapping Population at 0 mM and 75 mM NaCl.

	Shoot length (cm)		Root length (cm)		Shoot fresh weight (g)		Root fresh weight (g)		
Genotype	**0 mM**	**75 mM**	**0 mM**	**75 mM**	**0 mM**	**75 mM**	**0 mM**	**75 mM**	
ITMI-77	19.82	18.82	3.72	3.12	0.19	0.16	0.06	0.04	
ITMI-8	26.10	22.78	7.60	5.84	0.25	0.21	0.11	0.06	
ITMI-6	24.600	22.92	4.20	3.70	0.28	0.25	0.11	0.07	
ITMI-50	20.92	19.78	5.08	4.50	0.13	0.12	0.04	0.03	
ITMI-51	23.04	18.40	4.38	3.20	0.15	0.12	0.04	0.03	
ITMI-117	16.52	14.94	2.70	2.02	0.16	0.15	0.03	0.02	
ITMI-21	24.62	23.08	3.44	3.06	0.18	0.12	0.02	0.01	
ITMI-75	23.62	21.84	4.08	3.14	0.23	0.20	0.06	0.04	
ITMI-44	22.34	20.20	2.66	2.42	0.16	0.13	0.02	0.01	
ITMI-3	29.96	25.06	9.42	5.90	0.50	0.28	0.11	0.60	
	Shoot dry weight (g)		**Root dry weight (g)**		**Chlorophyll (mg/g)**		**Sugar (g)**		
Genotype	**0 mM**	**75 mM**	**0 mM**	**75 mM**	**0 mM**	**75 mM**	**0 mM**	**75 mM**	**K^+:Na^+**
ITMI-77	0.02	0.01	0.01	0.008	0.69	0.63	0.60	0.76	1.04
ITMI-8	0.02	0.10	0.01	0.009	2.11	1.48	0.37	1.85	1.23
ITMI-6	0.02	0.01	0.01	0.008	2.11	2.01	0.50	0.68	1.35
ITMI-50	0.02	0.02	0.01	0.009	1.23	1.07	1.12	1.69	2.60
ITMI-51	0.03	0.02	0.01	0.010	2.33	0.62	1.68	1.97	2.69
ITMI-117	0.02	0.01	0.01	0.008	0.78	0.67	1.22	1.24	1.61
ITMI-21	0.03	0.20	0.01	0.017	1.54	1.19	1.32	1.40	1.03
ITMI-75	0.02	0.10	0.01	0.008	0.52	0.45	0.66	1.06	1.70
ITMI-44	0.02	0.10	0.01	0.007	0.73	0.73	0.50	0.51	1.77

The best top lines were then subjected to higher salinity level, 100 mM NaCl, and tested for protein, proline, and sodium oxide dismutase (SOD) levels (Table 112). Superoxide dismutase increased under stress condition, the value ranging from 80.47 to 28.86, in ITMI-8 and ITMI-77, respectively. The highest SOD value was in ITMI-8, followed by ITMI-51, ITMI-50, ITMI-6, ITMI-117, ITMI-3, ITMI-75, ITMI-21, ITMI-44, and ITMI-77. Similarly the proline and protein content also increased under stress conditions. Among all the lines, the best proline content was found in ITMI-3 (1,164.1) and the highest protein content was recorded in ITMI-8. K^+:Na^+ ranged from 1.00 to 1.69, where the highest value was observed in ITMI-51, followed by ITMI-50, ITMI-3, ITMI-75, ITMI-44, and ITMI-6. The performance of top ten selected lines was checked at both 75 mM and 100 mM salinity levels. The overall performance of the ten lines was found to ITMI-3, ITMI-22, ITMI-25, ITMI-31, ITMI-52, ITMI-59, ITMI-68, and ITMI-81.

Table 112. Mean evaluation of physiological parameters of top 10 tolerant lines at 100 mM NaCl (SOD = superoxide dismutase).

Genotype	SOD	Protein	Proline	SDW	K^+:Na^+
ITMI-77	28.863	951.562	951.562	0.019	1.000
ITMI-8	80.471	820.369	820.369	0.026	1.060
ITMI-6	60.510	166.067	166.067	0.016	1.110
ITMI-50	63.275	1,150.842	1,150.842	0.022	1.500
ITMI-51	64.314	345.419	345.419	0.016	1.690
ITMI-117	56.176	255.743	255.743	0.028	1.090
ITMI-21	32.392	114.586	114.586	0.019	1.000
ITMI-75	40.000	1,081.094	1,081.094	0.022	1.210
ITMI-44	29.235	242.457	242.457	0.020	1.120
ITMI-3	49.392	1,164.127	1,164.127	0.017	1.220

Estimating genetic diversity in the ITIM Mapping Population. SSR markers (*Xwmc-304*, *Xwmc-179*, *Xwmc-18*, *Xwmc-134*, *Xwmc-134*, *Xwmc-141*, *Xwmc-154*, *Xwmc-160*, *Xwmc-11*, *Xwmc-116*, and *Xwmc-84*) were used to assess the genetic diversity among the ten tolerant genotypes of the ITMI Mapping Population. All the SSR markers gave clear and polymorphic bands. The range of the bands was 100–800 bp. Genetic diversity of top 10 salinity-tolerant genotypes was estimated from a dendrogram and similarity matrix. Dendrogram and similarity matrix were constructed using amplification (bivariate 1–0) data generated by SSR primers.

Dendrogram. In the dendrogram, genotypes are grouped on the basis of their genetic similarities and differences, using UPGMA. Based on their genetic distance, the clustering pattern of the 10 wheat genotypes is divided into three main clusters A, B and C (Fig. 42). The dendrogram reveals that these ten genotypes are genetically diverse from each other. Among these genotypes, ITMI-21 is most diverse, not forming any cluster with any other genotype. Cluster A had four genotypes, ITMI-3, ITMI-51, ITMI-8, and ITMI-77. Out of these four, ITMI-77 is the more diverse and ITMI-3 and ITMI-51 had about 80% genetic similarity or 20% genetic diversity. The other main cluster (cluster B) contained five genotypes, ITMI-6, ITMI-44, ITMI-75, ITMI-50, and ITMI-17. Among these five genotypes, ITMI-6 is more diverse than other four genotypes. Although ITMI-44/ITMI-75 and ITMI-50/ITMI-17 showed the maximum genetic similarity of 80% or 20% genetic diversity.

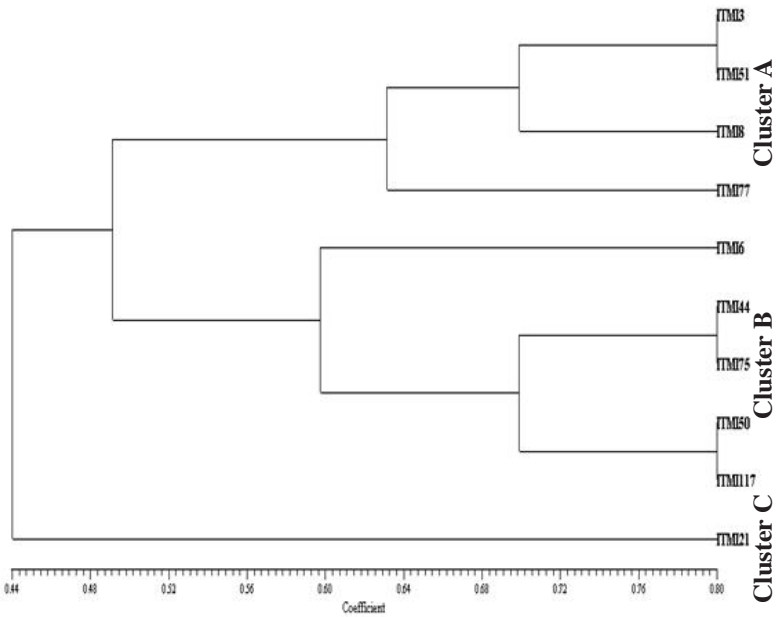

Fig 42. A dendrogram of 10 tolerant genotypes from the ITMI Mapping Population based on SSR markers.

Similarity matrix. A similarity matrix of top 10 lines based upon Nei and Li's similarity coefficient gives the degree of similarity among the genotypes (Table 113). Values range from 1–0, for which 1 represents 100% similarity and 0 represents 100% genetic diversity/distance. Ten microsatellite loci were used for this purpose. The range of genetic similarity was 20–80% among these genotypes. Maximum similarity was observed between ITMI-3 and ITMI-51, ITMI-44 and ITMI-75, and ITMI-50 and ITMI-17, and the minimum similarity and maximum genetic diversity was observed between ITMI-21 and ITMI-77.

Table 113. Similarity matrix among ten tolerant genotypes from the ITMI Mapping Population based on SSR markers

	3	6	8	21	44	50	51	75	77	117
3	1.00									
6	0.40	1.00								
8	0.60	0.40	1.00							
21	0.70	0.50	0.30	1.00						
44	0.60	0.60	0.60	0.30	1.00					
50	0.50	0.50	0.50	0.40	0.70	1.00				
51	0.80	0.40	0.80	0.50	0.60	0.50	1.00			
75	0.60	0.60	0.60	0.50	0.80	0.70	0.60	1.00		
77	0.50	0.30	0.70	0.20	0.70	0.60	0.70	0.50	1.00	
117	0.50	0.70	0.30	0.60	0.70	0.80	0.30	0.70	0.40	1.00

Conclusion. The salt tolerance potential of germ plasm was determined using the in vitro evaluation parameter K^+:Na^+ discrimination. The entire ITMI Mapping Population of 97 lines was subjected to hydroponic tests at 75 mol/m^3 NaCl, phenotypic characterization, and a molecular diversity estimation. For salinity tolerance, genotypes ITMI-51, ITMI-50, ITMI-75, and ITMI-44 were found to be most tolerant to salinity with high K^+:Na^+ values. In addition, ITMI-3, ITMI-8, and ITMI-6 were found to be tolerant because they show better performance for chlorophyll, sugar, shoot length, shoot fresh weight, root fresh weight, and dry mass.

A phenotypic study of the material revealed that ITMI-3, ITMI-22, ITMI-25, ITMI-31, ITMI-52, ITMI-59, ITMI-68, and ITMI-81 had good performance for plant height, grains/spike, spikelets/spike, spike length, and grain weight (Table 114). On the other hand, genotype ITMI-68 showed the highest grain weight (Table 114).

Table 114. Evaluation of phenological parameters of the top eight lines (pubescence; – (absent) or + (present)).

Entry	Pubescence	Plant height (cm)	Spike length (cm)	Grains/spike	Spikelets/spike	1,000-kernel weight (g)
ITMI-3	+	103.9	12.0	54	18	35.5
ITMI-22	+	101.8	9.8	50	21	41.0
ITMI-25	+	104.9	10.9	27	19	44.6
ITMI-31	+	97.5	12.9	38	22	40.0
ITMI-52	–	92.3	9.3	52	16	43.6
ITMI-59	+	104.4	13.8	35	20	38.8
ITMI-68	+	98.6	12.1	46	21	49.1
ITMI-81	+	91.5	11.3	51	19	48.3

From present study, we found that this experimental material provides a good source of tolerance to salinity and is agronomically good with a high level of genetic diversity, which is a prerequisite of any crop improvement program. We conclude, therefore, that this ITMI Mapping Population is a valuable source for genetic improvement of wheat for salinity tolerance.

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Optimization of high throughput DNA extraction from fresh leaf tissues of wheat for PCR assay.

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We have checked various protocols and their modifications that were developed and used to isolate quality DNA from wheat in the past (Murray and Thompson 1980; Dellaporta et al. 1983; Saghai-Maroof et al. 1984; Rogers and Bendich 1985; Doyle and Doyle 1990; Suman et al. 1999; Warude et al. 2003; Sarwat et al. 2006; Deshmukh et al. 2007). Three reported protocols (Na-bisulphite, CTAB, and SDS) were used (with some modifications) to isolate and analyze DNA from *T. aestivum* using fresh and dried leaf samples. The basic aim was to optimize a protocol that may be rapid and inexpensive with high quality and throughput.

The DNA isolated using various extraction protocols was compared from preparation in terms of quantity and quality. The DNA obtained was not of sufficient quantity, and the quality was very poor, especially in case of dried leaf tissues in all the tested protocols. The preparations (including DNA) in the test tubes were highly viscous and dirty brown in color, which showed no or very faint bands (or smears of the bands) upon gel electrophoresis and there were no amplification products after PCR analysis. However, the results from the modified CTAB buffer method were encouraging and were far better than the rest of the tested protocols especially in case of fresh leaf tissue without liquid nitrogen. We have stopped further testing for the protocols except CTAB procedure. The modified CTAB buffer method of genomic DNA extraction from fresh leaf tissues of *T. aestivum* as further tested and refined to compare its efficiency in terms of quantity and quality of the DNA for various tissue types. The DNA concentration was measured in a spectrophotometer (UV/VIS), and an absorbance, i.e., A260/A280 ratio of 1.3, was obtained indicating high levels of contaminated proteins and polysaccharides. Total DNA isolated from fresh leaves and dried-seed powder of T. aestivum was checked by means of agarose gel electrophoresis. High-molecular-weight DNA of larger quantities and of good quality was obtained from fresh leaves without using liquid nitrogen and dried seed samples (Figs. 1 and 2). The purity of the DNA samples was confirmed by absorbance (A260/A280) ratio, which was 1.8.

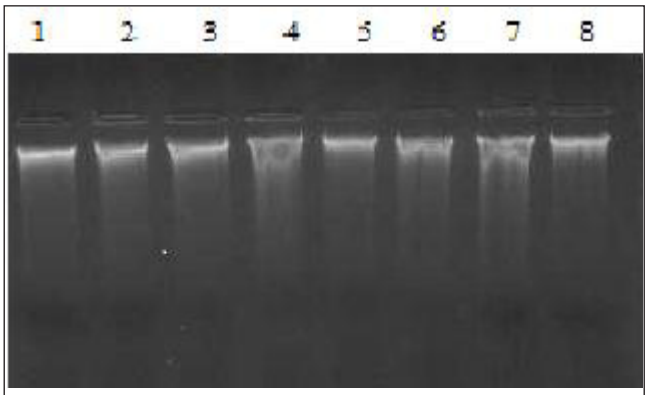

Fig. 1. Ethidium bromide-stained, agarose gel showing total DNA isolated from eight samples of fresh leaf tissue of *Triticum aestivum*.

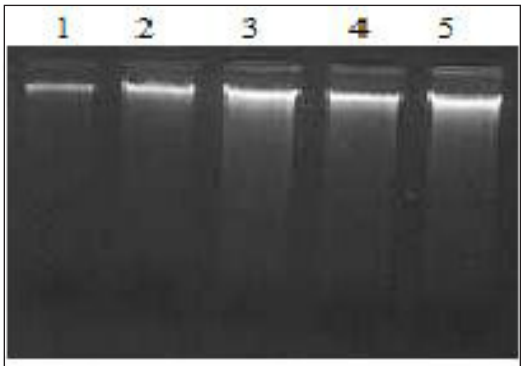

Fig. 2. Ethidium bromide-stained, agarose gel showing total DNA isolated from five samples of fresh leaves of *Triticum aestivum*.

DNA isolation is a primary and critical step for molecular analysis of any plant species. This process becomes even more difficult when the plant species contain high amounts of secondary metabolites and essential oils. These compounds are considered to be as contaminants that cause DNA degradation during preparation and therefore the extraction of genomic DNA from this plant is difficult. Polyvinylpyrrolidone (PVP), a compound known to suppress polyphenolic oxidation, has been used frequently in CTAB extraction protocols (Doyle and Doyle 1990). The modified CTAB buffer containing PVP was also employed to extract DNA from *T. aestivum* using liquid nitrogen (Hills and Van Staden 2002). However, Schneerman et al. (2002) reported that this compound did not significantly increase the yield or prevent contamination of the DNA. SDS-based extraction buffer is being used to break open the cells and isolate DNA, but the quality of DNA obtained is questioned due to precipitation of polysaccharides and proteins. In addition, the SDS might not bind with the proteins in the purification step, thus degrading the extracted DNA (Aljanabi et al. 1999; Deshmukh et al. 2007). Because SDS and

isoamylalcohol methods did not give significant results in either type of leaf tissues that we tested in the case of *T. aestivum*, it is hard to make any conclusive comments on their efficacy or effectiveness. However, the use of PVP in CTAB buffer did not improve the yield or quality rather we obtained significantly better results without its use in our experiment of DNA extraction.

Most of the protocols that we tested recommend extraction of DNA from fresh tissue, but for some areas of the world, the chemicals and resources that are routinely used in many protocols are too expensive to be used for routine DNA extraction. Therefore, it was necessary to establish an inexpensive and less time-consuming protocol for optimizing DNA extraction from fresh leaves of *T. aestivum*. We anticipate that this protocol will be adequate for extracting high-molecular-weight DNA from other species containing large amounts of secondary metabolites and essential oils.

The genetic characterization for improvement of cereals, including wheat, can be achieved by the use of molecular markers only if there is an efficient, rapid ,and less cost effective method of DNA extraction is available. To isolate high-quality DNA from leaf tissue of *T. aestivum*, various standard protocols were tested and modified. For DNA analysis, fresh and dried samples of wheat leaves were used. The DNA obtained from fresh-leaf tissue with a modified cetyltrimethylammonium bromide (CTAB) buffer protocol was of good quality, with no colored pigments or contaminants. We were able to obtain good quality DNA from fresh leaf tissue without using liquid nitrogen. A relatively large amount of DNA also was extracted from the dried tissue, but its quality was not as good as that from fresh leaves. The DNA extracted from fresh leaves was successfully amplified by PCR using STS markers. The same protocol will probably be useful for extracting high-molecular-weight DNA from other plant materials containing large amounts of secondary metabolites and essential oils.

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ITEMS FROM POLAND

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On variability of the weedy characteristics in a model grass, Brachypodium distachyon.

R. Kosina, B. Kłyk, and M. Florek.

At present, *Brachypodium distachyon* is known as an invasive weed in various world regions, e.g., South Africa, California, and Australia. Weedy plants exhibit special traits permitting their quick reproduction and dispersal. According to the description of weediness made by Ammann et al. (2000) and Basu et al. (2004), one can ascribe to the *B. distachyon* plant the following characteristics of weediness:

– germination in various habitats (rocky and sandy, podsol, and fertile),
– quick growth of seedling (several days),
– longevity of seed (we noted a good germination after 28 years of seed storage at room temperatures),
– a short period between vegetative and sexual phases (2–4 weeks, varuing for different types (Fig. 1A)),
– self-compatibility with possibility of chasmogamy (for some accessions we documented chasmogamy),
– adaptation to unspecialized pollinators (wind for chasmogamy),
– a large amount of seed produced (~40 seeds from one raceme spike, depending on the number of spikelets/spike), and
– the possibility of short and long dispersal (heavy diaspores and zoochory).

Some weed characteristics are not exhibited by *B. distachyon*. The plants do not produce seeds continuously. In the Kosina collection of 25 accessions, various forms are cultivated (Fig. 1). Some lines express a rigid spikelet rachilla (Fig. 1D), which is typical for cultivated forms, others have hairy spikelets adapted for zoochory. This mostly autogamic species creates its own population, which are composed of various pure lines. Many autogamic grasses, such as *Anisantha sterilis* (Green et al. 2001) or *Avena barbata* (Florek 2008) have similar microevolutionary potential. For such a breeding status, the selection can be very effective. Examples of various weedy characteristics of *B. distachyon* are provided (Fig. 1).

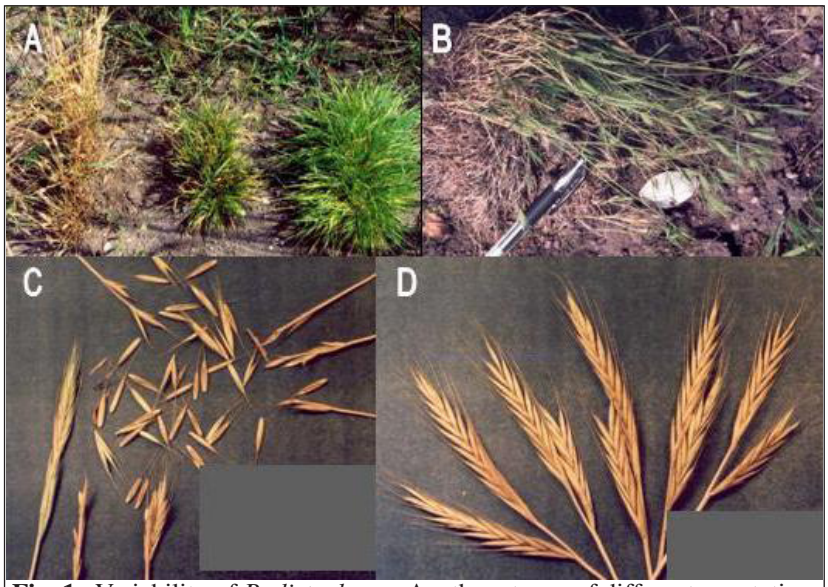

Fig. 1. Variability of *B. distachyon*. A – three types of different vegetation period (from the left, early, middle, and late); B – a tuft of grass with fertile spikelets during the second year of cultivation; C – a weedy type with a fragile rachilla; and D – a semi-cultural form with a rigid rachilla. According to Kłyk (2005).

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On wheat and Brachypodium distachyon caryopsis.

R. Kosina and P. Tomaszewska.

A wheat grain has some specific properties that can be used as a discriminatory tool in cereal taxonomy and in grain processing. The caryopsis is covered by several cell layers of the pericarp and is thicker in threshable wheats and thinner in unthreshable ones. The nucellar epidermis is highly reduced and joined with outer testa, which is sometimes distinctly suberinized. The aleurone is most often composed of single layer of proteinaceous cells (Fig. 2A), however, rarely, one can note different development of this tissue in the form of two or more layers of such cells (Fig. 2B). Starchy endosperm is composed of starch granules, the large, A type, and small, B type (Fig. 2C). Filling of endosperm cavity by starch can be considered as a spectacular developmental phenomenon (Fig. 2D); it is rare and was observed in *T. turgidum* subsps *durum* and *polonicum* or *T. aestivum* (Kosina 1979). The creation of the cavity is dependent on relations between development of outer parts of caryopsis and rate of starch synthesis. Transfer tissues (vascular bundle, pigment strand, nucellar projection), no doubt, play an important role here.

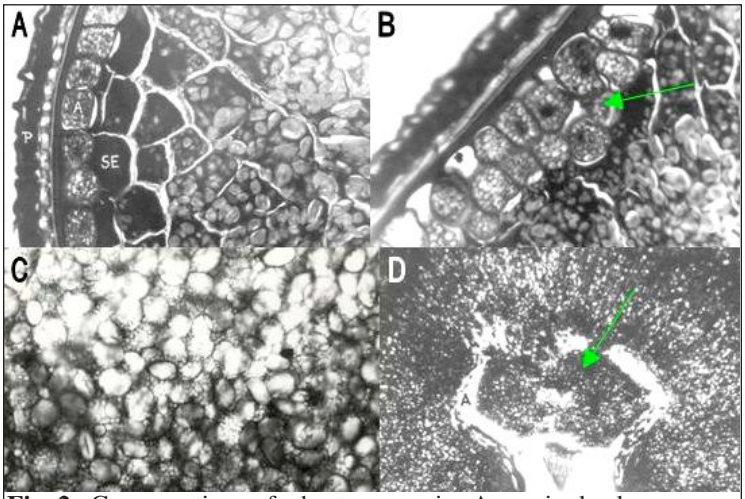

Fig. 2. Cross-sections of wheat caryopsis. A – a single aleurone layer (A) and distinct high-protein subaleurone endosperm (SE); B – two-layered aleurone (arrow); and C – starch grains of two sizes; D – an endosperm cavity filled by starch (arrow). A,B,D according to Kosina (1979).

Brachypodium distachyon is considered as a relative to Triticeae cereals, and its grain presents the same general pattern of development. However, the nucellar epidermis is extremely thick in this species when compared to other species of *Brachypodium* (Fig. 3A, yellow arrow). This thick layer is digested during seed germination . Within the system of transfer tissues, the vascular bundle is almost invisible and no cavity is created above the aleurone layer in a shallow crease (Fig. 3A, white arrow). The endosperm tissue is poorly filled with starch. Starchy cells also have thick walls decomposed along with starch during the seedling growth (Fig. 3B). All starch granules are of single type. The aleurone exemplified in Fig. 3B is formed by one layer of cells, but quite often this tissue is composed of 2–3 layers. Digestion of hemicelluloses of nucellar epidermis and starchy cell walls is slower than that of starch, and it is probably a trait characteristic for a wild grass.

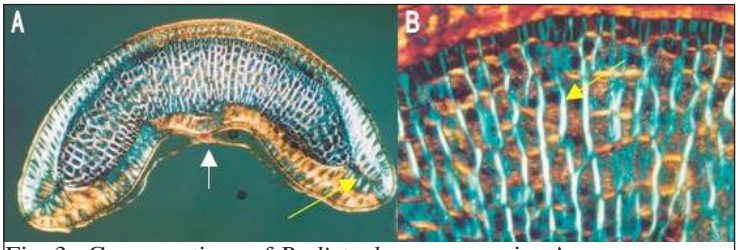

Fig. 3. Cross-sections of *B. distachyon* caryopsis. A – a poor system of transfer tissues (white arrow) and thick nucellar epidermis (yellow arrow) and B – a dorsal endosperm thick cell walls (arrow) and starch granules of one size.

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Microstructural differentiation in Brachypodium distachyon and its relatives – a case of the lemma.

R. Kosina and B. Kłyk.

Arithmetic average is the most common statistical method used to describe any unit in agronomy or biology. However, in fact other measures are of the same rank from the scientific point of view, such as variation of a given character and covariation of characters and its statistics coefficient of correlation and regression parameters. For the same set of *Brachypodium* OTUs (*B. distachyon*, *B. sylvaticum*, *B. retusum*, *B. pinnatum*, and *B. phoenicoides*) described by traits of abaxial epidermis of the lemma, the following statistics were calculated: arithmetic average, median, min-max values, coefficient of variation, coefficients of correlation, parameters of equation of regression (linear or curvilinear), and parameters of regression variation. Arrangements of the OTUs within an ordination space (nonmetric multidimensional scaling) were different for each group of parameters. The main conclusion is that each group of statistics is of equal value and independent for OTU characterization. For instance, arithmetic averages discriminated a *B. sylvaticum* group from other taxa quite well (Fig. 4). When using coefficients of correlation to characterize the OTUs, we obtained completely different arrangement of species (Fig. 5). Two accessions of *B. distachyon* are especially remarkable in this respect. They occupy two extreme points in the ordination space. Such a sharp intraspecific difference in traits interrelations is probably caused by genetic variation created among pure lines of this autogamic species.

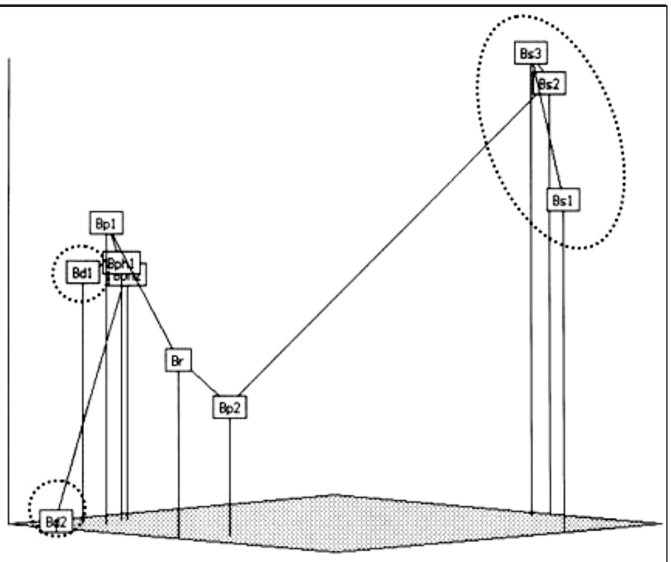

Fig. 4. A minimum spanning tree of *Brachypodium* OTUs in a nonmetric multidimensional scaling ordination space. OTUs are described by arithmetic averages. *B. sylvaticum* (Bs) and *B. distachyon* (Bd) are outlined (*B. retusum* (Br), *B. pinnatum* (Bp), and *B. phoenicoides* (Bph)).

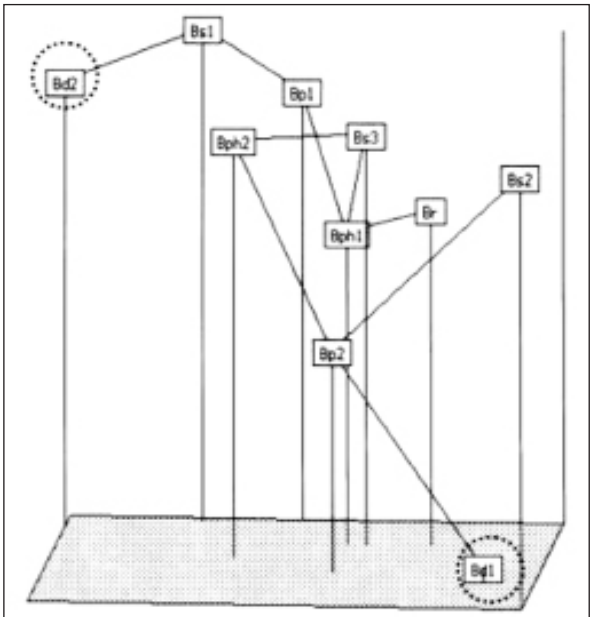

Fig. 5. A minimum spanning tree of *Brachypodium* OTUs in a nonmetric multidimensional scaling ordination space. OTUs are described by Pearson's coefficients of correlation. Accessions of *B. distachyon* (Bd) are outlined (*B. sylvaticum* (Bs), *B. retusum* (Br), *B. pinnatum* (Bp), and *B. phoenicoides* (Bph)).

Reproduction in Brachypodium distachyon and related species.

R. Kosina and B. Kłyk.

Differentiation of the mating system within a range of auto- and allogamy exists among species of the genus *Brachypodium*. Our study was made for accessions of the species *B. pinnatum*, *B. phoenicoides*, *B. sylvaticum*, *B. retusum*, and the model grass, *B. distachyon*. Morphometric analysis of the male structures proved that in *Brachypodium* two patterns of anther development were observed:

– long anthers with a large amount of small pollen grains in allogamic units and
– short anthers with a small amount of large pollen grains in autogamic units.

The OTUs of these two breeding patterns are well discriminated within an ordination space (Fig. 6, p. 251). *Brachypodium pinnatum* appeared as the most allogamic species. Others, such as *B. phoenicoides* and *B. sylvaticum*, are in the intermediate position between allo- and autogamy. Accessions of the model grass, *B. distachyon*, are in a distinct position in the diagram, which is described by smallest values of ordination axes. Distances between these accessions

are small; however, some chasmogamy, typical for allogamy, was also observed.

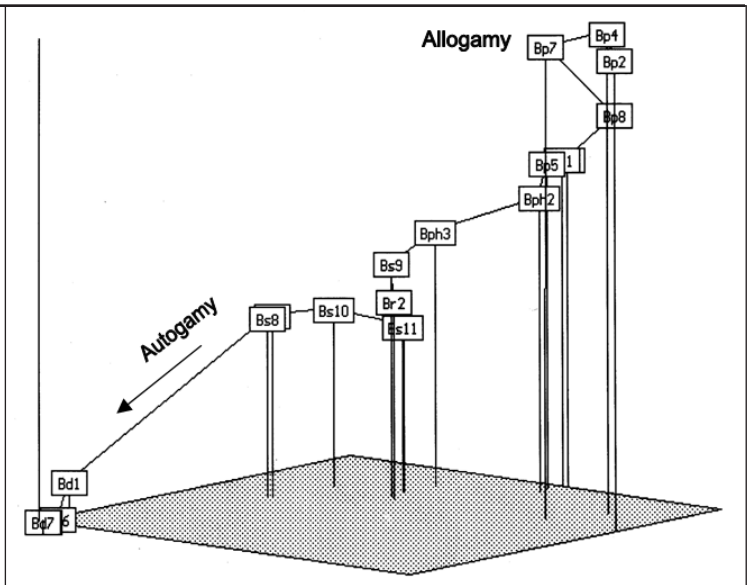

Fig. 6. A minimum spanning tree (mean taxonomic distance, nonmetric multi-dimensional scaling) of *Brachypodium* accessions described by traits of the mating system (*B. distachyon* (Bd), *B. sylvaticum* (Bs), *B. retusum* (Br), *B. pinnatum* (Bp), and *B. phoenicoides* (Bps)).

Nucleolar variation in Brachypodium distachyon.

R. Kosina and B. Kłyk.

An Ag-NOR technique plus DAPI staining were used for the identification of active rDNA loci. The research was conducted for root mitoses of several accessions of *B. distachyon*. Two unequal nucleoli are the most common arrangement and this suggests that two pairs of SAT chromosomes produce nucleolar proteins. Neighboring nuclei have the same nucleolar pattern, which proves the clonal nature of root nuclei. Nucleoli are mirrored in sister nuclei. Terminal Ag-NOR signals are typical for one pair of chromosomes and interstitial signals were observed in two other pairs. An important input into Ag-NOR variability is caused by association of NORs with telophase bridges. Active rDNA loci can be symmetrically located on a bridge (Fig. 7A) or a picture (Fig. 7B) can show distinct asymmetry, and Ag-NOR proteins can be stretched along a bridge. Finally, the Ag-NOR signal is included into one telophase nucleus and a sister nucleus is lacking it (Fig. 7C). The presented data prove an extreme cytogenetic potential existing in the species.

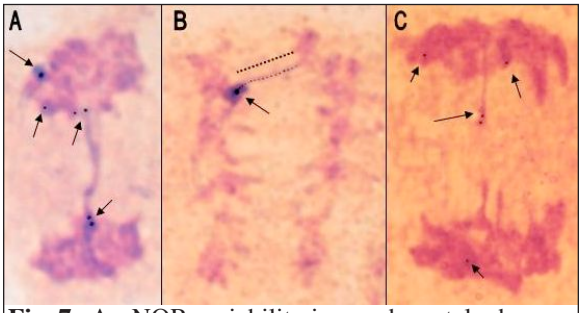

Fig. 7. Ag-NOR variability in anaphase-telophase nuclei of *B. distachyon*. Ag-NOR loci are pointed by arrows or a broken line A – telophase nuclei with an Ag-NOR bridge, B – an anaphase with a 'NOR-bridge', and C – a telophase with asymmetry of Ag-NOR signals.

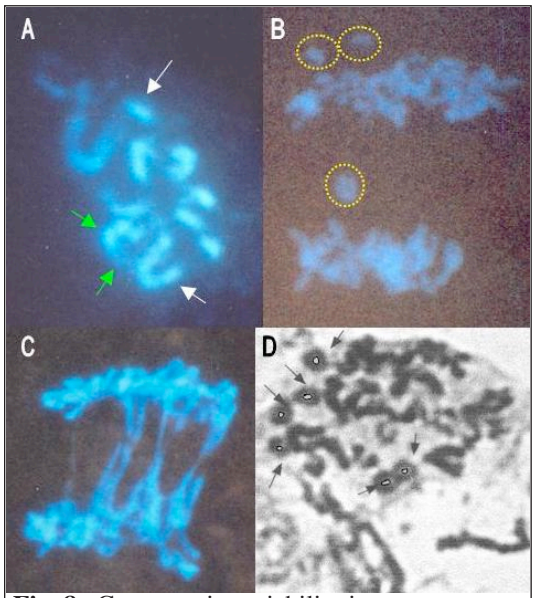

Fig. 8. Cytogenetic variability in *Brachypodium distachyon*. A – a bimodal (white arrows) and allocyclic (green arrows) karyotype; B – a telophase with laggards; C – anaphase-telophase multiple bridges; D – a late prophase with ring chromosomes (arrows).

On the cytogenetic variability in Brachypodium distachyon.

R. Kosina and B. Kłyk.

For several accessions of *B. distachyon*, DAPI karyotypes were studied. Some of them were diploid (Fig. 8A), and others were tetraploid. Many intermediate karyotypes, between 20 and 30 chromosomes, were documented. All the studied karyotypes were bimodal, composed of long, 3–4 pairs of chromosomes and short ones (Fig. 8A, white arrows). The long chromosomes appeared to be allocyclic (Fig. 8A, green arrows) with one decondensed arm. Small chromosomes have mostly strong DAPI fluorescence of an AT-rich heterochromatin. The genome of *B. distachyon* exhibited many disturbances (Fig. 8B, C, and D). There were noted laggards (Fig. 8B) and multiple bridges (Fig. 8C), sometimes numerous, associated

with rDNA and ring chromosomes (Fig. 8D, p. 252). The above-mentioned behavior creates unequal sister nuclei and their dysfunction finalized by apoptosis. This cytogenetic instability should be considered along with developmental anomaly of the grass caryopsis, which is visible in the form of mosaic of two endosperm phenotypes, starchy and aleurone cells. Both, cytogenetic and developmental anomalies suggest the activity of transposons in *B. distachyon*.

Nucleolar variability in a Triticum timopheevii subsp. timopheevii / Aegilops umbellulata amphiploid.

R. Kosina and K. Markowska.

For a '*T. timopheevii* subsp. *timopheevii* / *Aegilops umbellulata*' amphiploid and its parents, an Ag-NOR analysis in mitoses of main and lateral roots was performed. In addition, the status of Ag-nucleoli in interphase nuclei was studied in three forms of the amphiploid: control, roots from demethylated caryopses (5-azaC-I), and roots from caryopses harvested from mother plants, which were demethylated in the stadium of germinated caryopses and subsequently cultivated on plots (5-azaC-II). Polymorphism of amphiploid caryopses, light versus dark, is inherited from its paternal species. Sixty types of nucleoli arrangement were noted in the amphiploid (Fig. 9). The largest number of types is expressed in main roots from dark caryopses for the 5-azaC-II treatment. The NOR-activity of two unequal pairs of SAT-chromosomes is most probable in all the studied forms. Nucleoli of these two pairs can join independently giving two bodies of unequal size or nucleoli of two different chromosomes can be merged and two equal bodies are visible. These two types of nucleoli arrangement are most common in all studied plants. The number of nucleoli is within a range of 1–7, which means that in the amphiploid, some parental Ag-NOR loci are suppressed. Demethylation changes frequency of the most common type of nucleoli arrangement between the main and lateral roots when compared to the control and it is similar to the status noted for parental species.

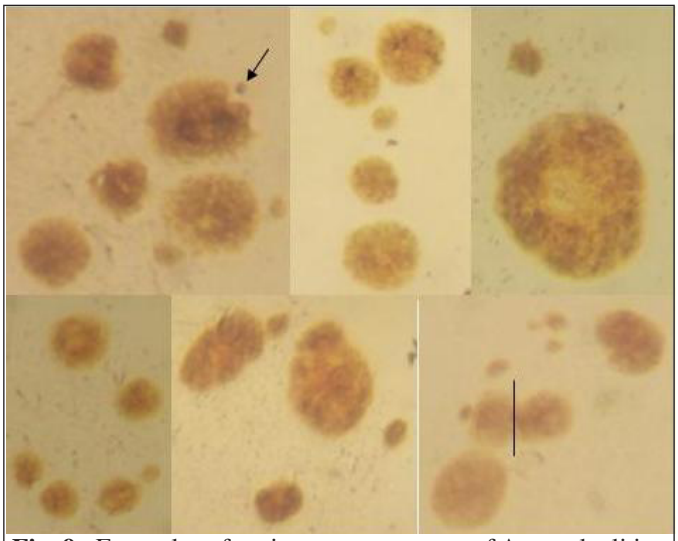

Fig. 9. Examples of various arrangements of Ag-nucleoli in the main roots of dark caryopses of the '*T. timopheevii* subsp. *timopheevii* / *Aegilops umbellulata*' amphiploid (5-azaC-II).

Lodicule micromorphology in an autogamic grass, Brachypodium distachyon.

R. Kosina and K. Pietrzak.

Grass lodicules play a decisive role in chasmogamic activity of these plants. Their structure and function is very original and complex (Kosina 2005, 2006). *Brachypodium distachyon* is, as a rule, recognized as an autogamic unit (Kłyk 2005); however, some chasmogamy was also noted for it (Kosina, unpublished

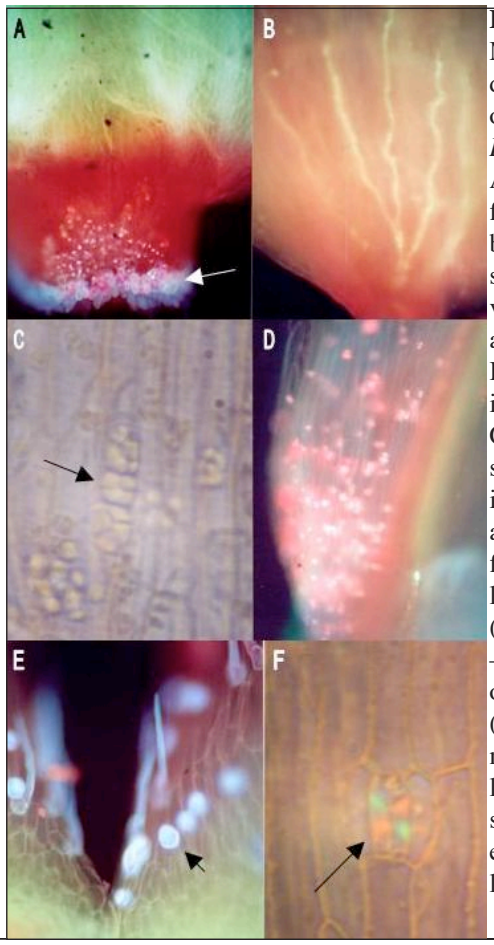

Fig. 10. Microstructural differentiation of lodicules in *B. distachyon*. A – aniline blue fluorescence of the base of lodicule showing four parts, various structurally and functionally; B – phloem veins in a cushion; C – composite starch granules in a lobe (before anthesis); D – light fluorescence of lipids in a lobe (after anthesis); E – blue fluorescence of round papillae (arrow) in two neighboring lodicules; F – a single stoma in epidermis of the lodicule lobe.

data). The description of *Brachypodium* lodicules was made by Kłyk (2005) and Pietrzak (2007). The most interesting properties of the *B. distachyon* lodicule are presented in Fig. 10 (p. 253). The lodicule is differentiated structurally and functionally along its own axis. At the base is a distinguished layer of cells with thick cellulosic walls (Fig. 10A, arrow, p. 253); however, the other parts of this organ are also differentiated developmentally, going toward the apex. In the lower part of the lodicule, a cushion, many thin phloem veins are developed (Fig. 10B, p. 253). The main metabolite in the upper part of lodicule, a lobe, are composite starch granules, which are observed before anthesis (Fig. 10C, p. 253). In addition, a lot of calcium oxalate crystals are noted around the border area cushion-lobe. After the anthesis, cells of the lobe contain many lipid globules (Fig. 10D, p. 253). In lodicules one can show some characteristics typical for leaves, such as short epidermal cells and stomata (Kosina 2010). In *B. distachyon*, short epidermal cells, such as papillae, were found (Fig. 10E, p. 253). Development of stomata in lodicules in *B. distachyon* (Fig. 10F, p. 253) is very rare. In a collection of more than 20 accessions of the species, only two expressed this trait, probably of mutational origin.

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Caryopsis microstructure in Triticum kiharae and T. fungicidum.

R. Kosina and M.K. Bureś.

Both *T. kiharae* (*T. timopheevii* subsp. *timopheevii* / *Ae. tauschii*) and *T. fungicidum* (*T. turgidum* subsp. *carthlicum* / *T. timopheevii* subsp. *timopheevii*) wheats are artificial amphiploids with highly sclerified spikes. Development of any caryopsis is dependent on the architecture of transfer tissues (nucellar projection and pigment strand) that are the main path for assimilates supplied into the endosperm. In *T. kihara*e (Fig. 11A), these tissues have larger volume and can be a better gate for assimilates. A vascular bundle is located below the pigment strand. In a ripe caryopsis, only the xylem vessels are recognizable, while phloem is obliterated. The xylem bundles have various numbers of vessels, and in *T. kiharae* it is composed of ~15 vessels, in *T. fungicidum* ~5. As a consequence of such a differentiation of transfer tissues and vascular bundle, the development of other tissues of the caryopsis is also variable. Differences are related to the nature of suberinized testa (Fig. 11 E and F, see arrows), thickness of nucellar epidermis (yellow layers) and aleurone cell shapes (stars). The ratio of starch protein is the most important parameter for wheat grain processing. This proportion is conditioned by the system of transfer tissues (Kosina 1988). Expression of a starch phenotype among aleurone cells is another

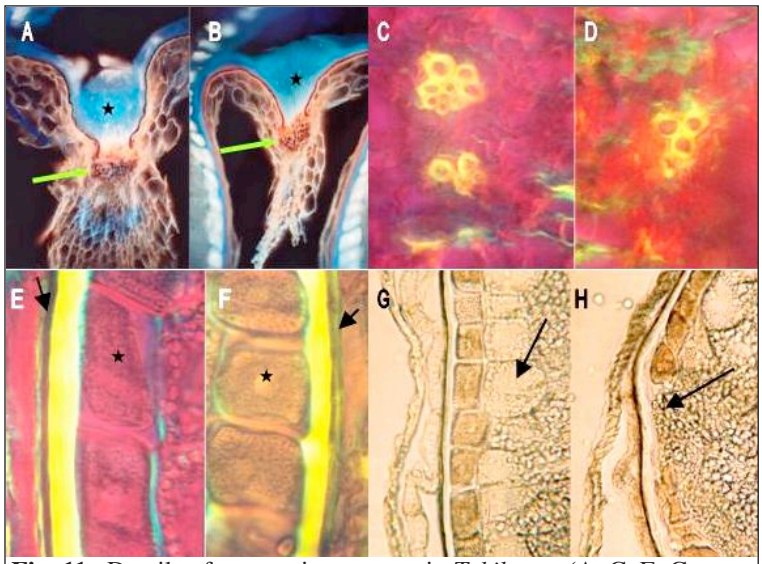

Fig. 11. Details of caryopsis structure in *T. kiharae* (A, C, E, G, and H) and *T. fungicidum* (B, D, and F). A and B – system of transfer tissues (blue nucellar projection – stars, and brown pigment strand – green arrows); C and D – xylem bundles (yellow); E and F – fragments of outer layers of caryopsis (arrows – suberized testa, yellow nucellar epidermis, stars – aleurone cells); G – high-protein subaleurone layer (arrow); and H – an island of starch cells (arrow) among aleurone cells.

observed phenomenon, which can be caused by somatic crossing-over, which is noted in grass endosperm surprisingly often (Kosina 2007).

Reference.

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Structural differentiation of embryo in the genus Brachypodium, including Brachypodium distachyon.

R. Kosina.

Measurements of scutellum, embryo axis and epiblast were used for the description of *Brachypodium* OTUs (Fig. 12). In an ordination space, embryos of *B. distachyon* are distinctly separated from other species; however, there is some overlapping of variation spheres of *B. distachyon* and *B. sylvaticum*. In the taxonomy of the genus *Brachypodium*, both species are recognized as extremes. There are even some proposals to discriminate *B. distachyon* in a separate section or a new genus *Trachynia*. *Brachypodium distachyon* is qualitatively distinguished from other species of the genus by morphology of its epiblast. In the diagram (Fig. 12), *B. distachyon*, *B. retusum*, *B. pinnatum,* and *B. phoenicoides* are at extreme points (see arrows). One can conclude that at least for some accessions, embryo characteristics well discriminate the species.

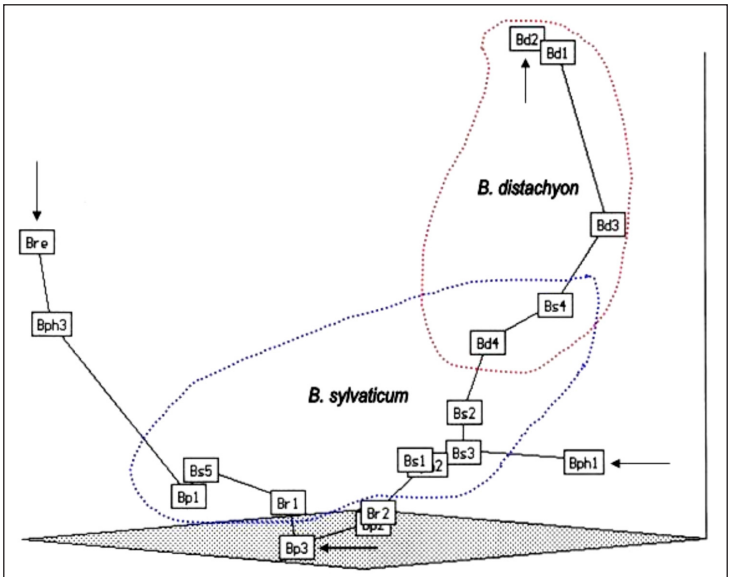

Fig. 12. A minimum spanning tree (mean taxonomic distance, non-metric multi-dimensional scaling) of *Brachypodium* accessions described by traits of the embryo (*B. distachyon* (Bd), *B. sylvaticum* (Bs), *B. retusum* (Br), *B. pinnatum* (Bp), and *B. phoenicoides* (Bph)).

Endosperm cytogenetics in 'Triticum / Aegilops tauschii' amphiploids.

R. Kosina.

Free nuclear endosperm of the amphiploids '*T. turgidum* subsp. *dicoccum* / *Ae. tauschii*', '*T. turgidum* subsp. *carthlicum* / *Ae. tauschii*', and '*T. turgidum* subsp. *turanicum* / *Ae. tauschii*' was studied by means of in vivo acridine orange fluorescence as well as by GISH and FISH methods (Kosina 1995). These forms were obtained from the Plant Germ-plasm Institute in Kyoto, Japan. Polyploidization of the syncythium was realized on two paths:

1. an increase in the volume of a given nucleus and amplification of rDNA signals in it and
2. an increase in the number of nuclei having the same number of rDNA loci.

Multiple bridges in anaphases are typical for these amphiploids. The cell cycle of groups of nuclei is synchronized

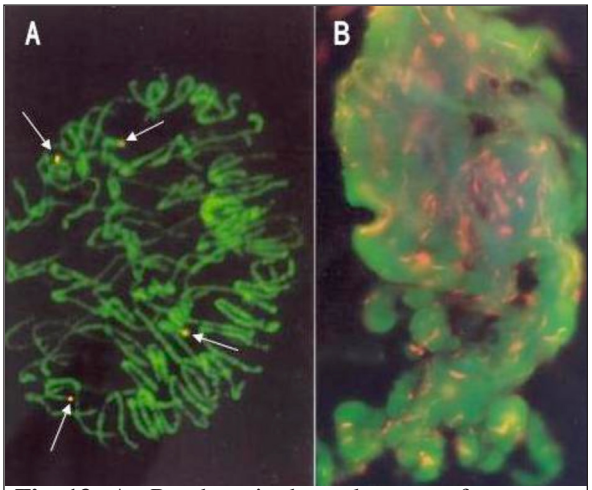

Fig. 13. A - Prophase in the endosperm of an amphiploid '*T. turgidum* subsp. *turanicum* / *Ae. tauschii*' with four rDNA loci (arrows) and B - an antipodal nuclear mass with highly amplified rDNA loci (red) in endosperm of *T. turgidum* subsp. *turanicum*.

is evidence of the clonal nature of syncythial endosperm. A karyokinetic spindle was disturbed and multipolar telophases were formed. The modal number of nucleoli was 4–6. In each nucleolus, one to several rDNA signals were observed (Fig. 13A, p. 255). Signals of rDNA were mirrored in telophase. However, some signals were also located on bridges or laggards and were lost giving an rDNA asymmetry in anaphase-telophase nuclei. The rDNA signals in a nucleolus decondense inside and outside of its body. Antipodal polytenic chromosomes create in the later stadia some nuclear masses with amplified rDNA loci, in amphiploids and in parental species (Fig. 13B, p. 255).

Reference.

Kosina R. 1995. Cytogenetyka molekularna amfiploidów: tetraploidy *Triticum* x *Aegilops squarrosa*. Sprawozdania Wrocławskiego Towarzystwa Naukowego 49B:57-60 (In Polish).

Nucleolar characteristics of endosperm in Triticeae.

R. Kosina.

Embryo sacs were excised from 3–5-day-old caryopses, and subsequently free nuclei of endosperm, were mounted on slides in acridine orange. This technique was applied for the following OTUs: *Ae. juvenalis*, an amphiploid *Triticum*/*Thinopyrum*/*Lophopyrum*, an amphiploid *Triticum*/*Aegilops*, *Critesion jubatum*, *C. bogdanii*, *C. bulbosum*, *Dasypyrum villosum*, *Elymus caninus*, *E. yezoënsis*, *E. mutabilis*, *E. hystrix*, *Elytrigia pungens*, *El. repens*, *Eremopyrum bonaepartis*, *Hordeum vulgare* subsp. *vulgare*, *H. vulgare* subsp. *spontaneum*, *Leymus arenarius*, *Lophopyrum elongatum*, *Secale sylvestre*, *S. montanum*, triticale, *T. fungicidum*, *T. kiharae*, and *T. aestivum*. The OTUs were described by 22 classes of distributions of nucleoli frequency. The best dendrogram was obtained for the Canberra distance and UPGMA clustering (Fig. 14). Diploids, such as species of *Secale* or *Dasypyrum*, presented short distribution and small variation of nucleoli contrary to some polyploid taxa located in lower position of the dendrograms. The lower cluster of the dendrograms is complex and it also contains some diploids like *H. vulgare*.

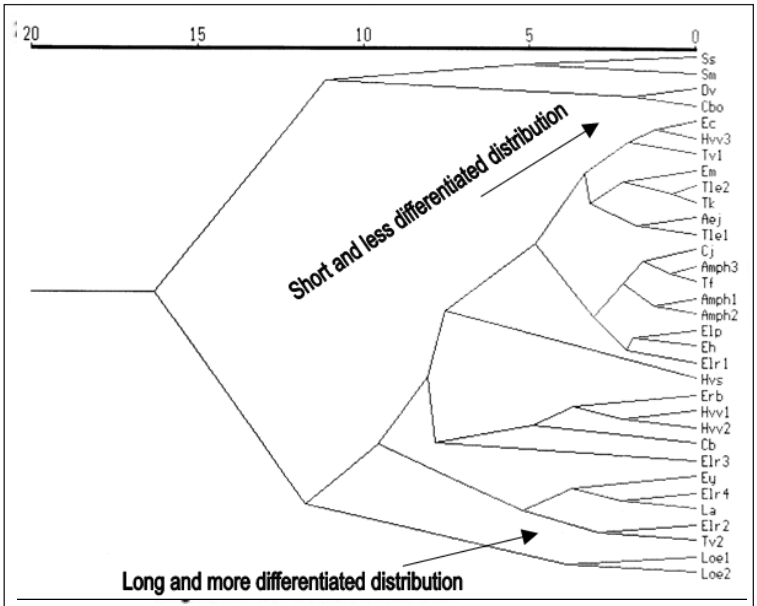

Fig. 14. A dendrogram of Triticeae OTUs characterized by distributions of nucleoli numbers in a free nuclear endosperm. *Ae. juvenalis* (Aej), an amphiploid *Triticum*/*Thinopyrum*/*Lophopyrum* (Amph1), an amphiploid *Triticum*/*Aegilops* (Amph2 and Amph3), *Critesion jubatum* (Cj), *C. bogdanii* (Cbo), *C. bulbosum* (Cb), *Dasypyrum villosum* (Dv), *Elymus caninus* (Ec), *E. yezoënsis* (Ey), *E. mutabilis* (Em), *E. hystrix* (Eh), *Elytrigia pungens* (Elp), *El. repens* (Elr1, Elr2, Elr3, and Elr4), *Eremopyrum bonaepartis* (Erb), *Hordeum vulgare* subsp. *vulgare* (Hvv1, Hvv2, and Hvv3), *H. vulgare* subsp. *spontaneum* (Hvs), *Leymus arenarius* (La), *Lophopyrum elongatum* (Loe1 and Loe2), *Secale sylvestre* (Ss), *S. montanum* (Sm), triticale (Tle1 and Tle2), *T. fungicidum* (Tf), *T. kiharae* (Tk), and *T. aestivum* (Tv1 and Tv2).

Microstructural variation in selected cereals under environmental stress.

R. Kosina.

Triticum amphiploids having genomes AAGGAA and AABBDD, and two cultivars of *Hordeum vulgare* (HV3 and HV5) and *Bromus secalinus* (BS) were cultivated in two extremely different environments: in a glasshouse with diurnal temperatures above 50°C in pots with pure sand and crucial irrigation (symbol s in Fig. 15, p. 256), and in outdoor podsol plots with diurnal temperatures of approximately 20–30°C and sufficient irrigation (symbol z in Fig. 15, p. 257).

OTUs (cereals) were described by eight characters of highly differentiated abaxial epidermis of palea and lemma as well as by four traits of lodicules. Both classes of characters (glumellae and lodicules) are well separated in den-

drograms (mean taxonomic distance, UPGMA), irrespective of their changes caused by experimental stress. In the dendrogram (Fig. 15), three groups of grasses, namely the amphiploids, *H. vulgare*, and *B. secalinus*, are distinctly separated. Appriopriate pairs (s vs. z) also are distinctly separated. Only the AGA amphiploid is differentiated more by the environmental stress. Development of the abaxial epidermis of palea and lemma was most often disturbed in amphiploids. Under drought conditions, high temperature, and starvation, the grass plant developed only one tiller with short spike or poor panicle. Tissues were highly sclerified. Under sufficient watering, the plants were often infested by fungi and setting of caryopses was defective. In conclusion, both environments can create a stress of various nature. Thus, the microstructure of cereals is shifted under heavy stress, but its general pattern is preserved. Then, this pattern can be a good basis for any taxonomic comparisons.

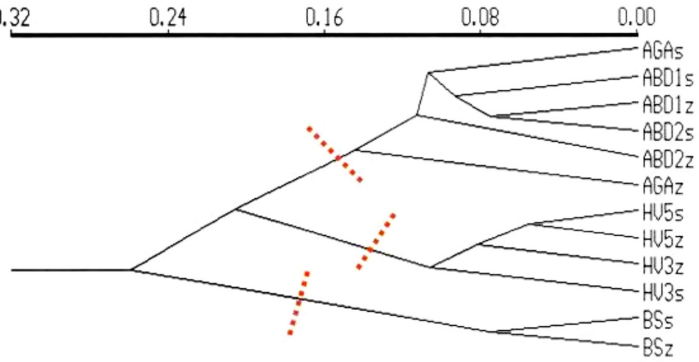

Fig. 15. A dendrogram (Canberra distance, UPGMA) of cereal OTUs described by glumellae and lodicule microstructure (*Triticum* amphiploids having genomes AAGGAA (AGA) and AABBDD (ABD1 and ABD2), and two cultivars of *Hordeum vulgare* (HV3 and HV5) and *Bromus secalinus* (BS)). Taxa are distinctly clustered (red dashed lines).

ITEMS FROM THE RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE FOR THE SOUTH-EAST REGIONS
Department of Genetics, Laboratory of Genetics and Cytology, 7 Toulaikov St., Saratov, 410010, Russian Federation.

The evaluation of spring bread wheat cultivars, NILs, and introgression lines in the hard, drought conditions of 2009–10.

S.N. Sibikeev, A.E. Druzhin, V.A. Krupnov, T.D. Golubeva, and T.V. Kalintseva.

For the recommendation of introgression lines with identified combinations of genes for resistance to pathogens in practical breeding some prebreeding research is necessary. These research includes determining resistance to abiotic stresses and bread-making qualities. The conditions of the growing periods of 2009 and 2010 allowed estimating the set of introgression lines for drought resistance. The two-year-old data for grain productivity in NILs in the extremely hard drought conditions have shown the following results. The combination of *Lr9+Lr19*-translocations in the genotypes of cultivars L503, Dobrynya, and line L2032, do not depress yielding ability, but *Lr19+Lr26* significantly improves grain productivity, and *Lr19+Lr24* and *Lr19+Lr25* significantly depresses yield ability. A neutral reaction for grain productivity in the introgression lines with substitution 6Agi (6D) is detected. The incorporation of genetic variability from *T. turgidum* subsps. *dicoccoides* and *dicoccum* to the spring bread wheat cultivars Saratovskaya 58 and Saratovskaya 55 (lines L196 and L2870) does not depress drought resistance, but incorporation of genetic variability from durum wheat (cultivars Saratovskaya zolotistaya, Lyudmila, and Saratovskaya 57) to bread wheat (lines L200/09 and L211/09), and their combination improves this trait. The NILs with combinations of translocations *Lr9+Lr19*, *Lr19+Lr24*, *Lr19+Lr25*, substitution 6Agi (6D), and also lines L196, L2870, L200/09, and L211/09 have good bread making quality at the level of cultivars. The NIL of L503 with combination of *Lr19+Lr26* translocations was exception in which the flour strength was reduced.

The evaluation of spring bread wheat introgression lines of the Genetics and Cytology Laboratory at ARISER in breeding for resistance to leaf and stem rust.

S.N. Sibikeev, A.E. Druzhin, L.I. Laikova (Institute of Cytology and Genetics, Novosibirsk, Russian Federation), D. Singh (KARI, Njoro, Kenya), and A.A. Morgounov (CIMMYT, Turkey).

In the 2010 growing season, a set of introgression lines was estimated for resistance to leaf and stem rusts on the experimental fields of the Institute of Cytology and Genetics (Academgorodok, Novosibirsk, Russia) and for resistance to race Ug99 + *Sr24* (TTKST) of stem rust in the KARI, Njoro, Kenya under natural epidemic conditions. We detected that the NILs with translocation combinations *Lr19+Lr24* and *Lr19+Lr26*, and also lines L196, L2870, L200/09, and L211/09, are resistant to leaf and stem rusts, including to Ug99. Thus, the efficiency of combinations *Lr19/Sr25+Lr24/Sr24* and *Lr19/Sr25+Lr26/Sr31* and also the unidentified leaf and stem rust genes in lines L196 and L2970 has been shown. In lines L196 and L2870, the probability is very high that the leaf and stem rust genes are linked, because during breeding of these lines, selections were conducted only for resistance to leaf rust.

The dynamics of population change Puccinia triticina at ARISER, Russian Federation, during 2008–10.

S.N. Sibikeev and A.E. Druzhin.

The climatic change in the Volga Region was all the more noticeable by its influence on the composition of the population *P. triticina*, which is considered one of the most virulent. Analysis of *P. triticina* population dynamics during 3 years (2008–10), showed that it is quite responsive to increases in air temperature. The study of leaf rust population composition was carried out in a greenhouse on NILs of Thatcher with differing *Lr* genes. Inoculations in the grenhouse were performed at the optimum temperature (20–22°C) using uridinospores that were collected in the field on susceptible cultivars of winter wheat. During 2008, the air temperature did not exceed the critical value for the pathogen (31°C) for virtually the entire season (Fig. 1); and a majority of virulent pathotypes were present in the population (Table 1).

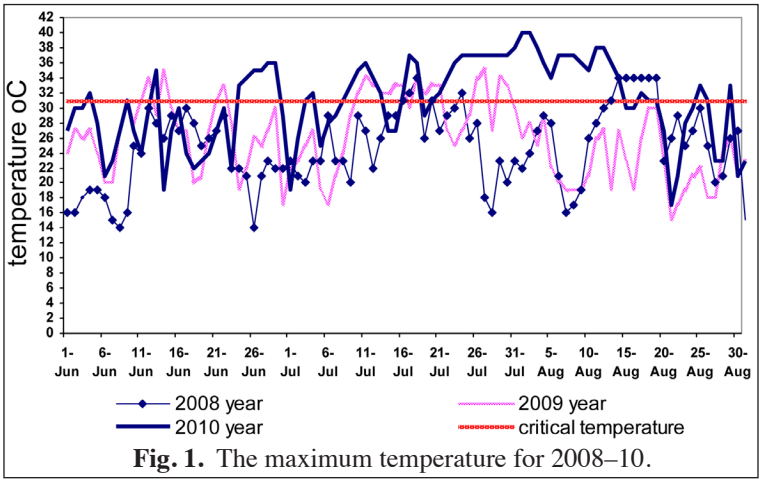

Fig. 1. The maximum temperature for 2008–10.

Since 2009, the has situation changed. The air temperature during the period of infection in field conditions is often higher than the critical indicator for the pathogen or is above the optimal value. This has led to the fact that in the population of the fungus eliminated or reduced their virulence the following pathotypes: pp11, pp14b, pp19, pp24, pp32, and pp40. In 2010, when temperatures during the vegetative period were very high (35-40°C) and in a hard drought (Fig. 1), significant changes were noticed

Table 1. The dynamics of change of the formula avirulence/virulence in populations of *Puccinia triticina* at the Agricultural Research Institute for the South-East Regions, Russian Federation, in 2008–10.

Year	Avirulence/virulence formula
2008	**9, 17a, 29, 28, 41, 42**/2a, 2b, 2c, 3a, 3bg, 3ka, 10, 11, 12, 13, 14a, 14b, 14ab, 15, 16, 18, 19, 20, 21, 22a, 23, 24, 25, 26, 27+31, 30, 32, 33, 34, 37, 38, 40, b, H
2009	**9, 11, 14b, 19, 24, 28, 29, 32, 40, 41, 42**/2a, 2b, 2c, 3a, 3bg, 3ka, 10, 12, 13, 14a, 14ab, 15, 16, 17a, 18, 20, 21, 22a, 23, 25, 26, 27+31, 30, 33, 34, 37, 38, b, H Infection type: 0; 1^-: 14b, 19, 32 22^+: 40 2^+3: 11
2010	**2b, 2c, 3a, 3bg, 3ka, 9, 10, 11, 12, 13, 15, 16, 17a, 19, 21, 24, 28, 29, 30, 32, 41, 42, H**/2a, 14a, 18, 20, 22a, 23, 27+31, 37, 38, 14b, 14ab, 33, 34, b Infection type: 0;1: 9, 21, 32 1^-: 2c, 12, 13, 29 11^+: 2b, 16 1^+2: 3a, 11 2^+: 3bg, 3ka, 10, 15, H 2^+3^-: 30

in the *P. triticina* population. In the pathogen population, there was eliminated or decreased virulence for the following pathotypes: pp2b, pp2c, pp3a, pp3bg, pp3ka, pp10, pp11, pp12, pp13, pp15, pp16, pp17a, pp19, pp21, pp24, pp30, pp32, and ppH. It is interesting that the following virulent pathotypes remained in the population: pp2a, pp14a, pp18, pp20, pp22a, pp23, pp27+31, pp37, pp38, pp14b, pp14ab, pp33, pp34, and ppb, which showed high adaptability to high temperature and were drought resistant.

Effects of interaction 6Agi (6D) chromosomes from Thinopyrum intermedium and Lr19 translocation from Th. elongatum on flour protein content spring bread wheat.

O.V. Krupnova, S.A. Voronina, V.A. Krupnov, and A.E. Druzhin.

On leached, chernozem soil with a crop rotation (a bare fallow–spring bread wheat), flour protein content varied from 13.9% up to 20.3% and gluten content from 30% up to 48%. In these conditions, near isogenic lines for chromosome 6Agi (6D) from *Th. intermedium* and an *Lr19* chromosome 7D translocation from *Th. elongatum* had a positive influence on flour protein content in spring bread wheat, both within a leaf rust epidemic and without.

In a population from crosses between parents Л1400R and 6Agi(6D) and Л1089 and *Lr19*-T7D, we selected recombinant inbred lines Л1204 and Л1205, which have the combination *Lr19*-T7D and 6Agi(6D). In a population from crosses between parents Л2032 (*Lr19*-T7D) and Л1400R, we are selected RILs Л108 and Л396, which have only 6Agi (6D). All four lines (Л1204 and Л1205, Л108, and Л396) are resistant to the Saratov population of a leaf rust and, on a grain yield and a flour protein yield per unit area, exceed that of the parents. For flour protein content, they are less than that of the parents. The mechanism of interaction, 6Agi(6D)/*Lr19* and *Lr19*/6Agi(6D), in a *T. aestivum* background, and the control of the decrease in flour protein content in the RILs, compared with the parents, are unknown.

Laboratory of Spring Durum Wheat Breeding, 7 Tulaikov Street, Saratov, 410010, Russian Federation.

A new spring durum wheat cultivar 'Nikolasha' has been released in the Russian Federation.

N.S. Vassiltchouk, L.A. Bespalova, G.I. Shutareva, A.N. Borovik, S.N. Gaponov, V.M. Popova, L.V. Yeremenko, T.M. Parshikova, and N.M. Tsetva, and P.P. Lukyanenko (Krasnodar Research Institute for Agriculture (KRIA), Wheat and Triticale Breeding Department, Krasnodar, 350012, Russian Federation).

The State Commission on the Test of Breeding Achievements approved a new cultivar of spring durum wheat named 'Nikolasha' (137/00-5) for use in agricultural production in 2009–10. Nikolasha appears well adapted to southern and southeastern areas of European part of the Russian Federation, such as the Krasnodar, Rostov, and Saratov regions. The cultivar was developed thanks to the joint breeding program between P.P. Lukyanenko Krasnodar Research Institute for Agriculture (KRIA) and Agricultural Research Institute for the South-East Regions (ARISER).

Cultivar Nikolasha was developed as a result of individual plant selection in the F_2 generation from the hybrid population obtained by crossing the line D-2033 with the cultivar Nick (D-2029) at ARISER. The line D-2033 was derived from a cross between two highly drought-resistant local lines Leucurum 1863 and Leucurum 1945. The cultivar Nick was derived from a cross between Saratovskaya zolotistaya and Altayskaya Niva. The local cultivar Saratovskaya zolotistaya has very high quality grain and pasta products. The cultivar Altayskaya Niva originated from the Altay region and is highly resistant to common bunt and loose smut. The elite plant was selected in the F_8 generation at KRIA in 2001. The field test of the line 137/00-5 was conducted in Krasnodar in 2004–05.

The spike of Nikolasha is white with white awns, pyramidal in shape, and of medium length (6–8 cm) and density (26–27 spikelets/10-cm rhachilla). Kernels are amber and vitreous. The 1,000-kernel weight was 38–46 g and test weight was 770–822 grams/L. Plants have good resistant to lodging. Plant height is 100–115 cm, which is 5 cm lower than that of the standard cultivar Novodonskaya. Plant heading is earlier than that of Novodonskaya by 1–2 days.

The cultivar is very drought resistant. Nikolasha has a high level of disease resistance, particularly to common bunt and loose smut; good field resistance to leaf, stripe. and stem rust; septoria leaf spot; and tolerant to root rot if sown after such fore crops as winter wheat and barley.

Nikolasha durum wheat is a widely adapted cultivar. The cultivar combines high potential productivity and drought resistance. In 2008, the yield in main trials at KRIA (Krasnodar) reached up to 6.28 t/ha against 4.74 t/ha for the check Kharkovskaya 17. In 2004–06, the average productivity of Nikolasha in the main trial was 5.14 t/ha, which was higher than that of the check cultivar Novodonskaya by 0.37 t/ha. In the Saratov field test in the 2010 spring wheat growing season when the hydrothermal coefficient for May–July in the Volga River Region was very low (0.1–0.2), which corresponds to an extremely strong drought, Nikolasha gave a grain yield of 0.75 t/ha, compared to 0.33 t/ha for the Saratovskaya zolotistaya check. This new cultivar has good physical grain parameters and strong gluten quality. For 2008–10, the average SDS-sedimentation index was estimated up to 50 mL, similar to that of Saratovskaya zolotistaya. Durum wheat Nikolasha is good achievement of ARISER and KRIA shuttle breeding program and according to the technological suitability for the pasta industry after the official testing it was also approved as an original cultivar for the dry, southeast areas of the Russian Federation (Saratov) in 2010 from the State Variety Testing Commission.

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Anther culture method of creating initial breeding stocks for triticale selection at ARISER.

T.I. Djatchouk, O.V. Khomyakova, V.N. Akinina, Yu.V. Italianskaya, N.F. Safronova, and L.P. Medvedeva.

The generation of doubled haploid (DH) plants via anther culture is an important biotechnological method, which permits significant shortening of the breeding process. This technique speeds up the time of cultivar development by several years. Different intervarietal and wheat-triticale hybrids (F_2–F_3 generation) based on the local triticale and wheat cultivars were used for haploid production in this study. The undoubled haploid plants were served by microclonal propagation using a somatic embryogenesis method.

The created DH lines were studied in a traditional breeding process. The winter hexaploid cultivar Student from the Volga region serves as standard cultivar. The triticale breeding program at ARISER works to solve the problems of reducing abiotic and biotic stress influence on the plant growth and increasing yield capacity and grain quality.

In a short time, using traditional and biotechnological approaches, some advanced DH lines of hexaploid triticale were developed. They differ from each other by several botanical and agronomical characteristics, yield capacity, quality of the grain, plant height, and vegetative period. In 2010, Sviatosar, a new winter triticale created by combining conventional and haploid breeding was submitted to the state variety tests. This cultivar was derived from cross of local line with the Krasnodar cultivar Strelets. The higher yield capacity of Svaiatosar is mainly due to a higher 1,000-kernel weight (Table 2).

Table 2. Grain yield, 1,000-kernel weight, and plant height of the new triticale cultivar Sviatosar.

	Grain yield (t/ha)					1,000-kernel weight (g)	Plant height (cm)
Cultivar	200	2008	2009	2010	Average	Average 2007–10	
Sviatosar	3.21	3.69	3.23	1.62	2.94	44.4	130
Student-St	2.81	3.17	2.89	1.08	2.48	38.2	130
LSD_{05}	0.36	0.38	0.30	0.30	0.30	2.4	—

Laboratory of Spring Bread Wheat Breeding, 7 Tulaikov Street, Saratov, 410010, Russian Federation.

Breeding of spring wheat in Saratov.

R.G. Sayfullin and F.V. Sirenko, Yu.V. Lobachev and L.G. Kurasova (Saratov State Agrarian University named after N.I. Vavilov, Department of Plant Growing, Plant Breeding and Genetics, Teatralnaya Square, 1, Saratov, 410012, Russian Federation).

In 2009–10, spring bread wheat cultivars from different wheat breeding centers of the Russian Federation, Germany, Belarus, and Kazakhstan were studied in the field trials at the Agricultural Research Institute for the South-East Region (ARISER, Saratov). The modern cultivars developed in the ARISER were used as a check. Grain yield of old Saratov cultivars (introduced into agricultural production in 1924–57) was 43.8% that of the modern cultivars. The closest yields to those the modern ARISER cultivars were those from Samara (Russia), the grain yield of which reached 66.9%. Yield capacity of cultivars from the relatively dry regions of Russia (Ufa, Orenburg, Kurgan, and Barnaul) and Kazakhstan was 53.9–55.1% that of the Saratov cultivars. Grain yield of Moscow Region's cultivars made up only 51.1%, whereas that of cultivars developed in the relatively moist regions of Germany and Belarus comprised 36.5% that of the Saratov cultivars (Table 3).

Table 3. Yield capacity of spring bread wheat cultivars produced by different wheat breeding centers in 2009–10.

Region where the cultivar was created	Grain yield capacity	
	t/ha	%
Saratov (modern cultivars)	1.78	100.0
Saratov (historically developed cultivars)	0.78	43.8
Samara	1.19	66.9
Ufa, Orenburg	0.98	55.1
Kurgan, Barnaul, Kazakhstan	0.96	53.9
Moscow	0.91	51.1
Germany, Belarus	0.65	36.5
LSD05	0.39	—

These data demonstrate that the bioclimatic potential of Saratov Region is most fully used by Saratov spring bread wheat cultivars. The cultivars created in other regions are less adaptive. The farther they are in their origin in time or space from the modern Saratov cultivars, the lower the yield capacity. To get optimal use from the bioclimatic potential of the region, the reach of regional breeding centers should be created and developed. The distance between them will depend on the agro-climatic differences between the regions. An increase of 10–15% of the modern local cultivars yiel capacity over those developed in neighboring regions may be used as an indicator of the working efficiency of any regional breeding center.

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Joint inheritance of resistance to leaf rust, spike productivity, and stem length in hybrid soft wheat plants.

V.G. Kyzlasov.

The soft wheat winter cultivar Moscovskaya 39 is characterized by a complex of valuable agronomic features. The cultivar is high-yielding and winter-hardy, and its grain quality is very good. However,Moscovskaya 39 is not resistant to leaf rust. Our aim was to provide resistance to leaf rust from a disomic substitution (2n = 42) wheat–*Aegilops* line (DSL) using a backcrossing technique. The disomic substitution line was selected from a hybrid population '*T. aestivum*/*Ae. speltoides*' (Kyzlasov et al. 2004) that is resistant to leaf rust.

The 'Moscovskaya 39/DSL' hybrid F_1, as well as the DSL itself, proved to be completely resistant to leaf rust. Resistance in the DSL is dominant. The 'Moscovskaya 39/DSL//Moscovskaya 39' F_1 hybrid segregated for resistance

to leaf rust in a ratio of 104 resistant plants : 115 affected plants ≈ 1 : 1. The experiment demonstrated that the resistant plants, in comparison with susceptible plants, had less productive spikes and longer stems (Table 1). The resistant plants had small caryopses, thin stems, narrow laminas, and longer glumes and lemmas.

When joining the features of high spike productivity and short stem with resistance to leaf rust in the same genotype, the author faced some problems because of their linked pattern of inheritance.

Table 1. Spike productivity and stem length in plants susceptible and resistant to leaf rust from a cross 'Moscovskaya 39/DSL//Moscovskaya 39'.

Leaf rust reaction	Spike productivity	Stem length (cm)
Resistant	1.8	119
Susceptible	2.1	101
Significance limit (0.05)	0.2	14

Reference.

Kyzlasov VG, Yatchevskaya GL, and Lazareva HN. 2004. Selection of soft wheat lines disomically substituted by chromosomes of *Ae. speltoides*. Ann Wheat Newslet 50:104-105.

Rye apomixis nonheritable by homozygous offspring.

V.G. Kyzlasov.

This report continues Kyzlasov (2010), which presents the results of a study of rye offspring obtained with no paternal parental participation. A reasonable opportunity for the creation of obligatory apomicts using polyploidization and duplication of homologous chromosomes of heterozygous genotypes is reported.

The germination capacity of the apomictic progenies studied was lower than that of normal rye by 20–30%. Sprouting was observed 2–5 days later than in the control group. Stooling was late as well. Slower plant growth was noted. Most plants died in the winter. A mere 7% of the progenies had survived by harvest time. The plants differed dramatically in their productive capacity, number of shoots/plant (1–30), stem length (30–120 cm), and spike and lamina size. Generally, strong inbreeding depression was manifested in the development of quantitative features, which means that the initial maternal plants, which produced apomictic offspring without pollination, had been heterozygous.

Surprisingly, recombinant plants with normally developed anthers and pollen, appeared among the apomictic progenies. Plants of spring type were found. The initial apomictic maternal plants had sterile pollen and all were winter type. These facts defy explanation, because spring type and pollen fertility are dominant features, whereas winter type and pollen sterility are recessive. As a result of reproducing plants with recessive features, no progeny with dominant features can appear. In the population studies, plants resistant to oidium and unable to produce stems, were found.

Before flowering, stamens were removed from 58 spikes of apomictic origin. One-half of the plants had sterile pollen in the F_3, the other half had fertile pollen. Emasculated spikes were covered with paper cages. Without pollination, practically no seed set in the emasculated flowers. Of 3,550 emasculated flowers, only three produced caryopses in the absence of pollination. Sucha negligibly low frequency of a feature development is statistically insignificant. The studied progenies did not inherit the apomictic reproduction pattern of the maternal plants. A noninheritable apomixis type was earlier described in soft wheat (Kyzlasov 2008).

Normal rye plants are always heterozygous. The studied offspring's failure to inherit apomictic reproduction pattern of their maternal plants can be explained by a transfer of the apomixis genes to homozygous state. We assumed (Maheshwari 1954) that the embryo sac oocyte without pollination can give rise to a diploid embryo due to chromosome endoduplication. The resulting progenies will be, in this case, fully homozygous. There are no reports about homozygous apomicts in the literature. Haploid organisms are fully homozygous. They also are unable to reproduce themselves via apomixis. The apomixis pattern described by the author in winter rye can be an effect of interaction of apomixis genes located in homologous chromosomes of heterozygous plants. Therefore, it is not inherited by homozygous progenies produced due to apomictic reproduction. Apomixis of this type is manifested in the phenotype of heterozygotes only. In homozygous plants, it disappears like the heterosis effect. Kyzlasov (2010) observed in apomictic reproduction, that apomictic progenies have to inherit their maternal plants ability to reproduce themselves via apomixis. However, they were not found to.

In another experiment, the formation of apomictic progenies was repeated in a hybrid population of 'F_2 winter rye R-1 with sterile pollen / spring rye R-2'. Apparently, there are carriers of pollen sterility genes in the population of spring rye R-2. Therefore, pollen appeared to be sterile in approximately 6% of the F_1 hybrid plants obtained. Without pollination, no seed formation was observed in the flowers of these plants. The other plants had fertile pollen. The second generation hybrid population had a segregation ratio by pollen viability of 118 plants with fertile pollen : 41 plants with sterile pollen ≈ 3 : 1 (Table 2). Formation of apomictic caryopses was revealed in the plants with sterile pollen without pollination. Their rate was approximately 10% of the total number of flowers in the spike

Table 2. Segregation pattern of an AaBb rye hybrid in F_2 for pollen sterility (+ = plants with fertile pollen, – = plants with sterile pollen).

	AB	Ab	aB	ab
AB	+	+	+	+
Ab	+	+	+	+
aB	+	+	–	–
ab	+	+	–	–

One-half of the apomictic progenies in the F_3 demonstrated fertile pollen, and the other half had sterile pollen. In the absence of flower pollination, 68 apomictic progenies in the F_3 produced no seeds, in the same manner as in the experiments of prior years. A model of formation of rye apomictic progenies with sterile pollen (aaBb) can be imagined as a result of allelic interaction between 'B' and 'b' genes in heterozygous state (B – b).

This apomictic reproduction type, revealed in rye, is supposed to be inherent to heterozygous plants only. A possibility of apomict formation through the interaction of genes located on homologous chromosomes of heterozygous organisms, is reported for the first time. In such cases, obligate apomicts can appear as a result of chromosome set doubling in genotypes heterozygous by apomixis genes, or unequal crossingover in heterozygous plants in meiosis, or a duplication of homologous chromosomes of heterozygous plants. Possibly, that is why the apomicts found in nature are usually polyploids or aneuploids with unbalanced chromosome number. In sexual reproduction also, flowering plants are known produce seeds entirely as a result of interaction of genes located in homologous chromosomes. If without the flower pollination, no seeds will appear.

These results are consistent with the hypotheses of apomictic plant species formation by means of hybridization and polyploidy (Strasburger 1905; Ernst 1918; Winkler 1908; Powers 1945). The data obtained substantiate the principles of the theory, now universally recognized, that apomixis is determined by the action of genetic factors (Petrov 1988).

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Research of the potassium maintenance in leaves of triticale seedlings in the presence of aluminum toxicity by means of ion-selective electrodes.

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Reaction of wheat and triticale plants to aluminum ions in a soil solution has been observed at very low aluminum concentrations. Some plants are able to grow in acclimation to aluminum toxicity, but is the growth of such plants accompanied by increased soil ion absorption, in particular potassium? Research of potassium movement in vegetation by ardent photometrics is expensive and labor-consuming and, because, of it its use is limited.

A fast and complete use of potassium ions in plant biomass by means of ionometry has been developed. The essence of the method consisted of the allocation of potassium from plants in two steps: first, the cut sheet within an hour per a solution of $CaCl_2$ (0.01 M, potassium of the apoplast), and second, after boiling the fabric sheet within 3 min in the same solution. After each stage, potassium ions were measured using a potash electrode (ELIT-031) on a Ekoniks EXPERT 001. This device allows to defining potassium maintenance in mg/L, and also to construct a model of dependence EMF from the concentration of potassium, on a preliminary constructed scale in a range of concentrations. After boiling, data of potassium level in the leaves was obtained. The triticale cultivar Legalo, after the addition of aluminun ions in the soil, was studied for the reaction of plants with the following scheme: control (0 mg/Al), Al4 ($AlCl_3$/100 g soil), K10 (KCl/100 g soil), and K10+Al4 (4 мg Al + 10 мg soil K/100 g). After 14 days, the plants were measured for maintenance of potassium before (potassium of apoplast) and after (general potassium) boiling.

The presence of aluminun ions in the soil sharply reduces apoplast potassium, whereas dependent simplast potassium fluctuates slightly (Fig. 1). The addition of potash salts to the soil does not activate potassium accumulation in the leaves of triticale seedlings. With the simultaneous addition to the soil of potash and aluminum salts, a decrease in the maintenance of potassium in the simplast is observed, which essentially stops the absorption of potassium by means of potash pumps and a strengthening of potassium in apoplast. The mechanism for the decrease in absorption of water and nutrients is the presence of aluminum ions, because aluminum toxicity has a negative influence on root metabolism. In the apoplast, the raised maintenance of potassium is observed. Potassium exit from the intercellular space is observed.

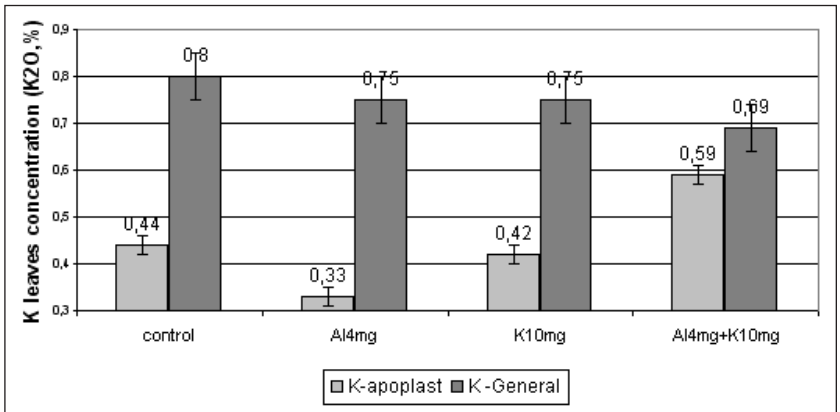

Fig 1. The potassium maintenance (K_2O, %) in seedlings leaves of the triticale cultivar Legalo.

Aluminum has an essential impact on seedling growth in triticale. Aluminum ions activate adaptable seedling growth; the dry weight increased 86%, whereas from potash salt use it was more than 57.6%, and from a potassium application in the presence of aluminum more than 56.4%. Potassium lowers the activation of growth in Legalo triticale. Growth did not caused a raised absorption of potassium ions. The absorption of potassium is dependent on metabolism by roots in the presence of aluminum ions (Poukhalskaya et al. 2008). Earlier, we observed similar growth activation of wheat plants in the presence of aluminum (Poukhalskaya et al. 2006).

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Influence of exogenous phytohormones on the functional activity of apical meristematic cells in wheat seedlings.

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The functioning of plant apical meristems is controlled by the hormonal regulatory system, which operates at all stages of plant ontogenesis. A topical problem is the identification and further study of molecular markers involved in the perception of a hormonal signal and its transmission to the plant cell genome.

Our preliminary work has found that the meristematic cells of the wheat apex are characterized by the presence of a marker protein called the proliferative antigen of initials (PAI), whose content in root and stem meristematic cells correlates with their mitotic index (i.e., it defines the extent of activity of these cells (Evseeva et al. 2009). The suggestion has been made that PAI is associated with the perception of an auxin or cytokinin signal and its transmission to the cell genome. Our aim was to examine the influenceof exogenous auxins and cytokinins on the functional activity of meristematic cells in the seedllings of wheat cultivar Saratovskaya 29.

The root system of 5-day-old seedlings was treated with solutions of indole-3-acetic acid (IAA; 1 and 0.1 mg/L) and 6-benzilaminopurine (6 BAP; 1 and 0.1 mg/L). The activity of meristematic cells was assessed by the results of determination of the cells mitotic index and by comparative immunochemical estimates of PAI content in these cells.

IAA at 1.0 and 0.1 mg/L enhanced the mitotic activity of the root meristematic cells 2- and 2.5-fold, respectively. The PAI content of the apical meristems changed insignificantly. In turn, in response to 6-BAP at 0.1 mg/L, cellular mitotic activity increased 2-fold and PAI content increased 1.2-fold. These results suggest that PAI involved in the perception of signals from gormones of the cytokinin series and their transmission to the plant cell genome.

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The programmed cell death in winter wheat suspension culture at low temperatures.

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Programmed cell death (PCD) is the genetically controlled process of the organized destruction of superfluous or defective cells (Krishnamurthy et al. 2000; Kingston-Smith et al. 2008). The mechanisms of PCD are well known in animals, whereas many features of this process in plants are needed to investigate. PCD in plants plays a crucial role in real-

izing of development program, response to pathogens and different abiotic stress (Heath 1998; Jones 2001; Gao et al. 2008). PCD in plant cells is accompanied by a number morphological and biochemical changes, just as in animal cells, and include chromatin condensation with subsequent nuclei disintegration and DNA fragmentation, concentration and vacuolization of the cytoplasm, protoplast condensation, release of cytochrome c from the mitochondria, activation of endonucleases and caspase-like proteins, generation of reactive oxygen species, and dependence of the death process on ATP level in the cell and protein synthesis de novo (Reape et al. 2008).

The available literature data about possibility of induction and development PCD process under cold conditions are not numerous (Koukalová et al. 1997; Ning et al. 2002). In these works, the possibility of PCD activation is investigated under low temperature treatment. Nothing is known about opportunity of subzero temperatures to cause PCD in plants. The aim of our work was to investigate conditions for PCD activation in a winter wheat suspension culture during treatment with low and subzero temperatures.

Materials and methods. Suspension-cultured cells of *T. aestivum* were grown in the dark at 26°C under continuous shaking in Murashige and Scoog (MS) medium containing sucrose (3%), thiamine (1.0 mg/L), pyridoxine (0.5 mg/L), nicotinic acid (0.5 mg/L), 2.4-D (2.5 mg/L), inositol (0.01%), and sodium dithiocarbamate (0.0005%). Suspensions were subcultured every 14 days using 2:7 dilutions. All treatments were carried out using log-phase cells 8 days after subculture. Suspension-cultured cells were subjected to cold hardening for 7 days at 8°C or 4°C and following short-term treatment (–8°C, 6 hours). After these treatments, suspension cells were moved under the control conditions (26°C) for 3, 6, and 10 days. Evans' blue staining of cell culture was used to determine the number of dead cells and cells with condensed protoplasts (Baker and Mock 1994). At least three independent experiments were performed with more than 500 cells counted per conditions. The quantity of stained cells and cells with condensed protoplasts were calculated using light microscope Axiostar plus (Carl Zeiss, Germany). Images were made using inverted fluorescent microscope AxioObserver Z1 (Carl Zeiss, Germany) with digital monochrome camera AxioCam MRm3 and the AxioVision Rel.4.7.2 software.

Results and discussion. Our experiments showed that reaction of suspension cultures hardened at different temperatures to transferring in the control conditions and following treatment with subzero temperatures differ greatly. About 15% of the cells were dying during culture treatment with 8°C, but during the following 10 days of the experiment at 26°C, cell death stopped (Fig. 1). Furthermore, the subsequent cold shock (the treatment with subzero temperature, CS) did not cause the mass mortality of suspension cells and during our experiment. The decrease in the quantity of living cells in the culture exposed to preliminary hardening at 8°C and then CS was only about 10–15% compared to the control culture (Fig. 1). The control culture treatment with subzero temperature caused the death of 15% of cells during exposure and 45% after transferring the culture in the control conditions (Fig. 1). The defense mechanisms became apparent in the suspension culture exposed preliminary cold hardening at 8°C. They allowed cells to withstand CS.

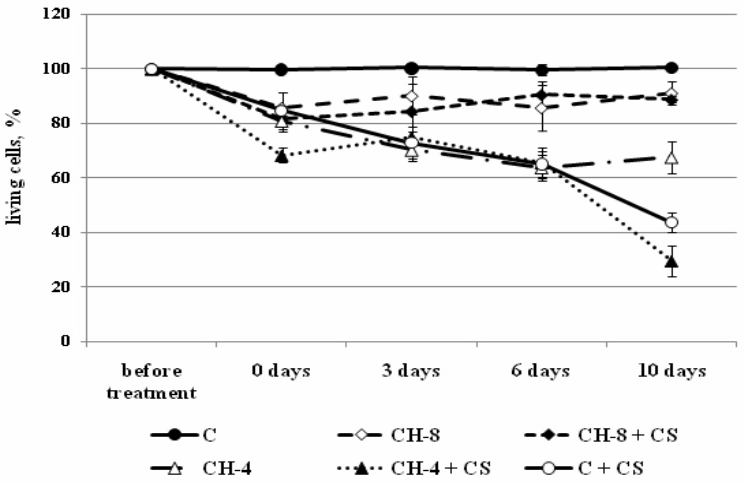

Fig. 1. The influence of subzero temperature (–8ºC, 6 h) on the dynamics of the cell death in the control and hardened suspension culture of winter wheat. C – control suspension culture without any treatment; CH-8 – cold hardening at 8ºC, 7 days; CH-4 – cold hardening at 4ºC, 7 days; CS – cold shock (treatment with subzero temperature) (M ± m; n=3–6).

Other tendency was observed in experiments at 4°C. The quantity of dead cells during this treatment was slightly greater than that in the culture hardened at 8°C (about 5%), but after transferring this suspension culture to the control conditions, the process of cell death continued and 70% of cells dyed during following 10 days of the experiment (Fig. 1). This quantity was greater than that of the respective percent of the dead cells in the control culture after the treatment with subzero temperature. In this connection, it is possible that metabolic state of the cells determined their

further existence (death program or adaptation). The process of PCD on the first stage is reversible, therefore after transferring the culture to the control conditions, those cells in which development of PCD has passed 'the point of no return' were dying during the 6 days of the experiment. At the same time, those cells in which the adaptation mechanisms have been formed or the development of PCD was at the reversible initial stages, returned gradually to the normal vital functions (O'Brien et al. 1998). The process of cell death caused the treatments with low and subzero temperatures to a have gradual, prolonged character; the process developed during several days and not at the same time as the CS treatment, but after it (Fig. 1). This fact allowed us to suppose the active character of the death in suspension culture. Thus, one of the important features characterizing active, genetically programmed cell death became apparent, the development of the process takes a long time. Reape et al. (2008) observed that PCD in plants is slower than in animals and develops during several hours, rarely during one day. In our experiments, PCD was connected with features of stress to low and subzero temperatures.

PCD in plants and animals depends on activity of many enzymes and protein and ATP synthesis (Williams and Dickman 2008). At subzero temperatures or the temperatures near 0°C, many enzymes in the cell denaturate because of a decrease in hydrophobic pressure providing their functional activity, in particular disintegration of the ATP-synthase complex (Finkelstein and Ptitsyn 2002). During cold denaturation of protein, the forming of 'boiling up' of a protein rather than 'molten globule' is observed is significant. Thus, the recovery of disturbed bonds in a spatial pattern takes much time after cold treatment and explains the slow character of the death process in our experiment. Koukalová et al. (1997) have shown the development of PCD under low temperature treatment of tobacco cell culture during 5 weeks.

The shrinkage of the cell and the condensation of the protoplast away from the cell wall is the one of more prominent features of PCD (Reape et al. 2008) and such changes are easy to observe in a light microscope (Fig. 2). The quantity of the cells with condensed protoplasts in the suspension culture hardened at 8°C was equal to that of the control level, whereas after the treatment with 4°C, cell death is accompanied by a 15–18% increase (Fig. 2). Subsequent treatment with subzero temperatures led to protoplast condensation both in the control culture and in the culture preliminary hardened at 4°C (Fig. 2), agreeing with the data of the cell death process after the treatment (Fig. 1, p. 266).

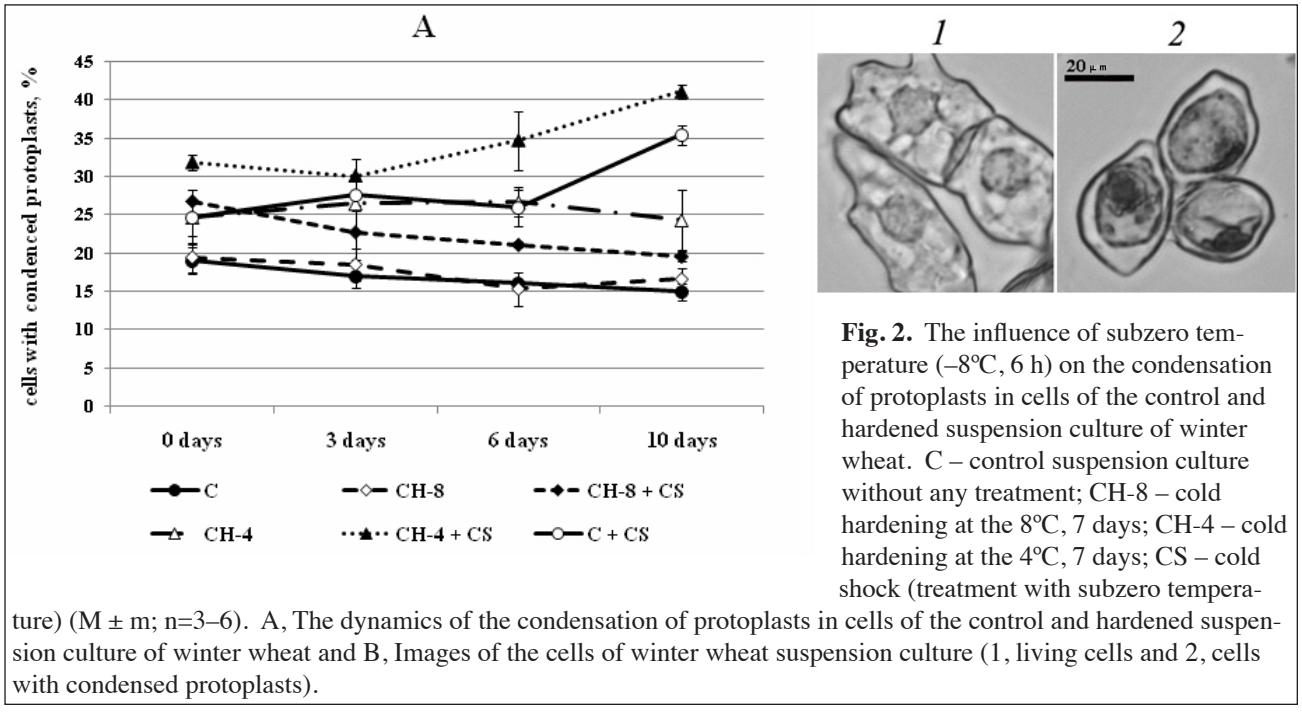

Fig. 2. The influence of subzero temperature (–8ºC, 6 h) on the condensation of protoplasts in cells of the control and hardened suspension culture of winter wheat. C – control suspension culture without any treatment; CH-8 – cold hardening at the 8ºC, 7 days; CH-4 – cold hardening at the 4ºC, 7 days; CS – cold shock (treatment with subzero temperature) (M ± m; n=3–6). A, The dynamics of the condensation of protoplasts in cells of the control and hardened suspension culture of winter wheat and B, Images of the cells of winter wheat suspension culture (1, living cells and 2, cells with condensed protoplasts).

These results allow us to conclude that low temperature may be both necessary for forming of mechanisms of low-temperature adaptation and a factor for PCD activation in suspension culture of winter wheat. At the same time, PCD under low temperature conditions is a slow process, which is accompanied by respective morphological changes.

Acknowledgements. The work has been performed, in part, with the support of Russian Foundation of Basic Research (08-04-01037 and 10-04-00921) and a Siberian Division of Russian Academy of Sciences Youth Grant.

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The antioxidant function of alternative oxidase and uncoupling proteins in winter wheat mitochondria under cold hardening.

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Cold hardening under low nonfreezing temperatures (first phase of hardening) attacks the ability winter crops to tolerate unfavorable freezing temperature. The acquisition of additional freezing tolerance is the second phase of hardening and takes place when plants are exposed under subzero temperatures (–2–3°C). Cold hardening of winter wheat is known tocause the activation of alternative oxidase (AOX) (one of terminal oxidases of mitochondrial electron transport chain, ETC) (Grabelnych et al. 2003, 2004; Sugie et al. 2006; Mizuno et al. 2008). The ability of alternative pathway (AP) relating to AOX functioning to respond to low-temperature conditions is one of the genetic factors determining cold/frost resistance in winter wheat (Sugie et al. 2006; Mizuno et al. 2008). One function of AOX in plant cells is the decrease of reactive oxygen species (ROS) formation (Popov et al. 1997; Maxwell et al. 1999; Moller 2001) that can be first line of mitochondria protection from oxidative stress (Moller and Kristensen 2004). The uncoupling proteins can carry out similar function in plant mitochondria (Kowaltowski et al. 1999; Considine et al. 2003). But, in contrast to AOX, uncoupling proteins are able to operate under increased ROS content (Rhoads et al. 2006). Sluse et al. (1998) have shown that an increase of free fatty acids (FFA) concentration blocked AOX activity causing activation of uncoupling proteins in vitro. We suppose that the in vivo increase of FFA content in mitochondria along with increase of ROS can regulate AOX and uncoupling proteins activities under stress (particularly, induced by low and subzero temperatures). Our aim was to study of AOX and uncoupling proteins activities under cold hardening in winter wheat seedlings and to detect theirs antioxidant function.

Materials and methods. Three-day-old etiolated seedlings of cold-resistant winter wheat cultivar Irkutskaya ozimaya were germinated on moist paper at 26°C and used as a control. For cold hardening, 2.5-day-old etiolated seedlings germinated at 26°C at 2–3°C for 7 days (first phase) and then placed in an incubator at –2°C for 2 days (second phase). The efficiency of cold hardening was estimated by synthesis of dehydrins. Mitochondria were extracted from shoots by differential centrifugation and purified on Percoll gradient (Pobezhimova et al. 2001). The isolated mitochondria were resuspended in the medium contained 40 mM MOPS-KOH buffer (pH 7.4), 300 mM sucrose, 10 mM KCl, 5 mM EDTA and 1 mM $MgCl_2$. The concentration of mitochondrial protein was analysed by Lowry. Integrity of mitochondrial outer membrane from was calculated on rate of ascorbate-dependent cytochrome-c-induced KCN-sensitive oxygen consumption in presence and absence of 0.04% Triton X-100 and was 92-93%. Mitochondrial activity was recorded polarograph-

ically at 26°C using a closed-type platinum electrode in a 1.4-ml cell. The reaction medium for AOX determination contained 300 mM sucrose, 20 mM MOPS-KOH buffer (pH 7.4), 5 mM $MgCl_2$, 10 mM EDTA, 0.1% bovine serum albumin (BSA) clear free fatty acids, 8 mM succinate (Suc), 5 mM glutamate (Glu), 3 mkM rotenone (Rot), 200 mkM ATP, 1 mM pyruvate, and 5 mM ditiotreitol. The concentrations of inhibitors of respiratory chain were: Rot (3 mkM), antimycin A (A-A) (20 mkM), benzhydroxamic acid (BHAM) (1 mM) and KCN (0.4 mM). The reaction medium for PUMP determination contained 150 mM sucrose, 10 mM Tris-HCl (pH 7.4), 65 mM NaCl, 5 mM EDTA, 0.33 mM EGTA, 8 mM Suc, 5 mM Glu, 3 mkM Rot, 200 mkM ATP, 1 mM BHAM, and 8 mkM linoleic acid (LA). ROS content in isolated mitochondria evaluated by 1 mkM H2DCF-DA (2',7'-dichlorofluorescein diacetate). Fluorescence of DCF was measured by using spectrofluorophotometer SHIMADZU RF-5301PC (Japan) with excitation and emission wavelengths set at 480 nm and 524 nm, respectively. All the experiments were performed on 3–6 separate mitochondrial preparations, arithmetic means and standard error are presented.

Results and discussion. First phase of cold hardening was accompanied by 32-41% decrease of state-3 respiration in winter wheat mitochondria whereas two phases of cold hardening lead to a 65–66% decrease in state-3 respiration. The decrease in the mitochondrial cytochrome pathway (CP) from 77% (control seedlings) to 53% and generation of ROS by mitochondria (a 1.5-fold increase in comparison with control) occurred during first phase of cold hardening (Fig. 3). At the same time, an approximately 1.8-fold activation of AP occured (with 22% to 40%) that was accompanied by synthesis of AOX stress isoforms. Still more ROS generation by mitochondria (2.8-fold) was observed under second phase of cold hardening) (Fig. 3) and at the same time the inhibition of AP (to 17%) and the increase of CP (to 73%) were observed. We suppose that the increase in ROS generation by winter wheat mitochondria under cold hardening is related to signal function of these molecules. AOX is protein of nuclear encoding, transmission of signal from mitochondria into nucleus and induction of nuclear genes consequently of mitochondrial signal pathway realization possible to allow plants to support cell homeostasis in changing environment (Rhoads et al. 2006). Activity of AOX may be able to estimate power of this signal pathway (Vanlerberghe et al. 2009).

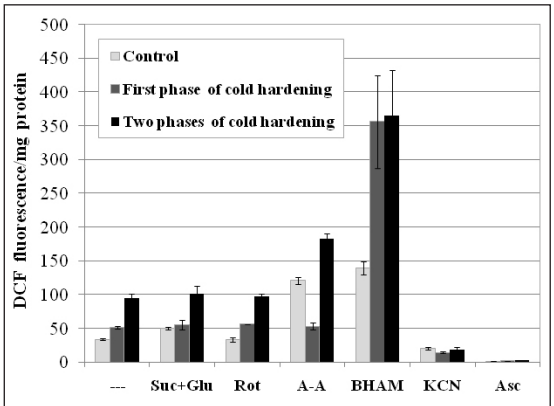

Fig. 3. The ROS content in mitochondria isolated from control and cold hardened seedlings of winter wheat (M±S.E; n=8–10). Control, before cold hardening; first phase of cold hardening, 2–3°C, 7 days; second phase of cold hardening, 2–3°C, 7 days + –2°C, 2 days; ---, without any additions; Suc + Glu, with 8 mM succinate and 5 mM glutamate added; Rot, 3 mkM rotenone added; A-A, 20 mkM antimycin A added; BHAM, 1 mM benzhydroxamic acid added; KCN, 0.4 мM KCN added; and Asc, 60 mM ascorbic acid added.

Succinate and respiratory inhibitors A-A and BHAM increased generation of ROS (1.5-, 3.6-, and 4.1-fold) in mitochondria from control seedlings while KCN inhibited generation of ROS by mitochondria (about 41%) (Fig. 3). These data agree with literature data about ability of A-A and hydroxamic acids to cause an increase of ROS generation by plant mitochondria (Popov et al. 1997). At the same, time suc and A-A did not cause an increase of ROS generation, but BHAM caused a 7-fold the increase in ROS generation in mitochondria from seedlings after first phase of cold hardening (Fig. 3). Taking into consideration that on this stage of cold hardening activation of AP occurs, we may conclude that antioxidant function of AOX is one of cause of the decrease of substrate- and A-A-dependent ROS generation in winter wheat mitochondria and greater ROS generation under addition of BHAM also supports this fact. The second phase of cold hardening also was accompanied the decrease of succinate-dependent ROS generation by mitochondria and lesser ability of A-A to generate ROS in comparison with control mitochondria (a 2-fold), but the effect of BHAM was similar to the control mitochondria (Fig. 3). These data show that antioxidant function of AOX during second phase of cold hardening is carried out in lesser degree than during first. Incubation of winter wheat mitochondria with ascorbic acid leads to full neutralization of ROS and Rot did not influence on ROS production of mitochondria (Fig. 3).

The accumulation of hydrogen peroxide in plant mitochondria during oxidation of suc and BHAM and A-A addition is related to significant increase of superoxide radical anions production (Popov et al. 1997). Superoxide radical anion is known to be an unstable compound and rapidly neutralized to hydrogen peroxide with the participation of superoxide dismutase. Hydrogen peroxide is more stable compound and can diffuse in cell on significant distance that may determine its ability to be a signal molecule.

The decrease of succinate-dependent ROS generation by mitochondria and lesser ability of A-A to produce of ROS during second phase of cold hardening (Fig. 3) may indicate on function of uncoupling proteins. We carried out analysis of state-4 respiration rate, respiration control by Chance-Williams (RC) and ADP/O ratio in winter wheat mitochondria from seedlings subjected to cold hardening. The rate of state-4 respiration in absence of LA was remained constant but the decrease of state-3 respiration rate occurred that was accompanied by the decrease of RC and ADP/O ratio in mitochondria from hardening seedlings. The decrease of ADP/O ratio was maximal under two phases of cold hardening (about 80%). We found that the addition of LA to mitochondria leads to stimulation of state-4 respiration: about 34%, 15%, and 47% in the mitochondria from control, hardened under low, and subzero temperatures seedlings, respectively. The decrease of RC and ADP/O ratio also was most expressed after two phases of cold hardening. The absence of significant stimulation of state-4 respiration in mitochondria after first phase of cold hardening possibly is explained by increase in these conditions of AOX activity. We estimated ROS in the mitochondria of control and hardened seedlings in presence of uncoupling proteins activators and inhibitors. Preliminary results show that activation of uncoupling proteins under incubation of mitochondria with LA effective decreases ROS generation by mitochondria whereas GTP (inhibitor of uncoupling proteins) vice-versa increases ROS.

Thus, first phase of cold hardening leads to inhibition of CP in winter wheat mitochondria, the increase of their ROS content and switch of electrons transport from CP to AP. Under this, likely, ROS carries out the function of signal molecules regulating expression and synthesis of AOX and activation of AP. Antioxidant function of AOX during first phase of cold hardening may present significant component of low-temperature adaptation of winter crops. Under more significant increase of level ROS in mitochondria (not damaging subzero temperatures) uncoupling proteins can replace AOX.

Acknowledgements. The work was performed, in part, with the support of President Russian Federation grant for support of young Russian scientists (1876.2007.4), interdisciplinary integration project of Siberian Division of RAS №45, and the Russian Foundation of Basic Research (№07-04-01055, №08-04-01037 и №10-04-00921).

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ITEMS FROM UKRAINE

PLANT PRODUCTION INSTITUTE OF ND. A. V. Y. YURYEV OF NAAS
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New morphological trait in the genus Triticum L.

O.V. Tverdokhleb.

In awned forms of the genus *Triticum*, awns usually are jagged in varying degrees. Smooth awns are relatively rare, they are found only in the cultivated tetraploid wheats *T. turgidum* subsps. *durum* and *turgidum* (Dorofeev 1972) and forms with pubescent awns still have not described in wheat (Tsvelev 1976; Dorofeev 1979). We found such forms in the progeny from a cross '*T. timopheevii* subsp. *timopheevii* / *T. turdigum* subsp. *durum* cultivar Spadshchyna (Fig. 1). In these forms, awn pubescence is a continuation of the pubescence from the top of the lemma and extends to a length of about 2.5 cm, regardless of awn length. In hybrid F_1 plants, the awns were jagged but not pubescent.

Fig. 1. Awn pubscence in the progeny from a cross '*T. timopheevii* subsp. *timopheevii* / *T. turdigum* subsp. *durum* cultivar Spadshchyna. Awn pubescence is a continuation of the pubescence from the top of the lemma and extends to a length of about 2.5 cm, regardless of awn length.

Of the 154 florets of hybrid F_1 plants pollinated with Spadshchyna, 22 seeds were obtained and 12 F_1BC_1 plants were grown. From 12 spikes in the F_2BC_1, four were fertile with seed set from 2.8 to 47.4%. All the spikes had light glumes with light awns and were slightly pubescent. When 25 seeds were sown, plants of F_3BC_1 were obtained, which were divided into five groups.

1. Spikes of dark coffee color, awned, glumes not pubescent, awns dark and pubescent. These five plants were derived from spontaneous pollination of the hybrid by pollen of *T. persicum*. Their fertility was close to zero; only one shriveled seed was found.
2. Spikes light with black pubescent awns, glumes not pubescent. This group included two plants with spike fertility of 18.2–25.0%.
3. Spikes light with black pubescent awns, glumes pubescent. We have assigned to this group five plants with a fertility of 19.2–34.2%.
4. Spikes with light pubescent glumes and awns. To this group were assigned eight plants with fertility from 2.6–3.1%.
5. Spikes light, no pubescence, glumes not pubescent. The group included five plants with a fertility from 2.6–9.4%.

Because all these hybrids have a *T. timopheevii* subsp. *timopheevii* cytoplasm, we concluded that mostof the plants obtained from a backcross with durum wheat and all plants from pollination by *T. persicum* had cytoplasmic male sterility. Sporadic plants with relatively high fertility obtained from backcrosses with durum wheat carried *Rf* genes inherited from *T. timopheevii* subsp. *timopheevii*.

Thus, awn pubescence may be combined with light and dark colored glumes, the presence or absence of pubescent glumes, dark and light colored awns, cytoplasmic male sterility, and presence of fertility restoration genes. Regarding the genetic nature of the pubescent awns, this feature is not evident in any of the parental forms or F_1 hybrids, but only appears in the progeny of step crossings and backcrosses. Its expression in *T. timopheevii* subsp. *timopheevii* apparently is suppressed by an inhibitor gene, which is not inherited in all progeny except descendants of backcrosses as a result of recombination. These plants manifest the awn pubescence.

Presence of awn pubescence in forms with enough fertility for distant hybrids, from 18–34%, it is possibility to obtain pubescent forms. We offer to combine these forms into a group of morphological races under the name convar. *pilosoaristatum* E. Tverdokhleb. Awn pubescence is a trait that may be easy recognized and can serve as a morphological marker in identifying wheat gene pool accessions. In particular, they can mark awned cultivars of wheat for ensure their protection using a DUS test. In the family Poaceae, this feature is well manifested in species of feather grass (*Stipa* L.). In the Triticinae subtribe, according to our observations, this feature is manifested in *Dasypyrum villosum* at the bottom of the awns as an extension of the glume keel pubescence by hard trichomes.

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ITEMS FROM THE UNITED STATES OF AMERICA

INDIANA

USDA–ARS AND PURDUE UNIVERSITY
Departments of Agronomy, Botany and Plant Pathology, Entomology, and the USDA–ARS Crop Production and Pest Control Research Unit at Purdue University, West Lafayette, IN 47907, USA.

C.E. Williams, S.E. Cambron, C. Crane, S.B. Goodwin, S. Scofield, B. Schemerhorn, R.H. Shukle, and J.M. Anderson (USDA–ARS); H.W. Ohm (Department of Agronomy); K. Wise (Department of Botany and Plant Pathology); and J. Stuart (Department of Entomology).

Wheat production.

According to the USDA National Agricultural Statistics Service, harvested wheat acreage in Indiana in 2010 totaled 250,000 acres. Acreage seeded to wheat in the autumn of 2009 was unusually low due to wet soil conditions in September and October, 2009; this significantly delayed harvest of corn and soybean and, thus, delayed and reduced seeding of wheat. Wheat production was down from 470,000 acres in 2009. Total production was estimated at 13.8 x 10^6 bushels, with an average yield at 60 bu/acre. Winter survival of wheat during the winter of 2009–10 was excellent, but average temperatures from February to mid-April were significantly below normal and soil moisture was higher than normal due

to frequent rainfall, resulting in delayed growth and development of wheat and limited uptake of nitrogen. Growth stage of wheat was 1 week later than normal at mid-April. However, from mid-April through June, temperatures were above normal and frequent rainfalls continued, so that wheat matured 1 week earlier than normal. Grain yields were below average, likely due to reduced plant development during the the autumn of 2009 and early spring of 2010.

Weather conditions were excellent for harvest of soybeans and corn in fall 2010, resulting in timely seeding of wheat and a return to typical acreage of wheat, estimated at 450,000 acres for the 2010–11 season. However, in contrast to normal weather/soil conditions in the sutumn in Indiana, rainfall during mid-August through October was unusually low. Thus, low soil moisture caused significantly variable and delayed emergence of wheat, resulting in little growth and tillering prior to onset of winter. Surprisingly, wheat survived the winter conditions quite well; very little winterkill.

Wheat disease summary.

Fusarium head blight was present in most areas of the state, but severity of the disease varied widely. Other fungal diseases including glume blotch and leaf blotch were moderately severe, and more so in southern Indiana. Powdery mildew developed early in the season on susceptible varieties, but declined with onset of warm conditions. Leaf and stem rusts developed late and were not severe.

Performance of new cultivars.

Herb Ohm.

Cultivar INW1021 yielded well in Indiana and nearby regions. INW1021 has moderate resistance to Fusarium head blight (*Fhb1*), soilborne wheat mosaic virus, and wheat spindle streak mosaic virus. The cultivar is adapted to southern Indiana and surrounding regions. INW1021 has survived winters very well in central and northern Indiana, but winters have been mild since 1996.

Cultivar INW0801, which has the gene *Bdv3*, also performed well. INW0801 is well-suited to southern Indiana and adjacent areas because yellow dwarf is present many years, and its early maturity is suited to doublecropping, seeding soybeans no-till after wheat harvest.

Breeding/genetics, combining multiple genes for resistance to foliar diseases, yellow dwarf, and Hessian fly in improved germ plasm and soft winter wheat cultivars adapted to Indiana.

Herb Ohm, Benjamin Campbell, Judy Lindell, Andy Linvill, Yanyan Liu, Dan McFatridge, Mahboobullah Nang, Wali Salari, Samantha Shoaf, Jin Sun, and Xiangye Xiao.

Fusarium head blight. We are backcrossing the combination of *Bdv3* and *Qfhs.pur-7EL* on 7DL (*Qfhs.pur-7EL* is more distal than *Bdv3*) into elite winter wheat lines. We are also combining these with *Bdv2*, which was moved from 7DL to 7BL, and *Fhb1*, on 3BS. We are also combining type-I FHB resistance, from combinations of three unrelated sources, with the type-II resistance to FHB.

Stem rust and stripe rust. We have identified and obtained germ plasm lines that have resistance to stem rust race TTKS (Ug99) and stripe rust. In collaboration with the USDA–ARS laboratory (Dr. Yue Jin) at St Paul, MN (Ug99) and at Purdue University for resistance to our local isolates of the causal fungal pathogens, we are mapping the resistance.

Marker-assisted selection. We have significantly expanded MAS as an integral part of the breeding program to combine a large number of desired QTL/genes for various important plant traits. MAS is a necessary technology to genotype parent lines for various desired traits and to plan parental combinations for efficiently combining a large number of desired plant traits.

Wheat management. In studies at Lafayette and Evansville, Indiana, in three seasons, 2008, 2009, and 2010, a second topdress of 45 #/acre N in early to mid-March (prior to Feekes growth stage 6 or 7), in addition to a first application of

95 #/acre N in early February, significantly increased grain yield, but had little negative effects on flour milling and baking qualities. We noted that in all three seasons, February–mid-April in one of the seasons, and February to mid-May in two of the seasons, conditions were more wet and cool than is typical in Indiana.

Personnel. Dan McFatridge, Technical Research Assistant with Herb Ohm, retired in December, 2010. Ph.D. students Joshua Fitzgerald, Jenae Skelton, and Rima Thapa joined the Herb Ohm laboratory in August 2010.

Publications.

Zhang X, Shen X, Hao Y, Cai J, Ohm H, and Kong L. 2011. A genetic map of *Lophopyrum ponticum* chromosome 7E harboring resistance genes to Fusarium head blight and leaf rust. Theor Appl Genet (in press).

Hessian fly/wheat interactions, effects of antinutrient and toxic proteins on Hessian fly (Diptera: Cecidomyiidae) larvae: potential for transgenic resistance in wheat to complement native resistance.

Richard Shukle (USDA–ARS), Subhashree Subramanyam (Department of Agronomy), and Christie Williams (USDA–ARS).

Results from a recent evaluation of 21 of the 33 resistance (R) genes in wheat to Hessian fly documented that only five would provide protection of wheat in the southeastern United States where Hessian fly is a major pest. These results confirmed the need for new approaches to deployment of R genes and discovery of novel genetically engineered approaches to resistance that will complement native resistance. We have developed an in planta translocation feeding assay for Hessian fly larvae to initially screen antinutrient and toxic proteins as candidates for transgenic resistance. Although some of the antinutrient/toxic proteins we have evaluated may not kill infesting Hessian fly larvae quickly enough to prevent damage to a specific plant, they should prevent larvae from completing their development and virulent genotypes from emerging into field populations. Results from these studies will enable transgenic resistance in wheat to Hessian fly and significantly enhance the durability of deployed R genes.

Genotyping virulence to H13 wheat in field collections of Hessian fly from the southeastern United States.

Richard Shukle (USDA–ARS), G. David Buntin (Department of Entomology, University of Georgia, Griffin, GA), Kathy Flanders (Department of Entomology Auburn University, Auburn, AL), Alisha Johnson (USDA–ARS), Francis Reay-Jones (Department of Entomology Clemson University, Clemson, SC), Dominic Reisig (Department of Entomology North Carolina State University, Raleigh, NC), Brandi Schemerhorn (USDA–ARS), and Jeffrey Stuart (Department of Entomology).

In the southeastern United States, the Hessian fly is a major pest of wheat and causes significant yield losses to the region. Hessian fly is primarily controlled through the use of resistant wheat cultivars that carry resistance (R) genes. Wheat containing the R gene *H13* has been found to provide effective protection against Hessian fly attack in the Southeast. However, successive yearly deployment of *H13* wheat lines will put a selection pressure on field populations that contain a low frequency of virulence, which will eventually drive the population to become resistant to *H13*. Using pheromone traps, samples of Hessian fly were taken from fields across North Carolina, South Carolina, Georgia, and Alabama. Virulence was assessed using PCR to amplify vH13 (gene for virulence in the insect to *H13*). Avirulent (susceptible to *H13*) and virulent (can overcome *H13*) Hessian fly genotypes differed in amplicon size due to an insertion within exon 2 of vH13 that leads to inactivation of the gene in the insect and resistance to the R gene. Using this method, field populations can be monitored regularly to survey the efficacy of any R gene's ability to protect wheat by detecting the frequency of virulence in Hessian fly. When additional avirulence genes are identified, this quick and easy genotyping method could replace the current detection system which requires more time, effort, money and flies.

Annotation of genes from Hessian fly (Diptera: Cecidomyiidae).

Richard Shukle (USDA–ARS), and Jacob Shreve and Jeffery Stuart (Department of Entomology).

The Hessian fly is the major insect pest of wheat in the southeastern United States and has traditionally been controlled through the utilization of Hessian fly-resistance (R) genes in wheat. Such R genes are a limited resource, and once deployed lose their field effectiveness with time. Using 21 of the named R genes, a recent evaluation determined that only five of the R genes tested were able to provide adequate protection for wheat. Thus, there is a need for novel genetically engineered resistance to this pest. One approach to genetically engineered resistance in wheat is the possible application of plant mediated RNAi to target Hessian fly genes essential in its biology and interactions with wheat. To identify efficacious targets for plant mediated RNAi in transgenic resistance we are utilizing the newly available Hessian fly genome sequence to annotate Hessian fly genes.

Publications.

Arrueta LD, Shukle RH, Weise IL, and Mittapalli O. 2010. Gene characterization of two digestive serine proteases in *Sitodiplosis mosellana*: Implications for alternative control strategies. The Can Entomol 142:532-545.

Behura SK, Shukle RH, and Stuart JJ. 2010. Assessment of structural variation and molecular mapping of insertion sites of Desmar-like elements in the Hessian fly genome. Insect Mol Biol 19:707-715.

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Shukle RH, Subramanyam S, Saltzman KA, and Williams CE. 2010. Ultrastructural changes in the midguts of Hessian fly larvae feeding on resistant wheat. J Insect Physiol 56:754-760.

Wheat resistance to Hesssian fly, characterizing wheat genes involved in defense against Hessian fly.

Christie Williams, Andrea Hargarten, Jill Nemacheck, Subhashree Subramanyam, and Jacob Shreve.

GDSL-lipase. We identified a GDSL-lipase gene (through microarray) that may be involved in delivery of defense molecules through the plant cuticle to Hessian fly larvae. Verified through qPCR that GDSL-lipase gene expression profile matches expectations for a gene that reorganizes cutin to allow defense molecules out of cell during the limited time frame when resistant cells are known to be permeable.

Class III peroxidase genes. Through qPCR, we verified that class-III peroxidase genes become up-regulated during induced resistance to Hessian fly, supporting speculation that they are responsible for increase in activity of reactive oxygen species noted to contribute to resistance.

Dirigent gene. Through microarray and qPCR, we characterized expression of a gene encoding a dirigent-like protein that appears to be involved in production of lignan defense molecules in response to Hessian fly.

Personnel. Andrea Hargarten has joined the lab as an ARS research technician.

Publications.

Anderson JM, Bucholtz DB, Sardesai N, Santini JB, Gyulia G, Williams CE, and Goodwin SB. 2010. Potential new genes for resistance to *Mycosphaerella graminicola* identified in *Triticum aestivum* x *Lophopyrum elongatum* disomic substitution lines. Euphytica 172:251-262.

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KANSAS

KANSAS STATE UNIVERSITY
Environmental Physics Group, Department of Agronomy, 2004 Throckmorton Plant Sciences Center, Manhattan, KS 66506-5501, USA.

Edema.

M.B. Kirkham.

Current research concerns edema, which is an abnormal accumulation of fluid in plant cells. The research is being carried out in association with Kimberly A. Williams and Sunghun Park in the Department of Horticulture, Forestry, and Recreational Resources, along with graduate student Qingyu Wu. Nicole Rud, another graduate student who also worked on the project, graduated in December, 2009. Edemata are a physiological disorder, not caused by any pathogen. They occur only under greenhouse conditions, and in the past, they have been thought be due to overwatering. Because wheat is usually grown in the field, edemata on wheat apparently have not been documented. We reported last year that lack of ultraviolet light was a cause for edemata (also called intumescences or enations) in tomato plants. The glass of greenhouses filters out ultraviolet light, which makes the plants susceptible to the intumescences. When we added back UV-B light to the tomato plants grown under greenhouse conditions, they did not develop the intumescences. Kirkham and Keeney (1974) associated the formation of enations on leaves of potato, which they observed under controlled environmental conditions, with the presence of abnormal amounts of ethylene, a gaseous hormone. We are carrying out research to determine the biochemical reason for the formation of the intumescences in tomato.

Reference.

Kirkham MB and Keeney DR. 1974. Air pollution injury of potato plants grown in a growth chamber. Plant Dis Rep 58:304-306.

News.

Ms. Kalaiyarasi Pidaran is continuing work toward the master's degree. Under greenhouse conditions, she is studying the effect of water deficit on sorghum hybrids varying in maturity.

The book on carbon dioxide, cited last year, will be published by CRC Press in late March, 2011 (see Publications, below). Here is an excerpt from the epilogue:

> "Because elevated carbon dioxide stimulates growth, yield is usually increased under elevated carbon dioxide. In a classic paper, Kimball (1983) analyzed more than 430 observations of the yield of 37 species grown with CO_2 enrichment, which were published in more than 70 reports of experiments carried out in a 64 year period beginning in 1918. His analysis showed that, with a doubling of atmospheric CO_2 concentration, yield probably will increase by 33%. In this book I have not cited papers dealing with models, except in passing. My focus has been on data published in refereed journal articles. However, Ken Caldeira at the

Carnegie Institution for Science in Stanford, California has modeled plant growth under elevated CO_2. He and his colleagues (Govindasamy et al. 2002) have found that "doubling the amount of carbon dioxide while holding steady all other inputs—water, nutrients, and so forth—yields a 70 percent increase in plant growth, an obvious boon to agricultural productivity" (Levitt and Dubner 2009, p. 185). This is an even greater increase than that documented by Kimball (1983). The year to year increases in crop yields that have been observed during the last 50 years, since Charles Keeling first started to record the CO_2 concentration in the atmosphere in 1958, probably are related, in part, to the increased CO_2 concentration in the atmosphere. If other factors controlling plant growth are neglected, we can calculate that yields are 7% more in 2008 than in 1958 due to the increase in atmospheric CO_2. The elevated levels of CO_2 in the air probably are adding to our food security without our recognizing it.

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Publications.

Douglas-Mankin KR, Precht K, Kirkham MB, and Hutchinson SL. 2010. Reclamation of abandoned swine lagoon soils using hybrid poplar in a greenhouse soil-column study. Internat J Agric Biol Eng 3:44-51.

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Kirkham MB. 2011. Review of book: Facts about Global Warming: Rational or Emotional Issue? by M Kutílek and DR Nielsen (Catena Verlag, Reiskirchen, Germany, 2010, 227 pp). CEP Newsletter, Center for Economic Policy, Prague, Czech Republic (In press).

Kirkham MB. 2011. Elevated Carbon Dioxide: Impacts on Soil and Plant Water Relations. CRC Press, Taylor and Francis Group (In press).

Kirkham MB and Liang GH. 2011. Review of book: From Dawn to Dawn: China's Journey to Agricultural Self-Sufficiency by TC Tso (Booklocker, Bangor, Maine, 2010, 260 pp). J Envir Quality (In press).

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Unger PW, Kirkham MB, and Nielsen DC. 2010. Water conservation for agriculture. *In:* Soil and Water Conservation Advances in the United States (Zobeck TM and Schillinger WF, Eds). SSSA Special Publication 60, Soil Science Society of America, Madison, Wisconsin. Pp. 1-45.

KANSAS STATE UNIVERSITY
Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Department of Agronomy, and the USDA–ARS Hard Red Winter Wheat Genetic Research Unit, Throckmorton Plant Sciences Center, Manhattan, KS 66506-5501, USA.

Notice of release of KS12WGGRC55 (TA5092) hard red winter wheat germ plasm homozygous for the ph1b gene.

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Kansas Agricultural Experiment Station announces the release of KS12WGGRC55 (TA5092) hard red winter wheat germ plasm homozygous for the *ph1b* gene for breeding and experimental purposes. KS12WGGRC55 is derived from the cross 'Overley/TA3809 F_2//Overley F_2/3/Amadina F_2', where TA3809 is a Chinese Spring stock homozygous for the *ph1b* mutant allele, which is a 70-Mbp deletion at the pairing homoeologous (*Ph1*) locus. In homozygous *ph1b* plants, homoeologous wheat chromosomes and, in 'wheat x alien' species hybrids, homoeologous wheat and alien chromosomes from related species can pair and recombine, allowing the production of wheat-alien recombinants. KS12WGGRC55 is homozygous for *ph1b*, which results in homoeologous chromosome pairing in about 46% of the pollen mother cells. The transfer of *ph1b* to adapted hard red winter wheats will accelerate the production and evaluation of wheat-alien recombinants under field conditions and their use in wheat improvement.

Small quantities (3 grams) of seed of KS12WGGRC55 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506.

Notice of release of KS12WGGRC56 (TA5619, TA5620, TA5621) stem rust-resistant wheat germ plasm.

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The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS12WGGRC56 wheat germ plasm with resistance to stem rust *Sr51* for breeding and experimental purposes. KS12WGGRC56 has the short arm $3S^sS$ derived from *Ae. searsii* translocated to the long arms of wheat chromosomes 3A, 3B, and 3D in the form of the Robertsonian translocations T3AL·$3S^sS$ (KS12WGGRC56-3AL, TA5619), T3BL·$3S^sS$ (KS12WGGRC56-3BL, TA5620), and T3DL·$3S^sS$ (KS12WGGRC56-3DL, TA5621), respectively. KS12WGGRC56-3AL is derived from the cross 'TA3809/TA6555 F_4', where TA3809 is the Chinese Spring stock homozygous for the homoeologous pairing mutant allele *ph1b* and TA6555 is a Chinese Spring–*Ae. searsii* disomic substitution line where the *Ae. searsii* chromosome $3S^s$ is substituting for the loss of wheat chromosome 3A (DS3S^s(3A). KS12WGGRC56-3BL is derived from the cross 'TA3809/TA6556 F_4', where TA6556 is a Chinese Spring–*Ae. searsii* disomic substitution line where the *Ae. searsii* chromosome $3S^s$ is substituting for the loss of wheat chromosome 3B (DS3S^s(3B); and KS12WGGRC56-3DL is derived from the cross 'TA3809/TA6557 F_4', where TA6557 is a Chinese Spring–*Ae. searsii* disomic substitution line where the *Ae. searsii* chromosome $3S^s$ is substituting for the loss of wheat chromosome 3D (DS3S^s(3D). The $3S^sS$ arm has a gene conferring resistance to stem rust (*Puccinia graminis* f. sp. *tritici* Eriks. & E. Henn.) races RKQQC and TTKSK designated as *Sr51* . The T3AL·$3S^sS$, T3BL·$3S^sS$, and T3DL·$3S^sS$ stocks are new sources of resistance to Ug99, are cytogenetically stable, and may be useful in wheat improvement.

Small quantities (3 grams) of seed of KS12WGGRC56 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506.

Noatice of release of KS12WGGRC57 (TA5617) stem rust-resistant wheat germ plasm.

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The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS12WGGRC57 hard red winter wheat germ plasm with the stem rust resistance gene *Sr52* for breeding and experimental purposes. KS12WGGRC57 is derived from the cross 'TA3060/TA7682 F_3', where TA3060 is a Chinese Spring wheat stock monosomic for chromosome 6D (CSM6D) and TA7682 is a Chinese Spring–*Dasypyrum villosum* disomic chromosome addition line for the *D. villosum* chromosome 6V#3 (DA6V#3). KS12WGGRC57 has the long arm 6V3#L derived from *D. villosum* translocated to the short arm of wheat chromosome 6AS in the form of a Robertsonian T6AS·6V#3L translocation. The 6V3#L arm in T6AS·6V#3L has a gene conferring resistance to stem rust (*Puccinia graminis* f. sp. *tritici* Eriks. & E. Henn.) (races RKQQC and TTKSK) designated as *Sr52*. *Sr52* is temperature-sensitive and is most effective at 16°C, partially effective at 24°C, and ineffective at 28°C. The T6AS·6V#3L stock is a new source of resistance to Ug99, is cytogenetically stable, and may be useful in wheat improvement.

Small quantities (3 grams) of seed of KS12WGGRC57 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506.

Notice of release of KS12WGGRC58 (TA5630, TA5625, TA5643) stem rust-resistant wheat germ plasm.

B. Friebe, W. Liu (Laboratory of Cell and Chromosome Engineering, College of Life Sciences, Henan Agricultural University, Zhengzhou, Henan 450002, PR China), D.L. Wilson, W.J. Raupp, M.O. Pumphrey (Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA), J. Poland and R.L. Bowden (USDA–ARS Hard Winter Wheat Genetic Research Unit), A.K. Fritz (Department of Agronomy), and B.S. Gill.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS12WGGRC58 wheat germ plasm with resistance to stem rust *Sr53* for breeding and experimental purposes. KS12WGGRC58 has a segment of the long arm 5M^{g}L derived from *Ae. geniculata* in the form of an interstitial translocation Ti5DS·5DL-5M^{g}L-5DL (KS12WGGRC58-Ti, TA5630) and terminal translocations T5DL-5MgL·5M^{g}S (KS12WGGRC58-T1, TA5625) and T5DL-5MgL·5M^{g}S (KS12WGGRC58-T2, TA5643). KS12WGGRC58-Ti is derived from the cross 'TA5599/Lakin F_3', where TA5599 is a wheat–*Ae. geniculata* terminal translocation stock consisting of part of the long arm of wheat chromosome 5D, part of the long arm of the *Ae. geniculata* chromosome arm 5M^{g}L, and the complete short arm 5M^{g}S, and Lakin is a Kansas hard red winter wheat cultivar. KS12WGGRC58-T1 and KS12WGGRC58-T2 are derived from the cross 'TA5599/TA3808 F_3' where TA3809 is the Chinese Spring stock homozygous for the homoeologous pairing mutant allele *ph1b*, with 5M^{g}L shortened by 10% and 20%, respectively, compared to that of TA5599. The 5M^{g}L arm has a gene conferring resistance to stem rust (*Puccinia graminis* f. sp. *tritici* Eriks. & E. Henn.) races RKQQC and TTKSK designated as *Sr53*. The Ti5DS·5DL-5M^{g}L-5DL and T5DL-5MgL·5M^{g}S stocks are new sources of resistance to Ug99, are cytogenetically stable, and may be useful in wheat improvement.

Small quantities (3 grams) of seed of KS12WGGRC58 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506.

Notice of release of KS12WGGRC59 wheat streak mosaic virus- and Triticum mosaic virus-resistant wheat germ plasm.

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The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS12WGGRC59 hard red winter wheat germ plasm with resistance to wheat streak mosaic virus and *Triticum* mosaic virus for breeding and experimental purposes. KS12WGGRC59 is derived from the cross 'TA3061/TA7700//TA3809 F_4', where TA3061 is a Chinese Spring wheat stock monosomic for chromosome 7D (CSM7D), TA7700 is a ditelosomic wheat–*Thinopyrum intermedium* addition line having the long *Th. intermedium* chromosome arm 7S#3L added to the wheat genome, and TA3809 is a Chinese Spring stock homozygous for the *ph1b* mutant allele. KS08WGGRC59 has the 7S#3L translocated to the short arm of wheat chromosome 7B in form of the Robertsonian translocation T7BS·7S#3L. The 7S#3L arm has a gene conferring resistance to Wheat streak mosaic virus (WSMV) and *Triticum* mosaic virus (TriMV) designated as *Wsm3*. *Wsm3* confers resistance to WSMV at 18°C and 24° and also confers resistance to TriMV at 18°C but is not effective against this virus above 24°C. The T7BS·7S#3L stock is a new source of resistance to WSMV and TriMV, is cytogenetically stable, and may be useful in wheat improvement.

Small quantities (3 grams) of seed of KS12WGGRC59 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506.

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NEBRASKA

UNIVERSITY OF NEBRASKA AND THE USDA–ARS GRAIN, FORAGES AND BIOENERGY UNIT.
Lincoln, NE, USA.

In 2010, 1,600,000 acres of wheat were planted in Nebraska and 1,490,000 were harvested with an average yield of 43 bu/acre for a total production of 64,070,000 bu. This crop would be considered a small crop. Autumn rains in 2009 prevented much of eastern Nebraska from harvesting corn and soybeans in time to plant wheat after the summer crop. In 2009, 1,700,000 acres of wheat were planted in Nebraska and 1,600,000 were harvested with an average yield of 48 bu/acre for a total production of 76,800,000 bu. In 2008, 1,750,000 acres of wheat were planted in Nebraska and 1,670,000 were harvested with an average yield of 44 bu/acre for a total production of 73,500,000 bu.

New cultivars.

In 2010, two new wheat cultivars were formally released. **NE01481**, to be marketed as **Husker Genetics Brand McGill**, in honor of a legendary professor of genetics at the University of Nebraska, was selected from the cross 'NE92458/Ike'. The pedigree of NE92458 is 'OK83201/Redland' and the pedigree of OK83201, an experimental line developed by Oklahoma State University is 'Vona//Chisholm/Plainsman V'. McGill was recommended for release primarily due to its superior adaptation to rainfed wheat production systems in eastern and west central Nebraska and its excellent resistance to wheat soil borne mosaic virus (WSBMV). McGill is moderately resistant to moderately susceptible to stem rust (caused by *Puccinia graminis Pers.: Pers. f. sp. tritici* Eriks & E. Henn.) in field nursery tests inoculated with a composite of stem rust races (RCRS, QFCS, QTHJ, RKQQ, and TPMK). In greenhouse tests, it is resistant to races TPMK, QFCS, and RCRS, but susceptible to race TTTT and RKQQ. It is moderately resistant to moderately susceptible to leaf rust (caused by *P. triticina* Eriks), and moderately susceptible to susceptible to stripe rust (caused by *P. striiformis* Westendorp f. sp. t*ritici*). McGill is susceptible to Hessian fly (*Mayetiola destructor* Say) and to wheat streak mosaic virus (field observations in NE). McGill has acceptable milling and baking end-use quality.

The second line is **NI04421**, which will be marketed as **Husker Genetics Brand Robidoux** in honor of a pioneer French trapper who had a trading post between Nebraska and Wyoming. Robidoux was selected from the cross 'NE96644/Wahoo (sib)' where the pedigree of NE96644 is 'Odesskaya P/Cody//Pavon 76/3*Scout 66'. Robidoux was released primarily for its superior performance under irrigation and rainfed conditions in western Nebraska (west of North Platte, where drought is common) and irrigated production sites in western Nebraska and eastern Wyoming. This cultivar seems to have good drought tolerance and does best in irrigated environments in the drier areas (eastern WY). Robidoux is moderately resistant to stripe rust (caused by *P. striiformis* Westendorp f. sp. t*ritici*), moderately resistant to moderately susceptible to stem rust (caused by *P. graminis Pers.: Pers. f. sp. tritici* Eriks & E. Henn.) in field nursery tests inoculated with a composite of stem rust races, moderately susceptible to leaf rust (caused by *P. triticina* Eriks). Robidoux is susceptible to Hessian fly (*M. destructor* Say) and to wheat streak mosaic virus. Robidoux is susceptible to common bunt (syn. stinking smut, caused by *Tilletia spp*.) and seed treatments are recommended. Where common bunt was present, Robidoux was the only line with the tell-tale odor and diseased kernels. The overall end-use quality characteristics for

Robidoux are acceptable and similar to many commonly grown wheat cultivars which are well received by the milling and baking industries.

Two additional lines are under increase for possible release in 2011 (NE03490 and NE04490), however, NE03490 is adapted to the same environments as Robidoux and NE04490 is adapted to the same environments as McGill. Hence, it is difficult to predict if these lines will have sufficient merit to be released.

Use of wheat synthetics to expand our genepool.

K. Onweller, R. Ward, P.S. Baenziger, Y. Jin, R. Bowden, S. Wegulo, C. Baker, R. Graybosch, and P. Byrne.

A collaborative effort with Colorado State University to use CIMMYT-developed wheat synthetic lines as sources for drought tolerance led us to further characterize six synthetic CIMMYT wheat lines. In our these studies, we discovered some lines were resistant to *P. graminis, P. striiformis*, and *Schizaphis graminum*. Two of the six lines possessed resistance to stem rust races in the Ug99 family. Studies to determine the identity of the genes are underway. Based on phenotyping of the synthetic parental lines at the Cereal Disease Laboratory in Minnesota, it has been hypothesized that the resistance in the synthetic parental lines may be from *Sr33*. *Sr45* will be tested for as well, as *Sr33* and *Sr45* are both derived from *Ae. tauschii* and are located on chromosome 1DS. Both genes have been shown to confer resistance to numerous races of stem rust, including Ug99. All synthetic lines exhibited seedling resistance and five exhibited adult resistance to *P. striiformis* race PST-100. Two different synthetic lines conferred excellent resistance to greenbug biotypes E, I, and K. A detailed inheritance study was undertaken with the assistance of Cheryl Baker (USDA–ARS, OK) to identify the genetic constitution of the resistance. Preliminary data suggest that single, dominant genes are acting in each synthetic line. In addition to resistance, the synthetic lines were assayed for high-molecular-weight glutenin and gliadin composition. The work revealed protein subunit compositions not commonly found in the Great Plains wheat cultivars.

Understanding the stem rust resistance in Gage wheat.

T. Kumsa, P.S. Baenziger, S. Wegulo, M. Rouse, and Y. Jin.

With the advent of stem rust race Ug99, understanding and developing better stem rust resistance is again in the attention of wheat community. In this project, we are interested in understanding the *Sr2* complex in Gage (a Nebraska cultivar released in 1965), which historically was superior to Scout 66 (a wheat cultivar that also carried the *Sr2* gene). Our goal is to understand the nature of Gage's superior resistance to stem when compared to that found in many other *Sr2* cultivars. With a newly developed marker csSr2, we confirmed the presence of *Sr2* in this cultivar. We are advancing generation to obtain $F_{2:3}$ families from crosses made between Bill Brown (susceptible cultivar) and Gage. These families will be used for phenotyping and genotyped to understand the *Sr2* complex. As part of this research, we also are collecting additional sources of resistance and pyramiding effort these genes. For example, using molecular markers it is hypothesized that some of the Nebraska lines contain both *Sr2* and *Sr24*. Crossing these lines to lines with *Sr36* and *Sr26* sources have been made to pyramid the resistance genes. We have collected useful germplasm for *Sr39*, *Sr40*, and *SrR*. Molecular markers and phenotyping will be used for selection and backcrossing.

Association mapping for important biotic and abiotic related traits in a structured wheat breeding population.

I. Salah, D. Wang, K. Eskridge, J. Crossa, and P.S. Baenziger.

The main objectives of this research are to apply association mapping and whole genome selection approaches to identify DArT and SSR markers associated with important traits in structured wheat breeding population and determine a marker-based kinship matrix and study the impact of selection (decreasing the number of lines as is commonly done in breeding programs) on genetic diversity. We grew 280 genotypes of hexaploid winter wheat plus two check cultivars in our preliminary nursery and harvested in nine environments during the 2009–10 season. Based on the phenotypic and molecular marker data, we clustered these lines into three groups. Then, we selected the best 57 genotypes from the 280 lines for advancement to the intermediate nursery (Nebraska Triplicate Nursery, year 2). We will evaluate the

57 genotypes using the same molecular markers and obtain new phenotypic data at similar locations throughout NE, but in replicated experiments. In the following year, approximately 25 lines will be advanced to the Nebraska Intrastate Nursery (year 3). We will also repeat this process for an additional 280 new genotypes in year 2, which will be advanced to 57 genotypes in year 3.

Preharvest sprouting derived from red/white wheat mating populations.

Juthamas Fakthongphan, R. Graybosch, and P.S. Baenziger.

Preharvest prouting (PHS) of wheat, the premature germination of wheat heads, takes place in a field under conditions of delayed harvest, high humidity, or wet conditions. This problem has a high economic impact on farmers and end-users. Wheat breeders have tried to diversify the wheat production system in Nebraska by introducing hard white winter wheat cultivars. T he grain yield potential and disease resistance have been increased but the current germ plasm of hard white winter wheat lacks some essential quality traits such as low levels of grain enzyme polyphenol oxidase, and resistance to PHS. Both traits will be important issues once the U.S. exports white wheat to the world markets. This research will focus on identifying red wheat parents capable of donating genes for tolerance to PHS, mapping or confirming which markers are applicable for the Great Plains hard white wheat gene pool, and analyzing the ABA sensitivity in these materials to correlate the misting assay for PHS to ABA response.

Modified food starches from waxy and partial waxy durum wheats.

L.E. Hansen, R. Graybosch, D. Jackson, and R. Wehling.

Partial waxy (reduced-amylose) and fully waxy (amylose-free) tetraploid wheats were developed by introgression of null alleles at the *Wx-A1* and *Wx-B1* loci from common hexaploid wheat. Purified starches were obtained from each genotype, and chemically modified by cross-linking with phosphorus (V) oxychloride, substitution with propylene oxide, and sequential cross-linking with phosphorus (V) oxychloride followed by substitution with propylene oxide. Functional properties were compared to blends of tetraploid waxy and wild-type starches of known amylose contents. Significant differences in functionality were observed amongst the genotypes and blends after each modification. Waxy (0% amylose) and wild-type (30% amylose) were very often at the extremes of the observed ranges of functional properties. In general, the functional properties of the chemically modified starches were dependent upon amylose content. Starches from *Wx-B1* null lines (24% amylose), were an exception. After substitution, such starches had the significantly highest value for RVA final viscosity, and generally performed in a manner similar to starch blends of 12–18% amylose.

Genetic improvement in U.S. hard winter wheats.

R. Graybosch and C.J. Peterson.

Data from USDA-coördinated winter wheat regional performance nurseries collected over the time period 1959–2008 were used to estimate genetic gain (loss) in grain yield, grain volume weight, days to heading, and plant height in winter wheats adapted to the Great Plains. In both the Southern Regional (SRPN) and Northern Regional Performance Nurseries (NRPN), linear regression revealed significant positive relationships between relative grain yields of advanced breeding lines and calendar year of the nursery trial. The estimated genetic gain in grain yield potential since 1959 was approximately 1.1% (of the control cultivar Kharkof)/yr for all entries in the SRPN, and 1.3%/yr if only the most productive entry was considered. For the NRPN, the estimates of genetic gain in grain yield were 0.79%/yr for all entries and 0.79%/yr for the most productive entry. Relative grain volume weights and days to heading have remained fundamentally unchanged since 1959, but relative plant heights have declined at rates of approximately 0.43%/yr in the SRPN and 0.32%/y in the NRPN. Linear regressions of relative grain yields versus year over the time period 1984–2008, however, showed no significant trend in the SRPN, and a very weak positive slope in the NRPN. Relative grain yields of Great Plains hard winter wheats may have peaked in the early to mid-1990s, and further improvement in the genetic potential for grain yield awaits some new technological or biological advance.

Fun with transgenic glutenins.

R. Graybosch, A. Blechl, B. Seabourne, and Y.R. Chen.

Quality and agronomic effects of three transgenic high-molecular-weight glutenin subunit (HMW-GS) events were characterized in advanced-generation breeding lines of hard winter wheat in three Nebraska crop years. Two of the transgenic events studied, Dy10-E and B52a-6, over-express HMW-GS 1Dy10, and the third event, Dx5+Dy10-H, over-expresses HMW-GS 1Dx5 and, to a much lesser extent, 1Dy10. In addition, novel proteins, possessing solubility characteristics defining them as HMW-GS, were present in Dx5+Dy10-H and B52a-6. Average grain yield of lines derived from the three transgenic events was statistically lower than that of a group of control cultivars and advanced breeding lines, but not lower than the mean of their respective non-transgenic sibs. Grain hardness was influenced by one of the events. Dx5+Dy10-H produced harder kernels than controls, its non-transgenic sister lines, and the two additional transgenic events. All three events produced doughs with unusual mixing properties, likely not directly useful in commercial applications. As a consequence, loaf volumes were depressed, but to variable degrees by the three events. The results indicated that over-expression of HMW-GS could eventually lead to improved bread-making quality by optimizing the level of over-expression or by development and characterization of additional events.

Breeding hopeful monsters (waxy wheats).

R. Graybosch, P.S. Baenziger, and F. Dowell.

Seed of the waxy wheat line NX04Y2107 was increased by UNL Foundation Seed and entered in the 2011 NE State Variety Trials. A second waxy line, NX05MD4180-6, was tested in both the 2010 NRPN and Uniform Eastern Soft Wheat Trial and advanced to state yield trials in NE and NY. Twenty-five waxy wheat lines of diverse parentage were selected for inclusion in advanced yield trials to be seeded in NE and OH. An additional 50 lines from 2010 field trials were advanced to a preliminary yield trial. Automated NIR-based seed sorting technology at the USDA–ARS Center for Grain and Animal Health Research has proven an invaluable aid in the breeding of waxy wheat. The technology allows automated segregation and recovery of waxy seed from segregating F_3 bulk populations.

Public private (University of Nebraska) collaborations.

In 2009, the University of Nebraska decided to sustain the wheat breeding project via enhanced collaborations with commercial companies spanning the value chain. The University of Nebraska–Lincoln (UNL) has had a long standing arrangement with BASF, providing access to the Clearfield technology. In 2009, UNL began a collaboration with ConAgra. In 2010, UNL developed a collaboration with Bayer Crop Science that allows nonexclusive access to UNL germ plasm and is in accordance with the principles for collaboration approved by the National Association of Wheat Growers and with the U.S. Wheat Associates Joint Biotechnology Committee. USDA–ARS projects at the University of Nebraska are not party to these agreements.

Personnel.

Anyamanee Auvachanon (currently a lecturer in Thailand), Neway Mengistu (currently a corn breeder with Pioneer Hibred), and Nicholas Crowley (currently a corn breeder with Pioneer Hibred) successfully completed their Ph.D. Juthamas Fakthongphan and Santosh Rajput began their Ph.D. program. Russell Ward and Sumardi bin Haji Abdul Hamid began their M.S. program. Dr. Devin Rose was hired with a joint appointment in the Food Science and Agronomy and Horticulture Departments as a cereal chemist who will oversee our wheat quality laboratory.

Publications.

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NEW YORK

BORLAUG GLOBAL RUST INITIATIVE
Cornell University, Ithaca, NY USA.

Message from Ronnie Coffman, Vice Chair of the Borlaug Global Rust Initiative (BRGI)

Dear friends and colleagues,

Thank you and commendations to the 250 participants from 33 different countries who attended this year's BGRI Technical Workshop in St. Paul, Minnesota, 13-16 June. We were there to network, share successes and challenges related to wheat rust, and learn from each other.

The meeting kicked off with the Field Day organized by our hosts at the USDA–ARS Cereal Disease Laboratory (CDL) and the University of Minnesota (UMN), Norman Borlaug's alma mater. The morning began with addresses from our chair, Jeanie Borlaug Laube, and the Honorable Minister of Agriculture of Bangladesh, Matia Chowdhury. Katherine Kahn, DRRW Program Officer at the Bill & Melinda Gates Foundation (BMGF), confirmed DRRW Phase II funding—$40M over five years from the BMGF and the U.K. Department for International Development (DFID). Rob Bertram, of USAID, spoke about some of the new commitments his agency is making to combat threats to the world's food supply.

Most significantly, Dr. Edward Knipling of the USDA and Rob Bertram of USAID, the lead funding agencies, led the groundbreaking ceremony for the new USDA–ARS CDL greenhouse. This investment will enable CDL researchers to expand their capacity to analyze rust samples collected at home and abroad.

Partners from the UMN and the CDL orchestrated the small grains field tour and demonstrations in the molecular diagnostic facilities on campus, as well as activities highlighting the University's rich history in rust research as E.C. Stakman's home and Borlaug's alma mater.

In the technical program that ensued at the Crowne Plaza Hotel on 14-16 June, speakers shared research findings in the areas of surveillance, molecular pathology, molecular breeding, and development and delivery of rust-resistant varieties, among other areas.

I was impressed by the 2011 Jeanie Borlaug Laube Women in Triticum Early Career and Mentor awardees who were announced during lunch on Tuesday (see related article below).

Another highlight of this year's program was the 'Competitive Graduate Student Symposium,' chaired by Bob McIntosh. Yuan Chai, Iago Lowe, and Jessica Rutkoski were selected based on the high quality abstracts they submitted for the poster session. They each gave a full talk in the plenary session, received free registration to the workshop, and a cash prize of $1,000. The session will recur each year in order to highlight the compelling research being conducted by the next generation of wheat rust workers. I know Dr. Borlaug would have been as pleased as I was to see such talent and leadership among the rising wheat and rust scientists.

Ambassador, Kenneth Quinn, from the World Food Prize Foundation, honored us by closing the meeting with a reminder of how we can all carry on Dr. Borlaug's vision of a more peaceful and food-secure world.

With the 2011 meeting behind us, I am looking forward to helping Dr. Wanquan Chen plan an equally inspired meeting in Beijing next year. Please make plans to join us the first week of September 2012 in the dynamic city of Beijing, immediately following the International Cereal Rusts and Powdery Mildew Conference.

Enjoy this quarter's newsletter. Keep up the good work!

Ronnie Coffman, Vice Chair
Borlaug Global Rust Initiative

The Jeanie Borlaug Laube Women in Triticum Awards.

The 2011 Jeanie Borlaug Laube Women in *Triticum* (or WIT) awardees were honored on 14 June, 2011 at the BGRI Technical Workshop during a special luncheon seminar in which Lucy Gilcrist gave a talk about her experiences as a woman in plant breeding research from 1960–80, and Hans Braun of CIMMYT gave his perspective on women's involvement in wheat breeding.

WIT Early Career Award. Five women scientists working in wheat, who ranged from advanced undergraduates to recent Ph.D. graduates and post-doctoral fellows, received 2011 Jeanie Borlaug Laube Women in Triticum (WIT) Early Career Awards. 'All of the WIT awardees would have made my father proud', said Jeanie Borlaug Laube, the daughter of Nobel Laureate Dr. Norman E. Borlaug and chair of the BGRI, for whom the awards are named, in announcing the awards. 'We are building a wheat-secure future with women scientists who are outstanding in wheat fields, molecular

laboratories, nurseries, or wheat-filled greenhouses.' Award winners received support to attend the annual BGRI Technical Workshop, and a training program at CIMMYT in Obregon, Mexico.

Awatif Abd El Lateef Farag Alla, from Sudan, who is conducting her Ph.D. research in plant breeding, genetics, and physiological dissection of heat and drought tolerance at ICARDA in Syria, under the guidance of Francis Ogbonnaya and Osman S. Abdalla, is working on improving wheat production in the face of global climate change.

Caixia Lan, who earned her Ph.D. in 2010 in Crop Genetics and Breeding from the Institute of Crop Science at the Chinese Academy of Agricultural Sciences, served as a lecturer in the College of Plant Science and Technology of Huazhong Agricultural University in July 2010 and worked on molecular breeding for wheat diseases resistance. Caixia continues her focus on adult-plant resistance today as a post doctoral researcher in Ravi Singh's spring bread wheat breeding program at CIMMYT in Mexico, where she works with Sybil Herrera.

Ida Paul, from South Africa (who was not able to attend the workshop), is a small grain pathologist at the Agricultural Research Council Small Grain Institute where she serves as program manager for the crop protection division. She manages 17 research projects throughout South Africa of which 13 are related to the protection of wheat against pests and diseases. Additionally, she is the main investigator in two research projects that optimizes the use of fungicides in wheat and barley. Ida received her Ph.D. in Environmental Studies from the University of Pretoria in 2006.

Silvia Barcellos Rosa, a native of Brazil who is pursuing her Ph.D. on leaf rust resistance, is supervised by Brent McCallum at Agriculture and Agrifood Canada, and Anita Brule-Babel at the University of Manitoba, Winnipeg. Silvia is particularly interested in non race-specific genes as promising sources to control leaf rust.

Stephanie Walter, from Germany, is a post-doctoral researcher in Mogens Hovmoller's group at Aarhus University in Denmark. Stephanie, whose Ph.D. was in the field of cellular and molecular biology, is working to dissect the genome of stripe rust and discover effectors that play a key role in the interaction between the wheat host and the stripe rust pathogen.

WIT Mentor Award. During the luncheon, the first WIT Mentor Award was presented to Leslie Boyd, research group leader and cereal rust pathologist at the John Innes Centre, in Norwich, UK. This award recognizes mentors of both genders who have proven to be excellent models for women working in *Triticum* and its nearest relatives. Recipients of the WIT Mentor Award receive a cash honorarium as well as the honor of organizing a session at the subsequent year's BGRI technical workshop.

Lesley was recognized for the support she gives to young female researchers in cereal sciences. As a scientist, she is passionate about her own research and instinctively supports the research and passion for science in others, female and male, young and more mature. 'Passions should be nurtured, not trampled upon,' said Boyd. Currently, Dr. Boyd is investigating the genetics and modes of action of resistance in wheat to fungal diseases that include yellow rust, stem rust, and blast of wheat. Her work covers both aspects of classical genetics of durable forms of disease resistance in wheat, as well as molecular and cellular dissection of the mechanisms behind resistance, including non-host resistance.

One of Boyd's former students, Hale Ann Tufan, from Turkey, was a 2010 recipient of the WIT Early Career Award.

For more information about the awards or to apply for the WIT Early Career Award or to or to submit a WIT Mentor Award nomination, visit http://www.bgriwit.org. The deadline for applications is 1 October, 2011.

From the BGRI blog.

Video highlights from the BGRI workshop in St Paul Minnesota are posted on the BGRI blog: Matia Chowdury, Dave Hodson, and Kenneth Quinn (http://globalrust.org).

Wheat briefs.

The Ug99 threat: disease movement and solutions. During the week of 13 June, wheat disease researchers from around the world attended the annual meeting of the Borlaug Global Rust Initiative, held in Minnesota. On Wednesday morning during a break from the proceedings, Ronnie Coffman, director of Cornell University's Durable Rust Resistance in Wheat project, spoke with Delta Farm Press about Ug99's progression, expectations for research, and the need for agricultural research funding.

Science in Africa: The Wheat Stalker. Scientists are fighting damaging wheat fungi from East Africa, but breeding new crops won't help unless farmers plant them.

Bill Gates Speaking at Chicago Council on Global Affairs. U.S. and Canadian wheat farmers lost 40 percent of their crop in the 1950s to wheat rust. Today, a form of rust called Ug99, first seen in Uganda, has spread up to the Middle East, down to South Africa, and is now threatening India. Our foundation has joined USAID, DFID, and others in funding research against this disease, but more funds are needed. It's crucial for avoiding disaster, not just from this disease, but also from the ones to come.

Improving wheat for food security. An agreement between the Ministers of Agriculture of the G20 on 23 June, 2011, in Paris underlines the importance of increasing world agricultural production, in particular that of wheat, to resolve the challenges of hunger and food price volatility. Already very active on this issue, INRA, together with other national and international research and funding organizations from about 10 countries, will launch the International Research Initiative for Wheat Improvement (IRIWI) this year.

Upcoming events and deadlines.

2nd International Plant Phenotyping Conference, 5-7 September 2011, Jülich, Germany.
https://www.congressa.de/phenosymp2011/

Women in *Triticum* Awards Deadline.
1 October, 2011 is the deadline to apply for the WIT Early Career Award or to submit a WIT Mentor award. For more information about the awards or to apply, visit http://www.bgriwit.org.

Recent publications.

Liu W, Rouse M, Friebe B, Jin Y, Gill BS, and Pumphrey MO. 2011. Discovery and molecular mapping of a new gene conferring resistance to stem rust, *Sr53*, derived from *Aegilops geniculata* and characterization of spontaneous translocation stocks with reduced alien chromatin. http://globalrust.org/traction/permalink/references1614

Rouse MN, Wanyera R, Njau P, and Jin Y. 2011. Sources of resistance to stem rust race Ug99 in spring wheat germplasm. http://globalrust.org/traction/permalink/references1613

Singh RP, Hodson DP, Huerta-Espino J, Jin Y, Bhavani S, Njau P, Herrera-Foessel S, Singh PK, Singh S, and Govindan V. 2011. The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. http://globalrust.org/traction/permalink/bgriiwc173

Strategies to reduce the emerging wheat stripe rust disease. Summary of International Wheat Stripe Rust Symposium, Aleppo, Syria, April 2011. http://icardablog.files.wordpress.com/2011/06/icarda-stripe-rust-research-to-action-report_low-res.pdf

People in the news.

Hodson on the move. David Hodson, currently employed by the FAO in Rome, will relocate in August to CIMMYT and be based in Addis Ababa, Ethiopia. Hodson is the international focal point for stem rust surveillance and will carry this role with him in his new location.

Dubcovsky wins fellowship to help feed the world. Wheat geneticist Jorge Dubcovsky is one of two plant biologists at UC Davis to be among the first-ever class of HHMI–GBMF Investigators, funded jointly by the Howard Hughes Medical Institute and the Gordon and Betty Moore Foundation. Professor Dubcovsky and Simon Chan, assistant professor in the

Department of Plant Biology, are among 15 recipients nationwide of the new awards program, to be supported with $75 million from the two organizations over the next five years. From Plant Sciences Weekly Newsletter, 17 June, 2011.

Felister Mbute Nzuve receives African Women in Agricultural Research and Development fellowship. Felister Mbute Nzuve received an African Women in Agricultural Research and Development (AWARD) grant to support her PhD research on stem rust. Nzuve's work focuses on characterizing new genes (seedling and APR) against Ug99 and breeding for rust resistance. She is conducting her research at the Kenya Agricultural Research Institute in Njoro with CIMMYT wheat breeder Sridhar Bhavani.

AWARD is a professional development program that strengthens the research and leadership skills of African women in agricultural science, empowering them to contribute more effectively to poverty alleviation and food security in sub-Saharan Africa. In selecting Nzuve, the organizers recognize her important research, leadership potential, and ambition to bring measurable change for the poor in rural communities. Nzuve also was offered a travel fellowship from BGRI. AWARD is a project of the CGIAR gender and diversity program and is funded by the Bill & Melinda Gates Foundation and the U.S. Agency for International Development. For more information on AWARD visit http://www.awardfellowships.org/.

Online resources.

Identification and management of stem rust on wheat and barley. This extension publication addressing the identification and management of stem rust was published in March 2011. While focused on the U.S. and Canada, it provides an illustrated overview of stem rust and it's affect on wheat and barley. A pdf version of the flyer is posted on the USDA website (http://www.ars.usda.gov/SP2UserFiles/Place/36400500/Stem_Rust_Man_National.pdf).

A companion brochure, Identifying rust diseases of wheat and barley, is available on the BGRI website (http://www.globalrust.org/traction/permalink/Pathogen210).

Slide presentations from the BGRI Technical Workshop. Many of the slide files from the workshop presentations are posted online at the BGRI website (http://globalrust.org/traction/permalink/about206).

From the field.

The International Winter Wheat Improvement Program (IWWIP) traverses eastern Europe. Every two years, the IWWIP conducts a traveling seminar to evaluate germ plasm, assess current practices and relations, and develop an improved game plan for the future. This spring the IWWIP Traveling Seminar, co-sponsored by the subregional office of the United Nations Food and Agriculture Organization for Central Asia, attracted 46 researchers from 17 countries and traveled through Turkey, Bulgaria, and Romania – covering a total of more than 2,000 km.

New cultivars and mindset in Nepal. On 16 May, 2011, a workshop in Kathmandu attracted 80 farmers interested in wheat cultivars, quality seed production, and raising wheat production and profitability. The event, titled 'Wheat Seed Production and Rusts Disease Management Day', was organized by the Nepal Agriculture Research Council, the National Agricultural Research and Development Fund, Nepal's Ministry of Agriculture and Cooperation, and CIMMYT.

The objectives of the day were to: 1) generate awareness of new agronomically superior Ug99-resistant cultivars among farmers; 2) involve farmers in quality seed production and dissemination for the next crop cycle; and 3) disseminate information about wheat production technology available to small scale farmers.

Tackling complexity in winter wheat. Winter wheat constitutes a staple food in the Central and West Asia and North Africa (CWANA) region, where it is grown on around 18 x 10^6 ha in wide-ranging cropping systems.Wheat can be found in climates that span cold, dry environments; temperate areas with heavy rainfall; and irrigated, high-yielding lands constrained by different biotic and abiotic stresses. These varied landscapes contribute significantly to the grain's diversity and complexity. To address the constraints upon and future outlook of this multifaceted crop, wheat researchers convened at the 1st Regional Winter Wheat Symposium on 25-27 July, 2011, in Tabriz, Iran. The event drew more than 100 participants from 12 countries in the CWANA region.

Mobile seed marketing in Africa. On 1 May, 2011, the busy streets of Morogoro, Tanzania, were treated to a surprising sight, owing to the unconventional promotional efforts of Tanseed International Ltd. Staff of this Tanzanian seed company drove a vehicle topped with Tanseed drought-tolerant cultivars through the city's crowded streets during the nation's Worker's Day Celebration.

Iran and CIMMYT partnership strengthened. CIMMYT and Iran have revitalized their long-standing and prosperous relationship. During a recent visit there, CIMMYT Director General Thomas Lumpkin and Global Wheat Program Director Hans-Joachim Braun signed the coöperative annual work plan. The memorandum, signed on Iran's behalf by Dr. Jahangir Pour-Hemmat, Deputy Minister of Jihad-e-Agricultural and Head of the Agricultural Research Education & Extension Organization, commits both parties to joint work on high-yielding, stress-tolerant and disease resistant wheat and triticale cultivars.

Linking research to development. Collaborative research in Egypt is providing a model for other countries with similar challenges. The Food Security Project is helping to increase wheat yields in irrigated systems. The Egypt–ICARDA wheat improvement project is developing improved varieties that combine high yield, disease resistance and good grain quality. Farmers involved in the two projects have reported excellent results from the 2010–11 season, wheat yields increased by 25% in El Sharkia Governorate and 17% in Assiut Governorate. Using improved technologies, farmers in El Sharkia achieved a 20% saving in irrigation water. The Water Benchmark Project is testing further improvements in the raised-bed planting technique and other measures to increase water productivity. Field trials of new wheat and legume cultivars have also been encouraging, with high yields and high levels of disease resistance.

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Editor's notes.

The Borlaug Global Rust Initiative facilitates the evolution of a sustainable international system to contain the threat of wheat rusts and enhance wheat productivity to withstand future global threats to wheat. Any person or institution with an interest or stake in wheat rust research and development is welcome to be a member of the BGRI, just send a message to BGRI@cornell.edu indicating your interest, and you will be added to our email distribution list. For more information about the BGRI, wheat rust projects, and who's who in the wheat rust world, visit the BGRI websitehttp (http://global-rust.org).

This quarterly newsletter is edited by Cally Arthur and sent to members of the BGRI. Suggestions on format and content are always welcome by the editor, at BGRI@cornell.edu or callyarthur@cornell.edu.

BGRI members are encouraged to contribute to the newsletter. Submissions may be technical communications on wheat breeding and rust pathology issues; announcements of meetings, courses and electronic conferences; book announcements and reviews; websites of special relevance to wheat and the rusts; announcements of funding opportunities; requests to other readers for information and collaboration; and feature articles or discussion issues brought by subscribers.

VIRGINIA

VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY
Department of Crop and Soil Environmental Sciences, Blacksburg, VA 24061, USA.

C.A. Griffey, W.E. Thomason, J.E. Seago, M.D. Hall, S. Liu, W.S. Brooks, and P.G. Gundrum; R.M. Pitman, M.E. Vaughn, D. Dunaway, and T. Lewis (Eastern Virginia Agricultural Research & Extension Center, Warsaw, VA 22572, USA); and D.G. Schmale, III (Department of Plant Pathology and Weed Sciences, Virginia Tech, Blacksburg, VA 24061, USA).

2010 wheat production in the Commonwealth of Virginia.

W.E. Thomason, C.A. Griffey, and J.E. Seago.

Growing conditions. Mid-September produced a window with dry weather and favorable conditions for planting small grains and by 21 September, approximately 12% of the intended acres of barley were planted and 7% of wheat acres. Barley planting proceeded rapidly, and 50% of the crop was seeded by mid-October. Wheat growers had planted 20% of their intended acres by this time and dry weather forced some to delay until rainfall returned to the Commonwealth. By 10 November, wheat seeded was at 62% of acres, compared to 64% for the 5-year average. However, warm temperatures and favorable conditions resulted in emergence being rated at 43% compared to the 5-year average of 29%. Cold, wet weather in late November and December slowed growth dramatically and water-logging in parts of some fields resulted in dead spots. As of 15 December, the wheat crop was rated 36% fair and 47% good. Barley was estimated to be in better condition with 67% of the crop rated as good. Soggy, cold conditions persisted throughout the winter. Many producers had difficulty being timely with late winter nitrogen and herbicide applications due to snow and wet fields. However by late March, fieldwork was back in full swing. On 10 April 10, the wheat crop was rated 55% good and 36% fair. April was warmer and drier than normal (Figs. 1 and 2), allowing crop growth to progress favorably. But hot, dry, and windy conditions prevailed and by 10 May, approximately 70% of the wheat crop had headed, compared to a 5-year average of 38% by this date. Dry and unseasonably warm weather persisted during pollination and grain fill resulting in yields that were estimated to be 3 and 1 bu/acre lower than the 5-year average for wheat and barley, respectively. These weather conditions did lessen the impact of most foliar diseases and resulted in good test weight and overall good grain quality.

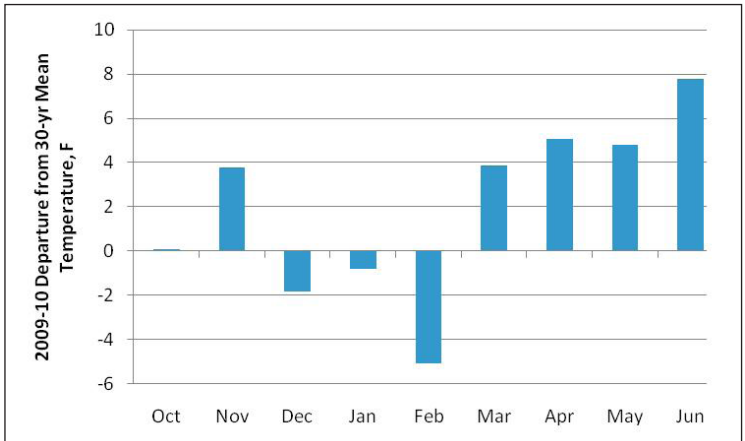

Fig. 1. Deviation of 2009–10 monthly average temperatures from 30-yr mean.

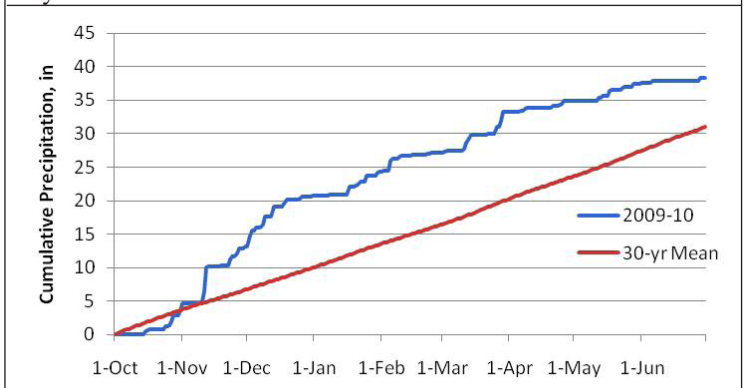

Fig. 2. Cumulative daily precipitation, 2009–10 season and 30-yr mean.

Disease and insect incidence and severity. Entries in Virginia's 2010 state wheat variety trials were rated (0 = no infection to 9 = severe infection) for disease severity at four locations. The prevalence and severity of powdery mildew (*Blumeria graminis*) were low (mean nursery score of 0.2) at Warsaw, VA, where only very susceptible lines had scores as high as 4. Mildew severity was highest at Blacks-

burg, VA, with lines having mean scores ranging from 0 to 9 with an overall nursery mean of 2.0. Leaf rust was prevalent and severe in many regions of the Commonwealth. Wheat entries received mean ratings from 0 to 9 at Blacksburg, Warsaw, and Painter with nursery means of 3.3, 2.3, and 1.7, respectively. Cultivars having only genes *Lr24* or *Lr26* were very susceptible to leaf rust. Race surveys conducted by the USDA–ARS Cereal Disease Lab on 39 isolates from five regions in Virginia indentified eight races of leaf rust. Five races having virulence for gene *Lr26* were identified and included MCRKG (in two regions), MCTSB (two regions), MFBJG (one region), TCRJG (one region), and TCRKG (four regions). Race MFBJG identified in Painter, VA, has virulence for genes *Lr24* and *Lr26*. Race MLDSD having virulence for gene *Lr9* and race TNRJJ having virulence for genes *Lr9* and *Lr24* were identified in Blacksburg, VA. Stripe rust was only found at three locations in 2010. Isolated infection foci were observed in wheat plots at Blacksburg and Painter, VA, and in a seed field at Mt. Holly, VA. Rust samples sent to Xianming Chen at Washington State University were identified as race PSTv46 having virulence for genes *Yr2*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, *Yr26*, *Yr27*, *Yr43*, *Yr44*, *YrTr1*, and *YrExp2*. Barley/cereal yellow dwarf virus infection was moderate at Blacksburg (0–5) and Painter (0–4), but severe at Suffolk, VA (0–9).

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service (http://www.nass.usda.gov/Statistics_by_State/Virginia/index.asp), in autumn 2009 Virginia wheat producers planted 180,000 acres (72,900 ha), which was 70,000 acres (28,350 ha) less than in autumn 2008. The estimated area harvested in 2010 was 160,000 acres (64,800 ha) which was 50,000 acres (20,250 ha) less than that harvested in 2009. The 2010 statewide average wheat yield was 51 bu/acre (3,427 kg/ha), which was 20 bu/acre (1,344 kg/ha) lower than the record yield set in 2008. Lower grain yields in 2010 resulted from the abnormally hot and dry weather during much of the grain-fill period. Overall wheat production in 2010 was 8.16 x 10^6 bushels (222,079 metric tons) compared with 19.9 x 10^6 bushels (541,000 metric tons) in 2008.

State cultivar tests. In the 2009–10 tests, a total of 83 entries were planted in seven environments across Virginia (http://www.grains.cses.vt.edu/). The test included 45 commercial cultivars and 38 experimental lines. No-till tests were conducted at Warsaw, Holland, and Shenandoah Valley and planted after corn. Mean grain yields varied from 63 bu/acre (4,233 kg/ha) at Suffolk, VA, to 102 bu/acre (6,853 kg/ha) at Blacksburg, VA, with an over locations mean yield of 79 bu/acre (5,308 kg/ha). Released cultivars Shirley, Pioneer 26R20, USG 3665, Dyna-Gro 9012, USG 3251, USG 3592, VA258, Pioneer 26R22, USG 3120, SS 8700, and USG 3201 all produced significantly higher yields than the overall trial average. Average grain yields among the 83 entries ranged from 68 bu/acre (4,569 kg/ha) to 86 bu/acre (5,778 kg/ha). Average test weight ranged from 58.4 lb/bu (752 kg/m^3) to 63.2 lb/bu (813 kg/m^3) with an overall trial average of 60.9 lb/bu (784 kg/m^3).

2010 Virginia Wheat Yield Contest Results. The 2010 contest was conducted statewide and the results are presented (Table 1). Top yields were 32.7 to 45.5 bu/acre (2,197–3,057 kg/ha) higher than the 2010 state average yield. Congratulations to our winners.

Table 1. 2010 Virginia wheat yield challenge winners.

Place	Grower	Farm	Yield bu/acre	Test weight	Planting date	Cultivar	Rate	Row width	Previous crop	Soil type	Tillage	Total N lb/acre	Seed treatment	Herbicides	Fungicides	Insecticides
1	Ronnie Russell	Corbin Hall Farm	96.5	60.0	12/21/09	Pioneer 26R15	24 seed/ft	7.0"	Corn	Eunola loam	No-till	125; 3 applications	n/a	Glyphosate (2 pt/acre); Harmony Extra (0.75 pt/acre); Osprey (4.75 oz/acre)		
2	James Townsend	Queenfield Farm	87.8	58.4	11/19/09	USG 3555	30 seed/ft	7.5"	Corn	Pamunkey	No-till	145; 3 applicatoin	Dividend Extreme	Finesse (0.4 oz/acre)	Headline (4 oz/acre)	Karate (1.25 oz/acre)
3	Richard Sanford	Sanford Farm	83.7	63.1	10/18/09	SS 560	196 lb/acre	7.5"	Corn	Suffolk	No-till	135; 3 applications	Raxil-Reldan-Thiram	Tilt (4 oz/acre)	Tile (4 oz/acre)	Warrior (1 oz/acre)

Release of hard red winter wheat cultivar Vision 30.

Vision 30 (PI 661153) hard red winter (HRW) wheat, was developed and tested as VA06HRW-49 and released by the Virginia Agricultural Experiment Station in March 2010. Vision 30 was derived from the cross '92PAN1#33/VA97W-414'. Vision 30 is a high-yielding, awned, semi-dwarf (*Rht2*) having mid-season spike emergence and resistance to powdery mildew. In Virginia, average (2007–09) grain yield of Vision 30 (5,301 kg/ha) has been similar to that of the soft red winter wheat check cultivar Renwood 3260 (5,536 kg/ha). Vision 30 was evaluated in the 2008 and 2009 USDA–ARS Uniform Bread Wheat Nursery and produced mean yields (4,992 and 4,690 kg/ha) that were similar ($P < 0.05$) to the highest yielding HRW wheat entry. In comparison to the hard wheat cultivar Lakin, Vision 30 has acceptable end-use quality on the basis of flour yield (69.9 versus 70.3/100 g), flour protein (10.7 versus 9.5 g/100 g), flour water absorption (59.8 versus 59.1 g/100g), dough mixing tolerance (3.3 versus 2.3), pup loaf volume (812 versus 803 cm^3), and crumb grain scores (3.3 versus 3.7). Marketing and distribution of Vision 30 will be handled by Virginia Identity Preserved Grains, LLC, West Point, VA. A seed sample has been deposited in the USDA–ARS National Center for Genetic Resources Preservation, and will become available for distribution after expiration of its U.S. Plant Variety Protection. Small quantities of seed for research purposes may be obtained from the corresponding author for at least five years from the date of this publication.

Release of hard red winter wheat cultivar Vision 40.

Vision 40 (PI 661154) hard red winter (HRW) wheat was developed and tested as VA06HRW-66 and released by the Virginia Agricultural Experiment Station in March 2010. Vision 40 was derived from the cross '92PIN#109/92PAN1#33'. Vision 40 is a high-yielding, winter hardy, awned, semi-dwarf (*Rht2*) having mid to late season spike emergence and moderate resistance to diseases prevalent in the mid-Atlantic area with the exception of Fusarium head blight. Vision 40 was the fourth highest yielding HRW wheat entry averaged over two years of the Uniform Bread Wheat Nursery grown at 11 test sites in ten states in 2008 and 12 test sites in nine states in 2009. In comparison to the hard wheat cultivar Lakin, Vision 40 has acceptable end use quality on the basis of flour yield (70.2 versus 70.3 g/100 g), flour protein (9.5 versus 9.5 g/100 g), flour water absorption (58.5 versus 59.1 g/100 g), dough mixing tolerance (1.7 versus 2.3), pup loaf volume (823 versus 803 cm^3), and crumb grain scores (3.6 versus 3.7). Marketing and distribution of Vision 40 will be handled by Virginia Identity Preserved Grains, LLC, West Point, VA. A seed sample has been deposited in the USDA–ARS National Center for Genetic Resources Preservation, and will become available for distribution after expiration of its U.S. Plant Variety Protection. Small quantities of seed for research purposes may be obtained from the corresponding author for at least five years from the date of this publication.

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WASHINGTON

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The mission of the lab is two-fold: conduct milling, baking, and end-use quality evaluations on wheat breeding lines, and conduct research on wheat grain quality and utilization. Our web site (http://www.wsu.edu/~wwql/php/index.php) provides great access to our research and methodology. Our research publications are available on our web site.

Morris and Engle lead the Pacific Northwest Wheat Quality Council, a consortium of collaborators who evaluate the quality of new cultivars and advanced breeding lines. We also conduct the U.S. Wheat Associates' Overseas Varietal Analysis Program for Soft White and Club Wheat. Our current activities and projects include grain hardness and puroindolines, waxy wheat, polyphenol oxidase (PPO), arabinoxylans, SDS sedimentation test, and soft durums. Beecher and Luna are currently researching the genetic basis for noodle dough color stability.

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Table 1. Wheat descriptors with data currently in GRIN (February 2011).

Descriptor	Years	Location	Accessions evaluated
DISEASE DESCRIPTORS			
Barley Yellow Dwarf Virus	1985–92	Davis, CA	2,287
Barley Yellow Dwarf Virus	1988–94	Urbana, IL	17,517
Soilborne Mosaic Virus	1985–89	Urbana, IL	6,587
Soilborne Mosaic Virus	2000	Manhattan, KS	4,998
Leaf Rust	1983–89, 1991–95	Manhattan, KS	38,751
Leaf Rust – Adult	2000	Manhattan, KS	5,000
Stripe Rust – Adult	1984–2005	Mt. Vernon, WA	47,540
Stripe Rust – Adult	1984–2005	Pullman, WA	37,676
Stripe Rust – PST 17	1984–2005	Pullman, WA	24,662
Stripe Rust – PST 20	1984–95	Pullman, WA	12,508
Stripe Rust – PST 25	1984–95	Pullman, WA	1,682
Stripe Rust – PST 27	1984–95	Pullman, WA	14,511
Stripe Rust – PST 29	1984–95	Pullman, WA	14,259
Stripe Rust – PST 37	1984–2005	Pullman, WA	17,252
Stripe Rust – PST 43	1984–2005	Pullman, WA	16,285
Stripe Rust – PST 45	1984–2005	Pullman, WA	17,217
Stripe Rust – PST 78	2000–05	Pullman, WA	4,277
Stripe Rust – PST 80	2004–05	Pullman, WA	2,998
Stripe Rust – PST 100	2004–05	Pullman, WA	5,892
Stem Rust – Adult	1987–94	Rosemount, MN	8,078
Stem Rust – Adult	1987–94	St. Paul, MN	19,141
Stem Rust – HJCS	1987–92	St. Paul, MN	4,342
Stem Rust – QFBS	1987–92	St. Paul, MN	8,639
Stem Rust – QSHS	1987–92	St. Paul, MN	4,455
Stem Rust – RHRS	1987–92	St. Paul, MN	4,312
Stem Rust – RTQQ	1987–92	St. Paul, MN	8,973
Stem Rust – TNMH	1987–92	St. Paul, MN	4,402
Stem Rust – TNMK	1987–92	St. Paul, MN	8,938
Stem Rust – HNLQ	1987–92	St. Paul, MN	4,705
Stem Rust – RKQS	1987–92	St. Paul, MN	4,682
Stem Rust – Genes	1987–92	St. Paul, MN	1,018
Common Bunt	1981–2004	Aberdeen, ID & Pendleton, OR	25,245
Dwarf Bunt	1978–2009	Logan, UT	20,146

Descriptor	Years	Location	Accessions evaluated
DISEASE DESCRIPTORS			
Stagonospora nodorum blotch	1970–78	Bozeman, MT	8,095
Powdery Mildew	1996–2005	Kinston, NC	13,973
Fusarium Head Blight/Scab	1998–2002	Brookings, SD	4,084
INSECT DESCRIPTORS			
Hessian Fly – B	1983–94	W. Lafayette, IN	449
Hessian Fly – C	1983–94	W. Lafayette, IN & Manhattan, KS	24,165
Hessian Fly – E	1983–94	W. Lafayette, IN & Manhattan, KS	24,149
Hessian Fly – GP	1983–94	W. Lafayette, IN & Manhattan, KS	14,441
Hessian Fly – L	1983–97	W. Lafayette, IN & Manhattan, KS	8,315
Russian Wheat Aphid – Biotype 1	1988–95, 2005	Stillwater, OK & Ft. Collins, CO	41,161
Russian Wheat Aphid – Biotype 2	2003–08	Ft. Collins, CO	14,186
Cereal Leaf Beetle	1963–70	Indiana, Michigan	16,347
AGRONOMIC–QUALITY DESCRIPTORS			
Growth Habit	1987–10	Aberdeen, ID	55,532
Lysine Content	1966–69	Lincoln, NE	10,367
Awn Color	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	27,037
Awn Type	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	30,113
Glume Color	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	27,403
Glume Pubescence	1983–97	Aberdeen, ID & Maricopa, AZ	24,312
Heading Date	1983–94	Aberdeen, ID & Maricopa, AZ	18,365
Heading Date – related to check	1999–2004	Maricopa, AZ	46,831
Kernel Color	1983–94, 2005–10	Aberdeen, ID & Maricopa, AZ	53,108
Kernels/Spike	1983–94	Aberdeen, ID & Maricopa, AZ	3,666
Kernel Weight	1983–94, 2005–09	Aberdeen, ID & Maricopa, AZ	53,162
Leaf Pubescence	1983–94	Aberdeen, ID & Maricopa, AZ	20,888
Plant Height	1983–97	Aberdeen, ID & Maricopa, AZ	21,841
Plant Height – related to check	1999–2004	Maricopa, AZ	46,841
Rachis Length	1995	Maricopa, AZ	2,512
Shattering	1983–94	Aberdeen, ID & Maricopa, AZ	10,637
Spike Density	1983–98, 2007–09	Aberdeen, ID & Maricopa, AZ	22,963
Spikelets/Spike	1995	Maricopa, AZ	2,502
Spike Type	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	22,730
Straw Breakage	1983–94	Aberdeen, ID & Maricopa, AZ	16,829
Straw Color	1983–97	Aberdeen, ID & Maricopa, AZ	24,142
Straw Lodging	1983–94	Aberdeen, ID & Maricopa, AZ	23,075

The authors wish to acknowledge the important contributions of the NSGGRF staff in this effort, with special thanks to Scott McNeil, Karla Reynolds, Carol Mortenson, and Kay Calzada.

Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN): http://www.ars-grin.gov/npgs. Certain accessions may not be available from the National Small Grains Collection due to intellectual property rights, quarantine, or insufficient inventories. Accessions registered in the *Journal of Plant Registrations* or *Crop Science* are available by contacting the developers.

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period. .Note: There were no PI assignments in *Aegilops*, *Secale*, and *X Triticosecale* in the past year.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
658657	*Triticum aestivum* subsp. *aestivum*	Red Amber	United States	Michigan
658682	*Triticum aestivum* subsp. *aestivum*	MD01W233-06-1	United States	Maryland
659070	*Triticum turgidum* subsp. *durum*	Snowglenn	United States	Virginia
659083 PVPO	*Triticum aestivum* subsp. *aestivum*	Sabin	United States	Minnesota
659089 PVPO	*Triticum aestivum* subsp. *aestivum*	NC-Cape Fear	United States	North Carolina
659317	*Triticum aestivum* subsp. *aestivum*	CO03752	United States	Colorado
659318	*Triticum aestivum* subsp. *aestivum*	CO03754	United States	Colorado
659319	*Triticum aestivum* subsp. *aestivum*	CO03758	United States	Colorado
659320	*Triticum aestivum* subsp. *aestivum*	CO03761	United States	Colorado
659321	*Triticum aestivum* subsp. *aestivum*	CO03764	United States	Colorado
659322	*Triticum aestivum* subsp. *aestivum*	CO03765	United States	Colorado
659479 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Stout	United States	Kansas
659480 PVPO	*Triticum aestivum* subsp. *aestivum*	ONeal	United States	Montana
659483 PVPO	*Triticum turgidum* subsp. *durum*	Wales	United States	North Dakota
659484 PVPO	*Triticum turgidum* subsp. *durum*	Westhope	United States	North Dakota
659485 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Famoso	United States	Arizona
659486 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Caliente	United States	Arizona
659487 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Rockland	United States	Montana
659488 PVPO	*Triticum aestivum* subsp. *aestivum*	Edge	United States	North Dakota
659489 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Paloma	United States	
659490 PVPO	*Triticum aestivum* subsp. *aestivum*	Brogan	United States	North Dakota
659491 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Digger	United States	North Dakota
659492 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-Lyn	United States	North Dakota
659554	*Triticum aestivum* subsp. *aestivum*	Select	United States	South Dakota
659556	*Triticum aestivum* subsp. *aestivum*	Alvina	France	
659557	*Triticum aestivum* subsp. *aestivum*	Apexal	France	
659558	*Triticum aestivum* subsp. *aestivum*	Arcane	France	
659559	*Triticum aestivum* subsp. *aestivum*	Arcole	France	
659560	*Triticum aestivum* subsp. *aestivum*	Armur	France	
659561	*Triticum aestivum* subsp. *aestivum*	Belaviso	France	
659562	*Triticum aestivum* subsp. *aestivum*	Berlioz	France	
659563	*Triticum aestivum* subsp. *aestivum*	Boreal	France	
659564	*Triticum aestivum* subsp. *aestivum*	But	France	
659565	*Triticum aestivum* subsp. *aestivum*	Cargidoc	France	
659566	*Triticum aestivum* subsp. *aestivum*	Cargimarec	France	
659567	*Triticum aestivum* subsp. *aestivum*	Cargo	France	
659568	*Triticum aestivum* subsp. *aestivum*	Choisel	France	
659569	*Triticum aestivum* subsp. *aestivum*	Corot	France	
659570	*Triticum aestivum* subsp. *aestivum*	Cosmos	France	
659571	*Triticum aestivum* subsp. *aestivum*	Divio	France	

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period. .Note: There were no PI assignments in *Aegilops*, *Secale*, and *X Triticosecale* in the past year.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
659572	*Triticum aestivum* subsp. *aestivum*	Ducat	France	
659573	*Triticum aestivum* subsp. *aestivum*	Ecrin	France	Colorado
659574	*Triticum aestivum* subsp. *aestivum*	Epiroux	France	Virginia
659575	*Triticum aestivum* subsp. *aestivum*	Faust	France	Virginia
659576	*Triticum aestivum* subsp. *aestivum*	Fleurus	France	
659577	*Triticum aestivum* subsp. *aestivum*	Floreal	France	
659578	*Triticum aestivum* subsp. *aestivum*	Fluto	France	
659579	*Triticum aestivum* subsp. *aestivum*	Fortin	France	
659580	*Triticum aestivum* subsp. *aestivum*	Friedland	France	
659581	*Triticum aestivum* subsp. *aestivum*	Gavroche	France	
659582	*Triticum aestivum* subsp. *aestivum*	Hamilcar	France	
659583	*Triticum aestivum* subsp. *aestivum*	Hickling	France	
659584	*Triticum aestivum* subsp. *aestivum*	Horace	France	
659585	*Triticum aestivum* subsp. *aestivum*	Iena	France	
659586	*Triticum aestivum* subsp. *aestivum*	Jano	France	
659587	*Triticum aestivum* subsp. *aestivum*	Magister	Netherlands	South Holland
659588	*Triticum aestivum* subsp. *aestivum*	Manital	France	
659589	*Triticum aestivum* subsp. *aestivum*	Martial	France	
659590	*Triticum aestivum* subsp. *aestivum*	Match	France	
659591	*Triticum aestivum* subsp. *aestivum*	Messidor	France	
659592	*Triticum aestivum* subsp. *aestivum*	Moulin	France	
659593	*Triticum aestivum* subsp. *aestivum*	Open	France	
659594	*Triticum aestivum* subsp. *aestivum*	Petrel	France	
659595	*Triticum aestivum* subsp. *aestivum*	Priam	France	
659596	*Triticum aestivum* subsp. *aestivum*	Rempart	France	
659597	*Triticum aestivum* subsp. *aestivum*	Rotonde	Netherlands	
659598	*Triticum aestivum* subsp. *aestivum*	Score	France	
659599	*Triticum aestivum* subsp. *aestivum*	Storch	Germany	
659600	*Triticum aestivum* subsp. *aestivum*	Tarquin	France	
659601	*Triticum aestivum* subsp. *aestivum*	Titien	France	
659602	*Triticum aestivum* subsp. *aestivum*	Ulm	France	
659603	*Triticum aestivum* subsp. *aestivum*	Unic	France	
659604	*Triticum aestivum* subsp. *aestivum*	Vasco	France	
659605	*Triticum aestivum* subsp. *aestivum*	Vizir	France	
659689	*Triticum aestivum* subsp. *aestivum*	NE01481	United States	Nebraska
659690	*Triticum aestivum* subsp. *aestivum*	NI04421	United States	Nebraska
659776 PVPO	*Triticum aestivum* subsp. *aestivum*	ND901CL Plus	United States	North Dakota
659783 PVPO	*Triticum aestivum* subsp. *aestivum*	CJ	United States	
659784 PVPO	*Triticum aestivum* subsp. *aestivum*	SY Goliad	United States	
659787 PVPO	*Triticum aestivum* subsp. *aestivum*	TV8861	United States	
659788 PVPO	*Triticum aestivum* subsp. *aestivum*	W930070B1	United States	
659789 PVPO	*Triticum aestivum* subsp. *aestivum*	W990624B1	United States	
659807 PVPO	*Triticum aestivum* subsp. *aestivum*	Everest	United States	Kansas
659808 PVPO	*Triticum aestivum* subsp. *aestivum*	Arcadia	United States	
659809 PVPO	*Triticum aestivum* subsp. *aestivum*	SY Gold	United States	
659810 PVPO	*Triticum aestivum* subsp. *aestivum*	SY605 CL	United States	

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PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
659811 PVPO	*Triticum aestivum* subsp. *aestivum*	Greer	United States	
659812 PVPO	*Triticum aestivum* subsp. *aestivum*	25R40	United States	Indiana
659813 PVPO	*Triticum aestivum* subsp. *aestivum*	25R34	United States	Indiana
659814 PVPO	*Triticum aestivum* subsp. *aestivum*	25R30	United States	Indiana
659818 PVPO	*Triticum aestivum* subsp. *aestivum*	SY 9978	United States	
659820 PVPO	*Triticum turgidum* subsp. *durum*	Desert King-High Protein	United States	
659821 PVPO	*Triticum aestivum* subsp. *aestivum*	W000537N1	United States	
659822 PVPO	*Triticum aestivum* subsp. *aestivum*	W020053D1	United States	
659823 PVPO	*Triticum aestivum* subsp. *aestivum*	W010476N1	United States	
660056	*Triticum aestivum* subsp. *aestivum*	T3-1	United States	Washington
660057	*Triticum aestivum* subsp. *aestivum*	41	United States	Washington
660058	*Triticum aestivum* subsp. *aestivum*	10-1	United States	Washington
660059	*Triticum aestivum* subsp. *aestivum*	28-1	United States	Washington
660060	*Triticum aestivum* subsp. *aestivum*	103	United States	Washington
660061	*Triticum aestivum* subsp. *aestivum*	24	United States	Washington
660062	*Triticum aestivum* subsp. *aestivum*	23	United States	Washington
660063	*Triticum aestivum* subsp. *aestivum*	5-3	United States	Washington
660064	*Triticum* hybrid	28-14-2	United States	Washington
660065	*Triticum* hybrid	29-4-1	United States	Washington
660066	*Triticum* hybrid	26-3-4	United States	Washington
660067	*Triticum* hybrid	32-6	United States	Washington
660068	*Triticum aestivum* subsp. *aestivum*	16-1	United States	Washington
660069	*Triticum aestivum* subsp. *aestivum*	12-3	United States	Washington
660070	*Triticum aestivum* subsp. *aestivum*	20-1	United States	Washington
660071	*Triticum aestivum* subsp. *aestivum*	25-4	United States	Washington
660072	*Triticum aestivum* subsp. *aestivum*	2-1	United States	Washington
660073	*Triticum aestivum* subsp. *aestivum*	5-1	United States	Washington
660074	*Triticum aestivum* subsp. *aestivum*	2	United States	Washington
660075	*Triticum aestivum* subsp. *aestivum*	24-1	United States	Washington
660076	*Triticum aestivum* subsp. *aestivum*	23-2	United States	Washington
660077	*Triticum aestivum* subsp. *aestivum*	C3-1	United States	Washington
660078	*Triticum aestivum* subsp. *aestivum*	22-3	United States	Washington
660079	*Triticum aestivum* subsp. *aestivum*	1-2	United States	Washington
660080	*Triticum aestivum* subsp. *aestivum*	22-2	United States	Washington
660081	*Triticum aestivum* subsp. *aestivum*	25-1	United States	Washington
660082	*Triticum aestivum* subsp. *aestivum*	25-3	United States	Washington
660083	*Triticum aestivum* subsp. *aestivum*	6-1	United States	Washington
660084	*Triticum aestivum* subsp. *aestivum*	12	United States	Washington
660085	*Triticum aestivum* subsp. *aestivum*	20-1	United States	Washington
660086	*Triticum aestivum* subsp. *aestivum*	13-1	United States	Washington
660087	*Triticum aestivum* subsp. *aestivum*	9-1	United States	Washington
660088	*Triticum aestivum* subsp. *aestivum*	2-1	United States	Washington
660089	*Triticum aestivum* subsp. *aestivum*	22-2	United States	Washington
660090	*Triticum aestivum* subsp. *aestivum*	25-4	United States	Washington
660091	*Triticum aestivum* subsp. *aestivum*	6-2	United States	Washington
660092	*Triticum aestivum* subsp. *aestivum*	4-1	United States	Washington

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period. .Note: There were no PI assignments in *Aegilops*, *Secale*, and *X Triticosecale* in the past year.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
660093	*Triticum aestivum* subsp. *aestivum*	12-1	United States	Washington
660094	*Triticum aestivum* subsp. *aestivum*	5-1	United States	Washington
660095	*Triticum aestivum* subsp. *aestivum*	17	United States	Washington
660096	*Triticum aestivum* subsp. *aestivum*	17	United States	Washington
660097	*Triticum aestivum* subsp. *aestivum*	17-4	United States	Washington
660098	*Triticum aestivum* subsp. *aestivum*	12	United States	Washington
660099	*Triticum aestivum* subsp. *aestivum*	20-1	United States	Washington
660100	*Triticum aestivum* subsp. *aestivum*	4-1	United States	Washington
660101	*Triticum aestivum* subsp. *aestivum*	5-3	United States	Washington
660102	*Triticum aestivum* subsp. *aestivum*	3-3	United States	Washington
660103	*Triticum aestivum* subsp. *aestivum*	2-1	United States	Washington
660104	*Triticum aestivum* subsp. *aestivum*	K4-1	United States	Washington
660105	*Triticum aestivum* subsp. *aestivum*	20-1	United States	Washington
660106	*Triticum aestivum* subsp. *aestivum*	29-3	United States	Washington
660107	*Triticum aestivum* subsp. *aestivum*	23-2	United States	Washington
660108	*Triticum aestivum* subsp. *aestivum*	23-1	United States	Washington
660109	*Triticum aestivum* subsp. *aestivum*	2-1	United States	Washington
660110	*Triticum aestivum* subsp. *aestivum*	28-1	United States	Washington
660111	*Triticum aestivum* subsp. *aestivum*	10	United States	Washington
660112	*Triticum aestivum* subsp. *aestivum*	17-3	United States	Washington
660113	*Triticum aestivum* subsp. *aestivum*	3-2	United States	Washington
660114	*Triticum aestivum* subsp. *aestivum*	20-1	United States	Washington
660115	*Triticum aestivum* subsp. *aestivum*	25-1	United States	Washington
660116	*Triticum aestivum* subsp. *aestivum*	4-1	United States	Washington
660117	*Triticum aestivum* subsp. *aestivum*	10	United States	Washington
660118	*Triticum aestivum* subsp. *aestivum*	15-3	United States	Washington
660119	*Triticum aestivum* subsp. *aestivum*	5-1	United States	Washington
660120	*Triticum aestivum* subsp. *aestivum*	28-1	United States	Washington
660121	*Triticum aestivum* subsp. *aestivum*	11	United States	Washington
660122	*Triticum aestivum* subsp. *aestivum*	24-1	United States	Washington
660123	*Triticum aestivum* subsp. *aestivum*	6-1	United States	Washington
660124	*Triticum aestivum* subsp. *aestivum*	14-2	United States	Washington
660125	*Triticum aestivum* subsp. *aestivum*	3-2	United States	Washington
660256	*Triticum aestivum* subsp. *aestivum*	Sr22TB	Australia	New South Wales
660291	*Triticum aestivum* subsp. *aestivum*	Decade	United States	Montana
660539	*Triticum aestivum* subsp. *aestivum*	Milton	United States	Missouri
660540 MAP	*Triticum aestivum* subsp. *aestivum*	MN98550-5	United States	Minnesota
660541 MAP	*Triticum aestivum* subsp. *aestivum*	MN99394-1	United States	Minnesota
660543 PVPO	*Triticum aestivum* subsp. *aestivum*	UICF-Brundage	United States	Idaho
660544 PVPO	*Triticum aestivum* subsp. *aestivum*	UICF-Lambert	United States	Idaho
660546	*Triticum aestivum* subsp. *aestivum*	SRG	United States	Idaho
660547	*Triticum aestivum* subsp. *aestivum*	LHS	United States	Idaho
660548	*Triticum aestivum* subsp. *aestivum*	IDO671	United States	Idaho
660549	*Triticum aestivum* subsp. *aestivum*	IDO644	United States	Idaho
660550	*Triticum aestivum* subsp. *aestivum*	IDO599	United States	Idaho

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2009–February 2010. There were no PI assignments in *Aegilops* and *Secale* during this period. .Note: There were no PI assignments in *Aegilops*, *Secale*, and *X Triticosecale* in the past year.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
660551	*Triticum aestivum* subsp. *aestivum*	IDO686	United States	Idaho
660552	*Triticum aestivum* subsp. *aestivum*	IDO687	United States	Idaho
660553	*Triticum aestivum* subsp. *aestivum*	IDO702	United States	Idaho
660647	*Triticum aestivum* subsp. *aestivum*	NB085WS03690	United States	Montana
660648	*Triticum aestivum* subsp. *aestivum*	NB474-23	United States	Montana
660649	*Triticum aestivum* subsp. *aestivum*	NB475-12	United States	Montana
660650	*Triticum aestivum* subsp. *aestivum*	NB481-23-1	United States	Montana
660651	*Triticum aestivum* subsp. *aestivum*	NB489-54-1	United States	Montana
660652	*Triticum aestivum* subsp. *aestivum*	NB085WS03686	United States	Montana
660653 PVPO	*Triticum aestivum* subsp. *aestivum*	Striker	United States	North Dakota
660654 PVPO	*Triticum aestivum* subsp. *aestivum*	Boomer	United States	North Dakota
660663	*Triticum aestivum* subsp. *aestivum*	Diva	United States	Washington
660664 PVPO	*Triticum turgidum* subsp. *durum*	Tioga	United States	North Dakota
660666 PVPO	*Triticum aestivum* subsp. *aestivum*	Bridgeport	United States	New York
660667 PVPO	*Triticum aestivum* subsp. *aestivum*	Hopkins	United States	New York

IV. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2011 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11Th International Wheat Genetics Symposium held in Brisbane, Australia, and the 2009 and 2010 Supplements (*Annual Wheat Newsletter* 55:256-278, 56:256-278) are available from the Komugi (http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp) and GrainGenes (http://wheat.pw.usda.gov/GG2/*Triticum*/wgc/2008/) websites. The Wheat Gene Catalog is not included as part of the IWGS proceedings and, therefore, cannot be cited as part of them.

Section numbers given is this supplement are only approximate.
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Morphological and Physiological Traits

Pre-harvest Sprouting
QTL
'Argent (non-dormant, white seeded) / W98616 (dormant, white seeded)': 90 DH lines: Strong QTL on chromosomes 1A, 3A, 4A, and 7A and weaker QTL on 2B, 5B, and 6B, all from W98616 {10740}.

XX. Embryo Lethality
XX.1. Embryo lethality in wheat x rye hybrids
The Chinese Spring (Imperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, and R7) produced hybrid seeds with different proportions of differentiated embyos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74–100% differentiated embryos {10748}. Crosses of R2 with the CS nulli-tetrasomics gave differentiated embryos only with N6AT6B and N6AT6D, indicating the presence of a complementary factor *Eml-A1* chromosome 6A {10748}.

39. Height

39.2. reduced Height : GA-sensitive

Rht14. 6AS {10767}. ma: *Rht14* – 11.7 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht16* and *Rht18* {10767}.

Rht16. 6AS {10767}. ma: *Rht16* – 28.0 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht14* and *Rht18* {10767}.

Rht18. 6AS {10767}. ma: *Rht18* – 25.1 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht14* and *Rht16* {10767}.

43. Lack of Ligules

lg1. , 2BS {10767}.

XX. Lesian Mimicry

Lesian mimics that resemble the responses of plants to infection by pathogens have occur in many species ({10743} for examples).

lm {10743}. 1BL {10743}. **bin:** C1BL6-0.32 {10743}.
v: Ning 7840 {10743}. **ma:** Proximal to *Xgwm264.1-1*B {10743}.
Lm was positively associated with *QLr.pser.1BL* {10743}.

XX. Soft Glumes

sog. **bin:** C-2AS5-0.78. **dv:** Tm-9, a mutant of TA4342-96 {10769}.
ma: *Xgwm71-2A* – 3.3 cM – *sog* – 3.5 cM – *Xbcd120-2A* {10769}.

Sog. **dv:** *T. monococcum* subsp. *aegilopoides* TA4342-96 {10769}.
Replace the previous entry regarding the relationship to Tenacious Glumes with: 'The Soft Glume locus is not an orthologue of Tenacious Glumes {10769}'.

69. Stem Solidness

Qsst.msub-3BL. Add following the current entry:
Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines {10730}.

71.Tenacious Glumes

Tg1. **bin:** 2BS-3 1.00-0.84.

Tg2. **v:** TA 3419 = Tetra Canthatch / *Ae. tauschii* var. *meyeri* TA1599 {10769}.
ma: *Xgwm261*/*Xwmc503-2D* – 2.3 cM – *Tg2* – 5.9 cM – *Xfba88*/*Xfbc400-2D* {10769}.
Replace the note on the relationship with Soft Glumes with: 'The Tenacious Glume loci are not orthologues of the Soft Glume locus {10769}'.

75.Yield and Yield Components

75.1.2. 1,000-kernel weight

TaCwi-A1{10812}. **ma:** *Xbarc15* – 10.9 cM – TaCwi-A1-STS markers *Cwi21* and *Cwi22* – 17.6 cM – *Xgwm71-2AL* {10812}.
Based on the rice *GIF1* gene encoding a cell wall invertase (GenBank accession EU095553), common wheat *TaCwi-A1* was cloned, and two STS markers Cwi21 and Cwi22 were developed from the polymorphisms between two allelic variants. On average, *TaCwi-A1a* had 1,000-kernel weights 2.4 g higher than *TaCwi-A1b* {10812}.

TaGW2-6A {10781}. **ma:** *Xcfd80-6AS.2* – 0.6 cM – *TaGW2-CAPS* – 0.5 cM – *Xbarc146-6A.1*/*Xwms132.4-6A* {10781}.
Based on its OsGW2 orthologue in rice, this gene was characterized and mapped as a CAPS marker in wheat {10781}. SNPs in the promoter region allowed distinction of two haplotypes . Hap-6A-A was mainly present in southern Chinese wheats; Hap6A-G was present in varieties from central and eastern Europe. On average, Hap-6A-A had 1,000-kernel weights more than 3 g higher than that of Hap-6A-G {10781}.

75.12. Spike number per plant

QSn.sdau-BL {10784}. **ma:** *Xwmc657-4B* – 4.6 cM – *QSn.sdau-4*B – 1.6 cM – *Xgwm495-4B* {10784}.

QSn.sdau-BL was resolved as a single gene in Line 05210/Laizhou 953 {10784}. It was associated with decreased spike length and grain number per spike.

Proteins

79.5.6. Waxy Proteins

Wx-A1.

Wx-A1h {10763}. Null allele. **tv:** Buck Topacio {10763}.

This is probably a unique allele possessing a 1-bp deletion in exon 6 leading to frameshift and a stop codon: partial sequence GQ120523 {10763}.

Wx-B1. At the end of section add:

A dominant PCR marker for identifying heterozygotes at the *Wx-B1* locus is reported in {10732}.

79.5.8. Puroindolines and grain softness protein

Add note:

Lines possessing the alien-derived genes *Lr57* and *Yr40* lack puroindoline genes and therefore should be hard phenotypes {10770}.

79.5.12. Serine proteinase inhibitors

Serine proteinase inhibitors or serpins are salt soluble proteins (~43 kDa) representing about 4% of the total protein in wheat and barley endosperms. They may have a role in plant defense.

Srp-A1 {10754}. 5AL {10754}.

Srp-B1 {10754}. *Srp5B* {10754}. 5BL {10754}.

Srp-B1a {10754}. *Srp5Ba* {10754}.

v: Etawah {10755}; Federation {10755}; Frame {10755}; Pugsley {10754}; Stylet {10755}.

Srp-B1b {10754}. Null allele.

v: Correll {10755}; EGA Eagle Rock {10755}; Gladius 10755}; Yitpi {10755}.

This allele reduced milling yield by 0.4% {10755}.

Srp-D1 {10754}. 5DL {10754}.

79.3. Endosperm Storage Proteins

79.3.1. Glutenins

79.3.1.1 *Glu-1*

Glu-A1

Restore the following entries erroneously deleted in a previous update:

Glu-A1v {10327}. 2.1* {10327}. **v:** KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.

Glu-A1w {10327}. 2' {10327}. **v:** TRI14165/91 {10327}.

Add:

Glu-A1z {10805}. [*Glu-A1^{m}a* {10805}]. **dv:** PI 191146, *T. monococcum*. subsp. *monococcum* {10805}.

Glu-A1aa {10805}. [*Glu-A1^{m}b* {10805}]. **dv:** PI 190946, *T. monococcum*. subsp. *monococcum* {10805}.

Glu-A1ab {10805}. [*Glu-A1^{m}c* {10805}]. **dv:** PI 191098, *T. monococcum*. subsp. *monococcum* {10805}.

Glu-A1ac {10806}.	[*Glu-A^{u}1-I* {10806}].	**dv:** PI 428319, *T. urartu* {10806}.
Glu-A1ad {10806}.	[*Glu-A^{u}1-II* {10806}].	**dv:** PI 428232, *T. urartu* {10806}.
Glu-A1ae {10806}.	[*Glu-A^{u}1-III* {10806}].	**dv:** PI 428240, *T. urartu* {10806}.
Glu-A1af {10806}.	[*Glu-A^{u}1-IV* {10806}].	**dv:** PI 428335, *T. urartu* {10806}.
Glu-A1ag {10806}.	[*Glu-A^{u}1-V* {10806}].	**dv:** PI 538741, *T. urartu* {10806}.
Glu-A1ah {10806}.	[*Glu-A^{u}1-VI* {10806}].	**dv:** PI 428230, *T. urartu* {10806}.
Glu-A1ai {10806}.	[*Glu-A^{u}1-VII* {10806}].	**dv:** PI 428253, *T. urartu* {10806}.
Glu-A1aj {10806}.	[*Glu-A^{u}1-VIII* {10806}].	**dv:** PI 427328, *T. urartu* {10806}.
Glu-A1ak {10806}.	[*Glu-A^{u}1-IX* {10806}].	**dv:** PI 428327, *T. urartu* {10806}.
Glu-A1al {10806}.	[*Glu-A^{u}1-X* {10806}].	**dv:** PI 428256, *T. urartu* {10806}.
Glu-A1am {10806}.	[*Glu-A^{u}1-XI* {10806}].	**dv:** PI 428224, *T. urartu* {10806}.
Glu-A1an {10806}.	[*Glu-A^{u}1-XII* {10806}].	**dv:** PI 428228, *T. urartu* {10806}.
Glu-A1ao {10806}.	[*Glu-A^{u}1-XIII* {10806}].	**dv:** PI 538724, *T. urartu* {10806}.
Glu-A1ap {10806}.	[*Glu-A^{u}1-XIV* {10806}].	**dv:** TRI 6734, *T. urartu* {10806}.
Glu-A1aq {10806}.	[*Glu-A^{u}1-XV* {10806}].	**dv:** TRI 11494, *T. urartu* {10806}.
Glu-A1ar {10806}.	[*Glu-A^{u}1-XVI* {10806}].	**dv:** TRI 11495, *T. urartu* {10806}.
Glu-A1as {10806}.	[*Glu-A^{u}1-XVII* {10806}].	**dv:** PI 428217, *T. urartu* {10806}.
Glu-A1at {10806}.	[*Glu-A^{u}3-XVIII* {10806}].	**dv:** PI 428225, *T. urartu* {10806}.
Glu-A1au {10806}.	[*Glu-A^{u}3-XIX* {10806}].	**dv:** PI 538733, *T. urartu* {10806}.
Glu-A1av {10806}.	[*Glu-A^{u}3-XX* {10806}].	**dv:** PI 428196, *T. urartu* {10806}.
Glu-A1aw {10806}.	[*Glu-A^{u}3-XXI* {10806}].	**dv:** PI 538724, *T. urartu* {10806}.
Glu-A1ax {10806}.	[*Glu-A^{u}3-XXII* {10806}].	**dv:** PI 428191, *T. urartu* {10806}.
Glu-A1ay {10806}.	[*Glu-A^{u}3-XXIII* {10806}].	**dv:** TRI 6734, *T. urartu* {10806}.
Glu-A1az {10806}.	[*Glu-A^{u}3-XXIV* {10806}].	**dv:** TRI 11496, *T. urartu* {10806}.

Glu-B1

Amendment:

Glu-B1al. Replace '7+8*' with '7^{OE}+7^{OE}+8*'. Add {899} after 'Glenlea'.

Add to the existing note:

However, there is evidence that over-expression is due to duplication of subunit 7 {10196}. In regard to subunit 8*, evidence was presented to indicate that in Glenlea, one of the standard cultivars for the allele, this subunit is the same as subunit 8 {10808}.

Add:

Glu-B1br {10807}.	7.1+7.2+8* {10807}.	**v:** H45 {10807}.
Glu-B1bs {10807}.	7.3+7^{OE}+8* {10807}.	**v:** VQ0437 {10807}.
Glu-B1bt {10809}.	17'+18' {10809}.	**tv:** TGR-214 {10809}.
Glu-B1bu {10809}.	17'+18* {10809}.	**tv:** TGR-2246 {10809}.
Glu-B1bv {10809}.	13**+8* {10809}.	**tv:** TGR-003 {10809}.
Glu-B1bw {10809}.	8' {10809}.	**tv:** TGR-244 {10809}.
Glu-B1bx {10810}.	7+17 {10810}.	**v:** CWI-59797, *T. aestivum* subsp. *ferrugineum* {10810}.
Glu-B1by {10808}.	7b*+8 {10808}.	**v:** Eshimashinriki {10808}.
Glu-B1bz {10808}.	7^{OE} {10808}.	**v:** Darius {10808}; Cappelle-Desprez {10808}; Festin {10808}; Petrel {10808}; Attila {10808}.
Glu-B1ca {10808}.	6+8b* {10808}.	**v:** Nidera Baguette 10 {10808}; Apollo {10808}; Brimstone {10808}; Clément {10808}; Ruso {10808}; Pepital {10808}; Thesee {10808}.
Glu-B1cb {10808}.	7^{OE}+8 {10808}.	**v:** Demai 3 {10808}; ACA 303 {10808}; Courtot {10808}; Shinchunaga {10808}.
Glu-B1cc {10808}.	7^{OE}+8a* {10808}.	**v:** Pioneer {10808}; Klein Jabal 1 {10808}; ProINTA Redemón {10808}.
Glu-B1cd {10808}.	7^{OE}+8b* {10808}.	**v:** ACA 601 {10808}.
Glu-B1ce {10808}.	7+8a* {10808}.	**v:** Tasman {10808}; Jing 411 {10808}.

Glu-D1
Add:

Glu-D1bu {10810}.	2'+12 {10810}.	**v:** CWI-64806, *T. aestivum* subsp. *aestivum* {10810}.
Glu-D1bv {10810}.	2"+10 {10810}.	**v:** CWI-65297, *T. aestivum* subsp. *erythroleucon* {10810}.
Glu-D1bw {10810}.	2"+12 {10810}.	**v:** CWI-60509, *T. aestivum* subsp. *graecum* {10810}.

Glu-B1-1
Add:

Glu-B1-1ah {899}.	7^{OE}	**v:** Benkuti 1201 {10196, 10197}; Glenlea; Klein Universal II {10196}; Tezanos Pintos Precoz {10196}; Tobari 66 {10196}.
Glu-B1-1ai {10807}.	7.1 {10807}.	**v:** H45 {10807}.
Glu-B1-1aj {10807}.	7.2 {10807}.	**v:** H45 {10807}.
Glu-B1-1ak {10807}.	7.3 {10807}.	**v:** VQ0437 {10807}.
Glu-B1-1al {10809}.	17' {10809}.	**v:** TGR-214{10809}; TGR-2246 {10809}.
Glu-B1-1am {10809}.	13** {10809}.	**tv:** TGR-003 {10809}.
Glu-B1-1an {10808}.	7b* {10808}.	**v:** Eshimashinriki {10808}.

Glu-B1-2
Add:

Glu-B1-2ai {10809}.	8' {10809}.	**tv:** TGR-244 {10809}.
Glu-B1-2aj {10808}.	8a* {10808}.	**v:** Pioneer {10808}, Jing 411 {10808}, Tasman {10808}.
Glu-B1-2ak {10808}.	b*' {10808}.	**v:** Nidera Baguette 10 {10808} , ACA 601 {10808}.

Glu-A3
Replace:

Glu-A3g {00113, 00114}.	6+10+20 {00114}.	**v:** Glenlea {10185}. **tv:** Claro de Balazote.

with:

Glu-A3g {00113}		**v:** Glenlea {10185}.

Add:

Glu-A3r {03116}.	[*Glu-A3d'* {03116}].	**v:** Magistral hexaploid triticale {03116}.
Glu-A3s {00114}.	[*Glu-A3g* {00114}].	6+10+20 {00114}. **tv:** Claro de Balazote {00114}.
Glu-A3t {10805}.	*Glu-A3^{m}a* {10805}.	**dv:** PI 190947, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3u {10805}.	*Glu-A3^{m}b* {10805}.	**dv:** PI 190946, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3v {10805}.	*Glu-A3^{m}c* {10805}.	**dv:** BGE-020466, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3w {10805}.	*Glu-A3^{m}d* {10805}.	**dv:** PI 191097, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3x {10805}.	*Glu-A3^{m}e* {10805}.	**dv:** BGE-013624, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3y {10805}.	*Glu-A3^{m}f* {10805}.	**dv:** PI 191094, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3z {10806}.	*Glu-A^{u}3-I* {10806}.	**dv:** PI 428319, *T. urartu* {10806}.
Glu-A3aa {10806}.	*Glu-A^{u}3-II* {10806}.	**dv:** PI 428327, *T. urartu* {10806}.
Glu-A3ab {10806}.	*Glu-A^{u}3-III* {10806}.	**dv:** PI 428340, *T. urartu* {10806}.
Glu-A3ac {10806}.	*Glu-A^{u}3-IV* {10806}.	**dv:** PI 428322, *T. urartu* {10806}.
Glu-A3ad {10806}.	*Glu-A^{u}3-V* {10806}.	**dv:** PI 428188, *T. urartu* {10806}.
Glu-A3ae {10806}.	*Glu-A^{u}3-VI* {10806}.	**dv:** PI 428203, *T. urartu* {10806}.
Glu-A3af {10806}.	*Glu-A^{u}3-VII* {10806}.	**dv:** PI 428255, *T. urartu* {10806}.
Glu-A3ag {10806}.	*Glu-A^{u}3-VIII* {10806}.	**dv:** PI 428328, *T. urartu* {10806}.

Glu-A3ah {10806}.	*Glu-A^{u}3-IX* {10806}.	**dv:** PI 428256, *T. urartu* {10806}.
Glu-A3ai {10806}.	*Glu-A^{u}3-X* {10806}.	**dv:** PI 428217, *T. urartu* {10806}.
Glu-A3aj {10806}.	*Glu-A^{u}3-XI* {10806}.	**dv:** PI 428335, *T. urartu* {10806}.
Glu-A3ak {10806}.	*Glu-A^{u}3-XII* {10806}.	**dv:** PI 428186, *T. urartu* {10806}.
Glu-A3al {10806}.	*Glu-A^{u}3-XIII* {10806}.	**dv:** PI 428183, *T. urartu* {10806}.
Glu-A3am {10806}.	*Glu-A^{u}3-XIV* {10806}.	**dv:** TRI 11563, *T. urartu* {10806}.
Glu-A3an {10806}.	*Glu-A^{u}3-XV* {10806}.	**dv:** PI 427328, *T. urartu* {10806}.
Glu-A3ao {10806}.	*Glu-A^{u}3-XVI* {10806}.	**dv:** PI 428253, *T. urartu* {10806}.
Glu-A3ap {10806}.	*Glu-A^{u}3-XVII* {10806}.	**dv:** PI 538735, *T. urartu* {10806}.
Glu-A3aq {10806}.	*Glu-A^{u}3-XVIII* {10806}.	**dv:** PI 428225, *T. urartu* {10806}.
Glu-A3ar {10806}.	*Glu-A^{u}3-XIX* {10806}.	**dv:** PI 538733, *T. urartu* {10806}.
Glu-A3as {10806}.	*Glu-A^{u}3-XX* {10806}.	**dv:** PI 428196, *T. urartu* {10806}.
Glu-A3at {10806}.	*Glu-A^{u}3-XXI* {10806}.	**dv:** PI 538724, *T. urartu* {10806}.
Glu-A3au {10806}.	*Glu-A^{u}3-XXII* {10806}.	**dv:** PI 428191, *T. urartu* {10806}.
Glu-A3av {10806}.	*Glu-A^{u}3-XXIII* {10806}.	**dv:** TRI 6734, *T. urartu* {10806}.
Glu-A3aw {10806}.	*Glu-A^{u}3-XXIV* {10806}.	**dv:** TRI 11496, *T. urartu* {10806}.

Glu-B3
Add:

Glu-B3ab {10804}.	**v:** Hope {10804}; Nanbukomugi {10804}.
Glu-B3ac {10804}.	**v:** Thesee {10804}; ACA 801 {10804}; Klein Proteo {10804}.
Glu-B3ad {10804}.	**v:** AC Vista {10804}; Heilo {10804}; Opata 85 {10804}; Ruso {10804}.

Glu-D3
In the ***Glu-D3d*** entry, add 'Jufy-1 {10813}' to the standard stock list.

Add:

Glu-D3l {10804}.	**v:** Heilo {10804}; Jing 411 {10804}, Pepital {10804}; Thesee {10804}.
Glu-D3m {10804}.	**v:** Darius {10804}.

79.3.2. Gliadins

79.3.2.1. *Gli-1*

Gli-A1
In the appropriate entry, replace:
Gli-A1null with ***Gli-A1w*** and add a column stating 'null allele'.

Add:

Gli-A1x {10805}.	[*Gli-A1^{m}a* {10805}].	**dv:** PI 191146, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1y {10805}.	[*Gli-A1^{m}b* {10805}].	**dv:** PI 190947, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1z {10805}.	[*Gli-A1^{m}c* {10805}].	**dv:** PI 190946, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1aa {10805}.	[Gli-A1^{m}d {10805}].	**dv:** PI 191097, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1ab {10805}.	[Gli-A1^{m}e {10805}].	**dv:** BGE-020466, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1ac {10805}.	[Gli-A1^{m}f {10805}].	**dv:** BGE-013626, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1ad {10805}.	[*Gli-A1^{m}g* {10805}].	**dv:** BGE-013628, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A1ae {10811}.	[*Gli-A^{u}1-I* {10811}].	**dv:** PI 428333, *T. urartu* {10811}.
Gli-A1af {10811}.	[*Gli-A^{u}1-II* {10811}].	**dv:** PI 428319, *T. urartu* {10811}.
Gli-A1ag {10811}.	[*Gli-A^{u}1-III* {10811}].	**dv:** PI 428335, *T. urartu* {10811}.
Gli-A1ah {10811}.	[*Gli-A^{u}1-IV* {10811}].	**dv:** PI 428323, *T. urartu* {10811}.

Gli-A1ai {10811}. [*Gli-A^{u}1-V* {10811}]. **dv:** PI 428231, *T. urartu* {10811}.
Gli-A1aj {10811}. [*Gli-A^{u}1-VI* {10811}]. **dv:** PI 428194, *T. urartu* {10811}.
Gli-A1ak {10811}. [*Gli-A^{u}1-VII* {10811}]. **dv:** PI 428256, *T. urartu* {10811}.
Gli-A1al {10811}. [*Gli-A^{u}1-VIII* {10811}]. **dv:** PI 428234, *T. urartu* {10811}.
Gli-A1am {10811}. [*Gli-A^{u}1-IX* {10811}]. **dv:** PI 428320, *T. urartu* {10811}.
Gli-A1an {10811}. [*Gli-A^{u}1-X* {10811}]. **dv:** PI 428255, *T. urartu* {10811}.
Gli-A1ao {10811}. [*Gli-A^{u}1-XI* {10811}]. **dv:** PI 428241, *T. urartu* {10811}.
Gli-A1ap {10811}. [*Gli-A^{u}1-XII* {10811}]. **dv:** PI 428235, *T. urartu* {10811}.
Gli-A1aq {10811}. [*Gli-A^{u}1-XIII* {10811}]. **dv:** PI 428183, *T. urartu* {10811}.
Gli-A1ar {10811}. [*Gli-A^{u}1-XIV* {10811}]. **dv:** PI 428317, *T. urartu* {10811}.
Gli-A1as {10811}. [*Gli-A^{u}1-XV* {10811}]. **dv:** PI 427328, *T. urartu* {10811}.
Gli-A1at {10811}. [*Gli-A^{u}1-XVI* {10811}]. **dv:** PI 428327, *T. urartu* {10811}.
Gli-A1au {10811}. [*Gli-A^{u}1-XVII* {10811}]. **dv:** PI 428253, *T. urartu* {10811}.
Gli-A1av {10811}. [*Gli-A^{u}1-XVIII* {10811}]. **dv:** PI 428224, *T. urartu* {10811}.
Gli-A1aw {10811}. [*Gli-A^{u}1-XIX* {10811}]. **dv:** PI 538727, *T. urartu* {10811}.
Gli-A1ax {10811}. [*Gli-A^{u}1-XX* {10811}]. **dv:** PI 428211, *T. urartu* {10811}.
Gli-A1ay {10811}. [*Gli-A^{u}1-XXI* {10811}]. **dv:** PI 538724, *T. urartu* {10811}.
Gli-A1az {10811}. [*Gli-A^{u}1-XXII* {10811}]. **dv:** PI 428191, *T. urartu* {10811}.
Gli-A1ba {10811}. [*Gli-A^{u}1-XXIII* {10811}]. **dv:** TRI 6735, *T. urartu* {10811}.
Gli-A1bb {10811}. [*Gli-A^{u}1-XXIV* {10811}]. **dv:** TRI 11494, *T. urartu* {10811}.
Gli-A1bc {10811}. [*Gli-A^{u}1-XXV* {10811}]. **dv:** TRI 6734, *T. urartu* {10811}.
Gli-A1bd {10811}. [*Gli-A^{u}1-XXVI* {10811}]. **dv:** TRI 11496, *T. urartu* {10811}.

Gli-B1
In the appropriate entry, replace:
Gli-B1null with ***Gli-B1x*** and add a column stating 'null allele'.

Gli-D1
In the appropriate entry, replace:
Gli-D1null with ***Gli-D1o*** and add a column stating 'null allele'.

80.3.2.2. Gli-2
Gli-A2
In the appropriate entry, replace:
Gli-A2null with ***Gli-A2aj*** and add a column stating 'null allele'.

Add:
Gli-A2ak {10805}. [*Gli-A2^{m}a* {10805}]. **dv:** BGE 013630, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2al {10805}. [*Gli-A2^{m}b* {10805}]. **dv:** PI 094740, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2am {10805}. [*Gli-A2^{m}c* {10805}]. **dv:** PI 190942, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2an {10805}. [*Gli-A2^{m}d* {10805}]. **dv:** PI 190947, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ao {10805}. [*Gli-A2^{m}e* {10805}]. **dv:** PI 190946, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ap {10805}. [Gli-A2^{m}f {10805}]. **dv:** BGE 013626, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2aq {10805}. [*Gli-A2^{m}g* {10805}]. **dv:** PI 191095, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ar {10805}. [*Gli-A2^{m}h* {10805}]. **dv:** BGE 001937, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2as {10805}. [*Gli-A2^{m}i* {10805}]. **dv:** PI 191096, *T. monococcum* subsp. *monococcum* {10805}.

Gli-A2at {10805}.	[*Gli-A2^{m}j* {10805}].	**dv:** BGE 020466, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2au {10805}.	[*Gli-A2^{m}k* {10805}].	**dv:** BGE 001937, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2av {10805}.	[*Gli-A2^{m}l* {10805}].	**dv:** BGE 029108, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2aw {10805}.	[*Gli-A2^{m}m* {10805}].	**dv:** BGE 013627, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ax {10805}.	[*Gli-A2^{m}n* {10805}].	**dv:** BGE 001937, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ay {10811}.	[*Gli-A^{u}2-I* {10811}].	**dv:** PI 428333, *T. urartu* {10811}.
Gli-A2az {10811}.	[*Gli-A^{u}2-II* {10811}].	**dv:** PI 428320, *T. urartu* {10811}.
Gli-A2ba {10811}.	[*Gli-A^{u}2-II* {10811}].	**dv:** PI 428230, *T. urartu* {10811}.
Gli-A2bb {10811}.	[*Gli-A^{u}2-IV* {10811}].	**dv:** PI 428319, *T. urartu* {10811}.
Gli-A2bc {10811}.	[*Gli-A^{u}2-V* {10811}].	**dv:** PI 428239, *T. urartu* {10811}.
Gli-A2bd {10811}.	[*Gli-A^{u}2-VI* {10811}].	**dv:** PI 428336, *T. urartu* {10811}.
Gli-A2be {10811}.	[*Gli-A^{u}2-VII* {10811}].	**dv:** PI 428235, *T. urartu* {10811}.
Gli-A2bf {10811}.	[*Gli-A^{u}2-VIII* {10811}].	**dv:** PI 428234, *T. urartu* {10811}.
Gli-A2bg {10811}.	[*Gli-A^{u}2-IX* {10811}].	**dv:** PI 428183, *T. urartu* {10811}.
Gli-A2bh {10811}.	[*Gli-A^{u}2-X* {10811}].	**dv:** PI 428256, *T. urartu*{10811}.
Gli-A2bi {10811}.	[*Gli-A^{u}2-XI* {10811}].	**dv:** PI 428255, *T. urartu* {10811}.
Gli-A2bj {10811}.	[*Gli-A^{u}2-XII* {10811}].	**dv:** PI 428224, *T. urartu* {10811}.
Gli-A2bk {10811}.	[*Gli-A^{u}2-XIII* {10811}].	**dv:** PI 428208, *T. urartu* {10811}.
Gli-A2bl {10811}.	[*Gli-A^{u}2-XIV* {10811}].	**dv:** PI 428202, *T. urartu* {10811}.
Gli-A2bm {10811}.	[*Gli-A^{u}2-XV* {10811}].	**dv:** PI 428217, *T. urartu* {10811}.
Gli-A2bn {10811}.	[*Gli-A^{u}2-XVI* {10811}].	**dv:** PI 427328, *T. urartu* {10811}.
Gli-A2bo {10811}.	[*Gli-A^{u}2-XVII* {10811}].	**dv:** PI 428317, *T. urartu* {10811}.
Gli-A2bp {10811}.	[*Gli-A^{u}2-XVIII* {10811}].	**dv:** PI 428253, *T. urartu* {10811}.
Gli-A2bq {10811}.	[*Gli-A^{u}2-XIX* {10811}].	**dv:** PI 538742, *T. urartu* {10811}.
Gli-A2br {10811}.	[*Gli-A^{u}2-XX* {10811}].	**dv:** PI 428232, *T. urartu* {10811}.
Gli-A2bs {10811}.	[*Gli-A^{u}2-XXI* {10811}].	**dv:** PI 428188, *T. urartu* {10811}.
Gli-A2bt {10811}.	[*Gli-A^{u}2-XXII* {10811}].	**dv:** PI 428244, *T. urartu* {10811}.
Gli-A2bu {10811}.	[*Gli-A^{u}2-XXIII* {10811}].	**dv:** PI 538733, *T. urartu* {10811}.
Gli-A2bv {10811}.	[*Gli-A^{u}2-XXIV* {10811}].	**dv:** PI 428212, *T. urartu* {10811}.
Gli-A2bw {10811}.	[*Gli-A^{u}2-XXV* {10811}].	**dv:** TRI 6734, *T. urartu* {10811}.
Gli-A2bx {10811}.	[*Gli-A^{u}2-XXVI* {10811}].	**dv:** PI 428254, *T. urartu* {10811}.

Gli-B2
In the appropriate entry, replace:
Gli-B2null with ***Gli-B2au*** and add a column stating 'null allele'.

Gli-D2
In the appropriate entry, replace:
Gli-D2null with ***Gli-D2ae*** and add a column stating 'null allele'.

NEW SECTION: Abiotic Stess Responses

Dehydrin-response Element Binding Factors
DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers an othologous *Dreb1* gene series was placed on chromosomes 3A, 3B, and 3D {10729}. SNPs in *Dreb-B1* permitted mapping in chromosome 3BL in the ITMI (Opata 85 / W7984) mapping population.

Dreb-B1 {10729}. 3BL {10729}.
ma: *Xmwg818-3B* – 27.3 cM – *Dreb1* – 11.2 cM – *Xfbb117-3B* {10729}.

Dreb-B1a [{10729}]. **v:** Opata 85 {10729}.
Dreb-B1b [{10729}]. **v:** W7984 {10729}.

Pathogenic Disease/Pest Reaction

80. Reaction to *Blumeria graminis* DC.
80.1. Designated genes for resistance

Pm4d {10744}. 2AL {10744}. **bin:** 2AL1-0.85-1.00.
dv: *T. monococcum* subsp. *monococcum* Tm27 {10744}.
v: Tm27d2 = WW St 2022 / Tm27 // Amor = TRI 29584 {10744}.
ma: A 218-bp fragment was amplified with STS marker ResPm4 as were other *Pm4* alleles {10744}.

Pm17. **v:** McCormack {10758}; Tribute {10758}; TAM303 {10758}.

Pm41. **bin:** 0.63–1.00.

Pm44 {10790}. 3AS {10790}. **v:** Hombar {10790}.
ma: Flanked by SSR markers distally located in chromosome 3AS {10790}.

Pm45 {10791}. Pm57-6D {10790}. 6DS {10791}.
v1: Line NWG0099 {10791}.
v2: D57 {10791}.
ma: Close linkages are reported in the draft manuscript.

82. Reaction to *Fusarium graminearum*
82.2. Disease: Crown rot cuased by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species.

'Cansas / Ritmo': After *QFHS.whs-5BL* add insert: '(remaned *Qfhs.lfl-1BL* in {10768})'. Then continue at end of the paragraph '*Qfhs.lfl-1BL* was verified in $F_{4:7}$ lines and in detected Biscay, History, and Pirat {10768}.

'CS / CS (Sumai 3 7A)': *QFhb7AC*, nearest marker *Xwmc17-7A*, explained 22% of phenotypic variance for type-II and 24% of phenotypic variance for type-III resistance {10798}.

'Lang /*T. aestivum* subsp. *spelta* CSCR6': *Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495*; R^2 up to 0.49, validated in other crosses {10273}. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23 {10273}.

'Soissons (relatively resistant) / Orvantis (susceptible)': Add at end of paragraph: Increased susceptibility associated with the *Rht-D1b* allele was further confirmed in crosses of semi-dwarf cultivars Apachi, History, and Romanus {10793}.

83. Reaction to *Heterodera avenae* Woll.

QCre.pau-1A {10749}. 1AS {10749}. **dv:** *T. monococcum* subsp. *monococcum* Tm 14087 *QCre.pau-2A* {10749}.
ma: *QCre.pau-1A* was mapped in a 3.6 cM interval in a *T. monococcum* subsp. *aegilopoides* Tb 5088 / Tm 14087 RIL population and was flanked by *Xcfa2153-1A* and *BE444890* {10749}; $R^2 = 0.26$ {10749}.
QCre.pau-1A was transferred to tetraploid and hexaploid lines {10749}.

QCre.pau-2A {10749}. 2AS {10749}. **dv:** *T. monococcum* subsp. *monococcum* Tm 14087 *QCre.pau-1A* {10749}.
ma: *QCre.pau-2A* was mapped in a 4.00 cM interval flanked by *BE498358* and *Xwmc358-2A* {10749}; $R^2 = 0.13$ {10749}.

90. Reaction to Meloidogyne spp.
Root knot eelworm
Revise to:

Rkn1 [{632}]. *Rkn* {632}. 6D {10799}.
dv: *Ae. tauschii* G3489.
v: Prosquare, a synthetic hexaploid of 'Produra/*Ae. tauschii* G3489' {632}.

Rkn2 [{1621}]. Derived from *Ae. peregrina* {1621}. *Rkn-mn1* {1621}.
3B{590}. **v:** X8 = 'CS/*Ae. peregrina* No. 1//Rescler/3/Lutin' {1620}; X35 {1620, 1621}.
ma: Co-segregation with RAPD $OpY16_{1065}$ and close linkage with several markers including *Est-B5* {0103}; converted to SCAR Y16 {10486}; may be the same as *CreY* (see reaction to *Heterodera avenae*) on chromosome $3S^v$ from *Ae. peregrina* translocated to 3BL {10800}.

Add:

Rkn3 {10801}. Derived from *Ae. ventricosa*. 2NS translocation into 2AS {10801}.
v: VPM1, Lassik (PI 653535) {10801}.
ma: Resistances to *M. javanica* and *M. incognita* mapped to the 2NS translocation in BC_6F_3 near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation {10801}.

92. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

92.1. Genes for resistance

QTL

Add at the end of this section:

A summary of QTL analyses is provided in {10276}.

92.2. Sensitivity to SNB toxin

Insert at the beginning of this section:

A discussion on the origin and role of host-specific toxins is provided in {10276}.

Add:

Tsn1. **v:** Forno {10275}. **tv:** Add: Some *T. turgidum* subsp. *dicoccoides* accessions {10756}.
dv: Two *Ae. speltoides* accessions {10756}.
c: *Tsn1* has eight exons and a S/TPK-NBS-LRR structure; all three domains are required for function and the TSN1 protein does not interact directly with ToxA {10756}.

tsn1. **ma:** Add: This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B* {10274}.

Genotype list in {10274}.

Snn1. **bin:** 1BS.sat.18.
ma: *XksuD14.2-1BS* – 0.4 cM – *Snn1/XBE498831/XBF474204* – 0.4 cM – *Xpsp3000-1BS/XBE422980/XBE637568/ZBE605202* {10727}; *XksuD14.2* – 0.34 cM – *Snn1/XBE498831/XBF474204* – 0.12 cM – *XBF29322* – 0.04 cM – *Xpsp3000-1BS/XBE422980/XbE637568/XBF605202* {10727}.

Snn2. **ma:** *XTC253803* – 3.6 cM – *Snn2* – 0.4 cM – *Xcfd-2*D {10274}.

snn2. **v:** Add: Atlas 66 {10274}; Cheyenne {10274}; Chinese Spring {10274}; Jagger {10274]; Opata 85 {10274}; Salamouni {10274}; TAM 105 {10274}.

Snn3 {10728,10507}. Sensitivity to *SnTox3* is dominant {10728}.
5BS {10728,10507}. **bin:** 5BS-6 {10507}.
v2: Grandin Snn2{10728,10507}.
ma: *Snn3* – 1.4 cM – *Xcfd20-5BS* {10507}.

snn3. **v:** BR34 {10507}.

Snn4 {10275}. Sensitivity to SnTox4 is dominant {10275}. 1AS {10275}.
bin: 1AS3-0.86-1.00 {10275}.
v: Arina {10275}.
ma: *XBG262267/XBG262975* – 0.9 cM – *Snn4* – 1.6 cM – *Xcfd58.1-1AS* {10275}.

snn4. **v:** Forno {10275}.

QTL

'P91193D1 / P92201D5' RIL population: tested in the U.S.A. and Australia: *QSng.pur-2DL.1* from P91103D1, R^2 = 0.123 (Indiana) and 0.381 (South Perth); and *QSng.pur-2DL.2* from P92201D5, R^2 = 0.069 (Indiana) and 0.112 (South Perth) {10776}.

94. Reaction to *Puccinia graminis* Pers.

Sr2. **ma:** Add: Tightly linked CAPS marker csSr2 based on a SNP proved superior to *Xgwm533-3B* as a marker for *Sr2* {10786}.

Sr13. **bin:** 6AL-8. **tv:** Kronos {10777}; Medora {10777}; Sceptre {10777}.
ma: *CD926040 – Sr13 – BE471213* {10777}.

A gene in 'Khapstein/9*LMPG' and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However, the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance gene mapped in {10778} could not be *Sr13*.

Sr22. **bin:** 7AL-0.74-0.86. **v:** Recombinant line reported in {10772, 10773}.
ma: Multiplex marker cssu22 based on STS markers derived from cloned fragment csIH81 was developed in {10772}. This marker gave positive results for *Sr22* in all recombinant lines including those reported in {10773}.

Sr38. Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.

Sr39. Add at the beginning of notes:Lines with shortened alien segments are reported in {10741}.

Sr48. **ma:** Replace the first sentence with: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* –2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.

Sr50 [{10745}]. *SrR* {0377}. 1DS {10745}.
ad: CS + Imperial 1R {0377}. **v:** Line T6-1 AUS 91434 {10745}.
al: *S. cereale* cv. Imperial.
ma: Line T6-1 retains the rye marker AW2-5 {10745}.

In rye, *Sr50* may be allelic with *Sr31*; however, in wheat they can be regarded as separate loci. *Sr50* is located in a small interstitial segment not detected by GISH. Line T6-1 lacks the *Sec-1* allele from rye {10745}.

Sr51 {10803}. Homoeologous group 3 {10803}; $3S^{S}S$ {10803}.
3A (T3AL·$3S^{S}$S) {10803}. **v:** TA5619 {10803}.
3B (T3BL·$3S^{S}$S) {10803}. **v:** TA5620 {10803}.
3D (T3DL·$3S^{S}$S) {10803}. **v:** TA5621 {10803}.
3D (T3DS-$3S^{S}$S·$3S^{S}$L) {10803}. **v:** TA5622 {10803}.
al: *Ae. searsii* TA2355 {10803}.
ma: 3^{S}S-specific markers are provided in {10803}.

Sr52 {10774}. 6A (T6AS·6V#3L) {10774}.
v: TA5617 {10775}.
ma: 6V3- specific EST-STS markers are given in {10775}.

The seedling response conferred by *Sr52* is temperature-sensitive.

Sr53 {10789}. Derived from *Ae. geniculata*. 5D {10789}.
Ti5DS·5DL-$5M^{g}$L-5DL {10789}. **v:** TA5630 (U6154-124) {10789}.
T5DL-$5M^{g}$L·$5M^{g}$S {10789}. **v:** TA5625 (U6200-64) {10789}.
T5DL-$5M^{g}$L·$5M^{g}$S {10789}. **v:** TA5643 (U6200-117) {10789}.
al: *Ae. geniculata* TA10437 {10789}.

The three translocation lines are re-engineered derivatives of TA5599 (T5DL-$5M^{g}$L·$5M^{g}$S {10789}).

SrCad {10733}. 6DS {10733}.
v: AC Cadillac {10733}; AC Crystal {10733}; AC Foremost {10733}; AC Karma {10733}; AC Taber {10733}; AC 2000{10733}; Peace {10733}; 5700 {10733}.
ma: Lines with *Bt10* {10733}. *Xcfd49-6D* – 7.7 cM – *SrCad* – 1.5 cM – *FSD_RSA/Bt10* – 14.1 cM – *Xbarc301-6D* — 8 cM – *Xbarc173-6D* {10733}; *Xcfd49-6D* – 7.2 cM – *SrCad* – 1.8 cM – *FSD-RSA/Bt10* – 14 cM – *Xcfd75-6D* {10733}.

SrR. Delete current listing.

95. Reaction to *Puccinia striiformis* Westend.

95.1. Designated genes for resistance to stripe rust

Yr1. **ma:** Replace the present entry with: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* –2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.

Yr5. Add note: Allelic with *Yr7* and *YrSp* {10759}.

Yr7. Add note: Allelic with *Yr5* and *YrSp* {10759}.

Yr9. **v2:** Brigadier *Yr17* {10785}.

Yr17. **v2:** Brigadier *Yr9* {10785}.
ma: Add: SCAR markers SC-372 and SC-385 were developed in {10796}.

Yr35. **ma:** *Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B* {10780}.

Yr40. **ma:** Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.

Yr42. Add note: Associated with *Lr62* {10537}.

Yr46. Update to: 4DL. **bin:** Distal to 0.56.
ma: Change present entry to: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.

Yr49 {10746}. Adult plant resistance. 3DS {10746}.
bin: 3DS-6 (0.55-1.00). **v1:** 'Avocet S*3 / Chuanmai 18' AUS91433 {10746}.
v2: Chuanmai 18 Yr18 {10746}.
ma: *Xgpw7321-3D/Yr49* – 1 cM – *Xgwm161-3D* {10746}.

95.2. Temporarily designated genes for resistance to stripe rust

YrSp. Add note: Allelic with *Yr5* and *Yr7* {10759}.

95.3. Stripe rust QTL

'Alcedo (R) / Brigadier (S)': DH population: Two major QTL *QPst.jic-2DL* (R^2 up to 0.36) and *QPst.jic-4BL* (R^2 up to 0.29) for percent infection contributed be Alcedo {10785}. A seedling-expressed QTL was located at the same position in 2DL {10774}.

'Flinor (R) / Mingxian 169 (S)': Two independent QTL for high temperature (24/18C) seedling resistance located in chromosome 5BL, designated *QYr-tem-5B.1* (*Xbarc89 – Xgwm67*) and *QYr-tem-5B.2* (*Xbarc140n – Xwmc235*) and R^2 = 0.37 and 0.33, respectively {10797}.

'Kukri (MR) / Janz (MR)': DH population: Tested with pre- and post-2003 Australian Pst races in several environments. *QYr.sun-7B* (Kukri) and *Qyr.sun-7D* (= *Yr18*) (Janz) were consistent over environments; *QYr.sun-1B*, *-5B*, and *-6B* were detected in most environments, and *QYr.sun-3B* was identified in only one season. Two genes, *QYR.sun-1A* from Janz and *QYr.sun-2A* from Kukri, were detected only with pre- and post-2003 races, respectively, and likely contributed to differential responses of these cultivars to the two groups of races {10751}.

96. Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr10. **tv:** Altar 82 {10760}; Russello {10760}.
c: Add: A second CC-NBS-LRR gene, *RGA2*, is required for expression of *Lr10* in tetraploid and hexaploid wheats {10760}.

Lr12. **v2:** Caldwell *Lr14a* {10787}.

Lr14.
Lr14a. **v2:** Caldwell *Lr12* {10787}.

Add note at end of section: The *Lr14* region in tetraploid wheat harbours *Qlr.ubo-7B.2*, a gene that confers durable resistance in durums {10734, 10736} and that is present in many Italian, CIMMYT, and ICARDA durum cultivars {10736}. The relationship of this gene described as *Lr14c* (reference genotype Creso) in {10735} remains to be determined. Reasons for considering *Lr14c* as a unique allele are given in {10735}. In association mapping, the presence of *QLr.ubo-7B.2* was predicted with 96% accuracy based on appropriate alleles of *Xcfa2257.2*, *Xgwm344.2*, and *Xwmc10* in the distal region of chromosome 7BL {10736}.

Lr17.
Lr17a. **ma:** Add: *Lr17a* – 3.7 cm – *Xbarc212-2a* {10795}.

Lr18. Add note: A resistance gene, *LrTt2*, in line 842-2 was located on chromosome 5BL in a similar region to *Lr18*. The claim that *Lr18* and *LrTt2* were different based on different low seedling infection types, but the genetic backgrounds were different {10752}.

Lr21. **v:** Lovitt {10766}; McKenzie {10766}
Add to notes: Further haplotype analyses are reported in {10766}.

Lr25. **i:** Tc+Lr25 *Lr48* {10738}.
Add note: *Lr25* is closely linked with *Lr48* {10738}.

Lr35. Add note at the end of section: Lines with shortened alien segments are reported in {10741}.

Lr37. Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.

Lr39. 2DS {add: , 10731}.
ma: Four markers, *Xbarc124-2D*, *Xgwm210-2D*, *Xgdm35-2D*, and *Xcfd36-2D* were closely linked with the terminally located *Lr39* (formerly *Lr41*), but the gene order was inconsistent and no specific allele was associated with it {10731}.

Lr47. 7AS. **v:** Add: Bionta 2004 {10737}.

Lr48. , 4BS {10738}. **ma:** RAPD markers flanking *Lr48* at 2.7 and 8.6 cM are reported in {10738}.
Lr48 is closely linked with *Lr25* {10738}.

Lr53. **ma:** *Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6*B – 3.4 cM – *Xgwm50-6B* {10780}.
Lr53 was genetically independent of *Lr36* {10780}.

Lr57. **ma:** Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.

Lr59. Add note: Problems in recovering balanced recombinants are reported in {10762}.

Lr62 Add note: Associated with *Yr42* {10537}.

Lr67. **bin:** Distal to 0.56.
ma: add: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.

LrAlt {10739}. 2AS {10739}. **v:** *T. aestivum* subsp. *spelta* cv. Altgold {10739}.
ma: *LrAlt* – 1.8 cM – *Xbarc212-2A/Xwmc382-2A* – 2 cM – *Xgwm636-2A* {10739}.

LrWo {10747}. 5B (10747}. **tv:** Wollaroi AUS99174 {10747}.
ma: *Xgwm234-5B* – 7.2 cM – *LrWo* – 20.3 cM – *wPT-1420* {10747}.
The relationship of *LrWo* to *Lr52* was not established.

Add to the list: complex genotypes
Coker 9663 *Lr9 Lr10 Lr14a* {10742}
Pioneer 26R61 *Lr13 Lr14b Lr26* {10742}

Genotype lists: French cultivars {10792}. Add to European cultivars {……., 10794}.

96.3. QTL for reaction to *P. triticina*

Insert above *QLr.sfr-1B*:

QLr.pser.1BL {10743}. 1BL {10743}. **bin:** 1BL6-0.32 {10743}.
ma: Proximal to *Xgwm264.1-1BL* {10743}.
Associated with *lm* producing a lesion mimic phenotype in the absence of disease {10743}.

After the entry for 'Avocet / Pavon' add:
'TA 4152-60 (MR) / ND495 (MR)': DH population: Five QTL for APR were identified in the field, viz. *QLr.fcu-3AL* ($R^2 = 0.18$), *QLr.fcu-3BL* ($R^2 = 0.19$), *QLr.fcu-5BL* ($R^2 = 0.07$), and *QLr.fcu-6BL* ($R^2 = 0.12$) from TA 4152-60 and *QLr. fcu-4DL* ($R^2 = 0.13$) from ND495 {10757}. The 3AL gene also conferred seedling resistance to some races and the 3BL gene conferred resistance to race MFPS {10757}.

Add:
Tetraploid wheat
Association mapping indicated genomic regions affecting leaf rust response in chromosomes 1A, 1B, 2A, 2B (*Lr13*, *Lr23* region), 3B, 5A, 5B, 6B, 7A, and 7B (see *Lr14*) {10736}.

97. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

97.1. Insensitivity to tan spot toxin

Tsn. **dv:** Two *Ae. speltoides* accessions {10756}.
tv: Add: Some *T. turgidum* subsp. *dicoccoides* accessions{10756}.
c: *Tsn1* has eight exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA {10756}.

93.3. Resistance to tanspot

TsrAri {10765}. Recessive. 3A {10765}.
v: Arina {10765}; Heines VII {10765}; Zenith {10765}.
Add: 'Batavia (S) / Ernie (R)': DH population tested over three years. Four (1A (Ernie), 7A, 2BS, 3BS (Batavia)), five (2BS, 5BL (E), 3D, 6A, 7D (B)), and four (2BS, 5BL (E) 1A, 6A (B)) QTL accounted for most of the variation in each

year. The greatest effect across years was the QTL on chromosome 2BS (R^2 = 0.382, 0.298 and 0.362, respectively). This QTL was validated in four additional populations {10782}.

'Wangshuibai / Ning 7840': RIL population: Race 1: *QTs.ksu-1AS*, R^2 = 0.39 (nearest marker *Xcfa2153-1A*) and *QTs.ksu-2BS*, R^2 = 0.04) (nearest marker *Xbarc2-2B*) {10753}.

XX. Reaction to Rhizoctonia spp.
Cause of Rhizoctonia root rot.
Rot1 {10761}. **v:** Scarlet-Rz1 {10761}.
Scarlet-Rz1 was produced by mutagenesis {10761}.

95. Reaction to *Schizaphis graminum* Rond. (Toxoptera graminum Rond.)
Gb2. **ma:** Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.
Gb3. **v:** TAM112 (10764}. **al:** Insave rye.
Gb6. **v:** N96L9970 {10764}.
ma: Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.

101. Reaction to *Tapesia* yallunda*e* (Anomorph: *Pseudocerosporella herpotrichoides*)
Add at end of section:
QPch.jic-5A {10771}. **bin:** 5AL-6; 0.68-0.78.
ma: Closely associated with *Xgwm639-5AL* {10771}.

102. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa*
Bt10. **v:** Present in lines with *SrCad* {10733}.
QTL
'Blizard (R) / 8405-JC3C (S)': DH population: Resistance and markers *Xgwm374-1BS*, *Xgwm364-1BS*, and *Xbarc128-1BS* were within a 3.9 cM interval {10783}.

106. Reaction to Wheat Streak Mosaic Virus
Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella*. See: Resistance to colonization by *Eriophyes tulipae*. According to {10226} WSMV may also be seed-borne. At least some sources of resistance to WSMV are also effective against *Triticum* mosaic virus.

Update:
Wsm1 {379, 440}. Derived from *Th. intermedium*.
4D = T4DL·4J^{S}S {391, 389}.
i: Karl*4/CI 17884 = PI 583794 = KS93WGRC27 {440}.
v: CI 17766 = B-6-37-1 {391, 800, 1543}; CI 17884 {391} KS90H445 {391}; KS90H450 {391}; CI 17883 {389}.
ad: CI 17881; CI 17886{391}.
su: 4J^{S}S (4A): CI 15092 {391}; 4J^{S}S (4D): CI 17882 and CI 17885 {391}.
ma: *Wsm1* cosegregated with a STS amplified by the primer set STSJ15 {1456}.
4D = T4DL·4DS-4J^{S}S {10788}. **v:** KS08WGGRC50 {10788}.
4A {800} = T4AL·4J^{S}S {391}.
6A = T6AS·4J^{S}L + T6AL·4J^{S}S {389}.
Wsm1 is located in 4J^{S}S (formerly 4Ai#2S). CI 17882, CI 17884, CI 17885, and KS90H445 also carry a 7S *Ae. speltoides* chromosome substituting for 7A (See Reaction to *Schizaphis graminum*).
Wsm1 also confers resistance to *Triticum* Mosaic Virus {10788}.
Wsm2. 3BS (10802}. **v:** CO960293-2 {10802}; Snowmass {10802}.
ma: *Wsm2* – 5.2 cM – *XSTS3B-55* {10802}; *Xbarc102-3B* – 1.6 cM – *Wsm2* {10802}.
Wsm2 confers resistance at temperatures below 19C {10802}.
Wsm3 {10775}. 7B (T7BS·7S#3L) {10775}. **v:** TA5624 {10775}.

XX. Reaction to Wheat Yellow Mosaic Virus

Vectored by *Polymyxa graminis*. MYMV is closely related to WSSMV, another bymovirus.

YmIb {10750}. 2DL {10750}.

v: Ibis {10750}; Jagger {10750}; KS 831957 {10750}; Madsen {10750}; Yumechikara {10750}.

ma: *Xwmc181-2D* – 12.4 cM – *YmIb* – 2.0 cM – *Xcfd16-2D* – 2.0 cM – *Xwmc41-2D* – 3.1 cM – *Xcfd168-2D* {10750}.

The relationships of *YmIb* to previously mapped gene in 2DL for resistance to WYMC and WSSMV in Yangfu 9311 {10258} and a Geneva derivative {0131} were not established.

References

Updates

10375. Correct author name from 'Laur' to 'Kaur' and delete 'Draft manuscript'.
10507. Correct page numbers to 682-693.
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10551. Replace with: Li G, Fang T, Zhang H, Xie C, Li H, Yang T, Nevo E, Fahima T, Sun Q & Liu Z 2009 Molecular identification of a new powdery mildew resistance gene *Pm41* on chromosome 3BL derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 119: 531-539.
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New

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V. ABBREVIATIONS USED IN THIS VOLUME.

PLANT DISEASES, PESTS, AND PATHOGENS:

BYDV = barley yellow dwarf virus
BMV = barley mosaic virus
CCN = cereal cyst nematode, *Heterodera avenae*
FHB = Fusarium head blight
RWA = Russian wheat aphid
SBMV = soilborne mosaic virus
SLB = Septoria leaf blotch
TMV = *Triticum* mosaic virus
WDF = wheat dwarf mosaic
WSBMV = wheat soilborne mosaic virus
WSMV = wheat streak mosaic virus
WSSMV = wheat spindle streak mosaci virus
WYMV = wheat yellow mosaic virus
E. graminis* f.sp. *tritici = *Erysiphe graminis* f.sp. *tritici* = the powdery mildew fungus
F. graminearum = *Fusarium graminearum* = head scab fungus
F. nivale = *Fusarium nivale* = snow mold fungus
H. avenae = *Heterodera avenae* = cereal cyst nematode
P. graminis = *Polymyxa graminis* = wheat soilborne mosaic virus vector
P. striiformis* f.sp. *tritici = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus
P. triticina = *Puccinia triticina* = *P. recondita* f.sp. *tritici* = leaf rust fungus
R. cerealis = *Rhizoctonia cerealis* = sharp eyespot
R. solani = *Rhizoctonia solani* = Rhizoctonia root rot
R. padi = *Rhonpalosiphum padi* = bird cherry-oat aphid
S. tritici = *Septorai tritici* = Septoria leaf spot fungus
S. graminearum = *Schizaphus graminearum* = greenbug
St. nodorum = *Stagonospora nodorum* = Stagonospora glume blotch
T. indica = *Tilletia indica* = Karnal bunt fungus

SCIENTIFIC NAMES AND SYNONYMS OF GRASS SPECIES (NOTE: CLASSIFICATION ACCORDING TO VAN SLAGEREN, 1994):

A. strigosa = *Avena strigosa*
Ae. cylindrica = *Aegilops cylindrica* = *Triticum cylindricum*
Ae. geniculata = *Aegilops geniculata* = *Aegilops ovata* = *Triticum ovatum*
Ae. longissima = *Aegilops longissima* = *Triticum longissimum*
Ae. markgrafii = *Aegilops markgrafii* = *Aegilops caudata* = *Triticum caudatum*
Ae. speltoides = *Aegilops speltoides* = *Triticum speltoides*
Ae. tauschii = *Aegilops tauschii* = *Aegilops squarrosa* = *Triticum tauschii*
Ae. triuncialis = *Aegilops triuncialis* = *Triticum triunciale*
Ae. umbellulata = *Aegilops umbellulata* = *Triticum umbellulatum*
Ae. peregrina = *Aegilops peregrina* = *Aegilops variabilis* = *Triticum peregrinum*
Ae. searsii = *Aegilops searsii* = *Triticum searsii*
Ae. ventricosa = *Aegilops ventricosa* = *Triticum ventricosum*
D. villosum = *Dasypyrum villosum* = *Haynaldia villosa*
S. cereale = *Secale cereale* = rye
T. aestivum* subsp. *aestivum = *Triticum aestivum* = hexaploid, bread, or common wheat
T. aestivum* subsp. *macha = *Triticum macha*
T. aestivum* subsp. *spelta = *Triticum spelta*
T. militinae = *Triticum militinae*
T. monococcum* subsp. *aegilopoides = *Triticum boeoticum*
T. timopheevii* subsp. *timopheevii = *Triticum timopheevii*
T. timopheevii* subsp. *armeniacum = *Triticum araraticum* = *T. araraticum*
T. turgidum* subsp. *dicoccoides = *Triticum dicoccoides* = wild emmer wheat
T. turgidum* subsp. *dicoccum = *Triticum dicoccum*

T. turgidum* subsp. *durum = *Triticum durum* = durum, pasta, or macaroni wheat
T. urartu = *Triticum urartu*
Th. bessarabicum = *Thinopyrum bassarabicum*
Th. elongatum = *Thinopyrum elongatum* = *Agropyron elongatum*
Th. intermedium = *Thinopyrum intermedium* = *Agropyron intermedium*

Scientific journals and publications:

Agron Abstr = Agronomy Abstracts
Ann Wheat Newslet = *Annual Wheat Newsletter*
Aus J Agric Res = *Australian Journal of Agricultural Research*
Can J Plant Sci = *Canadian Journal of Plant Science*
Cereal Chem = *Cereal Chemistry*
Cereal Res Commun = *Cereal Research Communications*
Curr Biol = *Current Biology*
Eur J Plant Path = *European Journal of Plant Pathology*
Funct Integ Genomics = *Functional Integrative Genomics*
Ind J Agric Sci = *Indian Journal of Agricultural Science*
Int J Plant Sci = *International Journal of Plant Science*
J Agric Sci Technol = *Journal of Agricultural Science and Technology*
J Cereal Sci = *Journal of Cereal Science*
J Hered = *Journal of Heredity*
J Phytopath = *Journal of Phytopathology*
J Plant Phys = *Journal of Plant Physiology*
Mol Gen Genet = *Molecular and General Genetics*
Nat Genet = *Nature Genetics*
PAG = Plant and Animal Genome (abstracts from meetings)
Phytopath = *Phytopathology*
Plant Breed = *Plant Breeding*
Plant, Cell and Envir = *Plant, Cell and Environment*
Plant Cell Rep = *Plant Cell Reporter*
Plant Dis = *Plant Disease*
Plant Physiol = *Plant Physiology*
Proc Ind Acad Sci = *Proceedings of the Indian Academy of Sciences*
Proc Natl Acad Sci USA = Proceedings of the National Academy of Sciences USA
Sci Agric Sinica = *Scientia Agricultura Sinica*
Theor Appl Genet = *Theoretical and Applied Genetics*
Wheat Inf Serv = *Wheat Information Service*

Units of measurement:

bp = base pairs
bu = bushels
cM = centimorgan
ha = hectares
kDa = kiloDaltons
m^2 = square meters
m^3 = cubic meters
μ = micron
masl = meters above sea level
me = milli-equivalents
mL = milliliters
mmt = million metric tons
mt = metric tons
Q = quintals
T = tons

MISCELLANEOUS TERMS:

Al = aluminum
AFLP = amplified fragment length polymorphism
ANOVA = analysis of variance
A-PAGE = acid polyacrylamide gel electrophoresis
APR = adult-plant resistance
AUDPC = area under the disease progress curve
BC = back cross
BW = bread wheat
CHA = chemical hybridizing agent
CMS = cytoplasmic male sterile
CPS = Canadian Prairie spring wheat
DH = doubled haploid
DON = deoxynivalenol
ELISA = enzyme-linked immunosorbent assay
EMS = ethyl methanesulfonate
EST = expressed sequence tag
FAWWON = Facultative and Winter Wheat Observation Nursery
GA = gibberellic acid
GIS = geographic-information system
GM = genetically modified
GRIN = Germplasm Resources Information Network
HPLC = high pressure liquid chromatography
HMW = high-molecular weight (glutenins)
HRSW = hard red spring wheat
HRRW = hard red winter wheat
HWSW = hard white spring wheat
HWWW = hard white winter wheat
ISSR = inter-simple sequence repeat
IT = infection type
kD = kilodalton
LMW = low molecular weight (glutenins)
MAS = marker-assisted selection
NSF = National Science Foundation
NILs = near-isogenic lines
NIR = near infrared
NSW = New South Wales, region of Australia
PAGE = polyacrylamide gel electrophoresis
PCR = polymerase chain reaction
PFGE = pulsed-field gel electrophoresis
PMCs = pollen mother cells
PNW = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada)
PPO = polyphenol oxidase
QTL = quantative trait loci
RAPD = random amplified polymorphic DNA
RCB = randomized-complete block
RFLP = restriction fragment length polymorphism
RILs = recombinant inbred lines
RT-PCR = real-time polymerase-chain reaction
SAMPL = selective amplification of microsatellite polymorphic loci
SAUDPC = standardized area under the disease progress curve
SCAR = sequence-characterized amplified region
SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis
SE-HPLE = size-exclusion high-performance liquid chromatography
SH = synthetic hexaploid

SNP = single nucleotide polymorphism
SRPN = Southern Regional Performance Nursery
SRWW = soft red winter wheat
SRSW = soft red spring wheat
STMA = sequence tagges microsatellite site
SWWW = soft white winter wheat
SSD = single-seed descent
SSR = simple-sequence repeat
STS = sequence-tagged site
TKW = 1,000-kernel weight
UESRWWN = Uniform Experimental Soft Red Winter Wheat Nursery
VIGS = virus-induced gene silencing

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VIII. VOLUME 58 MANUSCRIPT GUIDELINES.

Manuscript guidelines for the *Annual Wheat Newsletter*, volume 57. The required format for Volume 58 of the *Annual Wheat Newsletter* will be similar to previous editions edited from Kansas State University.

CONTRIBUTIONS MAY INCLUDE:

—Current activities on your projects.
—New cultivars and germ plasm released.
—Special reports of particular interest, new ideas, etc., normally not acceptable for scientific journals.
—A list of recent publications.
—News: new positions, advancements, retirements, necrology.
—Wheat stocks; lines for distribution, special equipment, computer software, breeding procedures, techniques, etc.

FORMATTING & SUBMITTING MANUSCRIPTS:

Follow the format in volume 44–57 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Limited editing is done. Use Microsoft Word™ or send an RTF file that can be converted. Use Times 12 CPI and 1.0" (2.5 cm) margins. Please include a separate .jpg or equivalent file of any graphic in the contribution. Submit by E-mail to jraupp@k-state.edu.

DISTRIBUTION:

The only method of distribution of Volume 58 will be electronic PDF either by email or through download from the GrainGenes database (http://wheat.pw.usda.gov/ggpages/awn/). The volume can be found in both PDF and HTML formats. The HTML files can be read with any internet browser.

The *Annual Wheat Newsletter* will continue to be available (Vol. 37–57) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.