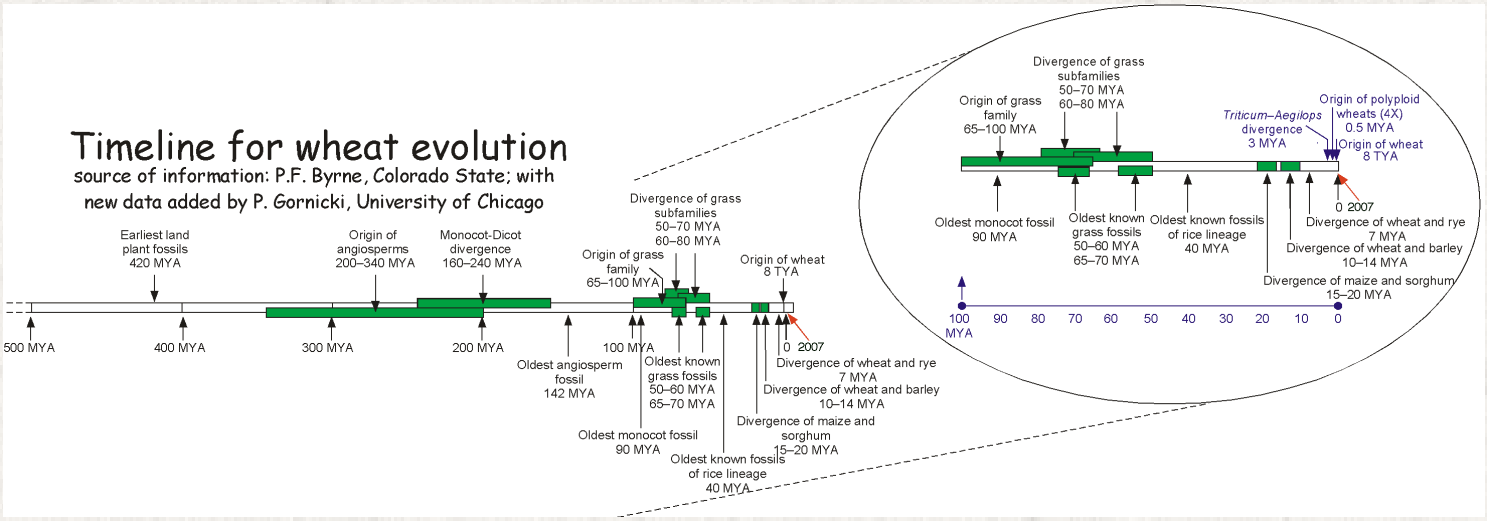
ANNUAL WHEAT NEWSLETTER

Volume 60



Contribution no. 15-029-B from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

ANNUAL WHEAT NEWSLETTER

Volume 60

Edited by W.J. Raupp, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506-5502 USA. Facilities during manuscript editing were provided by the Plant Pathology Department and the Wheat Genetics Resource Center, Kansas State University.

15 August, 2014

Contribution no. 15-029-B from the Kansas Agricultural Experiment Station, Kansas State University, Manhattan.

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I. ANNOUNCEMENTS

ISSS Workshop on Seed Longevity
SEEDS FOR FUTURE GENERATIONS – DETERMINANTS OF LONGEVITY

IPK Gatersleben, Germany.
5–8 July, 2015.

Topics

- Seed banking – state of the art
- Role of pre- and post-harvest environmental factors on seed longevity
- Genetics of inter- and intra-specific variation of seed survival
- Physiology and biochemistry behind seed ageing – deleterious effects vs. repair mechanisms

Rationale

Plant genetic resources play a major role for global food security. Worldwide, 7.4 x 10^6 accessions are stored in about 1,750 *ex situ* genebanks. Because the majority of global genebank holdings are stored as seed, seed longevity is of exceptional importance for germplasm conservation. Great differences between plant species are recognized. In addition, a huge variation within a species is present. However, a deficit exists in understanding the biology behind long and short seed life. A seed longevity workshop will focus on all aspects of seed ageing/conservation, concentrating on the molecular mechanisms of biochemistry, physiology, biophysics, and genetics of seed survival. Hence, the workshop will bring together scientists involved in seed science and seed banking.

With a total inventory of 150,000 accessions of 3,212 plant species and 776 genera, the genebank at IPK in Gatersleben, Germany, holds one of the most comprehensive collections worldwide. Therefore, IPK would be a predestined host for an initial workshop. Summer 2015 may be an appropriate time. The workshop will allow participants to visit the genebank facilities, including the extensive seed regeneration activities (~ 8,000 accessions) in the fields and glasshouses of IPK.

Contact:

ISSS Seed Longevity Workshop
Leibniz Institute of Plant Genetics and Crop Plant Research
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Scientific Committee

Andreas Börner, Germany
Francoise Corbineau, France
William Finch-Savage, United Kingdom
Fiona Hay, Philippines
Henk Hilhorst, The Netherlands
Ilse Kranner, Austria
Oliver Leprince, France
Hugh Pritchard, United Kingdom
Wim Soppe, Germany
Christina Walters, United States

Local Organizing Committee

Ulrike Lohwasser, Manuela Nagel, Andreas Börner, Martina Liewald, Katrin Menzel, and Uwe Scholz.

EWAC–EUCARPIA Cereals Section International Conference.

Lublin, Poland.
24–29 May, 2015.

We are pleased to announce that the joint EWAC–EUCARPIA Cereals Section International Conference will be held in Lublin, Poland, from 24 to 29 May, 2015. The conference will be a platform to share and exchange scientific experiences with researchers from different countries, focused on cereals genetic studies. During the last few years, we have observed the impressive progress in research concerning plant genetics and genomics, and we hope that this meeting will be an opportunity to discuss where we are now and where we are going to be in the future.

Please indicate your interest in receiving further information about Conference registration and accommodation by filling in the pre-registration form and returning it to the Conference Office via e-mail: ewac2015@up.lublin.pl by 30 September, 2014. Estimated deadline for registration and abstract submission will be February 2015. All details will be published consistently at the official EWAC website: www.ewac.eu. The conference will be held in Lublin – the main scientific and cultural center in Eastern Poland. If you would like to find more information about the city, please visit the official website www.lublin.eu/en.

The conference venue and accommodation place will be the Mercure Lublin Centrum Hotel (part of Accor Hotels) and estimated conference fee is about 550 € for full participation [http://www.accorhotels.com/gb/hotel-3404-hotel-mercure-lublin-centrum/].

The travelling information will be published in details in second circular. The citizens of majority of countries do not need a visa to enter Poland, however, if you would like to be sure if you are eligible, please visit Polish Ministry of Foreign Affairs website at http://www.msz.gov.pl/en/p/msz_en/travel_to_poland/entering_poland/.

The International Organizing Committee

Andreas Börner, Krzysztof Kowalczyk, Tatyana Pshenichnikova, John Snape, Victor Korzun, and Michał Nowak.

The Local Organizing Committee

Krzysztof Kowalczyk, Michał Nowak, Justyna Leśniowska-Nowak, Sylwia Okoń, Karolina Dudziak, and Magdalena Zapalska.

We hope you will save the date and look forward to welcoming you to Lublin next year!

In case of any questions concerning the conference, please do not hesitate to contact us at ewac2015@up.lublin.pl

BOOK ANNOUNCEMENT

Rye – Genetics, Breeding & Cultivation, 1st ed.

by Rolf H.J. Schlegel
ISBN-10: 1466561432; ISBN-13: 978-1466561434, CRC Press, Boca Raton, Taylor & Francis Group, Inc., New York, USA, 2013, pp 385

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 BRAZIL

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

Wheat in Brazil – 2013 crop year.

Eduardo Caierão, Ricardo Lima de Castro, Márcio Só e Silva, and Pedro Luiz Scheeren.

In the 2013 crop year, Brazilian wheat production was about 6 x 10^6 tons (Conab 2014), which is enough to supply 50% of the domestic demand (Table 1). 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 95.3% of the national production. Nonetheless, due to the characteristics of the cultivation system, average grain yield in this region is not the highest in the country.

Table 1. Cultivated area, total production and grain yield of wheat in Brazil in 2013 (* estimated value - March, 2014. Source: CONAB. 2014. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Available at: http://www.conab.gov.br/conabweb/index.php?PAG=131).

Region	Area (ha x 1,000)	Production (t x 1,000)	Grain yield (kg/ha)
North	—	—	—
Northeast	—	—	—
West-central	17.6	59.6	3,386.0
Southeast	88.1	210.6	2,390.0
South	2,104.1	5,257.7	2,499.0
Brazil [total]	2,209.8	5,527.9*	2,502.0*

In 2013, the wheat area cultivated was higher than in 2012 (2,209.8 versus 1,895.4). The total production and grain yield average/ha achieved in 2013 were 32.4% and 13.8% higher than that in 2012, respectively. Good weather conditions in the state of Rio Grande do Sul State important to the final wheat production in Brazil in the last crop season.

Reference.

CONAB. 2014. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. http://www.conab.gov.br/conabweb/index.php?PAG=131.

The history of wheat cultivars released from Embrapa in 40 years of research.

Eduardo Caierão, Pedro Luiz Scheeren, Márcio Só e Silva, and Ricardo Lima de Castro.

In 40 years of wheat genetic improvement, Embrapa developed over 100 new cultivars for different regions of Brazil. Too often, breeders demand information about the cultivars, such as year of release, name of precommercial line, genealogy, and the business unit responsible for the appointment, which are not always easily accessible and may be scattered in different papers. We conducted an historical survey of all cultivars released by Embrapa, aggregating into a single document the year of release, the name of pre-commercial line, the genealogy, and other information. Since 1974, Embrapa released 112 wheat cultivars (Table 2, pp. 6-8).

Table 2. Year of release, cultivar name, precommercial name, and genealogy of all wheat cultivars released by Embrapa, Passo Fundo, Brazil.

#	Year	Culivar name	Precommercial name	Genealogy
1	1975	CNT 1	PF 70225	PF 11-1000-62/BH 1146
2	1975	CNT 2	PEL 14049-68	IAS 16/Norin 26
3	1975	CNT 3	PF 70194	IAS 20/IAS 46
4	1976	CNT 4	PEL 13014-65	Lerma 50 /3/ IAS 31//IAS 20/Reliance
5	1976	CNT 5	PF 6946	IAS 46/BH 546
6	1976	CNT 6	PF 69162	IAS 20/IAS 50
7	1976	CNT 7	PF 70546	IAS 51 // IAS 20/ND 81
8	1976	CNT 8	PEL-SL-1268-69	IAS 20/ND 81
9	1977	CNT 9	PEL 72016	IAS 46/IAS 49 // IAS 46/Tokai 66
10	1977	CNT 10	PEL 72018	IAS 46/IAS 49 // IAS 46/Tokai 66
11	1978	Moncho BSB	—	Wren/Gaboto//Kalyansona/Blue Bird, Moncho Sib
12	1979	Trigo BR 1	PF 70402	IAS 20/IAS 50
13	1979	Trigo BR 2	PF 7158	IAS 50/4/IAS 46/3/Vilela Sol*4//Egypt101/Timstein
14	1979	Trigo BR 3	PF 72518	IAS 50/4/IAS 46/3/Vilela Sol*4//Egypt101/Timstein
15	1979	Trigo BR 4	PF 73226	IAS 20*3/Sinvalocho Gama
16	1980	Trigo BR 5	PF 74354	IAS 59 // IAS 52/Gasta
17	1980	Trigo BR 6	PEL 73538	IAS 20/Toropi
18	1981	Trigo BR 7	PF 72206	IAS 20/Toropi
19	1983	Trigo BR 8	PF 75171	IAS 20/Toropi // PF 70100
20	1983	Trigo BR 9 - Cerrados	R 30469-77	BH 1146/IRN 595-71
21	1983	Trigo BR 10 - Formosa	R 30147-77	D6301/Nainari 60//Weique/Red Mace/3/Ciano*2//Chris, Alondra 4546 Sel
22	1984	Trigo BR 11 - Guarani	MS 7810	Bluebird//Tobari 66/8156
23	1985	Trigo BR 13	PF 782027	IAS 51 // IAS 20/ND 81, CNT 7 Sel
24	1985	Trigo BR 14	Multilinha*	IAS 63/Alondra Sib // Gaboto/Lagoa Vermelha
25	1985	Trigo BR 15	PF 79300	IAS 54*2/Tokai 80 // PF 69193
26	1985	Trigo BR 12 - Aruanã	—	Bucky/Maya 74 Sib/4/Blue Bird//HD 832-5-5-Olesen/3/Ciano/Penjamo
27	1986	Trigo BR 16-Rio Verde	PF 79678	PF 70402/Alondra Sib//PAT72160/Alondra Sib
28	1986	Trigo BR 19	PF 79502	CNT 1/CNT 10
29	1986	Trigo BR 17 - Caiuá	MS 7878	Tezanos Pinto Prec//IRN 46/Ciano/3/II-64-27
30	1986	Trigo BR 18 - Terena	PF 781148	Cruzamento desconhecido
31	1987	Trigo BR 20-Guató	PF 81189	BH 1146*3/Alondra Sib
32	1987	Trigo BR 21-Nhandeva	PF 79475	Cajeme 71/PF 70553
33	1987	Trigo BR 22	PF 7942	PF 81130/CNT 10
34	1987	Trigo BR 23	PF 8215	Corre Caminos/Alondra Sib /3/IAS54-20 /Cotiporã//CNT 8
35	1988	Trigo BR 24	PF 8150	IAS 58*2/Eagle
36	1988	Trigo BR 25	PF 81230	BH 1146*3/Alondra Sib
37	1988	Trigo BR 27	PF 80271	RC 7201/BR 2
38	1988	Trigo BR 28	PF 81330	IAS 55/PF 70553
39	1988	Trigo BR 32	PF 82345	IAS 60/Indus //IAS62/3/AlondraSib/4/IAS 59
40	1988	Trigo BR 26 - São Gotardo	CPAC 831243	Kavkaz/Buho Sib//Kalyasona/Blue Bird,Veery Sib
41	1988	Trigo BR 29 - Javaé	MS 8166	Siskin Sib/Pavon Sib

Table 2. Year of release, cultivar name, precommercial name, and genealogy of all wheat cultivars released by Embrapa, Passo Fundo, Brazil.

#	Year	Culivar name	Precommercial name	Genealogy
42	1988	Trigo BR 30 - Cadiuéu	MS 81128	Ciano/8156//Tobari/Ciano/4/NO/3/II-12300// Lerma Rojo 64/8156/5/Pavon Sib
43	1988	Trigo BR 31 - Miriti	Veery 1	Kavkaz/Buho//Kalyansona//BB, Giennson 81
44	1989	Trigo BR 34	PF 839204	Alvarez 110/2*IAS 54/6/Toropi /4/TZPP/ Sonora 64 //Napo /3/Ciano /5/PF 6968
45	1989	Trigo BR 35	PF 83144	IAC 5*2/3/CNT7*3/Londrina//IAC5/ Hadden
46	1989	Trigo BR 33 - Guará	CPAC 841222	Buckbuck Sib/Bluejay Sib
47	1990	Trigo BR 36-Ianomami	PF 84588	Jupateco 73*3/Amigo
48	1990	Trigo BR 37	PF 84431	Mazoe/F13279 // Pelado Marau
49	1990	Trigo BR 38	PF 83348	IAS 55*4/Agent//IAS 55*4/CI 14123
50	1991	Trigo BR 42-Nambi-quara	PF 85634	Jupateco 73*6//Lagoa Vermelha*5 /Agatha
51	1991	Trigo BR 43	PF 853031	PF 833007/Jacuí
52	1991	Trigo BR 39 - Paraúna	CPAC 841244	Dove Sib/Pewee Sib
53	1991	Trigo BR 40 - Tuiúca	MS 208-84	Anahuac 7/Huacamayo Sib
54	1991	Trigo BR 41 - Ofaié	GD 833	BH 1146*6/Alondra Sib
55	1992	Embrapa 15	PF 85137	CNT 10/BR 5//PF 75172/Tifton 72-59 Sel
56	1992	Embrapa 16	PF 86238	Hulha Negra/CNT 7// Amigo/CNT 7
57	1992	Embrapa 10 - Guajá	MS 21169-85	CNT 8*3/Sonora 64
58	1993	Embrapa 24	PF 87128	Tifton 72-59 Sel/PF79763/3/Nobeoka Bozu /3*Londrina//B7908
59	1993	Embrapa 21	CPAC 86133	PAT 10/Alondra Sib//Veery 5
60	1993	Embrapa 22	CPAC 841153	Veery Sib/3/KLTO Sib/PAT 19//Mochis/Jup. 73
61	1994	Embrapa 27	PF 869107	PF 83743/5/PF 83182/4/CNT10*4//Lagoa Vermelha*5/Agatha /3/ Londrina*4/Agent // Londrina*3/Nyu Bai
62	1995	Embrapa 40	PF 84316	PF 7650/NS 18-78 // CNT 8/PF 7577
63	1995	Embrapa 41	CPAC 88118	PF 813/Polo 1
64	1995	Embrapa 42	CPAC 88130	LAP 689/MS 7936
65	1996	Embrapa 52	PF 86242	Hulha Negra/CNT 7//Amigo/CNT 7
66	1996	BRS 49	PF 90120	BR 35/PF 83619//PF 858/PF 8550
67	1997	BRS 119	PF 9198	PF 82252/BR 35//Iapar 17/PF 8550
68	1997	BRS 120	PF 91205	PF 83899/PF 813//F27141
69	1999	BRS 176	PF 86247	Hulha Negra/CNT 7//Amigo/CNT 7
70	1999	BRS 177	PF 92093	PF 83899/PF 813//F27141
71	1999	BRS 179	PF 92140	BR 35/PF 8596/3/PF 772003*2/PF 813//PF 83899
72	1999	BRS 207	CPAC 91086	Seri 82/PF 813
73	2000	BRS 192	PF 93167	PF 869114/PF 8722
74	2000	BRS 194	PF 92231	CEP 14/BR 23//CEP 17
75	2000	BRS 193	PF 95068	Anahuac 75/PF 869100
76	2001	BRS 208	WT 96053	CPAC 89119/3/BR 23//CEP 19/PF 85490
77	2002	BRS 209	PF 940384	Jupateco 73/Embrapa 16
78	2002	BRS Angico	PF 960198	PF 87107/2*IAC 13
79	2002	BRS Figueira	PF 950262	Coker 762*2/CNT 8
80	2002	BRS Timbaúva	PF 950419	BR 32/PF 869120
81	2002	BRS 210	WT 96061	CPAC 89119/3/BR 23//CEP 19/PF 85490
82	2003	BRS 234	PF 950407	BR 35//Embrapa 27/Buck Ombu/3/PF 87511
83	2003	BRS Buriti	PF 950400	Embrapa 27/Klein Orion

Table 2. Year of release, cultivar name, precommercial name, and genealogy of all wheat cultivars released by Embrapa, Passo Fundo, Brazil.

#	Year	Culivar name	Precommercial name	Genealogy
84	2003	BRS Camboatá	PF 970151	PF 93232 Sel 14
85	2003	BRS Guabijú	PF 970141	PF 86743/BR 23
86	2003	BRS Louro	PF 970128	PF 869114/BR 23
87	2003	BRS Umbu	PF 960243	Century/BR 35
88	2003	BRS 220	WT 98109	Embrapa 16/TB 108
89	2004	BRS Camboim	PF 980144	Embrapa 27*4/K. Cartucho//PF 869114/BR 23
90	2004	BRS Canela	PF 979064	BRS 120PF 91204*2//Anahuac 75
91	2004	BRS Guatambu	PF 970285	Amigo/2*BR 23
92	2004	BRS Tarumã	PF 970343	Century/BR 35
93	2004	BRS 229	WT 96168	Embrapa 27*3//BR 35/Buck Poncho
94	2005	BRS Guamirim	PF 990407	Embrapa 27/Buck Nandu//PF 93159
95	2005	BRS 254	PF 973047	Embrapa 22*3/Anahuac 75
96	2005	BRS 264	CPAC 98222	Buck Buck/Chiroca//Tui
97	2005	BRS 248	WT 99207	PAT 7392/PF 89232
98	2005	BRS 249	WT 00124	Embrapa 16/Anahuac 75
99	2007	BRS Pardela	WT 02094	Trigo BR 18/PF 9099
100	2007	BRS Tangará	PF 003295-A/B	BR 23*2/PF 940382
101	2008	BRS 276	PF 980537	Embrapa 27*3/Klein H3247 a 33400PF 93218
102	2008	BRS 277	PF 990423	OR 1/Coker 97.33
103	2009	BRS 296	PF 990283	PF 93232/Cook*4/VPM1
104	2010	BRS 327	PF 030027	CEP 24 Sel/BRS 194
105	2011	BRS Gaivota	WT 05106	PF 940301/PF 940395
106	2012	BRS 328	PF 023186-C=A	Klein H 3394 a 3110/PF 990744
107	2012	BRS 331	PF 015733-C	PF 99602/WT 98109
108	2012	BRS 374	PF 040310	PF 88618/Coker 80.33//Frontana/Karl
109	2012	BRS Parrudo	PF 070478	WT 98109/TB 0001
110	2012	BRS Gralha Azul	WT 07105	Jupateco F3/Embrapa 16//BRS Camboatá/LR 37
111	2013	BRS Marcante	PF 080310	PF 980533/PF 970227//BRS Guamirim
112	2013	BRS Sabiá	WT 08111	BRS 210/PF 980583

Performance of wheat cultivars in Rio Grande do Sul State, Brazil, 2012.

Ricardo Lima de Castro, Eduardo Caierão, Márcio Só e Silva, and Pedro Luiz Scheeren (Embrapa Trigo), and Jacson Zuchi and Rogério Ferreira Aires (Fepagro Nordeste, C.P. 20, 95.000-000 Vacaria, Rio Grande do Sul, Brazil).

The Brazilian Commission of Wheat and Triticale Research (CBPTT) annually conducts the State Test of Wheat Cultivars in Rio Grande do Sul State (EECT-RS) to support the identification of cultivars. This work had the objective to evaluate wheat cultivar grain yield performance of the EECT-RS in 2012. The yield grain performance of 32 wheat cultivars (Ametista, BRS 327, BRS 328, BRS 331, BRS 374, BRS Guamirim, CD 114, CD 121, CD 122, CD 123, CD 124, CD 1550, Fundacep Bravo, Fundacep Horizonte, Fundacep Raízes, JF 90, Marfim, Mirante, Quartzo, TBIO Alvorada, TBIO Iguaçu, TBIO Itaipu, TBIO Mestre, TBIO Pioneiro, TBIO Seleto, TBIO Sinuelo, TBIO Tibagi, TEC Frontale, TEC Triunfo, TEC Vigore, and Topázio e Turquesa) was studied in 13 environments (Cruz Alta – season 1, Cruz Alta – season 2, Júlio de Castilhos, Não-Me-Toque, Passo Fundo – seasons 1 and 2, Sertão, Vacaria, Augusto Pestana, Eldorado do Sul, Independência, and São Borja e São Luiz Gonzaga) in the state of Rio Grande do Sul in 2012. The experiments were in a randomized block design with three or four repetitions. Each plot consisted of five 5-m rows with a 0.2-m spacing between rows and a plant density of ~330 plants m^2. Grain yield data (kg/ha) were subjected to individual analyses of variance (for each environment) and to grouped analyses of variance (for all environments). The grouped analysis of variance was performed after the verification of homogeneity of residual variances, employing the mixed model (fixed

cultivar effect and randomized environment effect). The grain yield performance of wheat cultivars was evaluated by analysis of adaptability and stability, employing the method of distance from the ideal cultivar, weighted by the coefficient of residual variation, proposed by Carneiro (1988). In this analysis, the ideal cultivar was considered as the cultivar with high grain yield, high stability, low sensitivity to adverse conditions of unfavorable environments, and able to respond positively to improvement of favorable environments. The general average of the EECT-RS in 2012 was 3,699 kg/ha. The experiment conducted in Augusto Pestana had the highest average of wheat grain yield of 5,575 kg/ha. The maximum of wheat grain yield was 7,021 kg/ha in Augusto Pestana (Quartzo cultivar). The Quartzo, TBIO Itaipu, and Mirante cultivars had adaptability and stability in favorable environments (environments with average of wheat grain yield higher than the general average). Cultivars TEC Triunfo and TEC Frontale were adaptable and stable in unfavorable environments (environments with average of wheat grain yield lower than the general average). In general, for the average of all environments, cultivars TBIO Sinuelo (4,286 kg/ha), TBIO Mestre (4,121 kg/ha), and BRS 327 (3,950 kg/ha) came closest to the definition of the ideal cultivar.

Reference.

Carneiro PCS. 1998. New methodologies for analyzing the stability and adaptability of behavior (PhD thesis in Genetics and Breeding). Federal University of Viçosa, 168 pp.

Wheat crop in the state of Rio Grande do Sul, Brazil, 2012.

Ricardo Lima de Castro, Eduardo Caierão, Aldemir Pasinato, Pedro Luiz Scheeren, and Márcio Só e Silva.

The state of Rio Grande do Sul is one of the main wheat-producing states in Brazil. Our objective was to analyze the wheat crop in Rio Grande do Sul in 2012. In 2012, Rio Grande do Sul harvested 961,502 ha of wheat (50.3% of the total area harvested in Brazil) producing 1,866,254 tons of wheat (42.2% of the Brazilian production) with an average grain yield of 1,941 kg/ha (369 kg/ha below the Brazilian average of 2,310 kg/ha). Among the geographical mesoregions in Rio Grande do Sul (Fig. 1), the RS Northwest mesoregion harvested the largest wheat area, 761,248 ha (79.2% of the cropped area in the state), and had the largest production, 1,385,194 tons of wheat grain (74.2% of the state production) (Table 3). However, the average of wheat grain yield obtained in this mesoregion was the lowest of the State, 1,820 kg/ha (121 kg/ha below the state average) (Table 3). The RS Western Center mesoregion harvested 81,298 ha of wheat (8.5% of the cropped area in the state), produced 206,772 tons of wheat grain (11.1% of the state production), and had the highest average wheat grain yield in the state (2,543 kg/ha, 602 kg/ha above the state average) (Table 3). The wheat crop in Rio Grande do Sul in 2012 was hampered by adverse weather, such as a late frost, strong winds, and hail. Comparing the wheat crop data with the results of the State Test of Wheat Cultivars in Rio Grande do Sul State (EECT-RS) in 2012, we observed that the average of wheat grain yield of commercial crops was 1,758 kg/ha below the average of the EECT-RS (3,699 kg/ha).

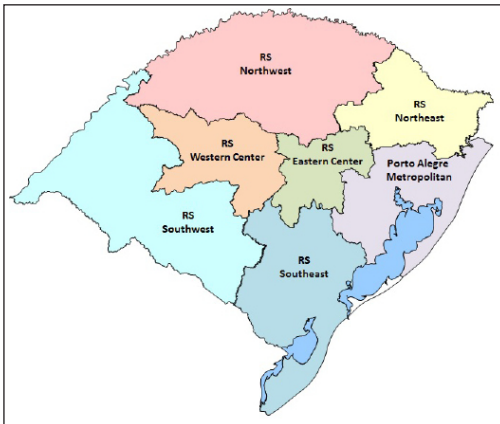

Fig. 1. Mesoregions in the state of Rio Grande do Sul, Brazil.

Table 3. Area harvested, production, and average of grain yield of wheat per mesoregion in the state of Rio Grande do Sul, Brazil, in 2012 (Source http://www.sidra.ibge.gov.br/bda/tabela/listabl.asp?z=t&o=11&i=P&c=1612 (In Spanish, English translation of web site available)).

Mesoregion	Area harvested		Production		Grain yield
	ha	%	tons	%	kg/ha
RS Northwest	761,248	79.2	1,385,194	74.2	1,820
RS Northeast	45,125	4.7	112,437	6.0	2,492
RS Western Center	81,298	8.5	206,772	11.1	2,543
RS Eastern Center	13,393	1.4	25,586	1.4	1,910
Porto Alegre Metropolitan	1,078	0.1	2,253	0.1	2,090
RS Southwest	49,160	5.1	112,364	6.0	2,286
RS Southeast	10,200	1.1	21,648	1.2	2,122
Rio Grande do Sul state	**961,502**	**100.0**	**1,866,254**	**100.0**	**1,941**

Reference.
IBGE. 2014. Sistema IBGE de Recuperação Automática - SIDRA. Available at < http://www.sidra.ibge.gov.br/bda/tabela/listabl.asp?z=t&o=11&i=P&c=1612 >, 28 March 2014. Note: Bank of aggregate data studies and research conducted by IBGE.

ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK GATERSLEBEN
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A. Börner, F. Arana-Ceballos, A. Bakhsh, Yu.V. Chesnokov, A.M. Castro, G. Gerard, E.I. Gordeeva, C. Jaenicke, T. Kartseva, E.K. Khlestkina, S. Landjeva, J. Ling, U. Lohwasser, V. Morozova, M. Nagel, S. Navakode, S.V. Osipova, A.V. Permyakov, M.D. Permyakova, T.A. Pshenichnikova, M.A. Rehman Arif, M.S. Röder, A. Sanabria, A. Shishparenok, L.V. Shchukina, M.R. Simon, A.V. Simonov, O.G. Smirnova, M. Taylor, Chr. Volkmar, Chr. K. Zaynali Nezhad, and D. Zanke.

Grain size QTL region QTgw.ipk-7D in wheat: sequence analysis and synteny to related grass species.

The previously described QTL for 1,000-kernel weight *QTgw.ipk-7D* associated with microsatellite marker *Xgwm1002-7D* was originally detected in a BC_2F_3 advanced backcross population of the winter wheat cultivar Prinz and the synthetic wheat line W-7984 (lab designation: M6). We developed near-isogenic lines (NILs) carrying introgressions of M6 in the genetic background of Prinz with varying size on chromosome 7DS. The BC_4F_3 NILs had a 10% increase in 1,000-kernel weight compared to the control group and the recurrent parent Prinz. The same QTL was detected in another population of the winter wheat Flair and a synthetic wheat XX86. By using homozygous recombinant lines developed from both populations, it was possible to fine-map *QTgw.ipk-7D* to an interval of approximately 1 cM flanked by markers barc126, wmc405, and gwm44 on wheat chromosome arm 7DS. From a chromosome arm 7DS-specific BAC library (provided by J. Dolezel and H. Simkova), BACs covering the region of *QTgw.ipk-7D* were isolated, and their sequences were obtained by 454 sequencing. Of the sequenced BACs, new microsatellite markers were developed and used for anchoring the BACs to the genetic map. Finally, the region of *QTgw.ipk-7D* was delimited to 10 BACs carrying at least 12 predicted genes. Good synteny to the genomic sequences of rice, *Brachypodium*, and *Sorghum* was observed. A BAC contig covering the respective genomic region in barley was identified and also completely sequenced. A detailed comparison of the barley sequence to the wheat sequence with respect to genome evolution is currently conducted.

Genetic architecture of heading date in European winter wheat.

A genome-wide association study (GWAS) for heading date (HD) was performed with a panel of 358 European winter wheat and 14 spring wheat cultivars through the phenotypic evaluation of HD in field tests in eight environments in collaboration with breeding companies (2009 and 2010 in Andelu (FR), Seligenstadt (DE) and Wohlde (DE); 2010 in Janville (FR) and Saultain (FR)). Genotyping data consisted of 770 mapped microsatellite (SSR) loci and 7,934 mapped SNP markers derived from the Infinium 90K iSelect wheat chip. Best linear unbiased estimations (BLUEs) were calculated across all eight environments and ranged from 142.5 to 159.6 days after 1 January with an average value of 151.4 days. For association mapping, a mixed linear model corrected with a kinship matrix for population stratification was employed. Considering only associations with a –log10 (P-value) ≥ 3.0, a total of 358 SSR and 2,983 SNP marker-trait associations (MTAs) were detected. After Bonferroni correction for multiple testing, a total of 90 SSR and 438 SNP

MTAs remained significant. As candidate genes, the photoperiodism gene *Ppd-D1* and vernalization genes *Vrn-B1* and *Vrn-D1* were genotyped in all cultivars. Highly significant MTAs were detected for the *Ppd-D1* gene on chromosome 2D. Consistent associations were found on all chromosomes with the highest number of MTAs on chromosome 5B. Linear regression showed a clear dependence of the HD score BLUEs on the number of favorable alleles (decreasing HD) and unfavourable alleles (increasing HD) per cultivar, meaning that genotypes with a higher number of favorable or a low number of unfavorable alleles showed lower HD and, therefore, flowered earlier. Co-locating MTAs were detected for the *Vrn-A2* on chromosome 5A and for *Ppd-A1* on chromosome 2A and *Ppd-B1* on chromosome 2B. After the construction of an integrated genetic map of the SSR and SNP markers, and exploiting the synteny to sequenced species such as rice and *Brachypodium distachyon*, we were able to demonstrate that a marker locus on wheat chromosome 5BL with homology to the rice photoperiodism gene *Hd6* played a significant role in the determination of the heading date in wheat.

A novel flowering time QTL on chromosomes 4D and 7A.

Fine tuning of the initiation of reproductive period is important for optimizing grain yield in wheat. Precise genetic stocks were used to determine the chromosomal location and map the loci responsible for a few days difference in flowering time between two spring cultivars carrying dominant alleles at the *Vrn-1* locus. The plant material, consisting of inter-cultivar chromosome substitution lines in which individual chromosomes of the Russian variety Saratovskaya 29 (S29) were substituted by the homologous chromosomes of the late-heading, German cultivar Yanetzkis Probat (YP). A set of single-chromosome, recombinant lines was studied in contrasting environments in Novosibirsk (western Siberia), Sofia (southeastern Europe), and Gatersleben (western Europe). The substitution line S29 (YP 4D*7A), carrying the entire donor chromosome 4D and an additional fragment of chromosome 7A, showed the largest delay in flowering at all sites. Two QTL associated with flowering time were identified using a set of 110 recombinant, double-haploid lines obtained after crossing line S29 (YP 4D*7A) with the recipient S29. One QTL was mapped to chromosome 4D and was regarded as a photoperiod-response locus. The second QTL was associated with a polymorphism on the chromosome 7A fragment and represented an intrinsic earliness gene. This information could aid the subtle regulation of flowering in wheats tailored for growing in specific environments.

Genome-wide association mapping of tan spot resistance (Pyrenophora tritici-repentis) in European winter wheat.

Genome-wide association mapping revealed the genetic architecture of resistance to tan spot in a population of 358 European winter wheat and 14 spring wheat cultivars. All cultivars were genotyped with 732 microsatellite markers resulting in 770 mapped loci spread across all 21 chromosomes. Based on field data in two environments (2010 in Ahlum and Lafferde, carried out by B. Rodemann, Julius Kühn Institute, Braunschweig, Germany) and the resulting best linear estimations, a total of 90 MTAs were significant with –log10 (P value) ≥ 3.0 using a mixed linear model corrected with a kinship matrix. Although the inheritance pattern of resistance to tan spot appeared to be quantitative, a number of already known resistance or susceptibility loci were confirmed, such as *Tsn1* on chromosome 5B, *tsn2* or *tsn5* on chromosome 3B, and *Tsc2* or *Tsr6* on chromosome 2B. Additionally, evidence for novel loci was gathered. Additive effects of favourable or unfavorable alleles were observed and suggest the application of genomic selection as a possible strategy for further cultivar development.

Fusarium head blight inducible resistance.

The ITMI mapping population was tested for Fusarium head blight (FHB) tolerance during five years of trials under Argentinean conditions, including inoculums prepared with 67 of the more frequent isolates. Types I, II, and V resistance were tested. Tolerant RILs were identified by their low incidence, severity, and higher 1,000-kernel weight. In the subsequent three years, these tolerant lines were subjected to treatments with biotic and hormonal defence inductors, prior to *Fusarium* inoculation in order to assess the presence of inducible mechanisms of resistance. One line resulted with highly inducible type-II resistance after pretreatment with Jasmonic acid, because this type of tolerance can be switched on before FHB infections, providing a high level of protection. The detection of inducible defences could be useful because these types of mechanisms could be included in commercial wheat production priming the plants and bringing on a more sustainable FHB control.

Location of resistance to Mycosphaerella graminicola, plant height, and heading date through genome-wide association mapping in wheat.

Septoria leaf blotch, caused by *Mycosphaerella graminicola* (Fuckel) Schrot. (anamorph, *Septoria tritici* Rob. ex Desm), constitutes a major disease problem of wheat. This disease is widespread in wheat-growing regions all over the world and yield losses are often severe. Host resistance is the most effective and economic means to reduce yield losses from this disease, although so far, only a few genes have been identified mainly due to the high genetic variability of the pathogen. An important fact in the search for resistance to this disease is its possible association with plant height and heading date. Phenotypic studies have reported genetic association between these characters, whereas others argue that this association is due to epidemiological or environmental factors. On the other hand, only a few molecular works have determined the existence of linkage between those traits.

The test material consisted of two Argentinean spring wheat cultivars, susceptible to leaf blotch and used as controls, and 96 winter wheat accessions from 21 countries. Three field experiments were conducted at the Experimental Station J. Hirschhorn, Faculty of Agricultural and Forestry Sciences, National University of La Plata, Argentina, during 2012 and 2013 in a split-plot design. The entire collection was inoculated with two isolates from two locations in Argentina (Pla and Nueve de Julio), the conidial suspension was adjusted to 5×10^6 spores/ml and sprayed at the 2-leaf stage in both years. For two of the experiments, severity (expressed as necrosis) in seedlings was scored, and for the three experiments, heading date and plant height were evaluated. The percentage of necrosis, plant height, and heading date scores indicated a wide phenotypic variation of the cultivars ranging from 32.44% (most resistant) to 67.56% (most susceptible), 22.97 to 127.7 cm plant height, and 94 to 138 days-to-heading. A phenotype–genotype association analysis, employing the general linear model and the mixed linear model, was performed with software Tassel 2.1. Only loci significant with both models were considered.

QTL for *M. graminicola* resistance were detected on chromosome 1A (two) and 6B in both experiments, and 46 MTAs were significant in one of both experiments analyzed with the isolate from Pla. In addition, four significant MTAs on chromosome 1B (two), 2A, and 2D in the two experiments analyzed were effective against the isolate from Nueve de Julio, whereas 53 MTAs were significant in only one. For heading date, five significant MTAs were detected on chromosomes 1B, 2B, 4B, 5D, and 6A in the three experiments analyzed. Additionally, 13 other MTAs located on chromosomes 1A, 1B, 2B (two), 3B (three), 5D, 6A, and 6B (four) were significant in two of three experiments evaluated. For plant height, four significant MTAs were identified on chromosomes 2B, 3A, 4A, and 7A for the three experiments analyzed, whereas another eight MTAs located on chromosomes 1B, 3A, 6A, 6B (two), 7A, and 7B (two) were significant in two of the three experiments.

Additionally, a correlation analysis was performed, in which necrosis was negatively associated ($P < 0.01$) with both plant height ($r = –0.254$) and heading date ($r = –0.419$) for the Nueve de Julio isolate and with both plant height ($r = –0.094$) and heading date ($r = –0.188$) for Pla isolate, although this was only significant in the last case ($P < 0.05$).

Preliminary screening of wheat lines against stripe rust.

A set of 117, spring wheat genotypes assembled from the wheat collection at the Federal Genebank in Gatersleben, Germany, was planted at the PMAS-Arid Agriculture University research farms located at Koonth, Rawalpindi, Pakistan, in rain-fed conditions to test for their adaptability to grow in arid conditions and to disease resistance. The lines were grown in a randomized complete-block design with Chinese Spring planted between every 20 lines as a positive control. The only source of water was rain that occurred three times during the whole growing season, and all the lines showed 100% germination. These lines were evaluated for stripe rust resistance on a rating scale of 1–100% (% infected leaf area) in field where they showed mixed reactions. The mean infection of these lines ranged from 0 to 43%. Eight lines showed complete immunity to the stripe rust attack and did not show any sign of infection, whereas three lines had the highest reaction (43%) towards stripe rust. Thirthy-eight lines had infection between 0 and 5% and 22 lines showed an infection severity between 5 and 10%. The data will be used to map loci for stripe rust resistance. Furthermore, they will be compared with the historical data to locate stable loci for resistance against stripe rust. Overall, the panel proved effective to study abiotic stresses such as drought tolerance and biotic stresses such as stripe rust resistance.

Observations on Oscinella frit and various aphids in spring and winter wheat collections.

The Frit fly is an oligophagous fly assigned to the family Chloropidae and an important pest in wheat and maize. *Oscinella frit* has two generations, larvae penetrate into the stem core and crawl toward the tillering node. Only one larva lives in one stem. The female flies lay their eggs on stems of underdeveloped plants and on ears of spring crops. In wheat, various aphids cause damage by sucking the phloem on spikes and leaves. Major species are *Sitobion avenae*, *Metopolophium dirhodum*, and *Rhopalosiphum padi*.

The observed spring wheat collection, consisting of 111 different genotypes from 27 countries, was sown at Gatersleben in 2013. Using white dish traps in every plot, we caught adult flies and various stages of aphids to determine the activity of both pests. The white dish traps were controlled weekly, and an additional visual rating was used to identify aphid infestations on spikes and flag leaves. Sweep nets were used to catch aphids and flies for a complete determination of species. After sampling all traits, we calculated an association study to find out characteristic MTAs for resistance. For a potential resistance to *O. frit*, we detected 41 MTAs; for the aphids, we detected 44 MTAs on the different wheat chromosomes.

Secondary, observations were made in 2013 about potential resistance against aphids in a winter wheat collection consisting of 96 genotypes at Gatersleben and on a second experimental area provided by Limagrain GmbH in the proximity of Peine (Lower Saxony). We collected characteristic traits for an association study calculation to determine characteristic MTAs for the infestation with aphids on spikes and flag leaves. Major species found in winter wheat were *S. avenae* (67.5%), *R. padi* (18.8%), and *M. dirhodum* (13.7%).

Studies on frost tolerance in bread wheat using a genome-wide association mapping approach.

Frost tolerance in plants is decisive to increase yield security, but the molecular and genetic background for this trait is still poorly understood. Phenotyping a panel of up to 360 accessions was performed at several locations in Germany and Russia. Highly significant differences between locations, but also between tested genotypes, were observed. The genotyping employed an ILLUMINA infinium iSelect 90k wheat chip. The chip carries a total of 81,587 valid and functional SNPs. After a round of selections, 38,052 polymorphic markers were available for the analysis. For the population-tructure analysis, the software Structure was used. The Q-matrix for three groups was the best option. Results were validated using an evolutionary tree calculated by the PAUP software, which also showed three clusters. The detailed analysis shows three subgroups of North American, Russian, and North and Middle European samples. Furthermore, the kinship matrix was inferred in Tassel 2.1. First results of model comparison yield highly significant associations (LOD > 3).

Genotypic-phenotypic associations of traits contributing towards post-anthesis drought tolerance in spring wheat.

A spring wheat panel comprising 111 genebank accessions was sown at experimental fields of IPK during 2013. All genotypes were allocated randomly to experimental units replicated four times. After two weeks of anthesis, a foliar application of potassium iodide solution (KI 0.5%) was made to a single row of each double-row plot. Morphological, yield, and yield-component trait data of each genotype were recorded in parallel for desiccation and control. Highly significant differences were obtained for all traits (days-to-flowering, days-to-maturity, plant height, number of seeds and seed weight/spike, 1,000-kernel weight, seed area, spike length, and number of spikelets/spike) compared under chemical desiccation treatment and the control. The most tolerant accession did show tolerance indices of 94% and 95% for 1,000-kernel weight and seed area, respectively, although the accession most sensitive to desiccation stress exhibited a tolerance index of only 25% for 1,000-kernel weight. The number of spikelets/spike was positively correlated with number of seeds/spike, both under the control and desiccation treatments, although this trait was negatively correlated with 1,000-kernel weight under both control and stress. A strongly positive correlation was determined between 1,000-kernel weight and seed area, hence both parameters are the best indicator for post anthesis desiccation/drought tolerance. The identified tolerant and susceptible genotypes can be used for further population development and post anthesis drought-tolerance studies. Phenotypic and genotypic data will be analyzed to establish marker-trait associations and identify favorable alleles for further marker-assisted breeding.

Identification of QTLs associated with the lipoxygenase activity on the chromosomes 5D and 7D in hexaploid wheat.

Lipoxygenase (LOX; EC 1.13.11.12) catalyzes the addition of molecular oxygen to polyunsaturated fatty acids for the formation of fatty acid hydroperoxides. Lipoxygenase isozymes are involved in the processes of plant growth, development and defense against biotic and abiotic stresses. Using *Triticum aestivum–Aegilops taushii* introgression lines, we mapped minor QTL (LOD from 2.04 to 2.69) associated with the LOX activity in common wheat under stress.

Two QTL associated with the phenotypic expression of LOX activity were found on chromosome 5D. The first is related with the soluble enzyme activity in wheat seedlings germinated on 12% polyethylene glycol solution, which imitates the oxidative stress. This QTL is located on the long arm of chromosome 5D. The LOX biosynthesis gene, the vernalization responce gene *Vrn-D1*, and QTL of many wheat-development parameters are well know to be in a similar position. The second QTL associated with activity of membrane-bonded LOX in wheat seedlings germinated on 12% polyethylene glycol solution; it was located on the short arm of chromosome 5D. This locus may be responsible for the regulation of lipoxygenase isoenzyme activity, which besides plant defense may play a role in the formation of endosperm texture (softness or hardness). This assumption is based on the physiological and functional relationships between the puroindolines, being that lipid-transfer proteins are considered to be molecular markers of grain hardness, the lipid-degrading enzyme lipoxygenase, and the polar lipids of starch grains that serve as a preferable substrate for LOX. One of the known loci responsible for polar lipid levels, *Fpl-1*, was found on the short arm, but *Fpl-2* is on the long arm of chromosome 5D, and both may coincide with the LOX loci that were detected in this study. Now, grain hardness is considered to be mainly associated with allelic variation of puroindolins in locus *Ha* at the distal end of chromosome 5DS. However, other genes located on the short arm of chromosome 5D of hexaploid wheat possibly also are important in regulating grain texture.

On chromosome 7D, the phenotypic variation of LOX activity in leaves of wheat grown under drought were linked with a marker in the centromeric region. This QTL may be relevant for tolerance to both abiotic and biotic stresses, because the known locus is associated with resistance to Septoria tritici blotch in a similar position. Moreover, QTL associated with LOX activity on chromosome 7D probably also effect the endosperm texture, because it coincides with known loci of the variant form of puroindolin b, which were detected on all homoeologous group-7 chromosomes.

The antioxidant enzymes activity in leaves of inter-cultivar substitution lines of bread wheat with different tolerance to water deficit.

A set of bread wheat, inter-cultivar, single-chromosome substitution lines (ISCSLs) of wheat cultivar Janetzkis Probat (JP) in to the genetic background of Saratovskaya 29 (S29) were used to dissect drought tolerance as a polygenic trait. The drought tolerance associated with antioxidant protection mechanisms was studied. The recipient cultivar S29 is highly drought tolerant, whereas the donor JP is sensitive. Plants were grown under controlled conditions of either adequate or inadequate soil moisture. The activity of leaf catalase (CAT) and three enzymes involved in the ascorbate/glutathione cycle, ascorbate peroxidase (APX), glutathione reductase (GR), and dehydroascorbate reductase (DHAR), were measured. The yield components and indices of drought tolerance/susceptibility were studied in the same material. We found that substitutions of JP chromosomes 2A and 4D in the S29 genetic background were critical for drought tolerance of yield components and indices of drought tolerance/susceptibility. At the same time, the cumulative activity (CA) of CAT, DHAR, APX, and GR in leaves under drought consisted of 26% from the recipient in the line S29 (JP 2A) and 43% in the line S29 (JP 4D). All ISCSL from the homoeologous group-2 chromosomes manifested low leaf GR and CAT activities. The lowest leaf CAT activity, in line S29 (JP 4D), proves the presence of genes responsible for activity level of the enzyme on 4D chromosome, whereas the homoeologous group-2 chromosomes may carry the structural and (or) regulatory genes responsible for GR activity. If so, such genes should be amenable to standard mapping strategies. Under drought conditions, CA correlated positively with the retention of leaf moisture content and several indices of drought tolerance/susceptibility and may be considered as a reliable physiological indicator of drought tolerance in wheat.

The genetic control of root length and weight in bread wheat intercultivar substitutions and introgression lines in Chinese Spring (Synthetic 6x).

Root length and weight were studied in a set of intercultivar, single-chromosome, substitution lines of Chinese Spring (Synthetic 6x) (CS/Syn), where the donor of separate chromosome pairs was a synthetic hexaploid AABBDD (*Triticum dicoccoides*/*Aegilops tauschii*). These parameters were studied under normal and restricted water supply. We found that 1A substitution resulted in a substantial reduction of root size in plant. Substitution of chromosome 5D, on the contrary, led to a significant increase compared to the recipient and donor. For the next stage, a set of genotyped introgression recombinant lines CS (Syn 5D) was studied under the same conditions. The lines were studied after 30-days of vernalization, because the donor of chromosome 5D, synthetic 6x, has a winter growth habit. The greatest root weight and length as well as a number of days-to-flowering comparable to the 5D substitution line was detected in the introgression lines 5D-5, 5D-6, and 5D-10. These lines have a common introgression fragment in the long arm of chromosome 5D containing the gene *Vrn-D1*. The lines were additionally studied after 45- and 60-days of vernalization in order to associate vernalization requirements with root size. We found that, in both cases, these three lines had the most developed root system. Generally, drought depressed root development in all lines, but the greatest root weight and length were detected in the 5D chromosome substitution line and introgression lines 5D-5, 5D-6, and 5D-10. The data obtained may prove the existence of the locus responsible for root traits in this region of 5D chromosome.

Genome-wide association mapping reveals new aluminium-tolerance loci in bread wheat.

Aluminium (Al) stress in acid soils presents a major impediment for plant growth that eventually results in substantial yield loss. By and large, hexaploid wheats are moderately tolerant, and breeding new Al-tolerant cultivars depends explicitly on the discovery of novel loci or genes. Genome-wide association mapping was carried out utilizing a panel of 96 winter wheat accessions. Marker alleles occurring at low frequencies ($f < 0.05$) and markers with 20% missing data were excluded from the analysis. Aluminum tolerance was assessed using hematoxylin staining with root regrowth as the tolerance parameter. Marker-trait associations were identified by both mixed linear and general linear models based on the average phenotypic value over four experiments.

This study identified five MTAs that are highly significant ($p < 0.001$) or significant ($p < 0.01$) by both models on chromosomes 1AL, 1DL, 3BL, and 6AS. All five loci represent independent loci and are not in LD with each other. Except for the MTA on 1AL, all other mixed linear MTAs were confirmed by tje general linear model. Allelic effects ranged from ±0.22 to ±0.31. The MTA on chromosome 3B showed the highest allelic effect of all the MTAs. The MTA on chromosome 1D was allocated to the bin 1DL2-0.41-1.00 where pertinent Al-tolerance gene candidate, *wali5*, was previously identified. The novel loci identified on chromosomes 1D and 3B are strong candidates for future research, with the potential for developing tolerant wheat genotypes.

Seed longevity in Russian spring wheat.

An artificial-ageing method (AA) was applied in studies on seed longevity testing. This method implies processing plant seed with high temperature at 100% relative humidity for 72 hours. For bread wheat, the temperature is usually 42°C. Seed of some cultivars are not sensitive to the 42°C-AA test and require higher temperatures to achieve ageing, including Russian, spring wheat cultivars Saratovskaya 29 (S29) and Novosibirskaya 67 (N67). As shown earlier, seed of S29 and N67 require a 48°C-AA test to get at least one-fifth of the seed to lose their viability. However, the stable response to the adjusted AA-test conditions is observed on seeds harvested more than one year ago. Recently harvested seed can be much more sensitive to the AA test. For S29, one-fifth of the seed looses viability at 48°C (12- and 18-month-old seed), 46°C (3-month-old seed), or 44°C (2-month-old seed). Thus, the AA test on young wheat seed is not recommended. Furthermore, comparison studies using the AA test can be recommended only for seed of plants grown simultaneously under the same conditions. In our studies, seed of S29 were two-times more sensitive to the 48°C test if the experiment was performed on material grown in the field (in conditions of an extremely rainy summer), compared to those grown in the greenhouse. Following these recommendations, we applied a 48°C-AA test to 18-month-old seed of NILs of S29 harvested from plants grown simultaneously in the greenhouse. A significant difference was observed between S29 and the NILs differing from S29 by the *Pp* genes (purple pericarp), suggesting a relationship between the accumulation of anthocyanin pigments in pericarp and seed longevity.

The ecology and genetic mapping of QTL controlling economically valuable traits in hexaploid spring wheat grown in environmentally different regions of the Russian Federation.

For the first time, a set of 110 RILs of the spring wheat ITMI mapping population was evaluated in different eco-geographical regions of the Russian Federation. Thirty-nine economically important traits that manifest themselves at different stages of growth were examined in each eco-geographical locality under study for five years. A total of 186 QTL with LOD scores above 2.5 were identified out of which 97 reached LOD scores > 3.0. The QTL for traits studied mapped onall 21 chromosomes and manifested themselves under contrasting environmental conditions with varying degrees of reliability. The manifestation of the identified QTL has been shown to depend on the environment, but they interact and correlate with each other. The main loci controlled by the same QTL change depending on particular ecological-geographic environment. The complexity of environmental factors is assumed to determine the characters of co-adapted gene blocks formed during the evolution of each plant species, as well as the specific ones of the wheat genetic co-adaptation system. The identified QTL may be of interest for further experiments on the genetic control of the corresponding agriculturally valuable traits and for marker-assisted selection in wheat breeding.

Additionaly, QTL were revealed by growing the ITMI mapping population in the arid steppes of the Middle Volga region during three years. These QTL mainly determined the duration of the growing season, plant height, spike length, number of spikelets/spike, number of seeds/spike, and 1,000-kernel weight. A QTL with pleiotropic effects, which is localized on the distal end of the long arm of chromosome 2D, determines the wax bloom on the stem, spike, and flag leaf. A QTL for resistance to leaf rust was located at the distal end of the short arm of chromosome 3D, and probably is allelic to *Lr27*. On the short arm of chromosome 7D, a QTL associated with resistance to powdery mildew was detected, presumably *Pm38*.

Evaluation of bread wheat accessions for agronomic traits under Iranian conditions.

We evaluated a large number of bread wheat accessions, mainly from southwestern Asia, including Iran, Afghanistan, India, Turkey, Pakistan, and Iraq. About 60 accessions belong to bread wheat cultivars from the European countries. Our aim was to generate pure-line plant material suitable for eco-TILLING and association mapping. The seed for these genotypes mainly were received from the IPK–Gatersleben Genebank, Germany. The experiment was based on an augmented design in which three Iranian bread wheat cultivars were used as controls with replication in order to check the homogeneity of the experimental conditions. Traits such as days-to-flowering, plant height, peduncle length, spike length, awn length, glum color, seed length, seed weight, flag leaf length, and 1,000-kernel weight were recorded. In the first year, one single plant from each genotype was selected to develop a pure line form each genotype. Currently, the data recorded at the field experiments are being analyzed, which will help to classify the genotypes based on morphological traits. This experiment also continues this year as the third replication. These genotypes can be evaluated under different biotic and abiotic stress condition in Iran. The next step is the generation of genotyping data.

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ITEMS FROM INDIA

BHABHA ATOMIC RESEARCH CENTRE
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Induced mutation studies in Indian wheat using electron beam irradiation.

G. Vishwakarma, Vikas, A. Shitre, and B.K. Das, and V.C. Petwal (Raja Ramanna Centre for Advanced Technology, Indore, India).

Induced mutations using gamma rays commonly are used for improvement of agronomic and other characters in crop plants. In Indian wheat, gamma ray-induced mutations commonly are used. However, other physical mutagens, i.e., X- rays, electrons, protons, and ion beams, have reported producing novel and useful mutants. We initiated a study, in collaboration with the Raja Ramanna Centre for Advanced Technology, Indore, to observe the effects of electron-beam irradiation on germination and early seedling growth. Three wheat cultivars, MP3054, Unnath C306, and NIAW301, were irradiated with e-beam doses of 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, and 750 Gray. Seeds were sown in controlled growth chambers. Observations were taken 15 days after sowing. GR50 and LD50 are being studied with replication. Once the doses are standardized, we will proceed to irradiate bulk seed for a mutation-breeding approach for developing mutants having useful traits, such as earliness, reduced height, low PPO, low phytic acid, and rust resistance.

Identification of novel mutants in Indian wheat using gamma ray irradiation.

Vikas, G. Vishwakarma, A. Shitre, and B.K. Das, and G.A. Gadekar (Agriculture Research Station, Niphad, India).

For improvement of agronomic traits and rust resistance, popular wheat cultivars of the Peninsular zone (NIAW917, NIAW 34, and NIAW301) were irradiated with Gamma rays. Approximately 700 seeds were irradiated with three doses (250, 300, and 350 Gray). In the M_1 generation, 600 seeds/dose were sown, which had 40–50% germination. In a rare event, we obtained double-spike, putative mutants in the M_1 generation in these cultivars. In another experiment, in the cultivar HD2189, a putative mutant with two tillers at the early seedling germination stage also was obtained in the M_1. Seeds from individual plants were harvested, and.these will be grown in the M_2 generation for further confirmation and stabilization.

Molecular characterization of an early mutant line in the wheat cultivar C-306; a study of inheritance and identification of molecular markers for earliness.

G. Vishwakarma, Vikas, A. Shitre, and B.K. Das.

In our earlier experiment, we identified early mutants in the background of the Indian wheat cultivar C-306, known for its excellent Chapati-making quality. The mutant was 25 days earlier than the C-306 parent. We are now in the process of characterizing these mutants using AFLP- and AP–PCR-based molecular markers. We also are developing a mapping population for tagging the mutant allele(s) for earliness. Crosses were made between the mutant line (TWM-89-2) and C-306. The F_1 seeds were harvested and the population is being advanced for studying inheritance in the F_2 onwards. Genetic polymorphism also is being studied among the parent and mutant using molecular markers. The mutants also were evaluated at different geographical locations to study the effect of environment on the mutant trait.

Use of mutation and molecular techniques for improvement of earliness and rust resistance in the wheat cultivar C-306.

Vikas, G. Vishwakarma, S.G. Bhagwat, and B.K. Das.

C-306 is an excellent cultivar for Chapati-making quality. However, the cultivar is of long duration, which is affected by terminal heat stress, and is susceptible to rust. In order to improve these traits, induced mutation studies were undertaken. A 25-day, early mutant was identified in a gamma ray-mutagenized population. The mutant later was crossed with Unnath C306 (C306+*Sr24*/*Lr24*) and selections for earliness and rust resistance were made in the F_2. Rust resistance in a segregating population was screened by using a SCAR marker for *Sr24* and also confirmed using phenotypic observation of plant reaction to stem rust spore injection. The early and rust resistant plants were selected and, in the F_3, earliness and rust resistance were confirmed. We have identified a few plants that are early and have rust resistance. These lines will be further evaluated and used in breeding programs.

Validation and use of DNA markers for rust resistance genes and quality traits for improvement of Indian wheat.

B.K. Das, G. Vishwakarma, Vikas, A. Shitre, Suman Bakhsi, and S.G. Bhagwat.

In our efforts for improvement of Indian wheat for rust resistance and quality traits, we are using molecular markers in addition to conventional plant breeding approaches. The molecular markers for rust resistance genes (*Sr24*/*Lr24*, *Sr26*, *Sr2*, *Sr25*, *Sr31*, *Lr34*, and *Lr32*) were validated and are being used in our breeding programs. A marker for *Glu-D1d* (coding for HMW subunits 5+10), an important trait related to flour quality, also was validated and being used in marker-assisted selection in our populations. Selections have been made from different inter-cultivar crosses using some of these markers. We now have a few selections with these traits, and those are in advanced generations and being evaluated at different locations.

Studies to develop high-temperature stress tolerance in wheat: transfer of the reduced-height gene, Rht8, and its agronomic evaluation in a high-temperature environment .

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

An agronomically desirable plant type with tolerance to heat has become a necessity for sub-tropical wheat areas. Our earlier studies indicated that a 192-bp allele of the WMS261 marker was observed in Indian cultivars; however, it was not associated with height reduction or any yield advantage, indicating that the *Rht8* gene may be absent in Indian cultivars. To transfer the *Rht8* gene linked to WMS261, crosses were made between a donor parent and the tall cultivars MP3054 or Ajantha. In a cross with MP3054, the F_2 segregants with the 192-bp allele showed a significant height reduction and a higher spikelet density over the 174-bp allele. In a cross with the tall parent Ajantha, plants with a 165-bp allele have a culm height of 64.1±0.79 and a plant height of 73.7±0.87, whereas plants with the 192-bp allele have a culm height of 49.5±0.94 and a plant height of 58.0±1.06. Genotypes with the 192-bp allele showed average culm height reduction of 23% and a plant height reduction of 21.3% over those with the 165-bp allele. Further evaluation of genotypes with the 192-bp allele associated *Rht8* under high temperature will give more information for suitability of this gene in warmer areas.

Studies to develop high-temperature stress tolerance in wheat: canopy temperature depression measurements to select physiologically more efficient genotypes under high temperature.

Suman Bakshi, A. Shitre, S.G. Bhagwat, and B.K. Das.

Canopy temperature depression (CTD) is a well-established method to identify physiologically competent genotypes under stress conditions. However, the significance of this technique to understand the plant's capability to tolerate heat stress is not explored in wheat. Canopy temperature depression is an expression of the number of morpho-physiological

traits and is characteristic of each cultivar. We designed an experiment to determine CTD differences among genotypes and the optimum growth stage and time for CTD measurements for detecting genotypic differences under heat stress. The experiment, at the Gamma Field, Trombay, measured the canopy temperature of 17 cultivars in 2009–10. Genotypes were sown in randomized block design with four replicates. Regional climatic data for crop season was collected from the observatory. Canopy temperature depression readings were taken by an infrared thermometer (TI200). The canopy temperature measurements were made between 12:00 to 2:00 PM. Five readings were taken for each replicate. The CTDs were taken at growth stages tillering, boot, anthesis, and maturity. Air temperatures also were observed in the field at time canopy temperatures were measured. The mean air temperature varied from 32 to 36.5ºC during the days of measurement. Significant genotypic differences were observed for CTD from the air temperature at all growth stages. The average CTD over the season ranged from 14.4°C for genotype HD2687 to 9.9°C for Raj4037. Genotypes in early stages (tillering and boot) showed a greater decline in canopy temperature compared to genotypes at anthesis and seed setting. The CTD experiment was repeated in the winter of 2010–11 to determine the reproducibility of results. Twelve cultivars with early, medium, and long maturity were used. Initial results indicated significant differences within and among the groups. Further analysis and association with field data will help in ascertaining the genotypes maintaining low CTD and better performers under heat stress.

Studies to develop high-temperature stress tolerance in wheat: dry matter accumulation and mobilization efficiency of bread wheat cultivars in warm environment.

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

The grain yield of wheat is adversely affected by high-temperature stress in warm environments.Grain filling is preceded by two processes, dry matter accumulation and its translocation to the developing grain. These processes become more important when the wheat plant experiences high temperature stress during grain filling. Eight bread wheat cultivars were evaluated for dry matter accumulation and mobilization to the grain in warm environments for 2 years. The genotypes were planted in a randomized manner with five replications. Two tillers from each replication were cut from the base after ear emergence and to maturity at 10-day intervals. The tillers were separated into stem, leaves, chaff, and grain, air dried and weighed. The difference in the maximum dry weight and dry weight at harvest was used as the translocated amount. The results showed significant differences among genotypes for dry weight accumulation at the different growth stages. Among all the genotypes analyzed, HUW206 had the highest dry matter accumulated in both years (2011 and 2012). For the rate of mobilization of dry matter from stem, the cultivar WH542 was followed by HUW206 (25.5 and 22.0%) and PBW435 (20.7 and 21.3%) in years 2011 and 2012, respectively. Among the genotypes analyzed for dry matter mobilization, WH542, HD2687, HUW206, and PBW343 carried the T1B·1R translocation and Sonalika, PBW435, HD2189, and Ajantha did not. Among the T1B·1R group, HUW 206 showed the highest dry matter accumulation (634 mg (2011) and 529 mg (2012)), higher mobilization (58.6% (2011) and 56.1% (2012)), and highest grain yield/plot (117.0 g). Among the non-T1B·1R group, PBW435 had the highest dry matter accumulation (309 mg (2011) and 417 mg (2012)), higher mobilization (50.5% (2011) and 62.0% (2012)), and the highest grain yield/plot (279.6 g). This study showed differences among the genotypes for dry weight accumulation and mobilization in a warm environment. Optimization of both the processes will be desirable to enhance grain yield under heat-stress conditions.

News from our wheat research group.

Mr. Gautam Vishwakarma joined our wheat research group as a scientist after completion of a 1-year orientation course in Bioscience. He is working on using induced mutations and molecular markers for wheat improvement and understanding the mechanism of rust resistance genes in wheat.

Dr. S.G. Bhagwat, who led our wheat research group as Head of the Mutation Breeding Section, retired from Government service on superannuation.

ITEMS FROM ITALY

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Imola, Italy.

Response of 31 durum wheat cultivars to cereal soil-borne mosaic virus in 2013.

C. Rubies-Autonell (University of Bologna), A. Sarti (ASTRA), R. Canestrale (CRPV), and V. Vallega (CRA–QCE).

Thirty-one durum wheat cultivars were grown during the 2012–13 season in a field with a natural inoculum source of cereal soil-borne mosaic virus (CSBMV) at Cadriano, near Bologna, and evaluated for resistance on the basis of symptom severity, DAS–ELISA value, and agronomic performance. The cultivars, planted on 25 October, 2012, were grown in 10-m^2, solid-seeded plots distributed in the field according to a randomized block design with three replicates. Symptom severity was evaluated on two dates (21 March and 4 April) using a 0–4 scale. DAS–ELISA was performed on extracts from a bulk of the basal half of the second and third youngest leaves of 10 randomly chosen plants/plot collected on one date only (4 April, 2013). The trial included five cultivars that had not been tested before.

Cereal soil-borne mosaic virus pressure was relatively high, as testified by the high mean symptom scores (≥ 3.0) recorded for eleven of the 31 cultivars assayed (Table 1, p. 22). Low mean symptom scores (≤1.0), accompanied by low ELISA values, were recorded only for the cultivars Cesare, Dylan, Levante, Serafo Nick, and Monastir. The latter had not been tested for CSBMV before.

Mean ELISA value and mean symptom severity score were correlated significantly (0.861**). Symptom severity score was significantly correlated (P = 0.001) with all the agronomic characters investigated (Table 2, p. 22). A regression analysis estimated quite accurately the agronomic CSBMV effects corresponding to different symptom severity scores in the 2012–13 season. For instance, a mean symptom score of 3.5 was associated with grain yield, plant height, 1,000-kernel weight, and test weight reductions of about 62%, 33%, 23%, and 2%, respectively, as well as with a heading delay of about 6 days (Table 3, p. 23). As in previous experiments, results indicated that even mild symptoms cause appreciable grain yield losses.

Table 1. Response to cereal soil-borne mosaic virus of 31 durum wheat cultivars grown near Bologna, Italy, in 2012–13. Items with the same letter(s) are statistically similar. Symptom severity was rated on a 0–4 scale and are the mean of two dates.

Cultivar	Mean symptom severity score		ELISA value		Grain yield (t/ha)		Plant height (cm)		Kernel weight (g)		Test weight (kg/hl)		Days-to-heading (from 1 April)	
Achille	3.67	a	1.584	a	3.86	jk	68.3	kl	41.2	ik	79.6	af	42.3	bc
Achille	3.67	a	1.584	a	3.86	jk	68.3	kl	41.2	ik	79.6	af	42.3	bc
Anco Marzio	3.71	a	1.070	af	3.67	jk	78.0	hj	38.8	jk	79.1	af	41.0	cf
Athoris	1.67	cf	0.580	fk	7.96	ad	89.7	bf	53.9	cd	81.9	a	37.3	i
Cesare	0.75	gi	0.443	hl	8.22	ab	93.0	ad	50.5	df	80.4	ac	40.0	eh
Claudio	3.25	a	1.258	ad	2.61	kl	59.0	m	44.0	gj	79.0	af	42.0	bc
Colombo	2.04	cd	0.439	hl	6.64	dg	83.0	fh	50.8	df	79.9	ad	41.7	bd
Core	1.67	cf	0.410	il	6.51	dh	89.7	bf	53.1	cd	77.9	bf	33.0	l
Cuspide	3.50	a	0.966	bh	3.45	jl	71.7	jl	40.5	ik	77.2	cf	41.0	cf
Duilio	2.00	cd	0.682	ej	6.18	eh	84.3	eh	51.1	de	78.0	bf	34.0	jl
Dylan	0.50	hi	0.473	hl	8.14	ac	95.0	ad	49.6	df	79.3	af	39.3	gh
Emilio Lepido	2.34	bc	0.756	dj	5.68	fh	78.0	hj	47.6	eg	76.4	f	34.7	jk
Grazia	3.42	a	1.429	ac	2.28	l	68.0	kl	42.6	gj	77.8	bf	41.3	ce
Iride	1.46	cg	0.780	dj	7.07	bf	80.7	gi	47.0	eg	80.1	ad	34.0	jl
Kanakis	3.46	a	0.910	ci	2.68	kl	68.3	kl	37.2	k	76.5	ef	40.0	eh
Levante	0.94	fi	0.492	gl	7.86	ad	96.0	ac	49.8	df	80.3	ac	39.0	gh
Liberdur	3.71	a	1.363	ac	4.15	ij	72.0	jl	41.1	ik	78.5	bf	43.0	b
Magellano	3.58	a	1.351	ac	3.75	jk	64.3	lm	41.7	hk	78.9	af	44.3	a
Marco Aurelio	1.46	cg	0.247	jl	6.78	bf	94.3	ad	57.7	ac	78.4	bf	37.3	i
Massimo Meridio	1.08	eh	0.325	jl	6.71	cg	96.7	ab	59.0	ab	78.6	bf	37.3	i
Miradoux	2.96	ab	1.459	ab	2.84	jl	73.7	ik	42.8	gj	77.0	df	45.0	a
Monastir	0.17	i	0.034	l	8.85	a	95.0	ad	54.7	bd	78.8	af	36.7	i
Odisseo	3.54	a	1.170	ae	3.68	jk	70.7	jl	43.8	gj	78.3	bf	40.3	dg
Ramirez	1.09	eh	0.605	fk	6.86	bf	91.0	ae	42.5	gj	80.1	ad	38.7	h
Saragolla	1.92	ce	0.745	dj	6.71	cg	83.0	fh	47.7	eg	78.8	af	35.0	j
Sculptur	3.38	a	0.950	bi	5.23	hi	65.3	lm	45.7	fi	78.2	bf	39.7	fh
Serafo Nick	0.92	fi	0.512	gl	7.61	ae	99.0	a	60.3	a	80.5	ab	37.3	i
Simeto	3.08	ab	1.421	ac	4.11	ij	66.7	kl	54.7	bd	77.7	bf	39.0	gh
Svevo	2.09	cd	1.038	bg	5.35	gi	87.0	dg	47.5	eg	77.6	bf	33.3	kl
Tirex	1.25	dh	0.654	ek	7.23	be	88.3	cg	49.5	df	80.4	ac	33.7	jl
Trapezio	1.25	dh	0.111	kl	8.18	ab	98.7	a	47.5	eg	79.8	ae	39.7	fh
Yelodur	1.58	cg	0.580	fk	7.07	bf	87.0	dg	46.8	eh	77.9	bf	39.3	gh

Table 2. Simple correlation coefficients between mean symptom severity, ELISA value, and various agronomic characters for 31 durum wheat cultivars grown in a field with cereal soil-borne mosaic virus near Cadriano (Bologna), Italy, during 2012–13. ns = not significant.

	ELISA value		Grain yield		Plant height		Kernel weight		Test weight		Heading date	
Symptom severity	–0.861	**	–0.928	**	–0.912	**	–0.704	**	–0.474	**	0.545	**
ELISA value	—		–0.871	**	–0.866	**	–0.636	**	–0.348	ns	0.514	**

Table 3. Estimated effects of cereal soil-borne mosaic virus on grain yield, plant height, kernel weight, test weight, and heading date for different symptom severity scores (Cadriano (Bologna), Italy, 2012–13).

Disease score (scale 0–4)	Grain yield loss		Plant height reduction		1,00-kernel weight reduction		Test weight reduction		Heading date delay (days)
	t/ha	%	cm	%	g	%	kg/hl	%	
0.5	0.82	8.8	4.8	4.7	1.9	3.3	0.3	0.3	0.8
1.5	2.46	26.4	14.5	14.1	5.6	10.0	0.8	1.0	2.4
2.5	4.10	44.1	24.2	23.5	9.3	16.7	1.4	1.7	4.0
3.5	5.74	61.7	33.8	32.9	13.1	23.4	1.9	2.4	5.6

Effects of cereal soil-borne mosaic virus over 12 seasons.

V. Vallega (CRA-QCE), C. Rubies-Autonell (DSA), A. Sarti (ASTRA), and R. Canestrale (CRPV).

Various sets of durum wheat cultivars were evaluated for resistance to cereal soil-borne mosaic virus (CSBMV) on the basis of symptom severity, DAS–ELISA readings and agronomic performance at two fields with the virus situated near Minerbio and Cadriano (Bologna) in 12 seasons between 1996 and 2013. A total of 146 durum wheat cultivars were assayed in these trials. Five of the 18 trials programmed for this period (three of which were at Ozzano, also near Bologna) could not be carried out due to the lack of adequate funds and/or sufficiently uniform fields. Moreover, in the 2010–11 season, only symptom severity and ELISA data were collected. Each trial was comprised of 30–34 cultivars, grown in 10-m^2, solid-seeded plots distributed in the field according to a randomized block design with three replicates. In each season, symptom severity was evaluated on three or more dates using a 0–4 scale, where 0–1.0 = no or slight symptoms, 1.1–2.0 = mild mottling and stunting, 2.1–3.0 = mottling and stunting, and 3.1–4.0 = severe mottling and stunting with virus-killed plants. The symptom score data collected on various dates in each season were averaged for computations and presentation. Mean symptom scores above 3.0 were recorded for at least one cultivar in all trials.

Symptom severity score and grain yield were highly and significantly correlated in all seasons, thus offering the opportunity to estimate the effect of various levels of CSBMV symptom severity on grain yield under diverse conditions using simple linear regressions. On average, symptom severity scores of 3.5, 2.5, 1.5, and 0.5 were associated with grain yield losses of about 53, 38, 23, and 8%, respectively (Table 4). Symptom scores also were significantly correlated with the other four agro-biological characters investigated, but not in all seasons. By and large, symptom scores of 3.5 were associated with mean plant height, kernel weight, and test weight reductions of about 25, 20, and 10%, respectively, and with a heading delay of about 3 days.

Table 4. Estimated effects of cereal soil-borne mosaic virus on grain yield for different symptom severity scores in twelve seasons, (Minerbio 1996–97 and Cadriano 2001–13).

Season	Symptom severity score			
	0.5	1.5	2.5	3.5
1995–96	7.0	21.1	35.2	49.3
1996–97	10.4	31.2	52.0	72.7
2000–01	8.4	25.1	41.9	58.7
2001–02	6.7	20.1	33.5	46.9
2002–03	7.6	22.9	38.1	53.4
2003–04	7.2	21.5	35.9	50.2
2004–05	5.9	17.8	29.6	41.4
2006–07	9.6	28.7	47.8	66.9
2008–09	5.2	15.7	26.1	36.5
2009–10	7.7	23.2	38.6	54.0
2011–12	6.9	20.8	34.7	48.6
2012–13	8.8	26.4	44.1	61.7
Mean	7.6	22.9	38.1	53.4
Minimum	5.2	15.7	26.1	36.5
Maximum	10.4	31.2	52.0	72.7

Response to cereal soil-borne mosaic virus of 148 durum wheat cultivars assayed from 1996 to 2013.

V. Vallega (CRA-QCE), C. Rubies-Autonell (DSA), A. Sarti (ASTRA) and R. Canestrale (CRPV).

A total of 148 durum wheat cultivars were grown in different trials over 13 seasons (from 1996 to 2013) at two fields with cereal soil-borne mosaic virus (CSBMV) near Minerbio and Cadriano (Bologna). The cultivars were evaluated for resistance to CSBMV on the basis of agronomic performance (except in the 2010–11 season), symptom severity, and

DAS–ELISA readings. Five of the 18 trials programmed over the 1996–2013 period could not be carried out due to the lack of adequate funds and/or sufficiently uniform fields. Each trial was comprised of 30–34 cultivars. The data collected for each cultivar and for each of the three parameters in each season from 1995 to 2005 were indexed as a percent of the highest value observed among all the cultivars assayed in that season and then averaged to minimize the confounding effects of differences in disease pressure between years. For various reasons, including the lack of agronomic data for the 2010–11 season, the cultivars assayed in the subsequent trials could not be classified according to the same criteria. On the other hand, because the new entries were grown along with cultivars already assayed for CSBMV resistance in other seasons, there was ample opportunity to adequately classify their response to CSBMV by the use of numerous direct comparisons and, thus, produce a synoptic table comprising all the 148 cultivars assayed (Table 5 below, continued on p. 25). In this respect, cultivars Duilio, Dylan, Claudio, Creso, Grazia, Iride, Levante, Meridiano, Neodur, and Simeto were tested in eight or more seasons.

Based on the experience accumulated, the CSBMV responses (Table 5, pp. 24-25) should be considered merely indicative for cultivars assayed in only one season, and highly dependable for cultivars assayed in three or more seasons. We note that although nearly half of the 148 cultivars listed carry a major gene for CSBMV resistance, located on the short arm of chromosome 2B, only 29 were classified as resistant, and none proved immune to CSBMV infection.

Table 5. Response to cereal soil-borne mosaic virus of 148 durum wheat cultivars assayed in 13 trials near Bologna (Minerbio 1996–97 and Cadriano 2001–13), Italy, and the number of years in which each cultivar was tested.

Cultivar	Years	Cultivar	Years	Cultivar	Years	Cultivar	Years
Resistant				**Moderately resistant**			
Alemanno	2	Meridiano	8	Ariosto	1	Latinur	4
Ares	4	Monastir	1	Arnacoris	3	Marco Aurelio	2
Asdrubal	1	Nefer	1	Artemide	1	Massimo Meridio	2
Baio	1	Neodur	8	Athoris	1	Neolatino	4
Biensur	4	Parsifal	2	Avispa	3	Normanno	7
Campodoro	1	Pharaon	2	Brindur	1	Orfeo	1
Ceedur	1	Pietrafitta	2	Canyon	1	Peleo	1
Colorado	5	Provenzal	5	Catervo	1	Portofino	2
Dario	1	Ramirez	3	Cesare	2	Pr22d89	3
Dylan	9	Saragolla	6	Chiara	1	Preco	1
Giusto	1	Serafo Nick	2	Colombo	2	Rusticano	1
Hathor	1	Solex	7	Core	2	San Carlo	5
Levante	8	Tiziana	3	Cosmodur	2	Sfinge	1
Lloyd	3	Valerio	1	Duilio	13	Svevo	5
Louxor	1			Fiore	2	Tirex	5
				Flavio	2	Torrese	1
				Gianni	5	Trapezio	2
				Grecale	2	Valsalso	1
				Ignazio	1	Virgilio	1
				Imhotep	3	Vitomax	3
				Iride	12	Vitron	2
				Isildur	2	Yelodur	3
				K26	1		

Table 5. Response to cereal soil-borne mosaic virus of 148 durum wheat cultivars assayed in 13 trials near Bologna (Minerbio 1996–97 and Cadriano 2001–13), Italy, and the number of years in which each cultivar was tested.

Cultivar	Years	Cultivar	Years	Cultivar	Years	Cultivar	Years
Moderately susceptible				**Susceptible**			
Appio	2	Minosse	2	Achille	6	Karur	4
Aureo	1	Miradoux	2	Agridur	1	Liberdur	5
Claudio	11	Norba	1	Anco Marzio	7	Magellano	1
Colosseo	4	Ofanto	2	Balsamo	2	Marco	2
Creso	10	Perseo	1	Bronte	1	Odisseo	2
Dorato	1	Plinio	1	Cannavaro	1	Orobel	7
Duetto	2	Portobello	1	Cannizzo	3	Peres	1
Emilio Lepido	1	Principe	1	Capri	1	Platani	2
Ermecolle	1	Quadrato	4	Carioca	1	Portorico	5
Exeldur	2	Sorrento	1	Casanova	2	Pr22d40	1
Gardena	2	Torrebianca	5	Ciccio	5	Prometeo	2
Giotto	3	Tresor	2	Ciclope	1	Sculptur	3
Giove	1	Vendetta	2	Cirillo	3	Severo	2
Italo	2	Verdi	3	Concadoro	1	Simeto	13
Ixos	3	Virgilio	2	Cuspide	1	Sorriso	1
Mimmo	1	Zenit	2	Derrick	2	Trionfo	2
				Giemme	2	Tripudio	2
				Granizo	1	Vesuvio	3
				Grazia	10	Vetrodur	3
				Ismur	2	Vettore	2
				Kanakis	3	Vinci	1

Effects of late sowing on durum wheat cultivars grown in a field infected with cereal soil-borne mosaic virus.

F. Quaranta, A. Belocchi, M. Fornara, and V. Vallega (CRA–QCE).

Wheat soil-borne mosaic virus (WSBMV), vectored by the soil-dwelling protist *Polymyxa graminis* Led., was first identified in the USA and thereafter reported in most of the wheat-growing areas of the world including Italy. In 2005, following the results of sequence analyses, the soil-borne wheat mosaic virus isolates prevalent in North America, Europe, and Far East Asia have been subdivided into three distinct furovirus species denominated wheat soil-borne wheat mosaic virus, cereal soil-borne mosaic virus (CSBMV), and Chinese wheat mosaic virus (CWMV), respectively. We note, however, that the results of recombination studies and other considerations suggest that these three furoviruses, transmitted by the same vector, exhibiting an identical particle morphology and inducing the same symptomatology, could be regarded as strains of WSBMV.

Late sowing has been proposed as a means of controlling WSBMV, yet the agronomic effects of purposefully delaying the seeding of wheats grown in fields infected by WSBMV, CSBMV, or CWMV have not been actually investigated so far. To study such effects, the responses of five durum wheat cultivars resistant to CSBMV (Dylan, Levante, Meridiano, Neodur, and Saragolla) and of five susceptible ones (Achille, Anco Marzio, Cirillo, Grazia, and Simeto) were investigated during the 2012–13 season in a field with natural inoculum sources of CSBMV situated near Rome (Italy) on three sowing dates: 25 October (early), 16 November (optimal), and 13 December (late).

The cultivar were grown in 10-m^2 plots distributed in the field according to a modified split-plot design with three replicates. To reduce border effects, three rows of the cultivar Tirex (moderately resistant to CSBMV) were seeded around the blocks at the time of each sowing. Symptom severity was scored on various dates using a 0–4 scale, where 0.0–1.0 = resistant, slight, or no symptoms; 1.1–2.0 = mildly resistant, mild mottling, and stunting; 2.1–3.0 = mildly susceptible, mottling, and stunting; and 3.1–4.0 = susceptible, severe mottling and stunting, with virus-killed plants. Only the symptom scores recorded on 4 April, 2013. Weediness was recorded as the percent of the soil surface covered

by undesired plants. To normalize data for ANOVA, symptom score and weediness data were subjected to square root and arcsine transformation, respectively. Grain yield, plant height, day-to-head (from 1 April), test weight, 1,000-kernel weight, and number of fertile tillers/m^2 were measured according to the standard procedures. Kernel number/spike and kernel number/m^2 were calculated from the data recorded for grain yield, 1,000-kernel weight, and spike number/m^2.

Plots received 30 kg/ha of N and 77 kg/ha of P_2O_5 (as diammonium phosphate) before seeding and 50 kg/ha (1 March) and 40 kg/ha (14 April) of N (as ammonium nitrate). Weeds were controlled with glyphosate, applied 5 October, 2012, and by harrowing prior to each sowing. We note that according to the results obtained in numerous trials carried out in Italy, resistant and moderately resistant durum wheat cultivars suffer, on average, grain yield losses of about 8 % and 23 %, respectively when grown under conditions favorable for CSBMV infection.

Cereal soil-borne mosaic virus disease pressure was severe in the early sowing, and decreased in the optimal and late sowing, as testified by the mean disease scores recorded for the susceptible cultivars in the first (mean score = 3.0) , second (2.5), and last sowing (2.2). As might be expected, the performance of the resistant cultivars was best in the optimal sowing for practically all the characters examined. Indeed, only the mean 1,000-kernel weight of the resistant cultivars proved highest in the latest sowing. Conversely, the performance of the susceptible cultivars improved substantially from the first to the last sowing date in regard to all the characters examined (Table 6).

Table 6. Mean performance at early. optimal. and late sowing dates for five cereal soil-borne mosaic virus (CSBMV)-resistant and five CSBMV-susceptible durum wheat cultivars grown in an CSBMV-infected field near Rome (Italy) during 2012–13. For each parameter. values with the same letters are not significantly different at P ≤0.05 (Duncan Multiple Range Test).

Sowing time	Cultivars	Grain yield (t/ha)		Plant height (cm)		Test weight (kg/hl)		1.000-kernel weight (g)		Spikes/ m^2 (n)		Kernels/ spike (n)		Kernels/m^2 (n)	
Early (25 October)		0.92	b	71	b	72.2	b	33.2	c	168	b	13	b	2,728	b
Optimal (16 November)		2.27	a	78	a	78.1	a	40.0	b	235	a	24	a	5,614	a
Late (13 December)		2.37	a	78	a	77.5	a	42.2	a	239	a	24	a	5,621	a
	Resistant	2.42	a	79	a	76.9	a	39.7	a	255	a	24	a	5,960	a
	Susceptible	1.28	b	72	b	75.0	b	37.1	b	173	a	17	b	3,348	b
Early	Resistant	1.48	d	79	ab	73.3		33.1	e	246	ab	18	d	4,403	cd
	Susceptible	0.36	e	64	c	71.1		33.2	e	89	d	8	e	1,053	e
Optimal	Resistant	3.04	a	81	a	79.1		41.9	b	269	a	28	a	7,264	a
	Susceptible	1.51	d	76	b	77.1		38.0	d	201	c	20	cd	3,964	d
Late	Resistant	2.75	b	78	ab	78.1		44.2	a	248	ab	25	ab	6,214	b
	Susceptible	1.99	c	78	ab	76.9		40.1	c	229	bc	22	bc	5,028	c

At the optimal sowing date, the mean grain yield recorded for the susceptible cultivars (1.51 t/ha) was about 50% of that recorded for the resistant cultivars (3.04 t/ha). Susceptible cultivars produced far fewer spikes/m^2 and grains/spike than the resistant cultivars as a consequence of CSBMV infection, but their mean 1,000-kernel weight was affected little. We note that at the optimal sowing the performance of the susceptible cultivars was significantly inferior to that of the resistant cultivars for all the characters investigated, including weediness (34% versus 9%).

Early sowing allowed plants of the resistant cultivars to tiller profusely, but induced them to head too early, thus determing high spike-sterility rates and low grain yields (1.48 t/ha). The mean grain yield recorded for the susceptible cultivars in the early sowing (0.36 t/ha) was substantially lower, representing only about 24% of that recorded for the resistant cultivars. Susceptible cultivars suffered severe die-back and produced far less spikes (89/m^2) than the resistant cultivars (246/m^2). We note that symptom scores close to 4.0 were assigned to five of the plots sown with susceptible cultivars, and that such plots produced grain barely sufficient to perform test weight and 1,000-kernel weight measurements. Mean weediness was substantially higher for the susceptible cultivars (65%) than for the resistant cultivars (16%).

Late sowing lead to a shorter growth cycle and, as a consequence, resistant cultivars produced less spikes and less grain/spike compared with the optimal sowing, yet also decidedly heavier grains and a moderately high mean grain yields (2.75 t/ha). The mean grain yield recorded for the susceptible cultivars in the late sowing (1.99 t/ha) was significantly higher than that recorded for such cultivars in the early (0.36 t/ha) and the optimal (1.51 t/ha) sowing, yet markedly lower than that recorded for the resistant cultivars in both the late and optimal sowings. Indeed, the mean grain yield recorded for the susceptible cultivars in the late sowing was 72% of that recorded for the resistant cultivars in that same sowing, and 65% of that recorded for the resistant cultivars in the optimal sowing. The mean grain yield data was recorded for the resistant and susceptible cultivars in the three sowings (Fig. 1).

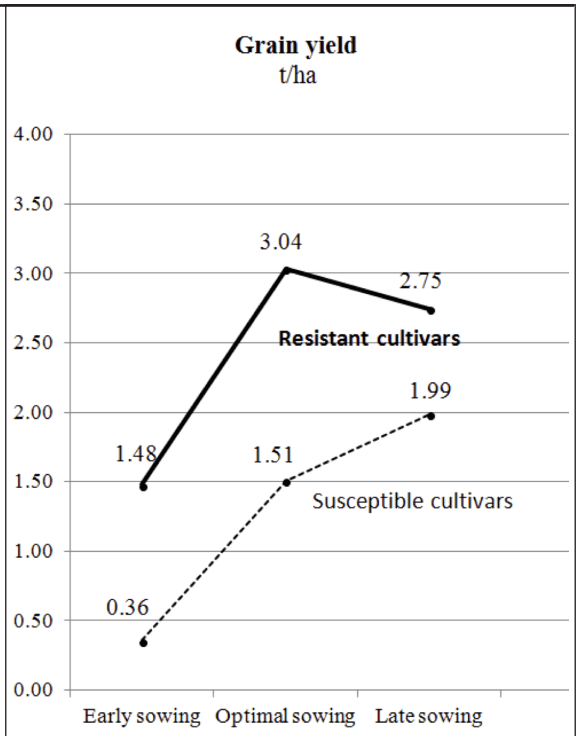

Fig. 1. Mean grain yield (t/ha) at early (25 October), optimal (16 November), and late (13 December) sowing dates for five cereal soil-born mosaic virus (CSBMV)-resistant and five CSBMV-susceptible durum wheat cultivars grown in an CSBMV-infected field near Rome (Italy) during the 2012–13 crop season.

We note that the highest grain yield recorded among susceptible cultivars in the late sowing (2.58 t/ha for the cultivar Anco Marzio) was lower than the lowest grain yield recorded among the resistant cultivars in the optimal sowing (2.78 t/ha for the cultivar Neodur). Also, it is important to note that the mean grain yield recorded in the optimal sowing (2.28 t/ha) for the 10 durum wheat cultivars investigated in this study was very similar and statistically not different from that recorded in the late sowing date (2.37 t/ha). Mean weediness in the late sowing was significantly higher for the susceptible cultivars than for the resistant (21% and 12%, respectively).

The data collected in 2012–13 suggest that purposefully delaying the sowing date of CSBMV-susceptible durum wheat cultivars in CSBMV-infected soils is advantageous only if resistant cultivars are not available. The data suggest that in those cases where the CSBMV response of the cultivars to be seeded is unknown, the mean grain yield expected as a result of purposefully delayed sowings is comparable to that which might be expected following optimal sowing; but evidently entails the risk of excessively delayed seedings as a result of unfavourable climatic conditions.

ITEMS FROM MEXICO

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.

Characteristics and description of phenotypic components of Quetchehueca Oro C2013 a new durum wheat cultivar for southern Sonora, Mexico.

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Abstract. Quetchehueca Oro C2013, a spring-type durum, originated from hybridizations and selections made from the cross 'Godrin/Gutros//Dukem/3/Thknee_11/4/Dukem_1//Patka_7/Yazi_1 /3/Patka_7/Yazi_1/5/Ajaia_12/F3Local(Sel. Ethio. 135.85)//Plata_13/3/Adamar'. The cross number and history selection is CDSS04B00367T-0TOPY-10Y-0M-4Y-0M-4Y-0B. This cultivar has an average height of 83 cm, 82 days to heading, and 125 days to physiological maturity. Plant growth habit is erect and shows null or low frequency of recurved flag leaves. The spike measures 7.0–8.5 cm and produces from 20 to 22 spikelets. In the mid-third of the ear, the glume shoulder is narrow and sloping, with a short and moderately curved beak. Ear glaucosity is strong, and awns are distributed the entire length and have a white color. Grain coloration, when treated with phenol, is nil or very light.

Introduction. Worldwide production of wheat in 2012 was 670.8 x 10^6 tons (FAO 2012). China was the main producer with 120.5, followed by India with 94.9. Mexico produced 3.3 x 10^6 tons, imported 4.04, and exported 835,908 (FAO 2011). Of the wheat-growing area in Mexico, 71.6% (350,785 ha) corresponded to the states of Sonora, North Baja California, and Sinaloa, during the autumn–winter crop season 2011–12, with an estimated value of USD$838 x 10^6 (SIAP 2014). Since the agricultural season 1994–95, durum wheat has been the dominant class grown in the state of Sonora. Important factors that contributed to shift from bread wheat to durum in this region were the implementation of domestic quarantine No. 16 (SARH 1987), which limited the cultivation of bread wheat in fields where Karnal bunt (*Tilletia indica*) had been detected at levels greater than 2% infected grains, the greater grain yield of durum wheat versus that of bread wheat, international export of durum, and resistance to leaf rust (*Puccinia triticina*) during the 1980s and 1990s. Altar C84 was the most grown 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 a 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 grown cultivar in southern Sonora from 2003–04 to 2008–09, reaching 119,327 ha (42.3%) during the last season (Table 1) (Fuentes-Dávila et al. 2010). Átil C2000, a high-yielding cultivar released in 2001, which became susceptible to leaf rust in 2001–02 (Figueroa-López et al. 2002), occupied 53,106.07 ha.

Table 1. Area (ha) and percentage of the total area grown with wheat during the 2008–09 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	Percent
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**	

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, whereas that for Átil C2000 increased (Table 2) (Fuentes-Dávila et al. 2011). During the 2010–11 crop season, 292,247 ha were grown with wheat in southern Sonora, 69.90% corresponded to durum wheat (predominating cultivars CIRNO C2008 (87,105 ha) and Átil C2000 (50,236 ha)), and the bread wheat cultivar Tacupeto F2001 (36,819 ha) (Table 3) (OEIDRUS 2011). CIRNO C2008 had a quick increase in area because it was publized as an improved Átil due to its resistance to leaf rust. In the 2011–12 crop season, CIRNO C2008 occupied 154,915 ha and 196,295 in 2012–13; however, a low incidence of yellow rust was detected in 2012–13. Therefore, more options for rust-resistant cultivars for this region must be increased so that they help contribute to the long-lasting use by wheat producers in Sonora and northwest Mexico and, at the same time, meet current minimum quality requirements for export.

Pedigree, selection history, and description of Quetchehueca Oro C2013. After evaluating grain yield since the 2009–10 agricultural season at the Norman E. Borlaug Experimental Station (CENEB), we proposed the release of the experimental durum wheat line 'Godrin/Gutros//Dukem/3/Thknee_11/4/Dukem_1//Patka_7/Yazi_1/3/Patka_7/Yazi_1/5/Ajaia_12/F3Local (Sel. Ethio. 135.85)//Plata_13/3/Adamar' as the cultivar **Quetchehueca Oro C2013** (Fuentes-Dávila et al. 2014). Quetchehueca Oro C2013 is a spring-type durum cultivar that originated from hybridizations made in

Table 2. Area (ha) and percentage of the total area grown with wheat during the 2009–10 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	Percent
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**	

Table 3. Area (ha) and percentage of the total area grown with wheat during the 2010–11 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	Percent
DURUM WHEAT		
CIRNO C2008	87,105	29.9
Átil C2000	50,236	17.3
Sáwali Oro C2008	14,353	4.9
Patronato Oro C2008	11,753	4.0
Júpare C2001	10,069	3.4
RSM Imperial C2008	7.149	2.4
CEVY Oro C2008	6,197	2.1
Río Colorado	5,111	1.7
Samayoa C2004	4,905	1.6
Rafi C97	1,806	0.6
RSM Chapultepec C2008	1,650	0.5
Others 1,210	0.4	0.20
Platinum	1,173	0.4
Aconchi C89	752	0.2
TOTAL	203,469	0.10
Altar C84	105	0.04
TOTAL	**178,806**	
BREAD WHEAT		
Tacupeto F2001	36,819	12.6
Kronstad F2004	18,681	6.4
Roelfs F2007	10,358	3.6
Navojoa M2007	8,046	2.8
RSM-Norman F2008	4,499	1.5
Cachanilla F2000	3,493	1.2
Rayón F89	2,576	0.9
Abelino F2004	1,355	0.5
Palmerín F2004	964	0.3
Others 538	0.1	
Oasis F86	319	0.1
TOTAL	**87,648**	

the Durum Wheat Breeding Program at CIMMYT. The cross number and history selection is CDSS04B00367T-0TOPY-10Y-0M-4Y-0M-4Y-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 4).

Table 4. Selection history and localities where cultivar Quetchehueca Oro C2013 was evaluated (F–W = Fall–Winter and S–S = Spring–Summer; RR = regular rainfed, NI = normal irrigation, and RI = reduced irrigation).

Activity	Locality	Season	Irrigation
Simple genetic cross	Cd. Obregon, Sonora	F–W/2003–04	NI
Top genetic cross	El Batan	S–S/2004	RR
F_1 generation	Cd. Obregon, Sonora	F–W/2004–05	NI
F_2 generation	Cd. Obregon	F–W/2005–06	NI
F_3 generation	Atizapan, Mexico	S–S/2006	RR
F_4 generation	Cd. Obregon	F–W/2006–07	NI
F_5 generation	Atizapan	S–S/2007	RR
F_6 generation	Cd. Obregon	F–W/2007–08	NI
Yield trials and spike selection by CIMMYT			
F_7 generation	El Batan	S–S/2008	RR
Spike selection by CIMMYT in different planting dates (15 and 30 November, 15 December, and 1 January.			
Yield trials by INIFAP	Cd. Obregon	F–W/2009–10	NI–RI
		F–W/2010–11	NI-RI
		F–W/2011–12	NI-RI

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 (Table 5, p. 31). Cultivar Quetchehueca Oro C2013 has an average of 82 days to heading with a range of 76 to 93. The biological cycle averages 125 days to physiological maturity; however, the cycle may be shortened due to the lack of cold hours if planting is late, and may average 113 days when sowing is at the end of December. Quetchehueca Oro C2013 has an average height of 83 cm (Fig. 1, left) with a maximum of 90 and minimum of 70. Plant growth habit is erect and shows null or low frequency of recurved flag leaves. Spike shape in profile view is tapering, density is dense, and the length, excluding awns, is medium; awns are longer than spikes. Spike glaucosity is strong, and awns are distributed throughout the entire length and are white. Glume shape is sloping (spikelet in the mid-third of spike), narrow, and not hairy on the external surface. The length of the beak is short and moderately curved. Grain is elongated (Fig. 1, right), and the length of brush hair in dorsal view is short. Grain coloration, when treated with phenol, is nil or very light.

Fig. 1. Quetchehueca Oro C2013 has an average of 82 days to heading with a range of 76 to 93. Plants are erect and present nil or a very low frequency of recuved flag leaves (left). Grain shape in the dorsal view (right), pubescence is short; grain color after treatment with phenol is nil or very light.

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Table 5. Characteristics and description of phenotypic components of cultivar Quetchehueca Oro C2013.

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

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Characteristics and description of phenotypic components of CIRNO C2008, a durum wheat cultivar widely adopted by farmers in southern Sonora, Mexico.

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

Abstract. CIRNO C2008, a spring-type durum, originated from hybridizations and selections made from the cross 'Sooty_9/Rascon_37//Camayo'. The cross number and history selection is CGS02Y00004S-2F1-6Y-0B-1Y-0B-0Y. This cultivar has an average height of 78 cm, 80 days to heading, and 122 days to physiological maturity. Plant growth habit is erect and shows null or low frequency of recurved flag leaves. The spike measures 6.5 to 9.0 cm long and produces from 18 to 20 spikelets. In the mid-third of the ear, the glume shoulder is medium and rounded, with a very short and straight beak. Spike glaucosity is strong, and awns are distributed the entire length and are brown. Grain coloration when treated with phenol is nil.

Introduction. Worldwide, production of wheat in 2012 was 670.8 x 10^6 tons (FAO 2012); China was the main producer with 120.5, followed by India with 94.9. Mexico produced 3.3 x 10^6 t, imported 4.04 t, and exported 835,908 t (FAO 2011). Of the area grown with wheat in Mexico, 71.6% (350,785 ha) corresponds to the states of Sonora, North Baja California, and Sinaloa, during the fall–winter crop season in 2011–12, with an estimated value of US$838 x 10^6 (SIAP 2014).

Since the 1994–95 agricultural season, durum wheat cultivars have become very important for international export in the state of Sonora, Mexico, from Altar C84 to Átil C2000, both of which became susceptible to a leaf rust race in 2001–02 (Figueroa-López et al. 2002). Despite the susceptibility, Átil C2000 occupied 53,106.07 ha in 2008–09, whereas the replacement cultivar, Júpare C2001, occupied 119,327.38 ha (Fuentes-Dávila et al. 2014). The commercial longevity of Júpare C2001 as a resistant cultivar to leaf rust has lasted from 2003–04 to 2008–09. The area sown with this cultivar decreased to 53,164 ha in 2009–10, and 10,069 in 2010–11 in southern Sonora.

Átil C2000 is a high-yielding cultivar (some fields yields have reached 11 t/ha), so many farmers prefer to apply fungicides for leaf rust control. This cultivar occupied 81,777 ha in 2009–10 and 50,236 ha in 2010–11; its relative, CIRNO C2008, newly released in 2008 for commercial cultivation, occupied 3,233 and 87,105 ha, respectively (Fuentes-Dávila et al. 2014). CIRNO C2008 had a rapid increase in area because it was publicized as the improved Átil due to its resistance to leaf rust, conferred by the progenitor Camayo, which has a resistant gene that is not present in any other commercial cultivar. Therefore, wheat farmers will not have to depend on fungicides in order to control the disease. In Mexico, and particularly in the northwestern part of the country, leaf rust is very important economically and, historically, is where it has caused yield losses ranging from 30 to 60%, depending on the cultivar and climatic conditions (Villaseñor et al. 2003). CIRNO C2008 occupied 154,915 ha in the 2011–12 crop season, and 196,295 in 2012–13. However, a low incidence of yellow rust was detected in 2012–13. Options of cultivars resistant to rusts for this region must be increased, so that they contribute to 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 CIRNO C2008. After evaluating grain yield since the 2006–07 agricultural season at the Norman E. Borlaug Experimental Station (CENEB), we proposed to release the experimental durum wheat line 'Sooty_9/Rascon_37//Camayo' as cultivar CIRNO C2008 (Félix-Fuentes et al. 2010). CIRNO C2008 is a spring-type durum cultivar, which originated from hybridizations made in the Durum Wheat Breeding Program of CIMMYT. The cross number and history selection is CGS02Y00004S-2F1-6Y-0B-1Y-0B-0Y. Shuttle breeding

was carried out between the experimental stations of El Batán, state of Mexico (B) (19°30'N and 2,249 masl), and the Yaqui Valley (Y) (27°20'N and 40 msnm), in Sonora (Table 6).

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 (Table 7). Cultivar CIRNO C2008 has an average of 80 days to heading with a range of 74 to 89. The cultivar has a biological cycle with an average of 122 days for physiological maturity; however,

Table 6. Selection history and localities where cultivar CIRNO C2008 was evaluated (F–W = Fall-Winter and S–S = Spring–Summer; RR = regular rainfed, NI = normal irrigation, and RI = reduced irrigation). The different planting dates for the INIFP yield trials were 15 and 30 November, 15 December, and 1 January.

Activity	Locality	Season	Irrigation
Simple genetic cross	Cd. Obregon, Sonora	F–W/2001–02	NI
F_1 generation	El Batan, Mexico	S–S/2003	RR
F_2 generation	Cd. Obregon	F–W/2003–04	NI
F_3 generation	El Batan	S–S/2004	RR
F_4 generation	Cd. Obregon	F–W/2004–05	NI
F_5 generation	El Batan	S–S/2005	RR
Yield trials and spike selection by CIMMYT	Cd. Obregon	F–W/2005–06	NI
Yield trials by INIFAP	Cd. Obregon	F–W/2006–07	NI–RI
		F–W/2007–08	NI–RI
		F–W/2008–09	NI–RI

Table 7. Characteristics and description of phenotypic components of cultivar CIRNO C2008.

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

the cycle may be shortened due to the lack of cold hours if planting is late, and may average 108 days when sowing is done at the end of December. CIRNO C2008 has an average height of 78 cm (Fig. 2, left), a maximum of 90 and minimum of 65. Plant growth habit is erect, and shows nil or low frequency of recurved flag leaves. The spike measures 6.5 to 9.0 cm long and produces from 18 to 20 spikelets (Fig. 2, middle).

Fig. 2. CIRNO C2008 durum wheat cultivar has an average height of 78 cm, erect plants, and no or a very low percent of recurved flag leaves (left). The spike shape is tapering in profile view, of medium density, and of medium length; the awns are longer than the spikes (middle). The grain shape is semi-elongated. In the dorsal view, pubescence is short (right) and grain color after treatment with phenol is nil.

Spike shape in profile view is tapering, density is medium, and the length excluding awns is medium; awns are longer than spikes. Spike glaucosity is strong, and awns are distributed in the entire length and are a brown color. Glume shape is rounded (spikelet in mid-third of spike), medium, and the hairiness on the external surface is absent or very weak. The length of the beak is very short and straight. Grain is semi-elongated (Fig. 2, right), and the length of brush hair in dorsal view is short. Grain coloration when treated with phenol is nil.

CIRNO C2008 has the registration TRI-124-240511 in the Mexican Catalogue of Plant Cultivars.

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 CIRNO C2008 originated.

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Characteristics and description of phenotypic components of Movas C2009, a durum wheat cultivar for northwest Mexico.

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Abstract. Movas C2009, a spring-type durum, originated from hybridizations and selections made from the cross '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'. The cross number and history selection is CDSS02B00720S-0Y-0M-8Y-1M-04Y-0B. This cultivar has an average height of 88 cm, 79 days to heading, and 120 days to physiological maturity. Plant growth habit is erect and shows null or low frequency of recurved flag leaves. The spike measures 7.0–8.0 cm long and produces from 18 to 20 spikelets. In the mid-third of the spike, the glume is strongly elongated, the shoulder is narrow and sloping, with a short and slightly curved beak. Spike glaucosity is medium, and the awns are distributed the entire length and have a light brown color. Grain coloration when treated with phenol is nil.

Introduction. Worldwide production of wheat in 2012 was 670.8 x 10^6 tons (FAO 2012); China was the main producer with 120.5, followed by India with 94.9. Mexico produced 3.3 x 10^6 t, imported 4.04 t, and exported 835,908 t (FAO 2011). Of the area grown with wheat in Mexico, 71.6% (350,785 ha) corresponded to the states of Sonora, North Baja California, and Sinaloa, during the 2011–12 fall–winter crop season, with an estimated value of US$838 x 10^6 (SIAP 2014).

Since the 1994–95 agricultural season, durum wheat cultivars have become very important for international export in the state of Sonora, Mexico. From Altar C84 to Átil C2000, Júpare C2001, and CIRNO C2008 (Fuentes-Dávila et al. 2014). Cultivar CIRNO C2008 went from 3,233 ha in 2009–10 to 87,105 ha in 2010–11, 154,915 ha in 2011–12, and 196,295 ha in 2012–13 in southern Sonora. However, a low incidence of yellow rust was detected in 2012–13.

One of the main objectives of the collaborative project on wheat breeding in northwestern Mexico 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, is to diversify the genetic resistance to rusts, and particularly to leaf rust, to avoid any epiphytotics.

Although CIRNO C2008 had a rapid increase in area since it was publicized as the improved Átil due to its resistance to leaf rust conferred by the progenitor Camayo, which has a resistant gene that is not present in any other commercial cultivar, the generation of resistant durum wheat cultivars to rusts for this region must be increased in order to reach the appropriate levels of diversification. Movas C2009 is one of several cultivars released for commercial cultivation in the last five years. The area grown with Movas C2009 in southern Sonora during the 2011–12 crop season was 18 ha (Table 8, p. 36) and 6,227 in 2012–13 (Table 9, p. 36).

Pedigree, history selection and description of Movas C2009. After evaluating grain yield since the 2007–08 agricultural season at the Norman E. Borlaug Experimental Station (CENEB), we proposed to release the experimental durum wheat 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' as cultivar **Movas C2009** (Félix-Fuentes et al. 2011). Movas C2009 is a spring-type durum cultivar, which originated from hybridizations made in the Durum Wheat Breeding Program of CIMMYT. The cross number and history selection is CDSS02B00720S-0Y-0M-8Y-1M-04Y-0B. Shuttle breeding was carried out between the experimental stations at El Batán, state of Mexico (B) (19°30'N and 2,249 masl); San Antonio Atizapán, state of Mexico (M) (19°17'N and 2,640 masl); and the Yaqui Valley (Y) (27°20'N and 40 masl), in Sonora (Table 10, p. 36).

Table 8. Area (ha) and percentage of the total area grown with wheat during the 2011–12 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	Percent
DURUM WHEAT		
CIRNO C2008	154,915	69.409
Átil C2000	11,343	5.082
Patronato Oro C2008	7,226	3.238
RSM Imperial C2008	3.236	1.450
Sáwali Oro C2008	2,183	0.978
RSM Chapultepec C2008	1,072	0.480
Samayoa C2004	990	0.444
CEVY Oro C2008	931	0.417
Júpare C2001	913	0.409
Platinum	335	0.150
Huatabampo Oro C2009	59	0.026
Movas C2009	18	0.008
TOTAL	**183,221**	
BREAD WHEAT		
Tacupeto F2001	17,278	7.741
Roelfs F2007	7,108	3.185
Kronstad F2004	6,671	2.999
Navojoa M2007	5,213	2.336
RSM-Norman F2008	2,665	1.194
Abelino F2004	740	0.332
Japaraqui F2003	244	0.109
Ónavas F2009	29	0.013
Tepahui F2009	17	0.008
Rayón F89	6	0.003
TOTAL	**39,971**	

Table 9 Area (ha) and percentage of the total area grown with wheat during the 2012–13 agricultural season in southern Sonora, Mexico.

Cultivar	Area (ha)	Percent
DURUM WHEAT		
CIRNO C2008	196,295.35	79.59
Movas C2009	6,227.00	2.52
Huatabampo Oro C2009	5,081.00	2.06
RSM Imperial C2008	4,494.30	1.82
Átil C2000	4,080.18	1.65
Patronato Oro C2008	3,182.57	1.29
Sáwali Oro C2008	1,180.00	0.48
RSM Chapultepec C2008	847.60	0.34
CEVY Oro C2008	184.54	0.07
TOTAL	**221,573.35**	
BREAD WHEAT		
Tacupeto F2001	8,823.71	3.58
Roelfs F2007	5,223.02	2.12
Kronstad F2004	4,166.04	1.69
Navojoa M2007	2,301.30	0.93
Villa Juárez F2009	1,479.00	0.60
Ónavas F2009	1,395.00	0.57
RSM-Norman F2008	1,236.00	0.50
Abelino F2004	159.50	0.06
Ocoroni F86	148.69	0.06
Tepahui F2009	92.00	0.04
Japaraqui F2003	20.00	0.01
TOTAL	**25,054.27**	

The most important phenotypic characteristics of this cultivar, according to the International Union for the Protection of New Varieties of Plants (UPOV, 1994), are shown (Table 11, p. 37). Cultivar Movas C2009 has an average of 79 days to heading with a range of 74 to 85. This cultivar has a biological cycle with an average of 120 days for physiological maturity; however, the cycle may be shortened due to the lack of cold hours if planting is late, and may average 110 days when sowing is done at the end of December. Movas C2009 has an average height of 88 cm (Fig. 3 (top), p. 38), a maximum of 100 and minimum of 75. Plant growth habit is erect, and shows nil or low frequency of recurved flag leaves. The spike measures 7.0 to 8.0 cm long and produces from 18 to 20 spikelets (Fig. 3 (middle), p. 38).

Table 10. Selection history and localities where cultivar Movas C2009 was evaluated (F–W = Fall-Winter and S–S = Spring–Summer; RR = regular rainfed, NI = normal irrigation, and RI = reduced irrigation). The different planting dates for the INIFP yield trials were 15 and 30 November, 15 December, and 1 January.

Activity	Locality	Season	Irrigation
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	El Batan	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

Table 11. Characteristics and description of phenotypic components of cultivar Movas C2009.

Structure	Characteristic	Description
Coleoptile	Anthocyanin coloration	Weak
First leaf	Anthocyanin coloration	Absent or very weak
Plant	Growth habit	Erect
	Frequency of plants with recurved flag leaves	Absent or very low
	Length (stem, ear, and awns)	Long
	Seasonal type	Spring
Culm	Hairiness of uppermost node	Absent or very weak
	Glaucosity of neck	Medium
Flag leaf	Glaucosity	Strong
	Glaucosity of blade	Weak
Awn	Anthocyanin coloration	Absent or very weak
	Color	Light brown
Awns at tip of spike	Length in relation to spike	Longer
Spike	Time of emergence	Medium
	Glaucosity	Medium
	Distribution of awns	Whole length
	Length excluding awns	Medium
	Hairiness of margin of first rachis segment	Absent or very weak
	Color (at maturity)	White
	Shape in profile view	Tapering
	Density	Medium
Lower glume	Shape (spikelet in mid-third of ear)	Strongly elongated
	Shape of shoulder	Sloping
	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)	Thin
Grain	Shape	Semi-elongated
	Length of brush hair in dorsal view	Short
	Coloration with phenol	Nil

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 medium, and awns are distributed the entire length and have a light brown color. Glume shape is strongly elongated (spikelet in mid-third of the spike), narrow, and hairy on the external surface. The length of the beak is short and slightly curved. Grain is semi-elongated (Fig. 3 (bottom), p. 38), and the length of brush hair in dorsal view is short. Grain coloration when treated with phenol is nil.

Movas C2009 has the registration TRI-118-270510 in the Mexican Catalogue of Plant Cultivars.

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 Movas C2009 originated.

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Fig. 3. Durum wheat cultivar Movas C2009 has an average height of 88 cm, 79 days to heading, and 120 days to physiological maturity. Plants are erect and present no or very low frequency of recurved flag leaves (top). The spike of Movas C2009 is tapering in profile, density is medium, and the length, excluding the awns is medium. Awns are longer than the spikes. Spikes measrue 7.0–8.0 cm and produce 18–20 spikelets (middle). Grain spahe of Movas C2009 is semi-elongated. In dorsal view, pubescence is short. Grain color after treatment with phenol is nil (bottom).

Characteristics and description of phenotypic components and quality of durum wheat cultivar Sáwali Oro C2008.

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Abstract. Sáwali Oro C2008, a spring-type durum wheat, originated from hybridizations and selections made from the cross 'Musk_1//ACO89/FNFoot_2/4/Musk_4/3/Plata_3// Crex/Alla/5/Olus*2/ Ilbor//Patka_7/Yazi_1'. The cross number and history selection is CDSS02Y00786T-0TOPB-0Y-0M-2Y-0M-0Y. This cultivar has an average height of 89 cm, 81 days to heading, and 122 days to physiological maturity. Plant growth habit is erect and shows no or low frequency of recurved flag leaves. The spike measures 8.0–8.5 cm long and produces from 19 to 20 spikelets. In the mid-third of the spike, the glume is elongated and the shoulder is narrow and rounded, with a very short and straight beak. Spike glaucosity is medium, and awns are distributed the entire length and have are light brown. Grain coloration when treated with phenol is nil or very light.

Introduction. The area used for wheat cultivation in Mexico in year 2012 was 578,836.38 ha. The state of Sonora covered 254,759.70 (44%), with a production of 1´784,562.72 t (SIAP 2014). The most important wheat-producing region in Sonora is comprised of the following districts of rural development: 148 Cajeme (Yaqui Valley) with 174,983 ha occupying 68.7% of the state area, and 149 Navojoa (Mayo Valley) with 49,018 ha occupying 19.2% of the state area. Since the 1994–95 agricultural season, durum wheat cultivars have become very important for international export in the state of Sonora, Mexico. From Altar C84 to Átil C2000, Júpare C2001, and CIRNO C2008 (Fuentes-Dávila et al. 2014). This last cultivar went from 3,233ha in 2009–10 to 87,105 in 2010–11, 154,915 in 2011–12, and 196,295 ha in 2012–13. However, low incidence of yellow rust was detected in 2012–13.

One of the main objectives of the collaborative project on wheat breeding in northwestern Mexico 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, is to diversify the genetic resistance to rusts, and particularly to leaf rust, to avoid any epidemics.

Although CIRNO C2008 had a rapid increase in area since it was publicized as the improved Átil, due to its resistance to leaf rust conferred by the progenitor CAMAYO, which has a resistant gene that is not present in any other commercial cultivar, the generation of resistant durum wheat cultivars to rusts for this region must be increased, in order to reach the appropriate levels of diversification. Sáwali Oro C2008 is one of several cultivars released for commercial cultivation in the last five years. The area grown with this cultivar in southern Sonora during the 2009–10 crop season was 4,761 ha, 14,353 ha in 2010–11 (Fuentes-Dávila et al. 2014), 2,183 ha in 2011–12, and 1,180 ha in 2012–13 (Felix-Fuentes et al. 2014).

Pedigree, history selection and description of Sáwali Oro C2008. After evaluations of grain yield carried out since the 2006–07 agricultural season at the Norman E. Borlaug Experimental Station (CENEB), we proposed to release the experimental durum wheat line 'Musk_1//ACO89/FNFoot_2/4/Musk_4/3/Plata_3//Crex/Alla/5/Olus*2/Ilbor//Patka_7/Yazi_1' as cultivar **Sáwali Oro C2008** (Figueroa-López et al. 2010). Sáwali Oro C2008 is a spring-type durum cultivar, which originated from hybridizations made in the Durum Wheat Breeding program of CIMMYT (Table 12). The cross number and history selection is

Table 12. Selection history and localities where cultivar Sáwali Oro C2008 was evaluated (F–W = Fall-Winter and S–S = Spring–Summer; RR = regular rainfed, NI = normal irrigation, and RI = reduced irrigation). The different planting dates for the INIFP yield trials were 15 and 30 November, 15 December, and 1 January.

Activity	Locality	Season	Irrigation
Top genetic cross	Cd. Obregon, Sonora	F–W/2001–02	NI
F_1 generation	El Batan, Mexico	S–S/2002	RR
F_2 generation	Cd. Obregon	F–W/2002–03	NI
F_3 generation	Atizapan, Mexico	S–S/2003	RR
F_4 generation	Cd. Obregon	F–W/2003–04	NI
F_5 generation	Atizapán	S–S/2004	RR
F_6 generation Yield trials by CIMMYT	Cd. Obregon	F–W/2004–05	NI
Yield trials by INIFAP	Cd. Obregon	F–W/2006–07	NI
		F–W/2007–08	NI
		F–W/2008–09	NI

CDSS02Y00786T-0TOPB-0Y-0M-2Y-0M-0Y. Shuttle breeding was carried out between the experimental stations of El Batán, state of Mexico (B) (19°30'N and 2,249 masl); San Antonio Atizapán, state of Mexico (M) (19°17'N and 2,640 masl); and the Yaqui Valley (Y) (27°20'N and 40 masl), in Sonora.

Phenotypic components. The most important phenotypic characteristics of Sáwali Oro C2008, according to the International Union for the Protection of New Varieties of Plants (UPOV 1994), are given (Table 13). Cultivar Sáwali Oro C2008 has an average of 81 days to heading with a range of 72 to 90. This cultivar has a biological cycle with an average of 122 days for physiological maturity, with a minimum of 110 and a maximum of 134. Sáwali Oro C2008 has an average height of 89 cm (Table 14, p. 41), a maximum of 95 and minimum of 75. Plant growth habit is erect, and shows none or a low frequency of recurved flag leaves. The spike measures 8.0 to 8.5 cm long and produces from 19 to 20 spikelets (Fig. 4, p. 41). Each spikelet produces three to five grains in the lower one-third of the spike with a predominance of four; from three to five in the middle one-third, with a predominance of four or five; and one to five in the upper one-third, with a predominance of four, three, or two.

Table 13. Characteristics and description of phenotypic components of cultivar Sáwlai Oro C2008.

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

Spike shape in profile view is parallel sided, density is medium and the length excluding awns is medium; awns are longer than the spikes. Spike glaucosity is medium, and awns are distributed the entire length and are light brown. Glume shape is elongated (spikelet in mid-third of spike), the shoulder is narrow and rounded, and the hairiness on the

Fig. 4. Durum wheat cultivar Sáwali Oro C2008 has an average height of 89 cm, 81 days to heading, and 122 days to physiological maturity. Plant growth habit is erect and shows no or low frequency of recurved flag leaves (top). Spikes of this cultivar are parallel sided in profile, medium dense, and the awns are longer than the spikes. Spike length, excluding the awns, measures 8.0–8.5 cm long and produces from 19 to 20 spikelets (middle). Grain shape is semi-elongated in the dorsal view, pubescence is medium. Grain coloration when treated with phenol is nil or very light (bottom).

external surface is absent. The length of the beak is very short and straight. Grain is semi-elongated (Fig. 4), 6.9 mm long by 3 mm wide, with an average weight of 50 mg. The length of brush hair in dorsal view is medium. Grain coloration when treated with phenol is nil or very light.

Quality. An important characteristic of the Mexican durum wheat which influences its demand abroad, is the high level of semolina extraction. Wheat semolina quality for pasta-making is determined by the content and quality of the protein and the pigment (Fig. 5) present in the grain endosperm of durum wheat. Sáwali Oro C2008 has a high protein content average (14%) and color Minolta b value of 27.8 (Table 14). This cultivar is consistently superior to cultivar check Júpare C2001 in protein content and yellow pigment in the grain endosperm. The grain of Sáwali Oro C2008 has an average specific weight of 83.2 kg/hL.

Sáwali Oro C2008 has the registration TRI-109-240209 in the Mexican Catalogue of Plant Cultivars.

Table 14. Characteristics of the industrial quality of Sáwali Oro C2008 and the check cultivar Júpare C2001.

Characteristic	Sáwali Oro C2008	Júpare C2001
Specific weight (kg/hl)		
Minimum	81.4	79.0
Average	83.2	83.6
Maximum	85.2	85.9
Grain protein (%)		
Minimum	12.6	12.9
Average	14.0	13.8
Maximum	15.0	15.1
Color (Minolta b value)		
Minimum	25.7	18.7
Average	27.8	20.7
Maximum	30.3	26.2

Fig. 5. Durum wheat cultivar Sáwali Oro C2008 produces a great concentration of pigment (right) compared to that of the check cultivar Júpare C2001 (left).

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Incidence of Karnal bunt in experimental plots sown with infected wheat seed during several crop seasons.

Guillermo Fuentes-Dávila.

Abstract. This work evaluated the effect of different quantities of infected seed/kg for sowing on the natural incidence of Karnal bunt. Experiments were conducted at the Norman E. Borlaug Experimental Station, in Sonora, Mexico. A set of treatments, which consisted of 5, 10, 100, 250, and 500 infected seeds/kg and an untreated, healthy check, was applied during the 1989–90 to 1993–94 crop seasons. Another set, consisting of 500, 1,000, 2,500, and 5,000 infected seeds/kg and the untreated, healthy check, with two replicated plots per season, was applied during 1991–92 to 1994–95. The experiments were established in the same land during the different crop seasons. For the first experiment, the healthy check showed the greatest number of infected grains in two crop seasons and was the second in two other seasons. The treatment with 500 infected seeds had the lowest number of infected grains in two crop seasons. For the second experiment, the healthy check showed the greatest number of infected grains in both replicates in the 1992–93 crop season, and in one in the 1994–95 crop season. The treatment with 5,000 infected seeds had the highest number of infected grains in both replicates in 1991–92, but the lowest one in both replicates in 1994–95 and in one replicate in 1992–93.

Introduction. Karnal bunt, caused by *Tilletia indica* Mitra (syn. *Neovossia indica* (Mitra) Mundkur), was first identified in India (Mitra 1931) and later in Mexico (Duran 1972), Pakistan (Munjal 1975), Nepal (Singh et al. 1989), Brasil (Da Luz et al. 1993), the United States of America (APHIS 1996), Iran (Torarbi et al. 1996), and the Republic of South Africa (Crous et al. 2001). More recently, the CIMMYT-blog/tag/karnal-bunt (CIMMYT 2011) states that 'Karnal bunt has long been present in Afghanistan, with favorable climatic conditions promoting occasional outbreaks, and a recent survey by ARIA indicated that several popular wheat varieties are susceptible to the disease. It is particularly prevalent in the eastern region bordering Pakistan, which has emerged in recent years as an important seed-producing area within Afghanistan'. Despite this, no public information is available regarding the history of Karnal bunt in that country, disease incidence, and the area affected.

Teliospores of *T. indica* are resistant to extreme cold, heat, chemical treatments (Smilanick et al.,1985), and can survive up to three (Bonde et al. 2004) to four years in field soil (Krishna and Singh 1982), making control difficult. Fairly good chemical control with fungicide applications during flowering can be accomplished (Salazar-Huerta et al. 1997); however, in northwest Mexico, due to quarantine regulations (SARH 1987), this measure is still not profitable for commercial use.

Although the effect of Karnal bunt on yield is not serious (Salazar-Huerta et al. 1997), the economic impact in flour quality, and the costs due to the quarantine measures established in northwest Mexico, are of great importance (Brennan et al. 1990). Such measures were imposed to avoid dissemination of the pathogen to other wheat-producing areas within and outside Mexico (SARH 1987). Regarding seed production and distribution, seed produced in the quarantined areas and destined for seed in such areas should comply with the norm of 0% damaged or infected grains of Karnal bunt and should be treated chemically as specified. Despite this, tolerance levels of 5, 10, and 25 infected grains were allowed in years of high incidence, with the objective to suffice the seed demand (García Valle 1991). Since 1981–82, when the Mexican Department of Agriculture and Water Resources established a systematic process of sampling in southern Sonora, disease incidence was observed to increase when weather conditions favored development and dissemination of the fungus (high relative humidity, cloudiness, and rain), whether or not the seed to be used for sowing was infected (García Valle 1991). At that time, a very economically important restriction imposed by the government, which accounted for about 29% of the total calculated annual loss caused by Karnal bunt in northwest Mexico (Brennan et al. 1990), was the quarantine of fields which showed more than 2% infected grain. This measure was highly debated and refuted by scientists, because a highly contaminated soil with teliospores of the causal agent and where wheat is the main crop, restrictions on sowing wheat would not serve as a control measure, mainly because of the longevity of the teliospores in the soil. Although this restriction is no longer in effect (SAGARPA 2002), our objective was to evaluate the effect of different quantities of infected seed/kg for sowing on the natural incidence of Karnal bunt. Part of this work was presented at the Annual meeting of the American Phytopathological Society (Fuentes-Dávila 1995, 1996).

Materials and methods. The Experiments were conducted at the Norman E. Borlaug Experimental Station, previously known as CIANO, located in the Yaqui Valley, Sonora, Mexico (27°20´N, 105°55´W, elevation 39 masl), during the 1989–90 to 1994–95 crop seasons, in block 910 in a clay soil with pH 7.8. Plots consisted of 10-m rows with 10 beds of two rows sown with the susceptible cultivar Bacanora T88 (Salazar-Huerta and Fuentes-Dávila 1993) at the rate of 75 kg/ha. A set of treatments, which consisted of 5, 10, 100, 250, and 500 infected seeds/kg and an untreated, healthy check, were sown in the 1989–90 to 1993–94 crop seasong, and another set, consisting of 500, 1,000, 2,500, and 5,000 infected seeds/kg and the untreated, healthy check, with two replicated plots per season, were sown during the 1991–92 to 1994–95 seasons. The different treatments were repeated using the same land during the time of the study so as to determine the effect of adding a certain amount of infected seed on the natural incidence of the disease. To minimize the spread of teliospores from one plot to another during the different crop seasons, treatments were separated by untreated buffer plots, with the dimensions already described, and sown with the same susceptible cultivar. Each experiment also was established in a strip starting with the untreated check and, then, from the lowest to the highest rate. In addition, the only agricultural practices performed were harrowing and bed formation. The entire plots were harvested and the number of infected grains was determined by visual inspection, counting the number of infected and healthy grains.

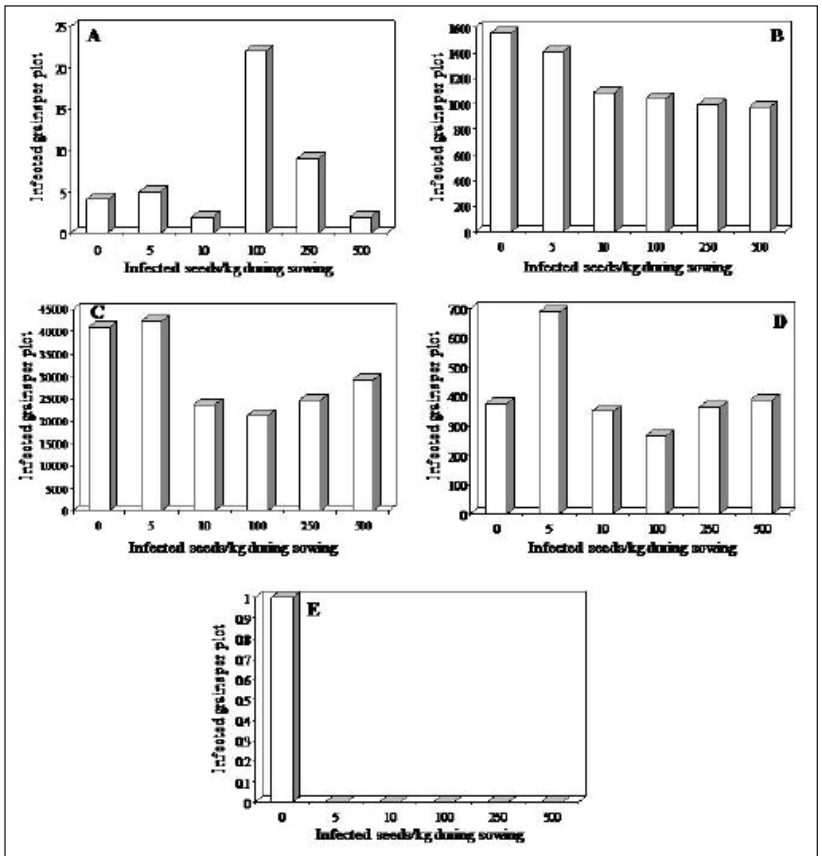

Fig. 6. Number of grains infected with Karnal bunt under natural infection from plots sown with 5–500 infected seed/kg of the susceptible cultivar Bacanora T88 in the Yaqui Valley, Sonora, Mexico, during the 1989–90 (A), 1990–91 (B), 1991–92 (C), 1992–93 (D), and 1993–94 (E) croping seasons.

Results. ***Low rates of infected seed.*** The total number of infected grain/plot was low during 1989-90 with a range of 2-22 (Fig. 6A). The greatest number of infected grains was obtained with the treatment of 100 seed/kg, however, the treatment

with 500 seed/kg had a little less than the check. In 1990–91, the range was 973–1,559, the check had the greatest number of infected grains and, as the rate increased, the number of infected grains decreased (Fig. 6B, p. 43). During 1991–92, disease incidence was even higher, with a range of 21,242–42,298, the highest being the treatment with 5 seed/kg followed by the check with 40,886, whereas the treatment with 500 seed/kg had 29,194 (Fig. 6C). During 1992–93, the range was 266–688; the treatment with 5 infected seed/kg had the greatest number of infected grains. The treatment with 100 infected seed/kg had the lowest number of infected grains, whereas the rest of the treatments were similar (Fig. 6D). During 1993–94, the only treatment that showed infected grains was the check with 1, and the rest did not show any infected grain (Fig. 6E).

High rates of infected seed. 1991-92. Replicate A. The total number of infected grains/plot was high during the 1991–92 growing season with a range of 4,126–5,523 (Fig. 7A). The greatest number of infected grains was obtained with the 5,000 treatment, followed by the 1,000 treatment. The check had the lowest number of infected grain. Replicate B. The outcome of this experiment was rather similar to replicate A; the highest number of infected grains was obtained with the treatment of 5,000, but followed by 500 (Fig. 7B). The check also had the lowest number of infected grains. 1992–93.

1992–93. Replicate A. The total number of infected grains/plot was moderate during this season with a range of 217–1,111 (Fig. 8A). The greatest number of infected grains was obtained with the check, followed by the plot with 1,000 infected grains. The lowest number of infected grains was obtained with the treatment of 5,000. ***Replicate B.*** As in the previous crop season, the outcome of this experiment was rather similar to replicate A; the highest number of infected grains was obtained with the check, but followed by the plot with 500 infected grains (Fig. 8B). The range was 221–921. The lowest number of infected grains was obtained with the treatment of 2,500 infected grains.

1994-95, Replicate A. No infected grains were found in any of the treatments of the two replicates in 1993–94 (Figs. 9A and 9B). The total number of infected grains/plot was high during this season, with a range of 5,052–10,190 (Fig. 10A, p. 45). The greatest number of infected grains was obtained with the check, followed by 1000. The lowest number of infected grains was obtained with the treatment of 5000. ***Replicate B.*** The greatest number of infected grains was obtained with the treatment of 1,000, followed by the check (Fig. 10B, p. 45). The lowest number of infected grains was obtained with the treatment of 5,000 infected grain.

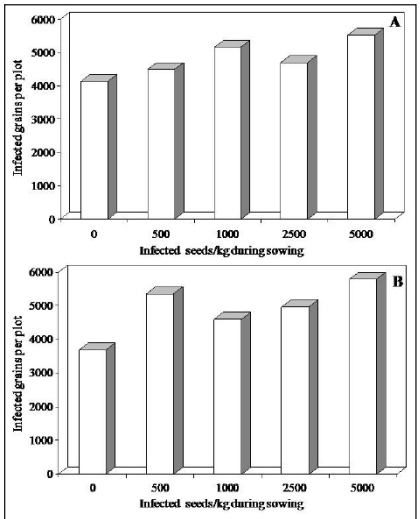

Fig. 7. Number of grains infected with Karnal bunt under natural conditions in plots sown with different numbers of infected seed/kg of the susceptible cultivar Bacanora T88 in the 1991–92 cropping season (A = replicate 1, B = replicate 2).

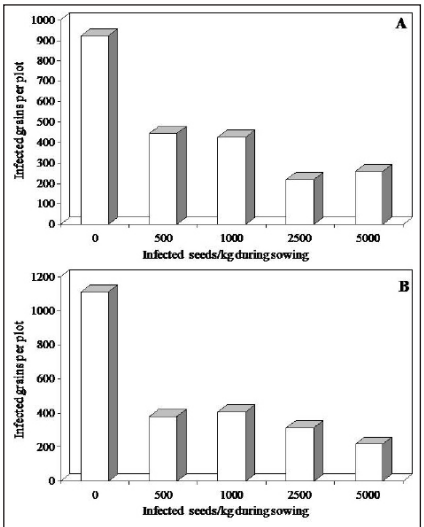

Fig. 8. Number of grains infected with Karnal bunt under natural conditions in plots sown with different numbers of infected seed/kg of the susceptible cultivar Bacanora T88 in the 1992–93 cropping season (A = replicate 1, B = replicate 2).

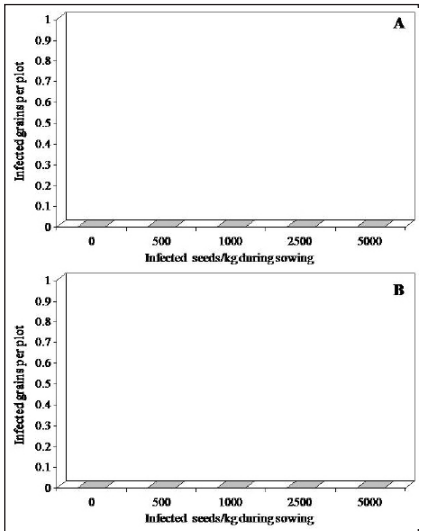

Fig. 9. Number of grains infected with Karnal bunt under natural conditions in plots sown with different numbers of infected seed/kg of the susceptible cultivar Bacanora T88 in the 1993–94 cropping season (A = replicate 1, B = replicate 2).

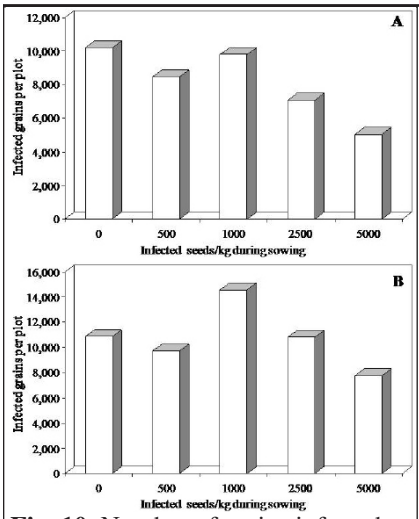

Fig. 10. Number of grains infected with Karnal bunt under natural conditions in plots sown with different numbers of infected seed/kg of the susceptible cultivar Bacanora T88 in the 1994–95 cropping season (A = replicate 1, B = replicate 2).

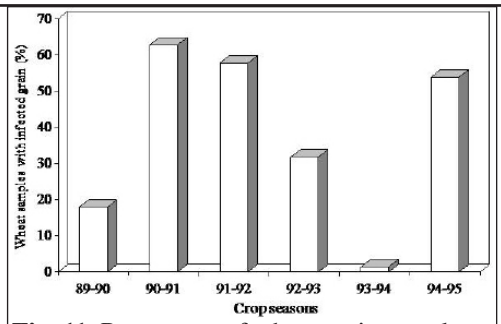

Fig. 11. Percentage of wheat grain samples infected with Karnal bunt during the 1989–90 to 1994–95 cropping seasons in the Yaqui Valley, Sonora, Mexico.

Karnal bunt incidence in the Yaqui Valley, Sonora, was low in 1989–90, high during 1990–91 and 1991–92, moderate during 1992–93, very low in 1993–94, and high again in 1994–95 (Fig. 11). Our results reflect those obtained in the surveysof the Department of Agriculture and the Local Councils of Plant Health in the Yaqui Valley during the 1989–90 to 1994–95 crop seasons. These results also confirm the observations and arguments that scientists have expressed in many meetings with plant health authorities of several countries. Based on the life cycle of *T. indica* and on accumulated experience, in an area where the soil is already contaminated with teliospores of *T. indica*, the use of infected seed for sowing, in this particular case ranging from 5 to 5,000 seeds/kg, does not influence a greater incidence of Karnal bunt.

Conclusions. Results of the experiments conducted during crop seasons 1989-90 to 1994-95, showed that using infected seed with karnal bunt for sowing, at rates ranging from 5 to 5000/kg, do not influence an increase on the incidence of the disease.

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ITEMS FROM PAKISTAN

NATIONAL AGRICULTURAL RESEARCH CENTER (NARC), ISLAMABAD
Wheat Wide Crosses and cytogenetics

ATTA-UR-RAHMAN SCHOOL OF APPLIED BIOSCIENCES (ASAB),
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Germplasm conservation prebreeding value addition for yield enhancement as a conduit to national food security for combating climate change and the 2050 vision.

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The importance of wheat as a food cereal is paramount, and the need to be on secure production grounds a national priority. Changing international scenarios around wheat production in light of productivity constraints and new sophisticated technologies necessitate that our researchers move with time and be proactive. This involves swift research program restructuring that generates outputs efficiently, is unique, and targets threats due to climate change that will impact food security issues in 2050, when a population surge touching 9.2 billion approximately 230 million of which will be Pakistan's share.

National wheat yields currently are 2.6 t/ha with annual productivity approaching 25 x 10^6 tones. Our 2015 goal is 30 x 10^6 tonnes and about 33 x 10^6 tones for 2030. Maximizing yields is a tall order, because a huge yield gap exists and the full varietal productivity potential near 9.0 t/ha is too distant. Despite cultivar releases that are high yielding, national yield levels remain stagnant, between 25–30 maunds/acre (2.5–3.0 t/ha) when the upper limit touchs about 8.4 t/ha, and close to 5 t/ha in irrigated and rainfed areas by progressive farmers. Policy setting and management play a vital role to counter this poor performance but, on the research horizon, stress constraints are a huge concern. The fear of seeing the migration of stem rust Ug99 in to Pakistan is one factor, another is the breakdown of yellow rust resistance that has occurred, and finally, the emergence of spot blotch in scattered locations in 2009 go hand in hand to motivate proresearchers to find solutions that can curb these new dangers. Exploiting genetic resources is a viable option and this taps the abundant genomic diversity of the annual and perennial Triticeae members across all three wheat gene pools.

Our Wide Cross Program is an offshoot of the CIMMYT program as Mujeeb-Kazi, who was the architect of the CIMMYT program and led it from 1979 until late 2004, has provided that program's basic outputs under the devolution concept that allowed CIMMYT to focus on their special tasks with our efforts to compliment the remaining wide cross activities. Over the years at CIMMYT, seed maintenance, viability, and distribution of stocks that earlier were major

gram mainstream activities have for some unknown reason weakened. Thus, we have increased our efforts in Pakistan to compliment the CIMMYT holdings so that stocks remain well authenticated and can be provided to researchers as user-friendly packages. Our efforts are categorized in this article by highlighting our holdings that have enormous national and international diversity exploitation value. We have gathered stocks from other sources, maintain them, and have them stored in the gene bank at the NARC. These stocks will, upon increase, become freely available under an MTA and shared after actual shipping costs are covered.

Our current focus during the on-going 2013–14 crop cycle is to have completed increase and storage of the germplasm (Table 1, p. 48) from which the NARC gene bank, after further increase, can distribute to users. The wide cross program will maintain a modest working collection.

Salient comments. The Wide Crossing Program covers various facets that embrace multidisciplinary aspects of wheat research and production geared to address food security issues that prevail within the country. Heavy reliance is given to harness novel genomic diversity that resides in the under-utilized Triticeae member resources. As a consequence, the program has embraced several multidisciplinary areas that can in a holistic manner deliver outputs that will augment wheat productivity specifics are as follows that are in force as a way forward:

Human resource development. This component is comprised of young professionals who are pursuing their academic degrees and conduct research on the programs genetic stocks, prebreding, and breeding materials aided by national support staff. The research directions currently are heavy on QTL and association mapping; digital imaging; application of allele-specific markers; utilizing genomic information from the WX germplasm; crop physiology targeted for heat, drought, and salinity tolerance traits; micronutrient profiles of iron, zinc, and phytic acid linked with phosphate uptake; and quality across complete rheology, but more on HMW (A-PAGE) and LMW (allele-specific markers).

Research area coverage. The multidisciplinary areas summarized above detail comprise cytology, cytogenetics, biochemical genetics, molecular genetics, doubled haploidy/tissue culture, crop physiology, prebreeding/breeding for major biotic and abiotic stresses, micronutrients, cereal quality, and the all-important water-use efficiency covering its availability and purity. Specific targets are to ensure that resistance/tolerance is available for all three rusts, Karnal bunt, heat/drought/salinity/sodicity blended with quality attributes across complete rheology parameters with a careful oversight that considers the lesser important stresses at this stage such as powdery mildew, spot blotch, and barley yellow dwarf virus, including aphids.

Keeping in view the current global scenario of technology development and availability of advances in genomic applications with availability of outsourcing opportunities around the 9K, 90K, and DArT genotyping platforms, our program focus has been intensified to concentrate on stringent phenotyping targets. This strategy has been adopted and partnerships are being established around relevant partners for relevant objectives.

Conclusions. The various articles that follow reflect our partners' contributions on various investigative areas that encompass the multidisciplinary research targets being evaluated.

Future awareness. After the emergence of the new stem rust race Ug 99 in 1999 in Uganda, its presence and anticipated spread became a serious threat to all neighboring countries and also for those in its migratory path. This led to the formation of the 'Global Rust Initiative' with the advocacy of late Dr. N.E. Borlaug. Variants of Ug99 developed and spread, but intensive global breeding efforts led to the release of numerous resistant cultivars to contain the pathogens possible damage on wheat productivity.

Recently, information has surfaced of stem rust infections in Ethiopia and Germany. This presence has been associated with climate change factors and, in Ethiopia, infections are not Ug99, whereas those in Germany are being studied. This presence will continue the vigilance by researchers to combat the new spread. Other minor diseases have an enormous potential to intensify and spread. Hence prebreeding, tapping the novel genomic diversity across all selected Triticeae members of the various gene pools, will be pivotal for maintaining yield output in the decades ahead and continuing our operating targets in anticipation that new alleles will be identified and pyramided to become a source of resistance that has durability.

Table 1. Germplasm maintained in NARC (2013–14), Islamabad, Pakistan

Germplasm	Detail	#	Germplasm	Detail	#
A-genome synthetics	2n=6x=42, AABBAA	194	Amphiploids		30
D-genome synthetics	2n=8x=42, AABBDD	1,014	Backcross 1	Self-fertile	19
Durums in synthetics	2n+4x=28, AABB	50	**Alien Addition Lines**		
Elite 1 DD synthetics	2n=6x=42, AABBDD	95	*Th. bessarabicum*	Complete, disomic	7
Elite 2 DD synthetics	2n=6x=42, AABBDD	34	*S. cereale*	Complete, disomic	7
DD Drought subset	2n=6x=42, AABBDD	23	*H. villosa*	disomic	6
DD Yellow Rust subset	2n=6x=42, AABBDD	40	**Translocation Stocks**		
DD Septoria subset	2n=6x=42, AABBDD	10	Seri 82 (T1BL·1RS and 1B)	10 of each	20
DD Scab subset	2n=6x=42, AABBDD	35	Bread wheat (T1BL·1RS and 1B)	17 wheats	34
DD Spot Blotch subset	2n=6x=42, AABBDD	34	Altar 84 (1B and T1BL·1RS)	10 of each	20
DD Salinity subset	2n=6x=42, AABBDD	13	Durum wheat (1B and T1BL·1RS)	6 wheats	12
DD synthetics (DArT)	2n=6x=42, AABBDD	241	**Genetic Stocks**		
DD Karnal subset	2n=6x=42, AABBDD	4	CS monosomics	Complete set	21
DD Waterlogging subset	2n=6x=42, AABBDD	4	Glennson monosomics	Complete set	21
Land Races : Pakistan	International Sub-Set	112	CS ditelocentrics		
Land Races : Core		200	CS nulli-tetrasomics		
Land Races : Iran			CS *phph*		
Land Races : Afghanistan			CS *PhPh*		
Pakistan's Historical set of Cultivars		115	CS *PhIPhI*		
Salinity tester set		24	Cappelli		
Wild Species			Cappelli *ph1cph1c*		
Ae. cylindrica			Solid stem		1
Ae. tauschii			Multiple ovaries		2
T. urartu			Long coleoptile		3
T. monococcum subsp. *aegilopoides*			Early flowering subset		8
T. monococcum subsp. *monococcum*			Crop Science Registrations		135
T. turgidum subsp. *dicoccum*			Wide cross bread wheat/synthetic		240
T. turgidum subsp. *dicoccoides*			Observation nursery	WXBWSHON	Varies yearly
T. aestivum subsp. *spelta*					
T. aestivum subsp. *sphaerococcum*					
T. turgidum subsp. *carthlicum*					
T. turgidum subsp. *polonicum*					
S. cereale					

Morphological and physiological characterization of BW/SH germplasm.

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For producing high-yielding wheat cultivars, the new D-genome diversity of synthetic wheats was utilized and improved advanced prebreding lines were selected. Fifty lines were studied further at the National Agricultural Research Center (NARC), Islamabad. Materials were observed for morphological and physiological parameters, such as canopy temperature, chlorophyll content, photosynthesis rate, transpiration rate, stomatal conductance (gs), internal CO_2, and water-use efficiency, that influence grain yield.

Seedling habit. Plant habit at growth stage GS:31 was observed according to Zadoks' scale (1974). Three different habits, erect (E), semi-erect (S), and prostrate (P), were noted.

Crop ground cover. The percentage of the soil surface enclosed by plant foliage is an imperative measure of crop establishment. Accessions with a high DGC are capable of capturing incident radiation, thereby escalating soil shading and declining soil evaporation, which elevates water-use efficiency and may improve competitiveness with weeds and potentially reduce soil erosion. DGC-based phenotyping was used on all 50 lines with the help of a DSC-S300 at a height of 1.5 m and Adobe Photoshop CS3 Extended software. Photoshop software includes the functionality required to perform and export the automated DGC used to determine DGC (Fig. 1).

Fig. 1. Original image before processing (top) and a black and white image of accession BW/SH 2 after Photoshop processing.

$$\%GC = (\text{Mean grey walue} / 255) \times 100$$

Leaf area. Leaf area was measured manually by measureing the length and width of flag leaf. The following formula was used for leaf area (Muller 1991):

$$\text{Leaf area} = \text{length} \times \text{width} \times 0.74$$

Waxiness. Existence of leaf and/or spike glaucousness is observed visually and recorded according to a 1–5 scale, where 1 = absent, 2 = low, 3 = medium, 4 = moderately high, and 5 = high waxiness (Rebetzke et al. 2012, Table 2, p. 50)

Digital imaging of seed. The phenology of seed was by digital analysis. Twenty-five seed from each accession were selected randomly and placed over a grid. Horizontal and vertical images were taken, and size, length, width perimeter, length-to-width ratio, and circularity calculated using the 'SMART GRAIN' software.

Physiological evaluation. ***Canopy temperature.*** Canopy temperature was measured during the boot stage on bright days during peak hours using an infrared thermometer MIKRON (I.R MAN) protocol (Pask et al. 2012).

Chlorophyll content measurement. Chlorophyll content at stage GS:32 was recorded by using a Minolta SPAD-502 instrument. Three readings were randomly recorded with arithmetic means.

Rate of photosynthesis, transpiration, internal CO_2, stomatal conductance from gas exchange, and water-use efficiency were recorded using an infrared gas analyzer (IRGA) on bright sunny days.

Multiple factor analysis. Morphological (plant habit, waxiness, digital ground cover percent, and leaf area), physiological (photosynthetic rate, rate of transpiration, internal CO_2, stomatal conductance, canopy temperature, and chlorophyll concentration index), and seed shape (area, perimeter, length, width, length/width ratio, circularity, and distance of intersection with center of gravity) parameters were analyzed as major factors along with sub-factors of each. We observed that all seed shape attributes have the same variability with leaf area and digital ground cover percent and are explained by multiple factor F1 (eigenvalue = 1.743). Variation in physiological characterization and plant habit are

explained by multiple factor F2 (eigenvalue = 1.093). Moreover, all the morphological, physiological, and seed shape attributes are explained with 38.668%, 23.289%, and 38.043%, respectively, by multiple factor F1 on the X-axis (Figs. 2 and 3).

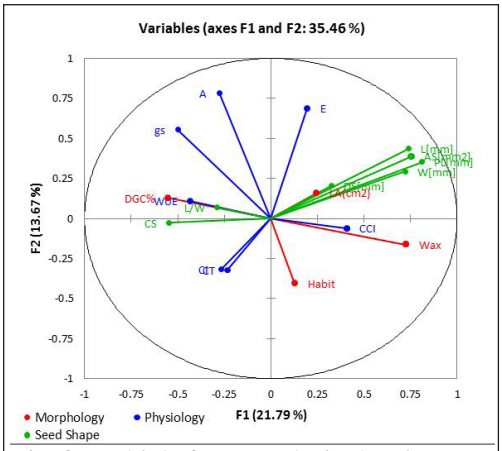

Fig. 2. Multiple factor analysis showing variability in all attributes analyzed.

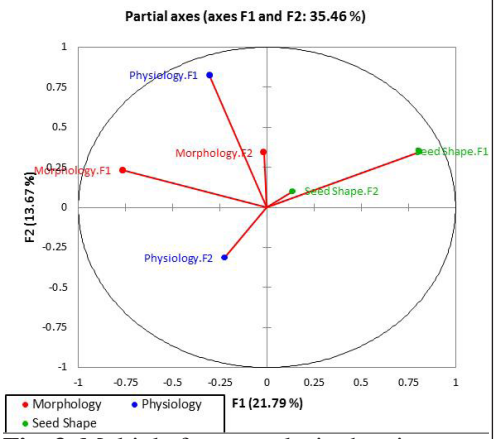

Fig. 3. Multiple factor analysis showing variability in subfactors.

Table 2. Pearson's correlation. Values in bold are different from 0 with a significance level of $\alpha = 0.05$. LA = leaf area (cm^2), Ci = internal CO_2, A = photosynthetic rate, E = transpiration rate, DI = gs = stomatal conductance from gas exchange, WUE = water-use efficiency, CT = canopy temperature, AS (mm^2) = seed area, PL = digital area of leaf (mm), L = seed length (mm), W = seed width (mm), L/W = length-to-width ratio, and CS = circularity, and DS = digital area of seed (mm).

	Wax	Habit	DGC%	LA (cm^2)	CCI	A	E	Ci	gs	WUE	CT	AS	PL	L	W	L/W	CS
Habit	0.203																
DGC%	–0.161	–0.091															
LA (cm^2)	0.024	–0.072	–0.242														
CCI	0.264	0.003	–0.179	–0.092													
A	–0.247	–0.038	0.158	–0.015	–0.138												
E	0.172	–0.100	0.063	0.114	–0.097	**0.476**											
Ci	–0.125	–0.119	0.083	–0.080	–0.034	**–0.515**	–0.222										
gs	**–0.349**	–0.151	0.240	–0.069	–0.112	**0.546**	**0.299**	0.397									
WEU	**–0.393**	0.051	0.085	–0.100	–0.017	**0.484**	**–0.522**	–0.246	0.280								
CT	–0.077	0.018	0.013	0.036	–0.058	–0.013	–0.233	–0.107	–0.162	0.175							
AS	**0.344**	–0.040	**–0.319**	0.083	**0.323**	0.057	0.230	–0.273	–0.140	–0.133	–0.276						
PL	**0.435**	–0.018	**–0.331**	0.085	**0.339**	0.023	0.222	–0.273	–0.175	–0.148	**–0.310**	**0.966**					
L	**0.381**	–0.084	**–0.291**	0.089	**0.349**	0.070	**0.309**	–0.190	–0.055	–0.188	**–0.327**	**0.937**	**0.952**				
W	**0.292**	–0.004	**–0.342**	0.152	0.230	0.010	0.114	**–0.280**	–0.209	–0.078	–0.216	**0.947**	**0.898**	**0.802**			
L/W	–0.019	–0.104	0.212	–0.151	0.047	0.089	0.197	0.227	**0.288**	–0.095	–0.050	**–0.409**	**–0.311**	–0.090	**–0.663**		
CS	**–0.480**	–0.052	0.198	–0.031	–0.228	0.118	–0.055	0.121	0.209	0.123	0.232	**–0.320**	**–0.552**	**–0.468**	–0.236	–0.187	
DS	0.240	**–0.339**	–0.060	0.204	0.199	–0.069	0.079	–0.058	–0.093	–0.106	–0.123	0.259	0.277	0.274	0.219	–0.022	–0.182

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Association analysis of agronomic traits in diverse wheat germplasm grown under water deficit conditions.

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Crop yield losses under water shortage require a genetic solution, because irrigation or other management practices cannot be considered as sustainable options for drought. Harnessing new alleles from the wheat wild relatives through interspecific and intergeneric hybridization are vital to achieve this goal (Mujeeb-Kazi et al. 2013). Various synthetic hexaploid wheats (derivatives) have resulted in significantly superior combinations of biotic/abiotic resistance/tolerance (Mujeeb-Kazi 2003). Association mapping (AM), which shows association between marker alleles and phenotypic traits, is now used extensively as an alternative approach to overcome the shortcomings of pedigree-based quantitative trait loci (QTL) mapping. The main theme in AM is to carry out genome-wide searches through panels of accessions having medium-to-high linkage disequilibrium (LD) levels for chromosomal regions harboring loci regulating the expression of particular phenotypic traits (Abdurakhmonov and Abdukarimov 2008; Sorrells and Yu 2009; Yao et al. 2009). We conducted a marker–trait association study based on the polymorphisms present at 101 SSR loci, each locus with at least two major alleles. We identified MTAs influencing agronomic performance of bread wheat germplasm, comprised of synthetic-derived (SBW) and conventional bread (CBW) wheat along with check cultivars (CCT), and grown across different soil moisture conditions. A series of chromosome areas significantly affected the variability of traits related to plant drought response, yield components (1,000-kernel weight), and grain yield are reported.

Comparisons among the three wheat groups are shown (Table 3). The SBW lines performed relatively much better than the corresponding check cultivars for most of the studied traits across both years. To sum up, we can say that SBW and CBW, collectively, were better in performance both under control irrigated and field-induced drought stress than the corresponding check cultivars. Furthermore, allelic introgression from *Ae. tauschii* into bread wheat did improve the expression of grain yield and related components. Therefore, synthetic-derived wheats are a promising source for improved yield and yield related traits. Water stress (drought), especially at anthesis, is considered the most important environmental stress factor in agriculture, resulting in decreased wheat yield. Drought stress affects the physiological processes in plants, including respiration, photosynthesis, and carbohydrate metabolism, ultimately reducing growth, grain set, and grain fill, resulting in reduced grain yield (Ji et al. 2010).

Table 3. Comparison of means among check cultivars (CCT) and synthetic-derived (SBW) and conventional (CBW) bread wheat under irrigated and drought stress.

Treatment	Germ-plasm	Plant height	Days-to-flowering	Days-to-physiological maturity	Spikes/ plant	Spike length (cm)	Grain/ spike	1,000-kernel weight (g)	Grain yield (g)
Irrigated	SBW	95.24	114.00	144.02	12.90	12.59	52.28	43.97	30.00
	CBW	93.92	116.85	146.15	12.24	12.35	53.35	43.16	27.98
	CCT	84.47	116.10	146.10	13.53	11.35	41.10	36.27	20.10
Stress	SBW	83.86	105.75	135.75	11.11	11.20	44.90	40.55	20.71
	CBW	82.22	108.58	137.95	9.97	11.14	45.84	38.93	17.71
	CCT	76.07	108.30	138.50	11.63	10.68	34.13	32.47	13.06
LSD for treatment		1.10***	0.83***	0.89***	0.47***	0.27***	1.45***	0.72***	1.32***
LSD for group		1.64***	1.25***	1.31***	0.60***	0.34**	1.81***	0.87***	3.10***
LSD for treatment*group		1.78***	1.39***	1.51***	0.80***	0.46***	2.36***	1.11***	3.10 NS

We compared the two model approaches for all studied traits (Table 4, p. 52). Higher MTA numberss (total 122) were found with the general linear model (GLM), whereas the mixed linear model (MLM) approach detected only 40 MTAs at $p < 0.05$. Consequently, the MLM approach detected 42.6% less MTAs than the corresponding GLM approach. Similarly, the number of MTAs at $p < 0.01$ was 40 and 27 with GLM and MLM approachs, respectively. Some markers

were associated specifically either to only one trait or to more traits. The number of significant MTAs that were similar in both approaches was 61 at $p > 0.05$ and 25 at $p < 0.01$. Some unique associations were found either only in the GLM or the MLM approach. The number of such unique MTAs at $p < 0.05$ was 61 (50.0%) for GLM and 9 (12.9%) for the MLM approach. At $p < 0.01$, the percentage of these specific MTAs in GLM was 37.5% (total 15), whereas MLM exhibited 7.4% (only two MTAs). At the same time, the effect was variable for individual studied traits and, in some instances, no prominent effects were observed for some of the studied traits. Similar findings have been discussed by Neuman et al. (2011) in their GWAS by genotyping a core collection (96) of wheat lines with DArT markers.

These results provide a stimulus for wheat breeders to exploit the germplasm for crop improvement. Developing improved cultivars with sufficient tolerance to drought stress and identifying osmotic stress related molecules and their roles in biochemical, physiological, and gene regulatory networks is necessary. Precise phenotyping is vital for screening larger core collection/mapping populations for exploring QTL and candidate genes to be used in plant breeding. This study adds strength for the genomic involvement capabilities to the A and B (S) resources via direct or synthetic hexaploids include tetraploids via pentaploid breeding and exploit the tertiary gene pool in a holistic manner for delivering practical outputs that are durable and an optimistic solution to address food security (Mujeeb-Kazi et al. 2013). Selection for high grain yield based on direct selection for grain weight is generally not desirable because of the limitations imposed by spike number/plant and grains/spike. Although some sort of compensation will always be there in any selection method, the major objective is to decrease it by finding the most appropriate yield component. Because synthetic-derived wheats maintain a comparatively high grain weight, especially under drought treatment, higher gain from selection would be expected when selecting for other components. Linkage mapping analysis in populations designed specifically for appropriate objectives will point out to what degree the AM identified regions play a role in particular genetic backgrounds.

Table 4. Comparison of the general linear model (GLM) and the mixed linear model (MLM) for calculation of associations between markers and traits.

Trait	No significant GLM at p ≤		No significant MLM at p ≤		Significant GLM and MLM at p ≤		GLM unique at p ≤		MLM unique at p ≤		MLM unique (%) at p ≤		GLM unique (%) at p ≤	
	0.05	**0.01**	**0.05**	**0.01**	**0.05**	**0.01**	**0.05**	**0.01**	**0.05**	**0.01**	**0.05**	**0.01**	**0.05**	**0.01**
Plant height	21	9	10	4	9	4	12	5	1	0	57.1	55.6	10.0	0.0
Days-to-flowering	8	2	6	1	3	1	4	1	2	0	50.0	50.0	33.3	0.0
Days-to-physiological maturity	21	7	17	8	16	7	5	0	1	1	23.8	0.0	5.9	12.5
Spikes/plant	14	3	8	4	8	3	7	0	1	1	50.0	0.0	12.5	25.0
Spike length	15	2	6	2	5	2	10	0	1	0	66.7	0.0	16.7	0.0
Grains/spike	8	3	5	2	4	2	4	1	1	0	50.0	33.3	20.0	0.0
1,000-kernel weight	20	11	10	4	8	4	12	7	2	0	60.0	63.6	20.0	0.0
Grain yield/plant	15	3	8	2	8	2	7	1	0	0	46.7	33.3	0.0	0.0
Total	**122**	**40**	**70**	**27**	**61**	**25**	**61**	**15**	**9**	**2**	**50.0**	**37.5**	**12.9**	**7.4**

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Available options to overcome food security issues in Pakistan in times of increasing water scarcity: I.

Zeshan Ali, A. Mohammad, M. Ahmad, Y. Riaz, R. Muhammad, Alvina Gul Kazi, H. Waheed, K. Anwaar, and A. Mujeeb-Kazi.

Wheat is recognized as the conduit to food security, and its ample production is significantly linked with water availability (Ali et al. 2013). Nearly all regions globally face water scarcity due to increasing population demands. Decline in this precious and limited resource is a major threat to the survival of mankind in terms of food security. Water resources are unevenly distributed globally; some regions face serious water shortages, whereas others have adequate water to sustain agricultural activities at an optimum (Pereira et al. 2002). Pakistan is a water-stressed country with an alarmingly low per capita water availability i.e. < 1,000 m^3 (Martin et al. 2006). Agriculture consumes most of Pakistan's available fresh water supplies (96%) for 86% of the total cultivable area (irrigated area) (Ali et al. 2014). The remaining 14% of the cultivable area is entirely rain-fed. Pakistan wheat production, targeting good agronomic practices, are hampered by water scarcity in irrigated and particularly in rain-fed agricultural areas. To ensure national food and fiber requirements by 2025 in connection with rapidly growing population, around 28–37 x 10^6 acre feet (MAF) of additional water will be required. Ensuring food security by maximizing wheat yield under declining available water assets is a challenging target that behooves national institutions to explore alternate water resources, e.g., reclamation of wastewater and rain water harvesting.

The Pakistan Agricultural Research Council (PARC), being an apex organization in rhw agriculture sector, was highly concerned about the gravity of water scarcity and the reclamation of wastewater for agricultural usage. Therefore, PARC initiated and developed a municipal wastewater reclamation facility at National Agricultural Research Center (NARC), Islamabad, to overcome water scarcity owing to its location in the rain-fed region. The municipal wastewater treatment facility (Bioremediation Orchard) is comprised of inter-connected constructed wetland and six detention ponds to cyclically treat wastewater through biological means under national environmental quality standards. Two large sedimentation ponds were constructed before the wastewater treatment facility to remove solid wastes. After sedimentation, wastewater was moved to the constructed wetland, which contained aquatic macrophytes, i.e., *Vetiver zizanoides*, *Phragmites australis*, and *Typha latifolia*, on top, and physical substrates beneath, i.e., gravel, boulders, brick pieces, sand, and crush. Wastewater treatment through a constructed wetland was a combination of physical and bioremediation processes. Effective microbe consortia (EM) also were applied in trickling filters of constructed wetland to support the wastewater treatment processes. Detention ponds contained floating aquatic plants, i.e., *Ceratophyllum demersum*, *Hydrocotyle umbellata*, *Pistia stratiotes*, *Lemna minor*, and *Eichhornia crassipes*, with phytoremediation being the dominant process for wastewater treatment. Some glimpses of this facility are illustrated (Fig. 4).

Fig. 4. The municipal wastewater treatment facility (Bioremediation Orchard) constructed wetlands (top left) with aquatic macrophytes *Pistia stratiotes* in a (upper left), *Hydrocotyle umbellata* (lower left), and *Lemna minor* (lower right) in detention ponds.

Water movement from sedimentation ponds to constructed wetland to detention ponds is under gravity with zero electrical or mechanical input. The whole bioremediation facility was underlined with UV stabilized polyethylene plastic sheets (500 microns thick) to avoid wastewater percolation to deeper soil profiles and the underground aquifer. This wastewater reclamation facility was spread over an area of 2.83 hectares operating at a hydraulic retention time

of 7 days. Treated water was approximately 0.67 x 10^6 gallons/day and irrigated 97.12 hectares through flood irrigation and 194.24 hectares through a high efficiency irrigation system. This technology was completely based on the indigenous resources and proved cost effective as well as environment friendly to overcome water scarcity within NARC premises (Farid et al. 2014). Comparison of untreated and treated wastewater characteristics are described (Table 5). Water quality in the reclaimed/treated water significantly improved with respect to the total coliforms, fecal coliforms, total hardness, chemical oxygen demand, biological oxygen demand, cadmium, and bicarbonate levels rendering this municipal wastewater fit for agricultural usage especially for wheat production in NARC with limited human and environmental health risks. Successful application of this wastewater reclamation technology at NARC and its subsequent utilization in wheat production has opened ways to overcome national water scarcity in rain-fed and irrigated areas. The adopted technology befits national agro-climatic regions and can greatly boost the area under cultivation particularly the rain-fed locations which will further help in ensuring food security in times of increasing water scarcity.

Table 5. Comparison of untreated and treated wastewater for wheat production at the municipal wastewater reclamation facility at the National Agricultural Research Center, Islamabad (NEQ = National Environmental Quality Standard).

Parameter	Unit	NEQ	Untreated wastewater	Treated wastewater
pH		6.5–8.5	8.4	7.5
Electrical conductivity	dS/m	0–3	1.206	0.740
Total dissolved solids	mg/L	0–2,000	884	560
Turbidity	FTU		201.00	19.03
Salinity	mg/L		0.9	0.3
Chloride (Cl^{-1})	mg/L	0–1,065	536.00	74.85
Calcium (Ca^{+2})	mg/L	200	84.10	42.02
Magnesium (Mg^{+2})	mg/L	150	67.00	32.19
Free CO_2	mg/L		0	0
Carbonate (CO_3^{-2})	mg/L	0–3	0.15	0.0
Bicarbonate (HCO_3^{-1})	mg/L	0–610	640	130
Nitrate (NO_3^{-2})	mg/L	0–30	12	6
Sulfate (SO_4^{-2})	mg/L	0–960	48.18	25.45
Chromium (Cr)	mg/L	1	0.10	0.04
Cadmium (Cd)	mg/L	0.1	0.09	0.03
Total coliforms	MPN/100 mL	0–1,000	≥1,600	110
Fecal coliforms	MPN/100 mL	0–1,000	≥1,600	80
Chemical oxygen demand	mg/L	150	192	45
Biological oxygen demand	mg/L	80	127	25

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Available options to overcome food security issues in Pakistan in times of increasing water scarcity: II.

Zeshan Ali, A. Mohammad, M. Ahmad, Y. Riaz, R. Muhammad, Alvina Gul Kazi, and A. Mujeeb-Kazi.

Variations in hydraulic retention time (HRT), type of constructed wetland, substrates/aquatic plants used in wetlands, and detention ponds can greatly influence the treatment efficiency of the bioremediation system (Ali et al., pp. 53-54, this publication; Ali et al. 2013; Farid et al. 2014). After successful completion of the municipal wastewater treatment project that generated 0.67 x 10^6 gallons/day, another bioremediation facility (The Bioremediation Garden) was designed

and developed to harvest wastewater generated by the NARC offices and its residential colony. The purpose of establishing this facility was to bring more acreage under an irrigated regime within the NARC research station in Islamabad. The engineering design for this facility varied from the earlier models, and contained only five detention ponds preceding the constructed wetland (Fig. 5). Detention ponds contained only *Pistia stratiotes* and *Eichhornia crassipes*, whereas the constructed wetland contained physical substrates coupled with *Phragmites australis* and *Typha latifolia*. This facility was over an area of 0.16 hectares treating 0.053 x 10^6 gallons/day and operated at an HRT of 5 days. The treated water is continuously utilized in the safe irrigation of the wheat crop within our NARC premises. Comparison of untreated and treated wastewater is shown (Table 6) and all investigated parameters are within national environmental quality standards in the treated water.

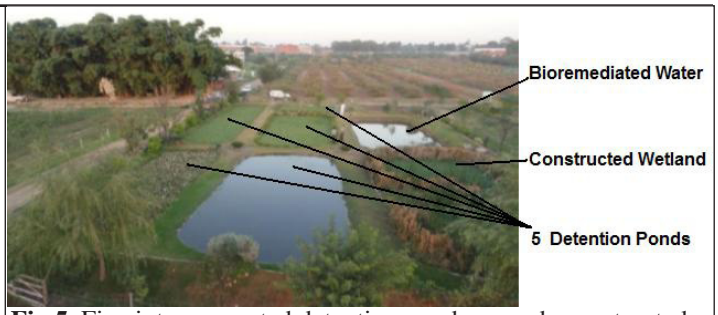

Fig 5. Five interconnected detention ponds precede constructed wetlands at the he Bioremediation Garden, National Agricultural Research Center, Islamabad.

Table 6. Comparison of untreated and treated wastewater for wheat production at the municipal wastewater reclamation facility at the National Agricultural Research Center, Islamabad (NEQ = National Environmental Quality Standard).

Parameter	Unit	NEQ	Untreated wastewater	Treated wastewater
pH		6.5–8.5	8.96	7.50
Electrical conductivity	dS/m	0–3	0.821	0.532
Total dissolved solids	mg/L	0–2,000	639	324
Turbidity	FTU		150.0	43.5
Chloride (Cl^{-1})	mg/L	0–1,065	236	47
Calcium (Ca^{+2})	mg/L	200	75	65
Magnesium (Mg^{+2})	mg/L	150	50.00	22.19
Free CO_2	mg/L		0	0
Carbonate (CO_3^{-2})	mg/L	0–3	0	0
Bicarbonate (HCO_3^{-1})	mg/L	0–610	450	320
Nitrate (NO_3^{-2})	mg/L	0–30	6.5	2.1
Sulfate (SO_4^{-2})	mg/L	0–960	41.0	30.5
Chromium (Cr)	mg/L	1	0.10	0.04
Cadmium (Cd)	mg/L	0.1	0.09	0.03
Total coliforms	MPN/100 mL	0–1,000	≥1,600	220
Fecal coliforms	MPN/100 mL	0–1,000	≥1,600	50
Chemical oxygen demand	mg/L	150	119	56
Biological oxygen demand	mg/L	80	98	66

Diverse, local aquatic flora is continuously monitored for phytoremediation potential and introduced in the existing detention ponds to optimize the bioremediation processes. Aptness of this wastewater treatment technology for national water scarce/limited regions is tremendous and urges ready devolution of this technology in our provincial areas such as Cholistan (Punjab) and Tharparkar (Sindh). These areas are truly rain-fed and currently suffering from famine like conditions leading to precious life losses. Increased wheat production in these areas only can be reached through increased fresh water supplies which currently are not feasible; however, biological reclamation of municipal wastewater may serve the purpose well. In Pakistan, 23 x 10^6 acre feet of wastewater is generated per annum, which, if treated wisely, can meet the national wheat crop irrigation demands. Allied research on wastewater quality, its biological treatment, and adequate utilization in wheat production can help meeting escalating population demands and ensuring food security issues imminent due to progressively declining water availability (Ali et al. 2013).

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Utilization and optimization of fourteen wheat quality standards for allocation of HMW glutenin subunits.

Hidayatullah, H. Ahmad, A. Ali, S.S. Lodhi, M. Jamil, Alvina Gul Kazi, and A. Mujeeb-Kazi.

Common wheat is a globally important agriculture crop that contributes significantly to human diet and is consumed in many diverse forms. Wheat is a staple food for about 40% of the world's population (Goyal and Prasad 2010; Peng et al. 2011). The wheat endosperm contains a major class of storage protein (glutenin) that plays a major role in bread making quality. These proteins are the foremost cause for the unique viscoelastic properties of wheat flour and dough. The polymeric glutenin proteins are separated into two subunit groups: high molecular weight glutenin subunits (HMW–GS) and low-molecular-weight glutenin subunits (LMW–GS), according to their motilities during sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS–PAGE).

HMW–GS have the largest effect on bread-making quality despite preserving only 10% of the total storage proteins, compared to the LMW–GS, which contribute about 40% of the total flour protein. The HMW–GS are encoded by dominant genes at the *Glu-1* locus, *Glu-A1*, *Glu-B1*, and *Glu-D1*, located on the long arms of chromosomes 1A, 1B, and 1D, respectively (Payne et al. 1984). Each locus contains two tightly linked genes (*Glu-1-1* and *Glu-1-2*) encoding two different types of subunits, one large (80–88 KDa) x-type and one small (67–73 KDa) y-type subunits (Mackie et al. 1996).

Bread wheat generally exhibits three to five HMW–GS that are separated by using SDS-PAGE (Payne et al. 1984). Variation in the number of these subunits results from some specific gene silencing. Apart from the silencing of specific genes that leads to variation in the subunit number, allelic variation in these subunits encoded by active genes results in proteins with different electrophoretic motilities (Payne 1987; Shewry et al. 2001). Such allelic variation composition at each locus was found to be strongly associated with the various HMW–GS.

Consequently, different subunits have been identified and characterized, and the significant association between some subunits and quality traits found (Gianibelli 2001). This information has been used for screening because these subunits are highly polymorphic in nature and not environmentally affected (Payne et al. 1981). The identification of specific HMW-GS alleles is, therefore, as an important target for improving wheat quality (Gale 2005).

An important area of our Wheat Wide Crosses and Cytogenetics program at the NARC, Islamabad, is the identification of specific HMW–GS alleles for quality improvement and selection of high quality genotypes for the major wheat breeding program. We made electrophoretic analyses on diverse wheat genotypes for optimizing and utilizing 14 different wheat standards to identify HMW–GS allelic variation (Table 7, Figs. 6 and 7, p. 57). These quality standards were used for allocating and optimizing allelic designations at the *Glu-1* loci using 7.5% gels. This base line standard array will be beneficial in our characterizing the large genomic stocks to be evaluated later (Figs. 6 and 7).

Table 7. Wheat standards used for allocating allele designations of high-molecular-weight glutenin subunits.

#	Stand cultivar	Subunit composition	Source
1	ACA 303	2* 7+8 5+10	Liu et al. 2008
2	Chinese Spring	N 7+8 2+12	Das et al. 2001
3	Amadina	1 7+9 5+10	Liu et al. 2008
4	Blue Sky	2* 7+8 5+10	Cornish 2005
5	Darius	2* 7+8 2+12	
6	Opata M-85	2* 13+16 2+12	Rabinovich et al. 2000
7	Gabo	2* 17+18 2+12	Branlard et al. 2003
8	Glenlea	2* 7+8* 5+10	Ng and Pogna 1989
9	Pavon	2* 17+18 5+10	Liu et al. 2008
10	Insignia	1 20 5+10	Branlard et al. 2003
11	Halberd	1 20 5+10	Anonymous 1998
12	Marquis	1 7+9 5+10	Graybosh 1992
13	Norin 61	2* 7+8 2.2+12	Hua et al. 2005
14	Seri M-82	1 7+9 5+10	Payne and Peña 2006

Seeds of these standards were obtained from CIMMYT, Mexico (Dr. R.J. Peña). These seeds have been planted in the Wheat Wide Crosses and Cytogenetics screen house NARC during the current growing cycle (2013–14) for increase and possible distribution at the national and international level.

Endosperm was used for the subunit assays with the corresponding embryos germinated and respective seedlings used to produce pure seed for future studies. All 14 standards, except Darius, matched their subunit

designation. We will maintain the entries in our wheat program. A 5-g sample of each entry will be supplied for storage in the NARC gene bank. Requests for 10 seed/sample will be sent upon covering shipping and handling costs.

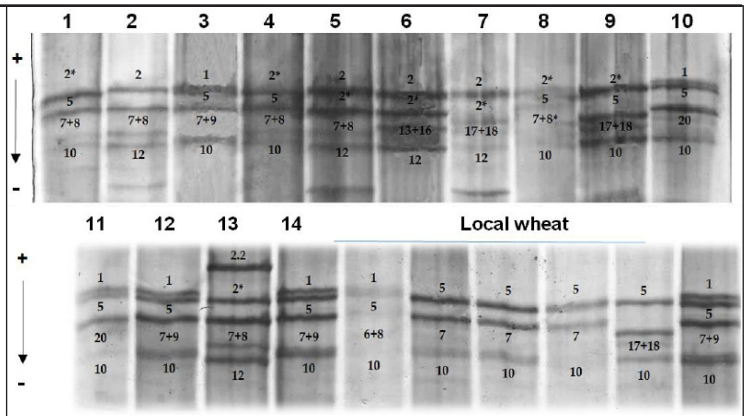

Fig. 6. Polyacrylamide gel electrophoresis profiles of high-molecular-weight glutenin subunit alleles of standard wheat cultivars.

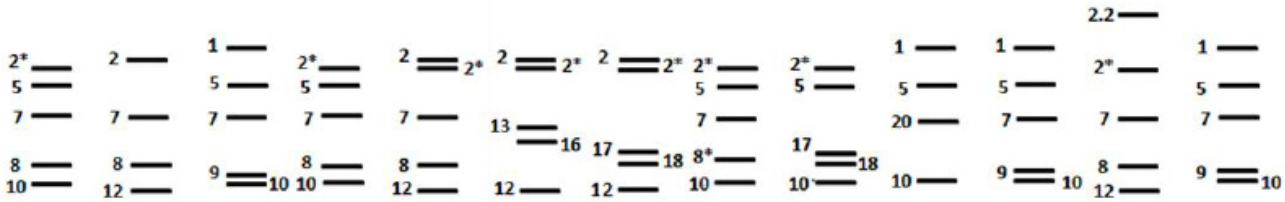

Fig. 7. Polyacrylamide gel electrophoresis profile of high-molecular-weight glutenin subunit alleles of standard wheat cultivars at the three *Glu-1* loci (L–R standards 1-14; because standards 10 and 11 are similar, cultivar 11 is not included.

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Genetic variation in diverse wheat germplasm for yield and yield-contributing traits.

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Wheat is the staple food for 35% of world's population (Ogbonnaya et al. 2013) and is, therefore, a key component of global food security (Mujeeb-Kazi et al. 2013). High wheat production may be achieved either by bringing more area under cultivation or enhancing yield per acre. Increasing the area under cultivation may possibly increase production but is not a feasible option, because global agricultural area is constantly decreasing due to urbanization, industrialization, soil salinization, and drought. Therefore, yield improvement is a plausible approach to enhance wheat production. Exploring the available genetic diversity can potentially lead to finding elite sources for inclusion in breeding for yield improvement. This study evaluated the extent of genetic diversity for individual yield traits in a diverse wheat germplasm.

The germplasm, consisting of 75 lines (Table 8), was evaluated under field conditions at National Agricultural Research Center (NARC), Islamabad, during the 2012–13 crop cycle in an augmented design. The material was hand-drilled in November 2012 in '6-m x 6-row' blocks with a row-to-row distance of 30 cm. The plant population/square meter square (plants/m^2) was 115. Standard cultural practices were followed to raise the crop to maturity. Data on days-to-maturity, plant height, tillers/plant, grains/spike, and spike length were recorded in March–April 2013 after physiological maturity. After harvesting, 1,000-kernel weight was recorded. Plant height was taken from the ground to the tip of top-most spike on three, randomly selected plants and averaged. Spike length was the average of three randomly selected plants. The number of spikes was taken from the three selected plants. Yield (g/m^2) was calculated by a formula ((yield (g/m^2) = number of plants/m^2 x number of tillers/plant x xumber of grains/spike x 1,000-kernel weight). Yield estimates for each genotype were g/m^2, using the number of plants/m^2 equal to 115 for all genotypes. The resulting data were extrapolated to t/ha. Data were analyzed in Excel 2010 for Summary Statistics. Traits showing considerably high genetic diversity were identified from the standard deviation.

Table 8. Germplasm type and number of genotypes evaluated for yield and yield-contributing traits. Source of germplasm is the CIMMYT and NARC Wheat Wide Crosses Programs.

Germplasm	# of genotypes
12x2	4
1x2	15
9x1	17
9x12	5
9x2	7
Ehydral	2
Kingbird	1
Mayoor/Ciano	2
Mayoor/Flycatcher	1
Mayoor/Opata	2
Nepal-AL	1
Sabuf/Ciano	4
Turaco/BCN	2
Turaco/Ciano	2
Turaco/Flycatcher	10
Total	**75**

Considerable genetic diversity was observed in almost all the quantitative traits under study (Table 9). The most notable variation was for plant height, grains/spike, grain yield, days-to-maturity, and 1,000-kernel weight. The higher the standard deviation of a trait, the higher was the genetic diversity of the material. This germplasm possesses enormous variation for these traits, which potentially can be utilized in future plant breeding. Decreased plant height is a desirable trait for abiotic stresses under irrigated planting, whereas reduced days-to-maturity is particularly important under terminal heat stress, which is vital under our conditions due to late wheat planting influenced by the cropping systems. Thousand-kernel weight supports overall yield potential of a cultivar.

Table 9. Variation in some quantitative traits of 75 wheat genotypes.

Variable	Mean	Minimum	Maximun	SD
Days-to-maturity	170.3	157.0	178.0	4.5
Plant height (cm)	99.9	68.0	131.0	9.3
Tillers/plant	9.9	7.0	14.0	1.5
Spike length (cm)	10.6	8.0	13.0	1.5
1,000-kernel weight (g)	37.3	28.0	50.0	4.3
Spikelets/spike	20.8	16.0	30.0	2.0
Grains/spike	62.3	48.0	90.0	6.1
Grain yield (g/m^2)	2,619.8	1,639.44	4,140.00	475.50
Grain yield (t/ha)	26.2	16.4	41.0	4.8

Recent findings on local wheat cultivars in Pakistan pinpoints the extent of variability and mean values obtained for a diverse set of wheat cultivars (Nawaz et al., 2013). Comparing our results to this study, we observed that our germplasm had promising wheat lines that outperformed. For example, cultivars Faisalabad-83 and SA-42 were outperformed by 46% for tillers/plant and 21.6% for grains/spike in our germplasm. Other traits, such as spikelets/plant, 1,000-kernel weight, and spike length, the best performing lines from our study out-performed the best (Nawaz et al. 2013) by 35%, 14%, and 11%, respectively.

Most notable results are those of grain yield (t/ha), which showed a remarkably high mean value compared to the current world record for wheat yield, i.e., 15.64 t/ha in the winter wheat cultivar Einstein, set by Mike Solari, a New Zealand farmer (http://www.farmersguardian.com/home/arable/arable-news/nz-farmer-beats-crop-world-record/31468).

The novel genetic diversity studied here is invaluable for breeding high yielding wheat cultivars for Pakistan, in particular, and globally via free germplasm exchange. The presence in the exploited germplasm has diversity from *Aegilops tauschii* (DD) and *Thinopyrum curvifolium* ($E^1E^1E^2E^2$), with several lines being resistant to other biotic stresses such as spot blotch, head scab, Karnal bunt, and *Septoria tritici*, making these lines a major parental source for recombination breeding around multiple stress resistance.

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Yield parameters of synthetic derivatives (bread wheat/synthetic hexaploid).

Farrukh Iqbal, M. Jamil, A.A. Napar, Z. Khan, S. Hussain, Alvina Gul Kazi, and A. Mujeeb-Kazi.

Synthetic derivatives of 269 lines were sown in the field at National Agricultural Research Center (NARC), Islamabad, during the 2012–13 crop cycle. Each line was grown in single, 1-m rows with a standard spacing. The rust-susceptible check cultivar Morocco, was sown after every 20 lines. Normal growing conditions were given and data was collected during May and after harvest. Only 260 of the 269 lines were successfully grown and data recorded for the following:

– Days-to-maturity was recorded when 50% of the plant color had turned golden brown.
– Fertile tillers of three plants were counted and averaged.
– Plant height (cm) was measured in centimeters from the ground to the tip of the spike (average for three spikes).
– Spike length (cm) of the main tiller of selected plants was measured from the base to the tip, excluding awns, and averaged.
– Spikelets/spike were counted from plants selected for spike length and averaged.
– Grains/spike of the main tiller were counted for each genotype after manual threshing.
– 1,000-kernel weight for each accession was determined by weighing 1,000-kernel samples from each line using an electronic balance.
– Karnal Bunt data was recorded by visual observation according to a scale of 1–5.

Data from 260 lines were recorded; 27 were selected on the basis of 1,000-kernel weight above 45 g (Table 10, p. 60). These 27 lines also are high yielding and will be used in further breeding programs. Entry number 23 has the highest weight and no rust, indicating resistance to biotic stress. Descriptive statistics were applied on 27 selected lines showing mean, standard error, mode, median, standard deviation, sample variance, range, minimum, maximum and sum of the data (Table 10). All selected lines had adult yellow rust scores ranging from 0 to 10 MRMS; only one plant was 60 MS.

Table 10. Descriptive statistics for in bread wheat/synthetic hexaploid derivatives.

Description	Mean	Standard Error	Median	Mode	Standard deviation	Sample variance	Range	Minimum	Maximum	Sum
Spike length (cm)	10.04	0.25	10	10	1.28	1.65	6	7	13	271
Plant height (cm)	90.22	1.28	91	82	6.68	44.71	23	79	102	2,436
Days-to-maturity	161.74	0.26	162	162	1.35	1.81	5	159	164	4,367
Tillers/plant	8.41	0.40	8	8	2.06	4.25	7	5	12	227
Spiklets/spike	20.15	0.28	20	19	1.43	2.05	5	18	23	544
Seeds/spike	58.11	1.65	61	61	8.59	73.87	30	44	74	1,569
1,000-kernel weight (g)	48.52	0.37	48	47	1.91	3.64	7	46	53	1,310

Exploitation of new genetic resources for water use efficiency and spot blotch (Cochliobolus sativus) resistance in bread wheat.

Muhammad Jamil, A. Ali, S. Hussain, A.A. Napar, K.F. Akbar, S. Asad, Alvina Gul Kazi, and A. Mujeeb-Kazi.

The food security vision for 2050 has put wheat production in the front line as the major conduit to provide for a global populace of 9.2 x 10^9. Thus, maximum yield is crucial and extremely challenging because the threat of climate change is significant. These changes can augment diminishing yield returns versus the influence of various abiotic (environmental) and biotic stresses. The latter encompass pathogen virulence shifts and migrations that lead to new stresses. One biotic stress that flared up in 2008–09 in parts of Pakistan was spot blotch. Two provinces of the country affected were the Upper Sindh and Lower Punjab. A major cultivar, Bhakkar, was consequently banned from subsequent cultivation and efforts to screen materials for resistance were initiated. We report our effort to assemble a wide germplasm array, including novel genomic diversity, as a first step to phenologically characterize a subset for future practical exploitation in the breeding targets.

One hundred lines of wheat diverse germplasm from CIMMYT nurseries 2012–13 were sown in three replicates then artificially inoculated with aggressive spore culture provided by the Crop Disease Research Institute at the National Agricultural Research Centre, Pakistan. This randomized complete block design and inoculation procedure followed that of Kumar et al. (2009). Data for plant habit was taken at growth stage GS:31 (Zadoks et al. 1974). At GS:32, the chlorophyll concentration index (CCI) was recorded using a Minolta SPAD-502 chlorophyll meter, and canopy temperature was measured by infrared thermometer MIKRON (IR-MAN) according to the set protocols by Pask et al. (2012). Using an infra-red gas analyzer, the rate of photosynthesis, transpiration rate, internal CO_2, and stomatal conductance was estimated.

Our results so far have enabled us to prescreen our germplasm on the basis of water use efficiency and chlorophyll concentration index. The purpose of the prescreening is to focus on broad-spectrum resistance regarding biotic and abiotic stress interactions. Because some master regulators relate biotic and abiotic stress responses in plants, a holistic approach must be used to identify and utilize broad spectrum stress tolerant genetic stocks (Atkinson and Urwin 2012).

For the phenological characters (Table 11, p. 61), we observed that the synthetic wheat line with *Ae. tauschii* has biotic and abiotic stress resistance in its pedigree; PBW343 and the back-cross derived line with Pastor are all abiotic stress tolerant, exhibit high water-use efficiency, and are candidate entries to be given high priority for biotic stress resistance utilization.

Significant correlation has been observed among rates of photosynthesis and transpiration, internal CO_2, and water-use efficiency (Table 12, p. 61). Plant habit also causes significant variation in stomatal conductance (Table 13, p. 61). Principal component and factor analysis for each generation are given (Table 14, p. 61).

In this ongoing study, the way forward will be disease scoring and genotyping through molecular marker application so that changes in these phenological characters during biotic stress can be mapped to explore the marker trait associations integrated with spot blotch resistance.

Table 11. Genotype from a set of 100 selected for eight with prominent attributes, especially water use efficiency.

Pedigree	#	Habit	Chlorophyll concentration index	Canopy temperature (°C)	Photosynthetic rate (μmol/m^2/s)	Transpiration rate (μmol/m^2/s)	Substomatal CO_2	Stomatal conductance	Water-use efficiency (μm CO_2/μm H_2O)
WBLL1*2/Kuruku//Heilo	45	2	49.03	20	14.31	1.30	27	0.10	11.01
PRL/2*Pastor	44	1	42.67	21	14.22	1.35	97	0.13	10.53
ROLF07*2/3/Prinia/Pastor//Huites	46	2	44.80	22	15.33	1.65	64	0.13	9.29
Kachu #1/Kiritati//Kachu	47	1	42.83	21	12.52	1.36	18	0.18	9.21
PBW343	43	1	43.30	22	9.82	1.11	101	0.08	8.85
D67.2/Parana 66.270//*Ae. tauschii* (320)/3/ Cunningham/4/VORB	16	1	43.27	20	13.35	1.54	53	0.10	8.67
Tacupetof 2001*2/Brambling//WBLL1*2/ Brambling	50	2	50.53	20	16.78	2.01	21	0.12	8.35
ROLF07*2/Diamondbird	65	2	44.07	20	13.71	1.65	56	0.08	8.31

Table 12. Correlation matrix (Pearson) for chlorophyll concentration index (CCI), canopy temperature (CT; °C), Photosynthetic rate (A; μmol/m^2/s), transpiration rate (E; μmol/m^2/s), substomatal CO_2 (C_I), and stomatal conducatance of H_2O (gs). Values in bold are different from 0 with a significance level alpha = 0.05.

Variable	Habit	CCI	CT	A	E	C_I	gs
CCI	0.119						
CT	–0.005	–0.098					
A	0.023	0.026	0.126				
E	0.048	–0.003	0.194	**0.566**			
C_I	–0.050	–0.066	–0.139	**–0.562**	–0.009		
gs	**0.257**	–0.136	0.127	0.066	0.093	0.000	
WUE	–0.033	0.038	–0.027	**0.569**	**–0.330**	**–0.620**	–0.019

Table 13. Single factor analysis of variance showing highly significant variation between habit and stomatal conductance

SOV	SS	MS	F	p
Habit	39.4139	19.70693	**15.25565**	**0.000002**
Error	125.3026	1.29178		
Total	164.7165			

Table 14. Principal component and factor analysis with eigenvalues and variability explained by each factor.

	F1	F2	F3	F4	F5	F6	F7	F8
Eigenvalue	2.218	1.555	1.197	1.130	0.865	0.649	0.370	0.015
Variability (%)	27.725	19.441	14.968	14.123	10.807	8.117	4.627	0.192
Cumulative %	27.725	47.166	62.134	76.257	87.064	95.181	99.808	100.000

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Seedling evaluation for salt tolerance in D-genome synthetic hexaploid wheats.

Zeeshan Khan, M. Jamil, A.A. Napar, F. Iqbal, J. Qazi, Alvina Gul Kazi, and A. Mujeeb-Kazi.

Common bread wheat is a hexaploid (AABBDD) originating by natural hybridization of *Triticum turgidum* (AABB) and *Aegilops tauschii* (DD) (Dvorak et al. 1998). To enhance diversity, D-genome, synthetic hexaploid wheats (SH) were developed (Ogbonnaya et al. 2013). Several superior SH combinations for both abiotic/biotic stress resistance/tolerance have been reported (Mujeeb-Kazi 2003). For diversity to salinity, heat and drought have surfaced as vital parameters to target for wheat varietal development due to prevalent environmental changes and need to maximize yield for tackling global food security issues.

Salinity tolerance in wheat varies greatly at different growth stages. Therefore, assessment of wheat salinity tolerance preferably should be carried out at important growth stages. This integrated approach will allow us to identify the wheat growth stage that greatly reduces the crop production. Salinity can cause a significant reduction in development of spike (Maas and Grieve 1990), tillering ability, spikelets/spike, and grains/spike (Grattan and Grieve 1992; Akram et al. 2002). Wheat yield starts to decline at 6–8 dS/m (Maas and Hoffman 1977).

In this initial study, a set of primary SH entries were screened. The germplasm used a set of 231 synthetic hexaploid wheats that have been genotyped with 2000 DArT markers, and the phenotypic data will be used for association mapping. This germplasm was sown at the Bio-Saline Agriculture Research Station, Pakka Anna, near Faisalabad, in the 2013–14 crop cycle and was planted in November 2013 (Fig. 8). This station is an ideal site for salinity screening. The water used for irrigation at this site also is saline, with an ECw range from 3–4 dS/m. The seed were sown in a randomized complete block design with three replications, a row-to-row distance of 30 cm, and a 1-m row length.

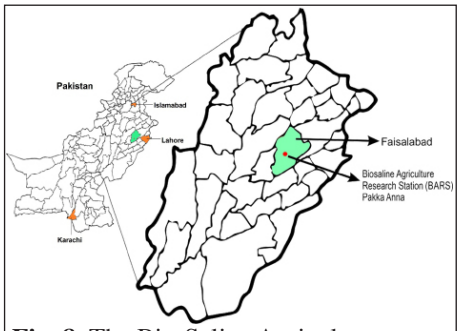

Fig. 8. The Bio-Saline Agriculture Research Station, Pakka Anna, near Faisalabad, Pakistan (longitude 73°05'E, latitude 31°24'N; elevation 190 m).

In vitro seedling growth was determined in an independent study carried out at Wheat Wide Crosses and Cytogenetic laboratory in NARC, Islamabad. Three treatments were used, one control (0 mM) and 2 NaCl treatments (75 mM and 150 mM). The top 19 genotypes are listed (Table 15, p. 63). The variability in frequency distribution is indicated in the histograms for height (Fig. 9, p. 63) and seedling weight (Fig. 10, p. 63) along with salt trait tolerance index (STTI). Pasban-91 and S-24 were used as tolerant checks and showed 17.91% and 41.37% STTI, respectively. PBW-343, with an STTI of 1.51%, was the susceptible check.

The centeral tendancy observed regarding seedling weight and height is that the treatments vary with the salt conentration.

An analysis of variance (Table 16, p. 64) for seedling height in 229 genotypes shows a highly significant variation in treatments and in genotypes along with their interaction, whereas the seedling weight was not significant.

Seedling height and the salt trait tolerance index show an 0.87 positive correlation coefficient, so regression highlights the relationship between seedling height and salt tolerance index with an $R^2 = 0.77$ variability explained.

Table 15. The top 19 of 226 genotypes with respect to the highest salt trait tolerance index (STTI %) for seedling height. * = *Aegilops tauschii* accession number of the WX working collection at CIMMYT, Mexico.

#	Germplasm	Pedigree	Genotype	Seedling height	STTI %
1	S-24	Local Check	2	2.00	41.37934
2	AUS30288	CROC_1/*Ae. tauschii* (466)*	12	5.83	35.71429
3	AUS34263	ARLIN_1/*Ae. tauschii* (225)	158	5.50	29.46429
4	AUS34262	ALTAR 84/*Ae. tauschii* (224)	157	5.00	27.77778
5	AUS34242	CPI/GEDIZ/3/GOO//JO69/CRA/4/*Ae. tauschii* (208)	137	4.50	26.73267
6	AUS34444	CROC_1/*Ae. tauschii* (210)	214	4.33	25.24272
7	AUS34264	GAN/*Ae. tauschii* (236)	159	4.50	24.54545
8	AUS33393	DVERD_2/*Ae. tauschii* (507)	95	2.50	23.07692
9	AUS30671	RASCON/*Ae. tauschii* (314)	76	3.67	21.56863
10	AUS34273	LARU/*Ae. tauschii* (309)	168	3.00	20.93023
11	AUS30664	GARZA/BOY//*Ae. tauschii* (281)	69	2.33	20.89552
12	AUS33398	CETA/*Ae. tauschii* (170)	100	2.50	20.83333
13	AUS34433	DOY1/*Ae. tauschii* (447)	203	3.50	20.00000
14	AUS34411	SORA/*Ae. tauschii* (211)	181	3.33	19.60784
15	AUS34443	CROC_1/*Ae. tauschii* (784)	213	3.16	19.58763
16	AUS34270	GARZA/BOY//*Ae. tauschii* (286)	165	3.00	19.14894
17	AUS34455	D67.2/P66.270//*Ae. tauschii* (213)	225	2.50	18.98734
18	AUS33405	GAN/*Ae. tauschii* (285)	107	3.16	18.44660
19	Pasban-90	Local check	1	2.00	17.91044

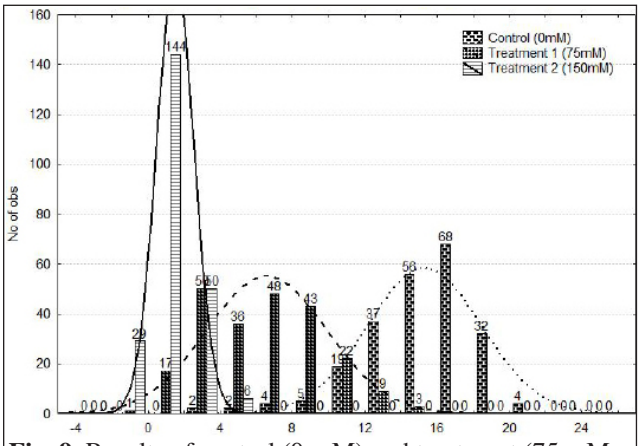

Fig. 9. Results of control (0 mM) and treatment (75 mM and 150 mM) effects on seedling height. In the control, (56+37) 93 genotypes ranged from 12 to 16 cm and (68+32) 100 genotypes ranged from 16 to 20 cm. In the 75 mM treatment (36+48) 84 genotypes ranges between 4–8 cm and (43+22) 65 genotypes ranged between 8–12 cm. In the 150 mM treatment, (144+50) 194 genotypes ranged from 0 to 4 cm and six genotypes were above 4 cm.

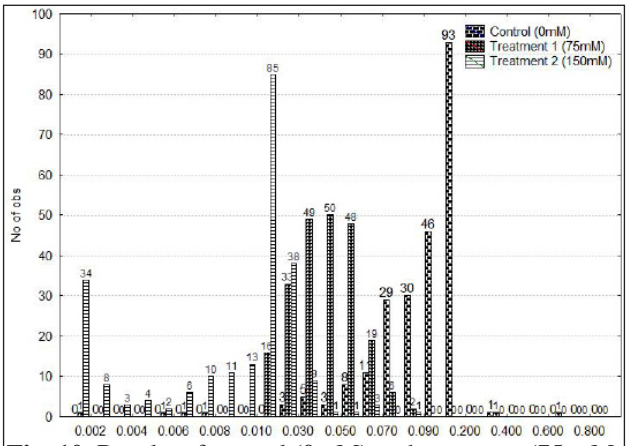

Fig. 10. Results of control (0mM) and treatment (75 mM and 150 mM) effects on seedling weight. In the control (29+30) 59 genotypes ranged between 0.07–0.09 g and (46+93) 139 genotypes ranged between 0.09–0.20 g. In the 75 mM treatment, (49+50) 99 genotypes ranged from 0.03–0.05 g and (48+19) 67 genotypes ranged from 0.05–0.07 g. In the 150 mM treatment, (85+38) 123 genotypes ranged between 0.01–0.03 g and nine genotypes are above 0.03 g.

The model equation for the salt trait tolerance index is:
STTI = 8.79+5.20*SH (cm)

From the equation obtained after regression analysis, we concluded that seedling height is directly proportional to the salt trait tolerance index (Fig. 11, p. 64).

Table 16. Analysis of variance highlighting significance in height of seedling; weight is nonsignificant.

		Seedling height (cm)				Seedling weight (g)			
	n	SS	MS	F	*p*	SS	MS	F	*p*
Genotype	228	8,771.7	38.5	16.26	0.00	1,150.93	5.04796	1.000689	0.487663
Treatment	2	66,218.4	33,109.2	13,991.82	0.00	11.26	5.63204	1.116476	0.327728
Genotype*treatment	456	6,206.0	13.6	5.75	0.00	2,300.45	5.04484	1.000072	0.494527
Error	1,374	3,251.3	2.4			6,931.12	5.04448		
Total	2,060	84,447.4				10,393.76			

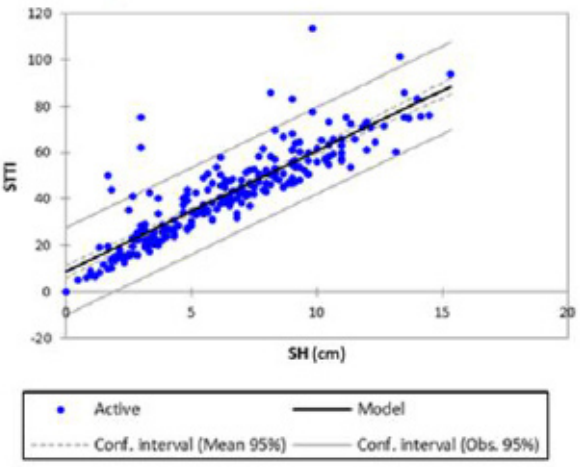

Fig. 11. Regression of salt trail tolerance index by seedling height (cm) ($R^2 = 0.770$).

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Digital imaging of selected landraces of Pakistan.

Sumaira S. Lodhi, Namra Haq, Peter John, Attya Bhatti, Alvina Gul Kazi, S. George, M. Jamil, and A. Mujeeb-Kazi.

Wheat improvement is based on harnessing genetic resource diversity that resides in the closely or distantly relatives of cereals within the primary, secondary, and tertiary gene pools. Detailed coverage on integrating such variability in wheat breeding programs was recently reviewed (Mujeeb-Kazi et al. 2013; Ogbonnaya et al. 2013). Germplasm within the primary gene pool is of high priority, because genetic affinity is high and recombination via homologous association is at a maximum. Landraces fall in this category and have been underutilized in wheat improvement. Reports from ICARDA showed the potential for barley landrace improvement, and we gain impetus from that effort to exploit the resources for wheat. This study covers a major segment of breeding value that targets seed size and shape.

Seed shape and size are one of the most important agronomic traits due to their effect on yield, eating quality, and market price. Plant research in genetics, functional analysis, and genomics can also benefit from quantitative evaluation of seed shape (Tanabata et al. 2012). In general, seed shape is scored in either manually or with computational methods. The manual method simply involves measuring seed length and width with callipers, but this method has a number of disadvantages. Computational methods, on the other hand, use digital imaging technology that enables one to automatically measure a variety of shape parameters of very small size in high-resolution images (Brewer et al. 2006; Bylesjö et al. 2008; Weight et al. 2008; French et al. 2009; Wang et al. 2009).

The progress in phenotyping is not at the same level as compared to high-throughput genotyping. More accurate, efficient, and high-throughput phenotyping in order to get maximum benefit from low-cost genotyping resources are needed (Houle et al. 2010). Photometric measurements or digital imaging provide briefer and cheaper phenotypic numbers and better elucidate the separate components of complex traits. Digital imaging is the process that converts images of plant organs into quantitative data. This process can increase the process of phenotyping, thus helping

to swiftly generate a large set of quantitative data. This method converts photographs into quantitative data based upon a measure of axes or pixel count. Digital imaging has the ability to demonstrate the dimensions of grain morphology contributing to grain weight and size. In wheat, these measurements might relate to traits such as yield or milling quality, which, in other ways, are quite costly to evaluate. Based upon this information, wheat seed shape might influence the possible endosperm to bran ratio. Thus, this process is important in providing us with the opportunity to evaluate the phenotypic and genetic components of seed, such as the wheat kernel.

We collected 211 landraces from different regions of Pakistan for this study (Table 17, pp. 65-69). All the accessions were photographed using a Nikon D5100 digital camera. Twenty-five sound and well developed seeds of each genotype were visually selected. Seeds were placed horizontally and vertically on black paper to provide color contrast (Figs. 12 and 13). Two photographs were taken at ~40 pixels/mm. All photographs were named according to accession and serial number.

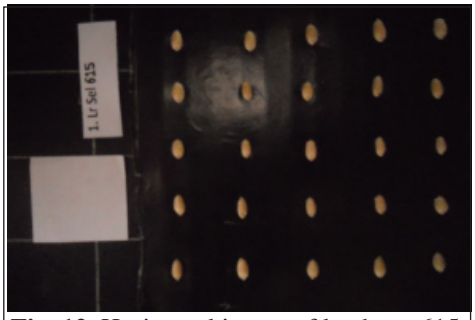

Fig. 12. Horizontal image of landrace 615.

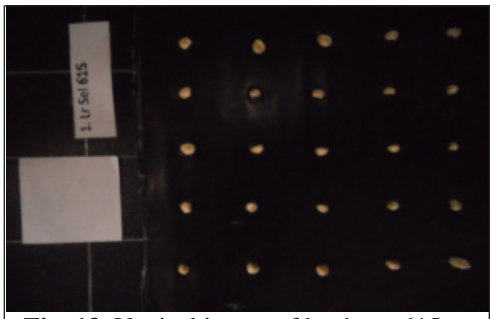

Fig. 13. Vertical image of landrace 615.

Table 17. Detail of landrace germplasm evaluated by digital imaging for seed shape and size.

#	Name	Detail
1	LRSEL 615	018836 *T. aestivum* PARC/MAFF 004290(01) 6/3/2001 Pakistan NWFP Swat Marghazar 1200
2	LRSEL 626	018849 *T. aestivum* PARC/MAFF 004297(04) 6/4/2001 Pakistan NWFP Chitral Bradam 1980
3	LRSEL 404	012103 *T. aestivum* PARC/JICA 003313(01) 6/1/1994 Pakistan NWFP Abbottabad Biroth 0920
4	LRSEL 406	012105 *T. aestivum* PARC/JICA 003315(01) 6/1/1994 Pakistan AJK Muzaffarabad Chattar 0750
5	LRSEL 620	018842 *T. aestivum* PARC/MAFF 004294(01) 6/4/2001 Pakistan NWFP Dir Darorah 1070
6	LRSEL 437	012219 *T. aestivum* PARC/JICA 003839(02) 7/1/1996 Pakistan NWFP Chitral Awilasht 2225
7	LRSEL 332	012012 *T. aestivum* PARC/JICA 003203(01) 6/1/1994 Pakistan NWFP Abbottabad Tarhanagala 1240
8	LRSEL 411	012116 *T. aestivum* PARC/ICARDA 003045(02) 5/1/1993 Pakistan Balochistan Kharan Karki/Kirichi 1250
9	LRSEL 619	018842 *T. aestivum* PARC/MAFF 004294(01) 6/4/2001 Pakistan NWFP Dir Darorah 1070
10	LRSEL 340	012021 *T. aestivum* PARC/JICA 003212(01) 6/1/1994 Pakistan NWFP Mansehra College Durai 0975
11	LRSEL 30	012010 *T. aestivum* PARC/JICA 003201(01) 6/1/1994 Pakistan NWFP Abbottabad Nawan Shehar 1135
12	LRSEL 321	011855 *T. aestivum* PARC/KUJ 002255(07) 10/1/1989 Pakistan AJK Muzaffarabad Pataka 0800
13	LRSEL 327	011931 *T. aestivum* PARC/NIAR 002827(02) 10/18/1991 Pakistan N. A. Gakuch Hatoon 1930
14	LRSEL 193	011521 *T. aestivum* PARC/IBPGR 001188(02) 10/1/1985 Pakistan Balochistan Awaran Jibri 1040
15	LRSEL 612	018833 *T. aestivum* PARC/MAFF 004288(06) 6/3/2001 Pakistan NWFP Swat Allahabad 1000
16	LRSEL 627	018850 *T. aestivum* PARC/MAFF 004297(05) 6/4/2001 Pakistan NWFP Chitral Bradam 1980
17	LRSEL 396	012079 *T. aestivum* PARC/JICA 003285(01) 6/1/1994 Pakistan F. A. Islamabad Pind begwal 0570
18	LRSEL 614	018835 *T. aestivum* PARC/MAFF 004289(02) 6/3/2001 Pakistan NWFP Swat Mena 1120
19	LRSEL 398	012081 *T. aestivum* PARC/JICA 003287(01) 6/1/1994 Pakistan F. A. Islamabad Pind begwal 0570
20	LRSEL 405	012104 *T. aestivum* PARC/JICA 003314(01) 6/1/1994 Pakistan AJK Muzaffarabad Kahala 0680
21	LRSEL 409	012114 *T. aestivum* PARC/ICARDA 003044(03) 5/1/1993 Pakistan Balochistan Kharan Chadman 1380
22	LRSEL 401	012084 *T. aestivum* PARC/JICA 003290(01) 6/1/1994 Pakistan F. A. Islamabad Karor 0990
23	LRSEL 394	012077 *T. aestivum* PARC/JICA 003283(01) 6/1/1994 Pakistan F. A. Islamabad Sary Chowk 0600
24	LRSEL 397	012080 *T. aestivum* PARC/JICA 003286(01) 6/1/1994 Pakistan F. A. Islamabad Pind begwal 0570
25	LRSEL 469	012284 *T. aestivum* PARC/JICA 003853(01) 7/1/1996 Pakistan N. A. Diamer Dazar 1595
26	LRSEL 455	012244 *T. aestivum* PARC/JICA 003691(01) 5/1/1996 Pakistan NWFP Buner Guswanda 0890
27	LRSEL 462	012269 *T. aestivum* PARC/JICA 003716(01) 6/1/1996 Pakistan NWFP Kohistan Patan 0820
28	LRSEL 634	018858 *T. aestivum* PARC/MAFF 004301(01) 6/4/2001 Pakistan NWFP Chitral Korepine 1500
29	LRSEL 402	012085 *T. aestivum* PARC/JICA 003291(01) 6/1/1994 Pakistan F. A. Islamabad Karor 1230
30	LRSEL 395	012078 *T. aestivum* PARC/JICA 003284(01) 6/1/1994 Pakistan F. A. Islamabad Pind begwal 0570
31	LRSEL 400	012083 *T. aestivum* PARC/JICA 003289(01) 6/1/1994 Pakistan F. A. Islamabad Karor 0990
32	LRSEL 485	012321 *T. aestivum* PARC/JICA 003892(01) 7/1/1996 Pakistan N. A. Ghanche Hushe 3280
33	LRSEL 457	012249 *T. aestivum* PARC/JICA 003697(01) 6/1/1996 Pakistan NWFP Swat Bekar 1430

Table 17. Detail of landrace germplasm evaluated by digital imaging for seed shape and size.

#	Name	Detail
34	LRSEL 459	012258 *T. aestivum* PARC/JICA 003705(01) 6/1/1996 Pakistan NWFP Swat Guza Sala 1200
35	LRSEL 625	018848 *T. aestivum* PARC/MAFF 004297(01) 6/4/2001 Pakistan NWFP Chitral Bradam 1970
36	LRSEL 236	011590 *T. aestivum* PARC/ICARDA/OSU 001306(01) 7/1/1986 Pakistan N. A. Gilgit Chalt 1660
37	LRSEL 314	011805 *T. aestivum* PARC/NIAR 002460(01) 5/1/1990 Pakistan N. A. Gilgit Masoth 1940
38	LRSEL 635	018859 *T. aestivum* PARC/MAFF 004301(03) 6/4/2001 Pakistan NWFP Chitral Korepine 1500
39	LRSEL 623	018846 *T. aestivum* PARC/MAFF 004296(01) 6/4/2001 Pakistan NWFP Dir Kotke 1280
40	LRSEL 6	011155 *T. aestivum* PARC/SVP 000197(01) 5/1/1981 Pakistan Balochistan Quetta Miangundi 1750
41	LRSEL 316	011807 *T. aestivum* PARC/NIAR 002461(01) 5/1/1990 Pakistan N. A. Gilgit Ali Abad 2180
42	LRSEL 581	018799 *T. aestivum* PARC/MAFF 6/2/2001 Pakistan NWFP 004277(01) Swat Shangla Pass 1940
44	LRSEL 244	011599 *T. aestivum* PARC/ICARDA/OSU 001315(05) 7/1/1986 Pakistan N. A. Gilgit Moor Khund 2480
45	LRSEL 461	012266 *T. aestivum* PARC/JICA 003714(01) 6/1/1996 Pakistan NWFP Dir Tormang 0950
46	LRSEL 638	018863 *T. aestivum* PARC/MAFF 004301(08) 6/4/2001 Pakistan NWFP Chitral Korepine 1500
48	LRSEL 195	011529 *T. aestivum* PARC/ICARDA 001210(02) 6/14/1986 Pakistan Balochistan Mastung Rangi Took 1860
49	LRSEL 308	011799 *T. aestivum* PARC/NIAR 002459(01) 5/1/1990 Pakistan N. A. Skardu Hanuchal 1420
50	LRSEL 163	011435 *T. aestivum* PARC/IBPGR 000610(07) 6/1/1982 Pakistan AJK Muzaffarabad Chibar 1550
52	LRSEL 309	011800 *T. aestivum* PARC/NIAR 5/1/1990 Pakistan N. A. 002459(02) Skardu Hanuchal 1420
53	LRSEL 307	011798 *T. aestivum* PARC/NIAR 002458(01) 5/1/1990 Pakistan N. A. Gilgit Parri 1350
54	LRSEL 145	011393 *T. aestivum* PARC/IBPGR 000593(04) 4/1/1982 Pakistan NWFP D.I. Khan Yarik 0300
55	LRSEL 151	011423 *T. aestivum* PARC/IBPGR 000604(03) 6/1/1982 Pakistan AJK Muzaffarabad Sharian 1250
56	LRSEL 310	011801 *T. aestivum* PARC/NIAR 002459(03) 5/1/1990 Pakistan N. A. Skardu Hanuchal 1420
57	LRSEL 311	011802 *T. aestivum* PARC/NIAR 002459(04) 5/1/1990 Pakistan N. A. Skardu Hanuchal 1420
58	LRSEL 389	012072 *T. aestivum* PARC/JICA 6/1/1994 Pakistan NWFP 003274(01) Nowsehra Pubbai 0290
59	LRSEL 392	012075 *T. aestivum* PARC/JICA 003277(01) 6/1/1994 Pakistan NWFP Nowsehra Pubbai 0290
60	LRSEL 385	012068 *T. aestivum* PARC/JICA 003268(01) 6/1/1994 Pakistan NWFP Malakand Durgai 0370
61	LRSEL 380	012063 *T. aestivum* PARC/JICA 003258(01) 6/1/1994 Pakistan NWFP Dir Rany 0830
62	LRSEL 190	011505 *T. aestivum* PARC/IBPGR 000936(06) 8/1/1983 Pakistan N. A. Gilgit Gulmit 2550
63	LRSEL 383	012066 *T. aestivum* PARC/JICA 003263(01) 6/1/1994 Pakistan NWFP Malakand Bat Khela 0670
64	LRSEL 384	012067 *T. aestivum* PARC/JICA 003266(01) 6/1/1994 Pakistan NWFP Malakand Durgai 0490
65	LRSEL 393	012076 *T. aestivum* PARC/JICA 003282(01) 6/1/1994 Pakistan F. A. Islamabad Sary Chowk 0600
66	LRSEL 312	011803 *T. aestivum* PARC/NIAR 002459(05) 5/1/1990 Pakistan N. A. Skardu Hanuchal 1420
67	LRSEL 408	012108 *T. aestivum* PARC/JICA 003320(01) 6/1/1994 Pakistan NWFP Abbottabad Turmothian 1280
68	LRSEL 152	011424 *T. aestivum* PARC/IBPGR 000605(01) 6/1/1982 Pakistan AJK Muzaffarabad Kucha 1010
69	LRSEL 379	012062 *T. aestivum* PARC/JICA 003256(01) 6/1/1994 Pakistan NWFP Dir Tamargarah 0770
70	LRSEL 386	012069 *T. aestivum* PARC/JICA 003270(01) 6/1/1994 Pakistan NWFP Mardan Rashakai 0320
71	LRSEL 387	012070 *T. aestivum* PARC/JICA 003271(01) 6/1/1994 Pakistan NWFP Mardan Rashakai 0320
72	LRSEL 388	012071 *T. aestivum* PARC/JICA 003272(01) 6/1/1994 Pakistan NWFP Mardan Rashakai 0320
73	LRSEL 334	012014 *T. aestivum* PARC/JICA 003205(01) 6/1/1994 Pakistan NWFP Abbottabad Tarhanagala 1240
74	LRSEL 362	012045 *T. aestivum* PARC/JICA 6/1/1994 Pakistan 003236(01) NWFP Swat Jaray 1230
75	LRSEL 685	018979 *T. aestivum* PARC/MAFF 004416(01) 4/28/2002 Pakistan NWFP Lakki Marwat Darra Jang 0470
76	LRSEL 331	012011 *T. aestivum* PARC/JICA 003202(01) 6/1/1994 Pakistan NWFP Abbottabad Nawan Shehar 1160
77	LRSEL 375	012058 *T. aestivum* PARC/JICA 003252(01) 6/1/1994 Pakistan NWFP Dir Talash 0890
78	LRSEL 358	012041 *T. aestivum* PARC/JICA 003231(01) 6/1/1994 Pakistan NWFP Swat Charbagh 1030
79	LRSEL 651	018880 *T. aestivum* PARC/MAFF 6/5/2001 Pakistan NWFP Chitral 004307(05) Green Lasht 1810
80	LRSEL 220	011571 *T. aestivum* PARC/ICARDA/OSU 001276(01) 7/22/1986 Pakistan N. A. Gilgit Hurmay 1850
81	LRSEL 246	011601 *T. aestivum* PARC/ICARDA/OSU 001318(01) 7/1/1986 Pakistan N. A. Gilgit Shakyot 1540
82	LRSEL 675	018926 *T. aestivum* PARC/MAFF 004360(01) 4/21/2002 Pakistan NWFP Lakki Marwat Basti Sultan Abad 0510
83	LRSEL 295	011783 *T. aestivum* PARC/NIAR 002598(07) 11/1/1989 Pakistan Balochistan Mastung Haji Ka 1720
84	LRSEL 333	012013 *T. aestivum* PARC/JICA 003204(01) 6/1/1994 Pakistan NWFP Abbottabad Tarhanagala 1240
85	LRSEL 319	011810 *T. aestivum* PARC/NIAR 002463(02) 5/1/1990 Pakistan N. A. Gilgit Rahimabad 1740
86	LRSEL 376	012059 *T. aestivum* PARC/JICA 003253(01) 6/1/1994 Pakistan NWFP Dir Talash 0890
87	LRSEL 245	011600 *T. aestivum* PARC/ICARDA/OSU 001317(01) 7/1/1986 Pakistan N. A. Gilgit Nafora Baseem 1320
88	LRSEL 496	013176 T. sp PARC/IBPGR 001189(04) 10/1/1985 Pakistan Balochistan Awaran Aladam 1100
89	LRSEL 234	011587 *T. aestivum* PARC/ICARDA/OSU 001295(01) 7/1/1986 Pakistan N. A. Baltistan Hajigam 2160
90	LRSEL 518	018688 *T. aestivum* PARC/PGRI 004104(01) 4/30/1999 Pakistan Punjab Chakwal Pind Kattha 0290
91	LRSEL 523	018693 *T. aestivum* PARC/PGRI 004109(01) 5/1/1999 Pakistan Punjab Chakwal Chakwal 0790

Table 17. Detail of landrace germplasm evaluated by digital imaging for seed shape and size.

#	Name	Detail
92	LRSEL 609	018830 *T. aestivum* PARC/MAFF 004288(03) 6/3/2001 Pakistan NWFP Swat Allahabad 1000
93	LRSEL 655	018884 *T. aestivum* PARC/MAFF 004308(03) 6/5/2001 Pakistan NWFP Chitral Kuragh 1910
94	LRSEL 616	018837 *T. aestivum* PARC/MAFF 004291(01) 6/3/2001 Pakistan NWFP Swat Islamapur 1090
95	LRSEL 621	018843 *T. aestivum* PARC/MAFF 004295(01) 6/4/2001 Pakistan NWFP Dir Chukiatan 1180
96	LRSEL 622	018844 *T. aestivum* PARC/MAFF 004295(04) 6/4/2001 Pakistan NWFP Dir Chukiatan 1180
97	LRSEL 242	011597 *T. aestivum* PARC/ICARDA/OSU 001314(03) 7/1/1986 Pakistan N. A. Gilgit Khaibar 2450
98	LRSEL 502	018667 *T. aestivum* PARC/MAFF 004271(01) 6/2/2001 Pakistan NWFP Swat Shangla 1600
99	LRSEL 357	012040 *T. aestivum* PARC/JICA 003230(01) 6/1/1994 Pakistan NWFP Swat Charbagh 1030
100	LRSEL 522	018692 *T. aestivum* PARC/PGRI 004108(01) 4/30/1999 Pakistan Punjab Chakwal Buchal Kalan 0680
101	LRSEL 247	011602 *T. aestivum* PARC/ICARDA/OSU 001319(02) 7/1/1986 Pakistan N. A. Gilgit Gitch 1660
102	LRSEL 438	012222 *T. aestivum* PARC/JICA 003841(01) 7/1/1996 Pakistan NWFP Chitral Hircheen 2830
103	LRSEL 342	012023 *T. aestivum* PARC/JICA 003214(01) 6/1/1994 Pakistan NWFP Mansehra Kotli Bala 0960
104	LRSEL 444	012228 *T. aestivum* PARC/JICA 003850(01) 7/1/1996 Pakistan NWFP Chitral Wadoos 1910
105	LRSEL 343	012025 *T. aestivum* PARC/JICA 003214(03) 6/1/1994 Pakistan NWFP Mansehra Kotli Bala 0960
106	LRSEL 674	018925 *T. aestivum* PARC/MAFF 004359(01) 4/21/2002 Pakistan NWFP Tank Pathan Colony 0490
107	LRSEL 443	012227 *T. aestivum* PARC/JICA 003849(01) 7/1/1996 Pakistan NWFP Chitral Gorapon 1685
108	LRSEL 417	012123 *T. aestivum* PARC/ICARDA 003066(04) 5/1/1993 Pakistan Balochistan Mastung Kolpur 1780
109	LRSEL 418	012144 *T. aestivum* PARC/SVP 000236(02) 6/1/1981 Pakistan Balochistan Ziarat Zandra 2100
110	LRSEL 281	011766 *T. aestivum* PARC/NIAR 002516(06) 10/1/1989 Pakistan N. A. Skardu Keris 2200
111	LRSEL 413	012119 *T. aestivum* PARC/ICARDA 003050(04) 5/1/1993 Pakistan Balochistan Kharan Baront 1250
112	LRSEL 359	012042 *T. aestivum* PARC/JICA 003232(01) 6/1/1994 Pakistan NWFP Swat Charbagh 1030
113	LRSEL 288	011776 *T. aestivum* PARC/NIAR 002591(02) 11/1/1989 Pakistan Balochistan Mastung Kahnak 1500
114	LRSEL 640	018865 *T. aestivum* PARC/MAFF 004302(02) 6/4/2001 Pakistan NWFP Chitral Chitral 1520
115	LRSEL 639	018864 *T. aestivum* PARC/MAFF 004302(01) 6/4/2001 Pakistan NWFP Chitral Chitral 1520
116	LRSEL 305	011796 *T. aestivum* PARC/NIAR 002456(01) 5/1/1990 Pakistan N. A. Chilas Ganni 1110
117	LRSEL 414	012120 *T. aestivum* PARC/ICARDA 003056(03) 5/1/1993 Pakistan Balochistan Kalat Jangan Wal 1830
119	LRSEL 210	011561 *T. aestivum* PARC/ICARDA/OSU 001264(01) 7/20/1986 Pakistan N. A. Gilgit Rai Kot 0950
122	LRSEL 381	012064 *T. aestivum* PARC/JICA 003260(01) 6/1/1994 Pakistan NWFP Dir Khal 0880
123	LRSEL 449	012233 *T. aestivum* PARC/JICA 003683(01) 5/1/1996 Pakistan NWFP Abbottabad Banda Sahib Khan 0910
124	LRSEL 645	018873 *T. aestivum* PARC/MAFF 004305(03) 6/5/2001 Pakistan NWFP Chitral Kosht 1600
125	LRSEL 617	018838 *T. aestivum* PARC/MAFF 004291(02) 6/3/2001 Pakistan NWFP Swat Islamapur 1090
126	LRSEL 399	012082 *T. aestivum* PARC/JICA 003288(01) 6/1/1994 Pakistan F. A. Islamabad Pind begwal 0570
127	LRSEL 679	018932 *T. aestivum* PARC/MAFF 004367(01) 4/21/2002 Pakistan NWFP Lakki Marwat Sarai Naurang 0560
128	LRSEL 296.	011787 *T. aestivum* PARC/NIAR 002450(01) 5/1/1990 Pakistan NWFP Malakand Malakand 0700
129	LRSEL 302	011793 *T. aestivum* PARC/NIAR 002452(04) 5/1/1990 Pakistan NWFP Swat Abuha 0810
130	LRSEL 652	018881 *T. aestivum* PARC/MAFF 004307(06) 6/5/2001 Pakistan NWFP Chitral Green Lasht 1810
131	LRSEL 636	018860 *T. aestivum* PARC/MAFF 004301(04) 6/4/2001 Pakistan NWFP Chitral Korepine 1500
132	LRSEL 328	011932 *T. aestivum* PARC/NIAR 002828(03) 10/20/1991 Pakistan NWFP Chitral Laspur Brook 2740
133	LRSEL 656	018885 *T. aestivum* PARC/MAFF 004308(04) 6/5/2001 Pakistan NWFP Chitral Kuragh 1910
134	LRSEL 301	011792 *T. aestivum* PARC/NIAR 002452(02) 5/1/1990 Pakistan NWFP Swat Abuha 0810
135	LRSEL 303	011794 *T. aestivum* PARC/NIAR 002453(01) 5/1/1990 Pakistan NWFP Swat Kandaray 1300
136	LRSEL 306	011797 *T. aestivum* PARC/NIAR 002457(01) 5/1/1990 Pakistan N. A. Chilas Governer Farm 1180
137	LRSEL 416	012122 *T. aestivum* PARC/ICARDA 003062(01) 5/1/1993 Pakistan Balochistan Quetta Hanna Lake 2000
138	LRSEL 658	018776 *T. aestivum* PARC/MAFF 004265(02) 6/1/2001 Pakistan NWFP Abbottabad Ferozabad 1240
139	LRSEL 153	011425 *T. aestivum* PARC/IBPGR 000605(02) 6/1/1982 Pakistan AJK Muzaffarabad Kucha 1010
140	LRSEL335	012016 *T. aestivum* PARC/JICA 003207(01) 6/1/1994 Pakistan NWFP Abbottabad Nika Pani 1195
141	LRSEL 135	011338 *T. aestivum* PARC/SVP 000431(01) 6/1/1981 Pakistan Balochistan Chagai Kitgai 0550
142	LRSEL 204	011547 *T. aestivum* PARC/ICARDA 001230(01) 6/17/1986 Pakistan Balochistan Pinhin Malang Abad 1380
143	LRSEL 351	012034 *T. aestivum* PARC/JICA 003224(01) 6/1/1994 Pakistan NWFP Mansehra Basi 1270
144	LRSEL 576	018794 *T. aestivum* PARC/MAFF 004273(01) 6/2/2001 Pakistan NWFP Swat Banjaar 1060
145	LRSEL 637	018861 *T. aestivum* PARC/MAFF 004301(06) 6/4/2001 Pakistan NWFP Chitral Korepine 1500
146	LRSEL 580	018798 *T. aestivum* PARC/MAFF 004276(01) 6/2/2001 Pakistan NWFP Swat Shangla Pass 2020
147	LRSEL 339	012020 *T. aestivum* PARC/JICA 003211(01) 6/1/1994 Pakistan NWFP Abbottabad Kalandar Abad 1250
148	LRSEL 320	011813 *T. aestivum* PARC/NIAR 002464(02) 5/1/1990 Pakistan N. A. Gilgit Juglote 1300
149	LRSEL 113	011312 *T. aestivum* PARC/SVP 000395(01) 5/1/1981 Pakistan Balochistan Chagai Lashkar Aab 0900

Table 17. Detail of landrace germplasm evaluated by digital imaging for seed shape and size.

#	Name	Detail
150	LRSEL 650	018879 *T. aestivum* PARC/MAFF 004306(08) 6/5/2001 Pakistan NWFP Chitral Burnes 1800
151	LRSEL 344	012027 *T. aestivum* PARC/JICA 003215(01) 6/1/1994 Pakistan NWFP Mansehra Rattar 1410
152	LRSEL 647	018875 *T. aestivum* PARC/MAFF 004306(01) 6/5/2001 Pakistan NWFP Chitral Burnes 1800
153	LRSEL 129	011332 *T. aestivum* PARC/SVP 000426(03) 6/1/1981 Pakistan Balochistan Ziarat Spinzandi 2280
154	LRSEL 348	012031 *T. aestivum* PARC/JICA 003218(01) 6/1/1994 Pakistan NWFP Mansehra Lilishan 1530
155	LRSEL 453	012238 *T. aestivum* PARC/JICA 003687(01) 5/1/1996 Pakistan NWFP Mansehra Hansherian 0850
156	LRSEL 578	018796 *T. aestivum* PARC/MAFF 004274(02) 6/2/2001 Pakistan NWFP Swat Rahimabad 1280
157	LRSEL 589	018809 *T. aestivum* PARC/MAFF 004280(02) 6/2/2001 Pakistan NWFP Swat Madyan 1340
158	LRSEL 25	011185 *T. aestivum* PARC/SVP 000220(01) 5/1/1981 Pakistan Balochistan Kharan 0800
159	LRSEL 72	011249 *T. aestivum* PARC/SVP 000261(05) 6/1/1981 Pakistan Balochistan Quetta Spezand 1710
160	LRSEL 587	018807 *T. aestivum* PARC/MAFF 004279(05) 6/2/2001 Pakistan NWFP Swat Khawaza Khala 1100
161	LRSEL 73	011252 *T. aestivum* PARC/SVP 000264(02) 6/1/1981 Pakistan Balochistan Quetta Near Lakh pass 1740
163	LRSEL 15	011171 *T. aestivum* PARC/SVP 000211(02) 5/1/1981 Pakistan Balochistan Kalat Halizai 1630
164	LRSEL 144	011392 *T. aestivum* PARC/IBPGR 000594(04) 4/1/1982 Pakistan NWFP D.I. Khan 0305
165	LRSEL 201	011543 *T. aestivum* PARC/ICARDA 001225(04) 6/17/1986 Pakistan Balochistan Quetta Baleli 1400
166	LRSEL 591	018811 *T. aestivum* PARC/MAFF 004281(01) 6/2/2001 Pakistan NWFP Swat Bahrain 1400
167	LRSEL 86	011274 *T. aestivum* PARC/SVP 000362(01) 5/1/1981 Pakistan Balochistan Pishin Sabura Post 2200
168	LRSEL 38	011200 *T. aestivum* PARC/SVP 000229(01) 5/1/1981 Pakistan Balochistan Pishin Barozai 1570
169	LRSEL 505	018671 *T. aestivum* PARC/PGRI 004082(01) 4/28/1999 Pakistan NWFP Chakwal Talial 0700
170	LRSEL 575	018793 *T. aestivum* PARC/MAFF 004270(03) 6/1/2001 Pakistan NWFP Mansehra Chappargram 1100
171	LRSEL 649	018877 *T. aestivum* PARC/MAFF 004306(03) 6/5/2001 Pakistan NWFP Chitral Burnes 1800
172	LRSEL 16	011172 *T. aestivum* PARC/SVP 000211(03) 5/1/1981 Pakistan Balochistan Kalat Halizai 1630
173	LRSEL 28	011188 *T. aestivum* PARC/SVP 000223(01) 5/1/1981 Pakistan Balochistan Chagai Nushki 1250
174	LRSEL 58	011229 *T. aestivum* PARC/SVP 000247(02) 6/1/1981 Pakistan Balochistan Loralai 1820
175	LRSEL 454	012240 *T. aestivum* PARC/JICA 003688(01) 5/1/1996 Pakistan NWFP Mansehra Khar Mang Bala 1300
176	LRSEL 594	018814 *T. aestivum* PARC/MAFF 004282(02) 6/3/2001 Pakistan NWFP Swat Rahmet 1540
177	LRSEL 143	011391 *T. aestivum* PARC/IBPGR 000595(02) 4/1/1982 Pakistan NWFP D.I. Khan 0360
178	LRSEL 212	011563 *T. aestivum* PARC/ICARDA/OSU 001266(01) 7/21/1986 Pakistan N. A. Gilgit Sakowar 1400
179	LRSEL 26	011186 *T. aestivum* PARC/SVP 000221(01) 5/1/1981 Pakistan Balochistan Kharan 1070
180	LRSEL 138	011341 *T. aestivum* PARC/SVP 6/1/1981 Pakistan Balochistan 000436(03) Chagai Kitaka 0950
181	LRSEL 586	018806 *T. aestivum* PARC/MAFF 004279(04) 6/2/2001 Pakistan NWFP Swat Khawaza Khala 1100
182	LRSEL 663	018894 *T. aestivum* PARC/MAFF 004311(01) 6/6/2001 Pakistan NWFP Chitral Bamburet 2010
183	LRSEL 664	018896 *T. aestivum* PARC/MAFF 004312(02) 6/6/2001 Pakistan NWFP Chitral Bamburet 1900
184	LRSEL 205	011549 *T. aestivum* PARC/ICARDA 001236(03) 6/18/1986 Pakistan Balochistan Pinhin Gawal 1570
185	LRSEL 76	011256 *T. aestivum* PARC/SVP 000265(05) 6/1/1981 Pakistan Balochistan Quetta 1720
186	LRSEL 95	011290 *T. aestivum* PARC/SVP 000377(01) 5/1/1981 Pakistan Balochistan Pishin Sheikh Wasil 1550
187	LRSEL 105	011303 *T. aestivum* PARC/SVP 000390(01) 5/1/1981 Pakistan Balochistan Chagai Peeshok 0850
188	LRSEL 7	011156 *T. aestivum* PARC/SVP 000198(01) 5/1/1981 Pakistan Balochistan Mastung Bolan 1630
189	LRSEL 209	011560 *T. aestivum* PARC/ICARDA 001261(01) 6/24/1986 Pakistan Balochistan Qila Saifullah – 1380
190	LRSEL 648	018876 *T. aestivum* PARC/MAFF 004306(02) 6/5/2001 Pakistan NWFP Chitral Burnes 1800
191	LRSEL 642	018868 *T. aestivum* PARC/MAFF 004303(03) 6/5/2001 Pakistan NWFP Chitral Kari 1510
192	LRSEL 666	018913 *T. aestivum* PARC/MAFF 004353(03) 4/20/2002 Pakistan NWFP D.I. Khan Darahan 0420
193	LRSEL 590	018810 *T. aestivum* PARC/MAFF 004280(03) 6/2/2001 Pakistan NWFP Swat Madyan 1340
195	LRSEL 583	018801 *T. aestivum* PARC/MAFF 004278(01) 6/2/2001 Pakistan NWFP Swat Sherai 1150
196	LRSEL 391	012074 *T. aestivum* PARC/JICA 003276(01) 6/1/1994 Pakistan NWFP Nowsehra Pubbai 0290
197	LRSEL 570	018788 *T. aestivum* PARC/MAFF 004269(01) 6/1/2001 Pakistan NWFP Mansehra Chattar Plain 1560
198	LRSEL 572	018790 *T. aestivum* PARC/MAFF 004269(03) 6/1/2001 Pakistan NWFP Mansehra Chattar Plain 1560
199	LRSEL 657	018886 *T. aestivum* PARC/MAFF 004309(01) 6/5/2001 Pakistan NWFP Chitral Cherun 1900
200	LRSEL 114	011313 *T. aestivum* PARC/SVP 000396(01) 5/1/1981 Pakistan Balochistan Chagai Isa Chah 0930
201	LRSEL 451	012235 *T. aestivum* PARC/JICA 003684(02) 5/1/1996 Pakistan NWFP Abbottabad Tanan Gali 1240
202	LRSEL 103	011301 *T. aestivum* PARC/SVP 000388(01) 5/1/1981 Pakistan Balochistan Chagai Cheattar 0850
203	LRSEL 62	011236 *T. aestivum* PARC/SVP 000253(01) 6/1/1981 Pakistan Balochistan Sibi Korjk 0190
204	LRSEL 111	011310 *T. aestivum* PARC/SVP 000394(03) 5/1/1981 Pakistan Balochistan Chagai Peeshuk 0910
205	LRSEL 510	018679 *T. aestivum* PARC/PGRI 004093(02) 4/29/1999 Pakistan Punjab Chakwal Chabbar 0765
206	LRSEL 511	018680 *T. aestivum* PARC/PGRI 004094(01) 4/29/1999 Pakistan Punjab Chakwal Buchal Khurd 0890

Table 17. Detail of landrace germplasm evaluated by digital imaging for seed shape and size.

#	Name	Detail
207	LRSEL 646	018874 *T. aestivum* PARC/MAFF 004305(04) 6/5/2001 Pakistan NWFP Chitral Kosht 1600
208	LRSEL 200	011537 *T. aestivum* PARC/ICARDA 001222(01) 6/16/1986 Pakistan Balochistan Quetta – 1540
210	LRSEL 659	018888 *T. aestivum* PARC/MAFF 004310(02) 6/5/2001 Pakistan NWFP Chitral Booni 2080
211	LRSEL 139	011342 *T. aestivum* PARC/SVP 000437(03) 6/1/1981 Pakistan Balochistan Chagai Kachao 1250

Smart Grain software (version 12) was used to analyze the seed images. This software helped us to calculate area, perimeter length, length, width, length-to-width ratio, circularity, and distance between IS and CG. To find out the appropriate combinations of studied attributes, principal component and bi-plot analyses were made using mean values. The Pearson correlation co-efficient revealed that highest correlation was observed between area and perimeter (89.9%) followed by perimeter and length (89.2%), area and length (85.9%), area and width (82.7%). Area was positively co-related with perimeter, length, and width, i.e., the greater the seed area, the greater the perimeter, length, and width. The Pearson correlation among the different seed variables is shown (Table 18).

Table 18. Pearson correlation matrix recorded for 200 Pakistani wheat landraces.

	Area	Perimeter	Length	Width	Length:width	Circularity	Distance
Area							
Perimeter	0.899						
Length	0.859	0.892					
Width	0.827	0.677	0.461				
Length:width	–0.067	0.121	0.428	-0.600			
Circularity	–0.109	–0.527	–0.350	0.063	–0.398		
Distance	0.063	0.174	0.267	–0.219	0.481	–0.299	1.000

The vector length shows the extent of variation explained by respective traits in the principal component analysis. The first two components showed 80.57% of the total variation. Considering PC1 and PC2, most of the components, such as area, perimeter, and length, contribute positively to PC1 (Fig. 14). The correlation matrix indicated that area, perimeter, and length were highly correlated, thus, they belonged to the same group. The length-to-width ratio, distance, and circularity form a group of negatively correlated entries.

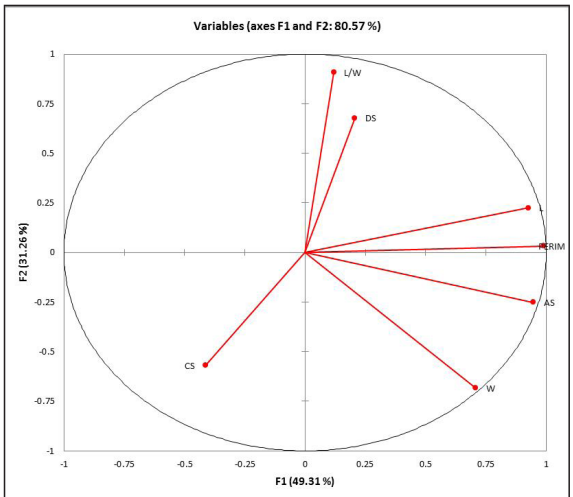

Fig. 14. Principal component analysis bi-plot of area (AS), perimeter (PERIM), length (L), width (W), the length-to-width ratio (L/W), circularity (CS), and distance (DS) on the first two principle components.

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Exploring the genetic diversity for yellow rust resistance and yield contributing traits in wheat landraces.

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With increasing population growth, wheat production is crucial. To accomplish this, additional genetic diversity for major biotic and abiotic stresses is needed. Hence, cultivar improvement with new allelic genetic diversity is an approach that has global interest (Mujeeb-Kazi et al. 2013; Ogbonnaya et al. 2013). Landrace diversity has been underutilized in wheat improvement but holds high value and also is receiving our attention. The performance of Pakistani wheat landraces for grain yield contributing traits in relation to yellow rust diversity is of interest and is a facet that has previously delivered many novel genes for resistance to diseases of wheat. (Repellin 2001).

This ongoing study was envisioned to characterize and evaluate for stripe rust resistance and yield contributing traits in a set of 174 wheat landraces that included some historical set of Pakistan's wheat cultivars. During the 2012–13 wheat growing season, a study conducted at Wheat Wide Crosses Program, National Agricultural Research Center (NARC), Islamabad, Pakistan, to assess genetic diversity for stripe rust resistance and yield-contributing traits. The germplasm was comprised of 174 Pakistani wheat landraces, including historical wheat cultivars acquired from the Plant Genetic Resources Programme, NARC, Islamabad. All accessions were planted in 1-m rows with a 30-cm row-to-row distance. The entire trial was bordered by a rust susceptible spreader (Morocco). Recommended cultural practices were uniformly followed.

Percent severity and reaction of each accession was estimated according to a Modified Cobb's Scale (Peterson et al. 1948; Roelfs et al. 1992). Stripe rust was scored at heading, when the susceptible spreader exhibited maximum disease severity. Data was recorded on plant height, number of spikes/plant, spike length, number of days-to-maturity, and 1,000-kernel weight. A coefficient of infection (CI) was computed by multiplying disease severity (DS) with constant values of infection type (IF). Constant values for infection types were used based on the following: resistance = 0.1, moderate resistance = 0.25, medium = 0.5, moderate susceptibility = 0.75, susceptibility = 1.0 (Pathan et al. 2006) (Table 19). Data on yield-contributing traits were then statistically analyzed for mean, standard deviation, standard error, and Pearson's correlation. Data was streamlined by transforming number of correlated variables into a smaller number of variables through principal component analysis.

Rust severity on the screened genotypes describes the resistance behavior. To calculate coefficient of infection (CI) the data on disease severity and host reaction was combined according to (Sajid et al. 2007). Genotypes with CI values of 0–20%, 21–40%, and 41–60% were considered as having high, moderate, and low levels of adult-plant resistance, respectively. The results revealed that disease stress was noticeably high, as shown by CI of susceptible spreader (Table 19, pp. 70-71). In first group, 102 accessions have CI values of 0–20%, and are considered resistant to relatively better resistance for stripe rust severity. Within the first group, the lowest CI values (0.5–1.0%) for six accessions (49, 58, 65, 71, 72, and 165) were resistant to rust. Forthy-four ccessions in the second group, with CI values of 21–40%, were estimated to be moderately resistant. The last group was comprised of nine accessions with CI values of 41–60%. Nineteen accessions showed stripe rust severity of more than 60% and were rated susceptible. Similarly,

Table 19. Adult-plant infection type and coefficient of infection in a subset of Pakistani landraces. For Reaction, R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

Genotype	Reaction	CI	Genotype	Reaction	CI	Genotype	Reaction	CI	Genotype	Reaction	CI
49	R	0.5	20	MR-MS	15.0	69	MS	22.5	158	MS-S	50.0
58	R	0.5	23	MR-MS	15.0	75	MS	22.5	77	S	50.0

Table 19. Adult-plant infection type and coefficient of infection in a subset of Pakistani landraces. For Reaction, R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

Genotype	Reaction	CI	Genotype	Reaction	CI	Genotype	Reaction	CI	Genotype	Reaction	CI
65	R	0.5	12	MR-MS	15.0	91	S	20.0	143	S	50.0
72	R	0.5	25	MR-MS	15.0	102	S	20.0	145	S	50.0
71	R	1.0	27	MR-MS	15.0	29	MR-MS	25.0	146	S	50.0
165	R	1.0	33	MR-MS	15.0	32	MR-MS	25.0	37	S	60.0
NARC-09	MR	1.25	40	MR-MS	15.0	34	MR-MS	25.0	96	S	60.0
NARC-11	MR	1.25	45	MR-MS	15.0	35	MR-MS	25.0	105	S	60.0
4	MR	1.25	61	MR-MS	15.0	67	MR-MS	25.0	106	S	60.0
14	R-MR	1.25	62	MR-MS	15.0	111	MR-MS	25.0	108	S	60.0
38	MR	2.5	63	MR-MS	15.0	125	MR-MS	25.0	112	S	60.0
80	MR	2.5	70	MR-MS	15.0	134	MR-MS	25.0	159	S	60.0
131	MR	2.5	79	MR-MS	15.0	135	MR-MS	25.0	170	S	60.0
142	MR	2.5	85	MR-MS	15.0	157	MR-MS	25.0	176	S	60.0
149	MR	2.5	92	MR-MS	15.0	184	MR-MS	25.0	182	S	60.0
150	MR	2.5	114	MR-MS	15.0	188	MR-MS	25.0	109	S	70.0
151	MR	2.5	116	MR-MS	15.0	199	MR-MS	25.0	178	S	70.0
153	MR	2.5	120	MR-MS	15.0	200	MR-MS	25.0	187	S	70.0
168	MR	2.5	127	MR-MS	15.0	43	MR-MS	30.0	104	S	80.0
15	MR-MS	2.5	129	MR-MS	15.0	177	MS-S	30.0	122	S	80.0
18	MR	5.0	154	MR-MS	15.0	22	S	30.0	44	S	100.0
56	MR	5.0	161	MR-MS	15.0	55	S	30.0	119	S	100.0
132	MR	5.0	173	MR-MS	15.0	88	S	30.0	133	S	100.0
141	MR	5.0	174	MR-MS	15.0	94	S	30.0	156	S	100.0
144	MR	5.0	183	MR-MS	15.0	100	S	30.0	Morocco	S	100.0
189	MR	5.0	186	MR-MS	15.0	107	S	30.0			
16	MR-MS	5.0	190	MR-MS	15.0	128	S	30.0			
41	MR-MS	5.0	194	MR-MS	15.0	137	S	30.0			
42	MR-MS	5.0	196	MR-MS	15.0	140	S	30.0			
66	MR-MS	5.0	9	MR-MS	20.0	197	S	30.0			
117	MR-MS	5.0	11	MR-MS	20.0	13	MS-S	40.0			
123	MR-MS	5.0	17	MR-MS	20.0	21	S	40.0			
162	MR-MS	5.0	19	MR-MS	20.0	50	S	40.0			
1	MR-MS	10.0	26	MR-MS	20.0	54	S	40.0			
2	MR-MS	10.0	39	MR-MS	20.0	64	S	40.0			
30	MR-MS	10.0	60	MR-MS	20.0	95	S	40.0			
31	MR-MS	10.0	76	MR-MS	20.0	99	S	40.0			
46	MR-MS	10.0	83	MR-MS	20.0	110	S	40.0			
47	MR-MS	10.0	103	MR-MS	20.0	118	S	40.0			
48	MR-MS	10.0	115	MR-MS	20.0	130	S	40.0			
87	MR-MS	10.0	124	MR-MS	20.0	136	S	40.0			
121	MR-MS	10.0	163	MR-MS	20.0	138	S	40.0			
126	MR-MS	10.0	166	MR-MS	20.0	148	S	40.0			
160	MR-MS	10.0	169	MR-MS	20.0	152	S	40.0			
167	MR-MS	10.0	181	MR-MS	20.0	155	S	40.0			
180	MR-MS	10.0	198	MR-MS	20.0	175	S	40.0			
185	MR-MS	10.0	52	S	20.0	84	S	50.0			
193	MR-MS	10.0	53	S	20.0	89	S	50.0			
3	MR-MS	15.0	82	S	20.0	113	S	50.0			
7	MR-MS	15.0	86	S	20.0	139	S	50.0			

Mirza et al. (2000) and Sajid et al. (2009) also conducted field evaluations of quantitative resistance to stripe rust, finding that the resistance level established on disease severity went from very low to very high among the evaluated genotypes.

Grain yield and yield-contributing traits are important for assessing yield potential (Zamarud et al. 2007). These traits are complex characteristics and known to be the cumulative outcome of different physiological processes. Principal component and factor analyses (Fig. 15) revealed that 57.07% of the variability was explained by the F1 and F2. Moreover, the F1, with an Eigenvalue of 2.089 explained the variation of days-to-maturity, spike length, and plant height, and the F2, with Eigenvalue of 1.335, described the variation in the coefficient of infection, spikes/plant, and 1,000-kernel weight (Table 20). According to Saif et al. (2013), 1,000-kernel weight was an important yield-contributing trait. The coefficient of infection is negatively correlated with all yield components (Table 21). Days-to-phenotypic-maturity was highly correlated with plant height and spike length. These results agree with those of Sunderman and Wise (1964).

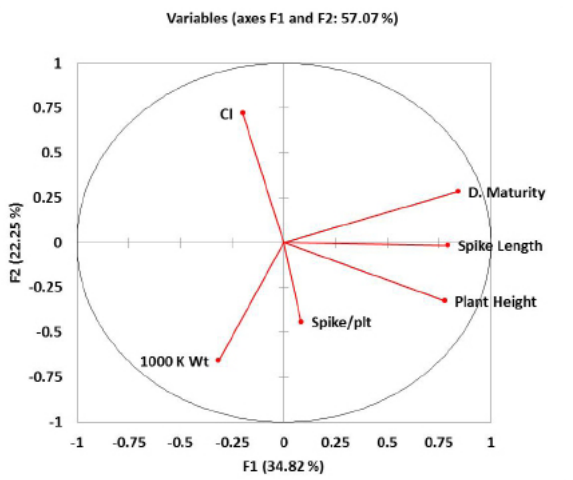

Fig. 15. Principal component analysis of the coefficient of infection (CI), days-to-maturity, spike length, plant height, spikes/plant, and 1,000-kernel weight in a subset of Pakistani landraces.

Table 20. Factors with Eigenvalues and % variability explained.

	F1	F2	F3	F4	F5	F6
Eigenvalue	2.089	1.335	1.081	0.708	0.470	0.316
Variability (%)	34.816	22.252	18.018	11.803	7.841	5.270
Cumulative (%)	34.816	57.068	75.086	86.889	94.730	100.000

Table 21. Pearson's correlation matrix (CI = coefficient of infection and DM = days-to-maturity).

Variable	Plant height	Spikes/ plant	Spike length	CI	DM
Spikes/plant	0.266				
Spike length	0.443	–0.070			
CI	–0.205	–0.073	–0.160		
DM	0.503	–0.097	0.546	0.012	
1,000-kernel weight	–0.030	–0.027	–0.103	–0.208	–0.328

These findings show that the genotypes had diversity to stripe rust resistance, ranging from resistant to moderately resistant and moderately resistant to susceptible genotypes. About 3% of the evaluated germplasm exhibited resistance, 59% were moderately resistant, and 33% were susceptibe. Landraces 49, 58, 65, 71, 72, and 165 were resistant and expected to have resistance genes. Landraces 4, 18, 38, 56, 80, 131, 132, 141, 142, 144, 149, 150, 151, 153, 168, and 189 may have different degrees of slow rusting. These genotypes can be used for upcoming breeding for stripe rust resistance after the ongoing confirmatory studies. Our Wheat Wide Crosses Program at the NARC has already acquired wheat landraces of different origins to carryout studies regarding genetic diversity for yellow rust resistance and yield-contributing traits. Our contention is that novel landraces may be an arsenal of unique genetic diversity for other new traits that need to be analyzed so multiple-value components can be blended swiftly. We are searching for resources that are rich in micronutrient profiles (Fe, Zn, and Phytase) and relate to PO_4 use efficiency with importance in place to climate change parameters (heat, drought, and soil variation to salinity/sodicity). Exploitation of landraces in wheat improvement will add to the in-place activities that embrace intraspecific, interspecific, and intergeneric programs.

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Analysis of genetic diversity and trait association under stripe rust pressure in 7th elite bread wheat yield trial (EBWYT) under agro-climatic conditions.

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The impact of CIMMYT's Wheat Breeding Program has been significant (Rajaram 1999). This study analyzed the genetic diversity, trait association and response against stripe rust in 24 genotypes of Elite Bread Wheat Yield Trial (EBWYT) contributed by CIMMYT (Table 22) with NARC-2009 as the commercial check. The experiment was

Table 22. Genotypes in 7th Elite Bread Wheat Yield Trial.

Entry	Pedigree
503	FRET2/Tukuru//FRET2/3/Munal #1
504	Kachu//WBLL1*2/Brambling
505	Kachu/Kiritati
507	Thelin#2/Tukuru//Kiritati
510	WBLL4/Kukuna//WBLL1/3/WBLL1*2/Brambling
511	FRET2*2/Brambling/3/FRET2/WBLL1//Tacupeto F2001/4/WBLL1*2/Brambling
512	Altar 84/*Ae. tauschii* (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/ Kachu/6/Kiritati//PBW65/2*SERI.1B
513	FRNCLN*2/Tecue #1
514	Milan/S87230//BAV92*2/3/Akuri
515	Kachu/Kinde
516	MUU/FRNCLN
517	MUU/KBIRD
518	Becard #1/4/Kiritati/3/2*SERI.1B*2//KAUZ*3/BOW
519	Becard/FRNCLN
520	WBLL1/Kukuna//Tacupeto F2001/4/Whear/Kukuna/3/C80.1/3*Batavia//2*WBLL1
521	Whear/Kukuna/3/C80.1/3*Batavia//2*WBLL1/4/Quaiu
522	WBLL1*2/Brambling//CHYAK
523	Becard//ND643/2*WBLL1
524	Attila/3*BCN*2//BAV92/3/Kiritati/WBLL1/4/Danphe
525	Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq
526	Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq
527	Kachu/Becard//WBLL1*2/Brambling
528	PFAU/SERI.1B//AMAD/3/Waxwing*2/4/Tecue #1
530	ND643//2*Attila*2/Pastor/3/WBLL1*2/Kuruku/4/WBLL1*2/Brambling

conducted in randomized complete block design with three replications at the National Agricultural Research Centre, Islambad, Pakistan, during winter 2012–13 crop season. Each plot consisted of four 4-m rows with a 30-cm row-to-row distance. The entire trial was bordered by a rust susceptible spreader (Morocco), which also was also planted after every 20th entry. The trial was subjected to constant recommended cultural practices. Percent severity of rust infection was taken according to a Modified Cobb's Scale (Paterson et al. 1948), and the reaction referred to the infection type on each genotype was estimated following Roelf et al. (1992) and Mcintosh et al. (1995). Rust notes for severity and infection type were taken together, with severity first. Stripe rust was scored at the heading stage when the susceptible spreader exhibited maximum disease severity. The coefficient of infection (CI) was calculated by multiplying disease severity (DS) with constant values for infection type (IF). Constant values for infection types were used based on the following scale: resistant = 0.1, moderately resistant = 0.25, medium = 0.5, moderately susceptible = 0.75, and susceptible = 1.0 (Pathan et al. 2006). Data was recorded on plant height (cm), spikes/plant, spike length (cm), days-to-maturity, 1,000-kernel weight (g), and and grain yield (kg/m^2).

Data on yield components was statistically analyzed and mean, standard deviation, standard error, and Pearson's correlation were estimated. Traits were analyzed by cluster and principal component analyses by using XLSTAT 3.06 software. A principal component analysis was used to streamline the data by transforming the number of correlated variables into a smaller number of variables. Cluster analysis classifies variables that are further grouped in to core groups and subgroups. Basic statistics also was computed for accessions in each cluster.

Variation in quantitative traits can be seen through descriptive statistics (Table 23). Thousand-kernel weight with a mean value of 42.0, ranges from 37.0 to 45.3 g and has a variance of 5.46. A narrow range with high variance indicates a greater variability among the genotypes. The mean value for the CI for stripe rust was 6.26, with high variability within the genotypes, and is low, highlighting most of the genotypes as stripe rust resistant. Days-to-maturity also showed a high level of variance, indicating the presence of early maturing genotypes. Selection can be made for heat-tolerant, early maturing lines. Spikelets/spike, spike length, and grain yield had low variance, describing the constant expression of the germplasm. High-yielding genotypes can be selected based on these characteristics as advocated by Ramzan et al. (1994). Such a substantial range of variation allows for a good foundation for a yield-maximization breeding target.

Table 23. Descriptive atatistics for six quantitative traits of 24 wheat genotypes. Traits are *Yr* CI = stripe rust coefficient of infection, DM = days-to-maturity, SPP = spikelets/plant, SPL = spike length (cm), TKW = 1,000-kernel weight (g), and GY = grain yield (kg/m^2). SE = standard error and SD = standard deviation.

Trait	Mean	SE	Median	Mode	SD	Variance	Range	Min	Max	Level (95%)
Yr CI	6.26	1.62	1.46	0	7.93	62.87	23.33	0.00	23.3	3.35
DM	164.90	0.81	166.20	168	3.98	15.80	12.67	156.00	169.0	1.68
SPP	9.10	0.15	9.00	9	0.75	0.56	3.00	8.00	11.0	0.31
SPL	10.15	0.19	10.00	10	0.95	0.91	3.33	8.33	11.7	0.40
TKW	41.97	0.48	42.33	44	2.34	5.46	8.33	37.00	45.3	0.99
GY	1.40	0.03	1.40	1.23	0.17	0.03	0.63	1.10	1.73	0.07

Days-to-maturity have a significantly positive correlation with spike length and a significantly negative correlation with CI for stripe rust (Table 24). Spikes/plant, spike length, 1,000-kernel weight, and grain yield showed positive correlations with the CI, presumably due to rust resistance and the slow-rusting behavior of the genotypes.

Table 24. Correlation coefficient (Pearson's Correlation) matrix shown for estimated traits. Traits are *Yr* CI = stripe rust coefficient of infection, DM = days-to-maturity, SPP = spikelets/plant, SPL = spike length (cm), TKW = 1,000-kernel weight (g), and GY = grain yield (kg/m^2).

Variable	*Yr* CI	DM	SPP	SPL	TKW
DM	–0.451				
SPP	0.081	0.015			
SPL	0.081	0.547	0.175		
TKW	0.369	–0.490	0.188	–0.128	
GY	0.234	0.217	0.281	0.144	–0.201

In the future, new, wide diversity is required that is present in wheat wild relatives (Mujeeb-Kazi et al. 2007). We have not identified any line with excellent yield potential, but within the best from the test group (Table 22, p. 85), few were selected for recombination stocks. New genomic diversity, coupled with multivariate cluster analysis of germplasm, might be helpful for identifying promising lines with respect to higher yield in the future.

Principal component and factor analysis (Table 25) revealed that factor F1 (Eigenvalue = 2.06) highlights the trend of variability in days-to-maturity, spike length, and 1,000-kernel weight and F2 (Eigenvalue = 1.53) depicts the extent of change in spikes/plant, grain yield, and the coefficient of infection of stripe rust (Fig. 16).

Table 25. Principal component and factor analysis.

	F1	F2	F3	F4	F5	F6
Eigenvalue	2.060	1.538	0.933	0.865	0.415	0.189
Variability (%)	34.329	25.634	15.553	14.413	6.922	3.148
Cumulative %	34.329	59.964	75.516	89.929	96.852	100.000

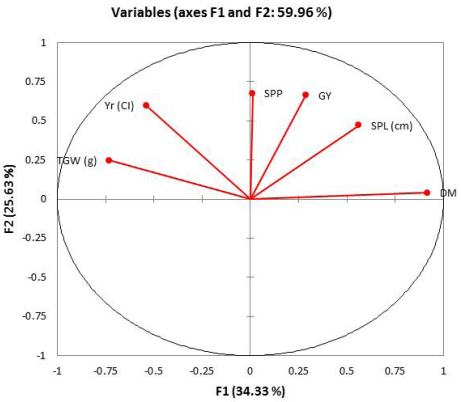

Fig 16. Principal component and factor analysis (TGW = 1,000-kernel weight, Yr (CI) = coefficient of variation for stripe rust, SPP = spikes/plant, GY = grain yield, SPL (cm) = spike length, and DM = (days-to-maturity).

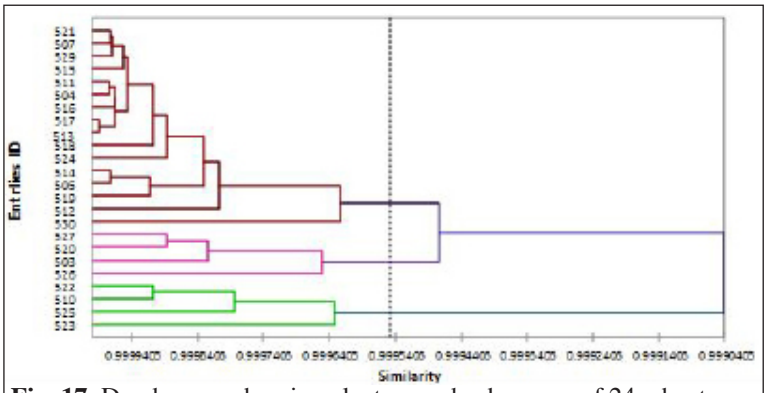

Fig. 17. Dendogram showing clusters and subgroups of 24 wheat genotypes.

Table 26. Cluster grouping of genotypes based on six quantitative traits.

Cluster	Frequency	Entries
1	4	503, 520, 526, 527
3	16	504, 505, 507,511, 512, 513, 514, 515, 516, 517, 518, 519, 521, 524, 529, 530
2	4	510, 522, 523, 525

The cluster analysis divides the 24 genotypes into three clusters showing high similarity within a cluster and high heterogeneity between clusters (Jaynes et al. 2003) (Fig. 17). Cluster one is composed of four genotypes with a medium stripe rust CI, a high number of spikes/plant, and a larger spike length (Table 26). The mean grain yield also is high in 16 genotypes of cluster 2 (Table 27). Cluster 3 is comprised of four genotypes having the lowest mean CI value for stripe rust. This cluster analysis indicates tremendous variation among genotypes of the three different clusters. Future selections from this germplasm can be made by keeping these three clusters in view. The applied value for breeders via clustering of germplasm by a multivariate approach appears to be the ability to select from specific clusters for breeding programs.

Table 27. Arithmetic means with standard deviation of each cluster for coefficient of variation for stripe rust (*Yr* (CI)), days-to-maturity (DM), spikes/plant (SPP), spike length (SPL (cm)), 1,000-kernel weight (TKW (g)), and grain yield (GY (kg/m^2)).

Cluster	*Yr* (CI)	DM	SPP	SPL	TKW (g)	GY (kg/m^2)
1	11.66+1.36	164.25+2.98	9.50+0.79	10.58+1.10	43.83+1.75	1.45+0.12
2	20.83+1.66	161.33+5.01	9.00+0.27	10.00+1.12	43.33+1.05	1.45+0.23
3	1.27+2.11	165.95+3.56	9.02+0.81	10.08+0.91	41.16+2.32	1.37+0.16

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Response of D-genome penetrance and expressivity on synthetic wheats for phenotypic traits and seed image analysis.

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As early as 1987, combining *Aegilops tauschii* accessions with *Triticum turgidum* cultivars was an effort launched by A. Mujeeb-Kazi at CIMMYT, Mexico. As a consequence, over the last few decades, synthetic wheats (SH) were developed that are beset with extensive user-friendly diversity for numerous biotic/abiotic stresses (Ogbonnaya et al. 2013). Over 1,000 synthetic wheats are available that harbor a genomic wealth that can unravel the basic information. We have focused on using SH-wheats that will elucidate how *Ae. tauschii* accessions are contributing to gene penetration and expressivity. We have selected material categorized as the same durum/different *Ae. tauschii* accessions to unravel how the D genome from different accessions has modified trait expressivity in a uniform AABB genomic profile. Initial data forms the basis of this brief study and will be expanded in the future on a larger scale.

Plant material. One-hundred seventeen, D-genome SH wheats developed from the combination of three durum wheats, Altar, Ceta, and D67.2, and different *Ae. tauschii* accessions; three original durum parents; four local checks, Pasban-90, S-24, Shorawaki, and PBW-343, were used. All the traits were recorded at different growth stages (Zadoks et al. 1974) (Table 28, p. 77). Traits studied were:

Plant habit. Recorded at GS-31 as prostrate, erect, and semi erect.

Anthocyanin pigment. Anthocyanins are pigmented compounds in plants that play a protective role under different stress conditions. Anthocyanin content tends to increase under drought, cold, UV-B irradiation, the presence of toxic metals in soils, and pathogen attack, and are found in different organs such as culm, leaf, auricle, pericarp, and coleoptiles. Recorded as either present or absent at GS-26 for all genotypes.

Leaf area index (LAI). The photosynthetic capacity of the crop is related to the total leaf area and the length of time that this area is maintained. Maintenance of the leaf area is essential for the production of the carbohydrates used for grain filling. Leaf area is influenced by the rates of leaf appearance, tiller production, and leaf expansion. Leaf area is measured as LAI. The LAI of a crop determines water-use efficiency. The higher the LAI, the more water used during the vegetative growth stage. In dryland crops, a large area of leaf in early vegetative growth may use water needed for flowering and grain fill. The leaf area of five random leaves from each genotype was measured. LAI has been calculated by the following formula of Muller (1991) at GS-41:

Leaf area index (cm^2) = Leaf length (cm) × leaf width (cm) × 0.74.

Table 28. Germplasm description used to study the response of D-genome penetrance and expressivity on synthetic wheats.

#	Entry	Pedigree	#	Entry	Pedigree
1	433	Altar 84/*Ae. tauschii* (1012)–	64	854	D67.2/P66.270//*Ae. tauschii* (634)
2	908	Altar 84/*Ae. tauschii* (1068)	65	855	D67.2/P66.270//*Ae. tauschii* (635)
3	1010	Altar 84/*Ae. tauschii* (1094)	66	260	D67.2/P66.270//*Ae. tauschii* (646)
4	3	Altar 84/*Ae. tauschii* (178)	67	823	D67.2/P66.270//*Ae. tauschii* (657)
5	5	Altar 84/*Ae. tauschii* (188)	68	861	D67.2/P66.270//*Ae. tauschii* (658)
6	8	Altar 84/*Ae. tauschii* (191)	69	261	D67.2/P66.270//*Ae. tauschii* (659)
7	12	Altar 84/*Ae. tauschii* (192)	70	865	D67.2/P66.270//*Ae. tauschii* (665)
8	17	Altar 84/*Ae. tauschii* (193)	71	866	D67.2/P66.270//*Ae. tauschii* (666)
9	20	Altar 84/*Ae. tauschii* (198)	72	867	D67.2/P66.270//*Ae. tauschii* (668)
10	23	Altar 84/*Ae. tauschii* (205)	73	875	D67.2/P66.270//*Ae. tauschii* (709)
11	33	Altar 84/*Ae. tauschii* (211)	74	803	D67.2/P66.270//*Ae. tauschii* (731)
12	48	Altar 84/*Ae. tauschii* (219)	75	804	D67.2/P66.270//*Ae. tauschii* (741)
13	49	Altar 84/*Ae. tauschii* (220)	76	884	D67.2/P66.270//*Ae. tauschii* (788)
14	52	Altar 84/*Ae. tauschii* (221)	77	885	D67.2/P66.270//*Ae. tauschii* (791)
15	57	Altar 84/*Ae. tauschii* (223)	78	887	D67.2/P66.270//*Ae. tauschii* (796)
16	64	Altar 84/*Ae. tauschii* (224)	79	888	D67.2/P66.270//*Ae. tauschii* (797)
17	918	Altar 84/*Ae. tauschii* (237)	80	889	D67.2/P66.270//*Ae. tauschii* (828)
18	464	Altar 84/*Ae. tauschii* (244)	81	895	Ceta/*Ae. tauschii* (1085)
19	80	Altar 84/*Ae. tauschii* (291)	82	440	Ceta/*Ae. tauschii* (1024)
20	551	Altar 84/*Ae. tauschii* (319)	83	962	Ceta/*Ae. tauschii* (683)
21	96	Altar 84/*Ae. tauschii* (328)	84	927	Ceta/*Ae. tauschii* (418)
22	97	Altar 84/*Ae. tauschii* (328)	85	930	Ceta/*Ae. tauschii* (442)
23	318	Altar 84/*Ae. tauschii* (333)	86	825	Ceta/*Ae. tauschii* (615)
24	923	Altar 84/*Ae. tauschii* (380)	87	955	Ceta/*Ae. tauschii* (680)
25	419	Altar 84/*Ae. tauschii* (502)	88	903	Ceta/*Ae. tauschii* (373)
26	572	Altar 84/*Ae. tauschii* (539)	89	578	Ceta/*Ae. tauschii* (1055)
27	993	Altar 84/*Ae. tauschii* (793)	90	449	Ceta/*Ae. tauschii* (166)
28	187	Altar 84/*Ae. tauschii* (JBANGOR)	91	448	Ceta/*Ae. tauschii* (1042)
29	186	Altar 84/*Ae. tauschii* (Y86-87 S401)	92	516	Ceta/*Ae. tauschii* (1043)
30	607	D67.2/P66.270//*Ae. tauschii* (1009)	93	517	Ceta/*Ae. tauschii* (1046)
31	608	D67.2/P66.270//*Ae. tauschii* (1015)	94	450	Ceta/*Ae. tauschii* (172)
32	610	D67.2/P66.270//*Ae. tauschii* (1017)	95	446	Ceta/*Ae. tauschii* (1030)
33	906	D67.2/P66.270//*Ae. tauschii* (1032)	96	477	Ceta/*Ae. tauschii* (371)
34	785	D67.2/P66.270//*Ae. tauschii* (1054)	97	454	Ceta/*Ae. tauschii* (200)
35	771	D67.2/P66.270//*Ae. tauschii* (1057)	98	483	Ceta/*Ae. tauschii* (445)
36	892	D67.2/P66.270//*Ae. tauschii* (1068)	99	513	Ceta/*Ae. tauschii* (1036)
37	894	D67.2/P66.270//*Ae. tauschii* (1074)	100	511	Ceta/*Ae. tauschii* (1031)
38	896	D67.2/P66.270//*Ae. tauschii* (1085)	101	515	Ceta/*Ae. tauschii* (1038)
39	899	D67.2/P66.270//*Ae. tauschii* (1090)	102	452	Ceta/*Ae. tauschii* (184)
40	909	D67.2/P66.270//*Ae. tauschii* (1093)	103	919	Ceta/*Ae. tauschii* (310)
41	584	D67.2/P66.270//*Ae. tauschii* (185)	104	921	Ceta/*Ae. tauschii* (345)
42	34	D67.2/P66.270//*Ae. tauschii* (211)	105	897	Ceta/*Ae. tauschii* (1090)
43	37	D67.2/P66.270//*Ae. tauschii* (213)	106	600	Ceta/*Ae. tauschii* (416)
44	44	D67.2/P66.270//*Ae. tauschii* (217)	107	429	Ceta/*Ae. tauschii* (540)
45	47	D67.2/P66.270//*Ae. tauschii* (218)	108	460	Ceta/*Ae. tauschii* (235)
46	50	D67.2/P66.270//*Ae. tauschii* (220)	109	1008	Ceta/*Ae. tauschii* (1093)
47	53	D67.2/P66.270//*Ae. tauschii* (221)	110	786	Ceta/*Ae. tauschii* (356)
48	614	D67.2/P66.270//*Ae. tauschii* (1039)	111	573	Ceta/*Ae. tauschii* (541)
49	59	D67.2/P66.270//*Ae. tauschii* (223)	112	640	Ceta/*Ae. tauschii* (299)
50	590	D67.2/P66.270//*Ae. tauschii* (239)	113	655	Ceta/*Ae. tauschii* (408)
51	223	D67.2/P66.270//*Ae. tauschii* (257)	114	485	Ceta/*Ae. tauschii* (450)
52	593	D67.2/P66.270//*Ae. tauschii* (260)	115	622	Ceta/*Ae. tauschii* (199)
53	781	D67.2/P66.270//*Ae. tauschii* (288)	116	479	Ceta/*Ae. tauschii* (391)
54	594	D67.2/P66.270//*Ae. tauschii* (301)	117	673	Ceta/*Ae. tauschii* (519)
55	224	D67.2/P66.270//*Ae. tauschii* (308)	118	Check	Pasban-90
56	595	D67.2/P66.270//*Ae. tauschii* (320)	119	Check	Shorawaki
57	596	D67.2/P66.270//*Ae. tauschii* (368)	120	Check	PBW-343
58	782	D67.2/P66.270//*Ae. tauschii* (400)	121	Check	S-24
59	599	D67.2/P66.270//*Ae. tauschii* (416)	122	Durum	Altar
60	603	D67.2/P66.270//*Ae. tauschii* (448)	123	Durum	Ceta
61	605	D67.2/P66.270//*Ae. tauschii* (497)	124	Durum	D67.2
62	847	D67.2/P66.270//*Ae. tauschii* (629)			
63	853	D67.2/P66.270//*Ae. tauschii* (633)			

Chlorophyll concentration index (CCI). Three measurements using a SPAD-502 leaf chlorophyll meter (Konica-Minolta, Osaka, Japan) from the random leaf blade were recorded. The crop ground cover, or the percentage of soil surface enclosed by plant foliage, is an important observation of crop establishment and early vigor. Genotypes with expansive early ground cover are able to better capture incident radiation, thus escalating soil shading and declining soil evaporation, which elevates the water-use efficiency and may have improved the competitiveness with weeds and potentially diminish soil erosion. Photographs of the ground cover of each genotype were taken at GS-32 with a digital camera and processed by using Adobe Photoshop CS3 Extended software (Fig. 18). The percent ground cover (%GC) has been calculated by the following formula:

Fig. 18. Crop ground cover images showing the prostrate foliar expanse.

$$\% \text{ GC} = (\text{mean grey value} / 255) \times 100$$

Digital imaging (DI) of seed. Seed shape and size are among the most important agronomic traits due to their higher effect on yield and grain quality. The DI technique was used to generate high-throughput photometric traits explaining various magnitudes of grain size and shape. DI has the ability to display the dimensions of grain morphology that are contributing to grain weight and size. Photograph of 25 well-developed seeds of each entries were taken. Seeds were placed horizontally with equal distances on black background to provide color contrast. Area size (mm^2), perimeter length (mm), length (mm), width (mm), length-to-width ratio, circularity, and distance between IS and CG were made and computed by the Smart Grain software version 1.1.

Statistical analysis and data interpretation indicate that the different *Ae. tauschii* accessions show their higher penetrance effect in the D-genome SH as observed via the digital imaging behavior of seed, plant habit, anthocyanin pigment, leaf area index, ground cover percentage (GC%), and CCI. The leaf area of Altar 84, Ceta, and D67.2 were 32.56, 25.53, and 35.96, respectively. The SHs ranged from 17.30 to 64.75, due to contributions from the D genome. The seed area of Altar 84, Ceta, and D67.2 were computed as 36 mm^2, 31 mm^2, and 32 mm^2, respectively, whereas the SHs varied from 19 mm^2 to 47 mm^2 (Fig. 19).

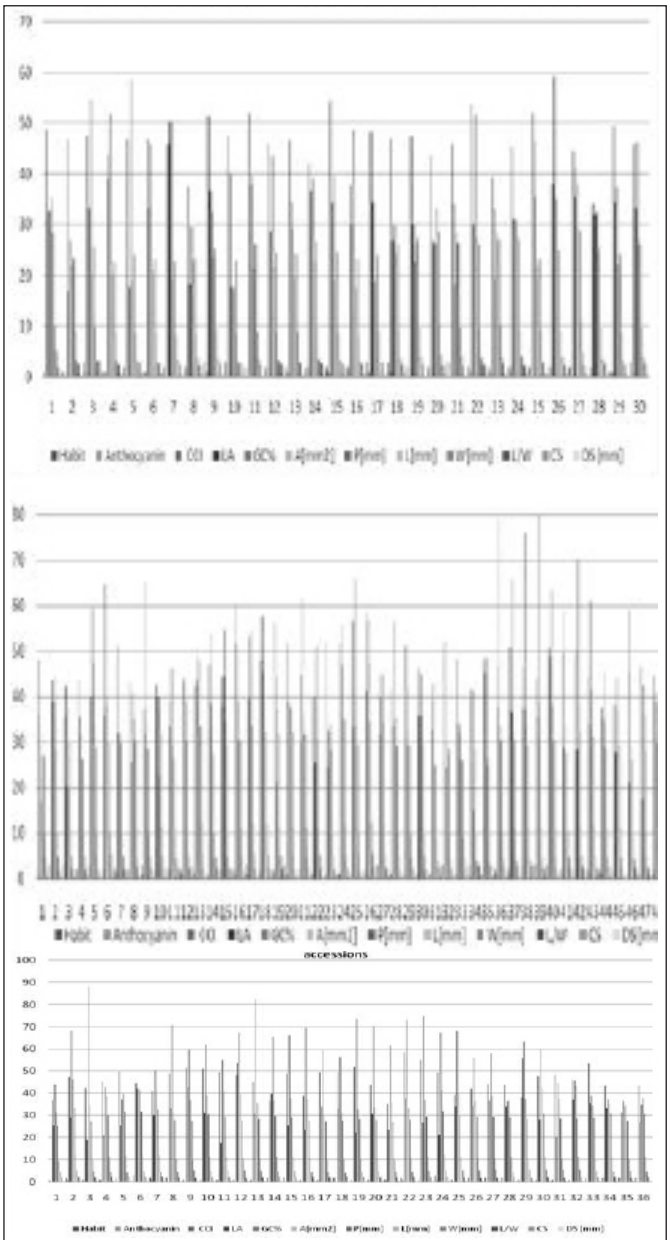

Fig. 19. Parameters showing genetic penetrance and expressivity in synthetic hexaploid wheat developed from the same durum cultivars (Altar 84 (top), D67.2 (middle), and Ceta (bottom) with different *Ae. tauschii* accessions.

The multiple factor analysis shows that the durum parents with all the attributes have different patterns of variability as expressed through partial axes. Subfactors of Ceta and Altar 84 are explained by the multiple factor partial axis F1 and subfactors of D67.2 are explained by F2 (Fig. 20).

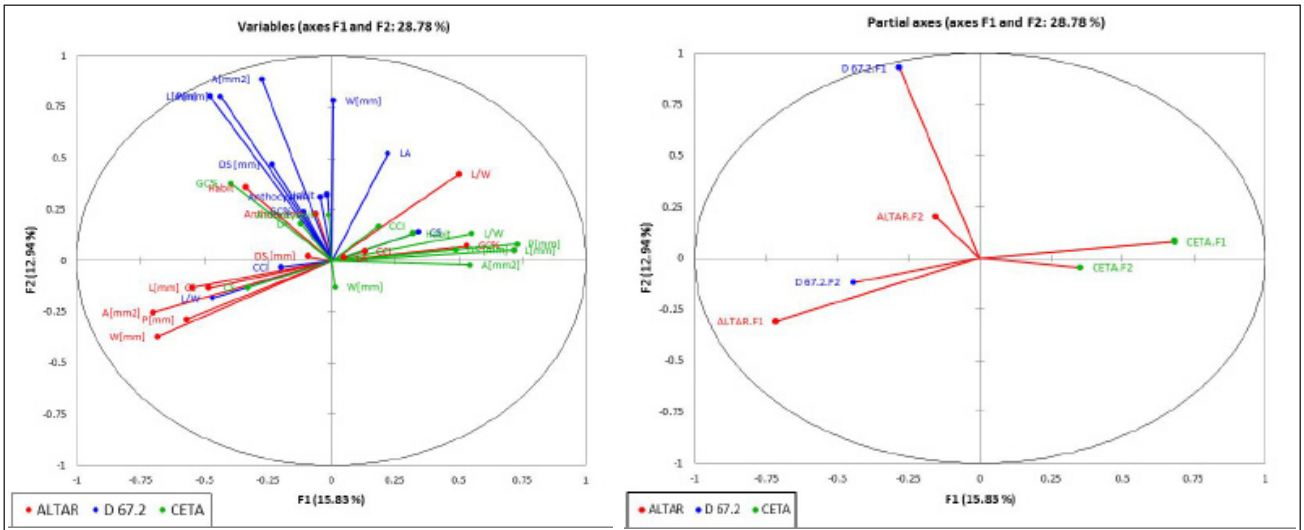

Fig. 20. Multiple factor analysis of different variables for Altar 84 and Ceta (left; axis F1 and F2: 28.78%) and PD67.2 (right; axis F1 and F2: 28.78%).

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Assessment of diverse bread wheat germplasm for drought tolerance via osmotic stress imposed during early seedling growth.

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Our annual wheat yields are severely affected by variable rain patterns that penalize or favor crop yields. Water shortages and climate change are two major factors that have forced us to maximize what productivity. Drought-tolerant wheat cultivars are paramount for providing food security in the future.

Drought stress is one of the most important abiotic stresses, generally accompanied by heat stress during the dry season. Drought is a global problem seriously influencing crop productivity. As a result of a possible climatic shift in the Indo-Gangetic Plains, which currently contributes 15% of the global wheat production, as much as 51% of the area is classified as heat stressed. This area could represent a significant reduction in wheat yield unless appropriate cultivars tolerant to abiotic stresses are adopted by farmers of this region. In Pakistan, this problem is multifaceted, because 20% of the cultivated area is rain-fed and is under the direct, severe threat of drought and heat. The remaining irrigated area is facing severe water availability problems. Coping with the consequences of climate change on agriculture requires unprecedented efforts toward the development of improved genetic resources more resilient to weather vagaries, particularly drought (Semenov and Halford 2009). Developing stress-tolerant cultivars is the most important goal of several breeding programs. However, success has been limited due to inadequate screening techniques, and clearly explains the lack of trait responsive tolerant genotypes. Yield has been the foremost criteria for such programs and is a very complex trait in terms of number of genes controlling it. Yield also is largely influenced by many environmental factors that cause selection for such traits to be less effective. Another problem is that, due to major environmental factors, the heritability of yield and its components also is very low (Ludlow and Muchow 1990). Drought-related traits

can, however, effectively be measured in off-season or in controlled laboratory conditions in early generations, which could be a cost-effective and user-friendly potential approach. Seedling emergence is a sensitive growth stage that is susceptible to water-deficit. Seed germination, seedling vigor, and coleoptile and root shoot length are well recognized prerequisites for the successful stand establishment of crop plants. Rauf et al. (2007) observed that in semiarid regions, low moisture is a restrictive factor during germination, hence, the rate and degree of seedling growth are extremely important in defining both yield and time of maturity. The availability of soil moisture has a major effect on germination and emergence. Besides reduction in total germination, relatively low soil moisture also causes a delay in seed emergence.

Selection for drought tolerance at an early stage in seedlings is most commonly carried out using chemical desiccators such as polyethylene glycol (PEG-6000). PEG also can be used to modify the osmotic potential of nutrient solution cultures and induce plant water-deficit in a relatively controlled manner (Lagerwerff et al. 1961). Rauf et al. (2007) evaluated 16 spring wheat genotypes at four PEG-6000 levels and noted a significant reduction in germination percentage, germination rate index, shoot length, root length, the fresh and dry weights of shoots and root, and the root:shoot ratio in all treatments except the control; the greatest decrease in these traits occurred with a 33% PEG concentration. Sayar et al. (2008) observed that a 25% PEG concentration decreased the germination by 9% in sensitive cultivars, whereas at 30% PEG, only a few seeds from drought-tolerant cultivars germinated. Bayoumi et al. (2008) assessed nine *Triticum aestivum* cultivars by using PEG at 0%, 15%, and 25%. PEG considerably reduced the shoot, root biomass, and coleoptile length in susceptible genotypes, whereas the reduction was less in the drought-tolerant genotypes.

Drought escape, due to a profound root system, enhances the ability of a plant to capture water from deeper layers of the soil and is a fundamental adaptation mechanism to drought. Root system characteristics are of fundamental importance for soil exploration and below-ground resource acquisition, and are strongly related to plant adaptation to suboptimal conditions, such as drought stress.

Our study was targeted to elucidate a rapid and upfront technique for screening wheat genotypes for drought tolerance in early seedling growth stages using PEG-6000 and also compute the associations between drought-related seedling traits. The study was in a growth room of the Wheat Wide Crosses and Cytogenetics laboratory, National Agricultural Research Centre (NARC), Islamabad, during early 2014. The experiment was laid-out in split-plots arranged in randomized complete blocks with three replications. Osmotic stresses were considered as the main plots and cultivars as subplots. Thirteen spring wheat genotypes, LC-2, LC-3, LC-4, LC-5, LC-6, LC-7 DL-1, DL-3 DL-6, SH.DR-24, SH.DR-42, NARC-09, and Durum-7, were studied to see the effect of osmotic stress imposed by using PEG-6000. Solutions were prepared according to weight-by-volume (w/v) as followe: T1 (control with distilled water), T2 (7.5% PEG solution), T2 (15% PEG solution), and T3 (25% PEG solution). For 15% PEG, 150 g of PEG was dissolved with stiring in 1,000 mL of distilled water. Similarly, for 25% PEG, 250 g of PEG was dissolved in 1,000 mL of distilled water. The temperature in growth room was kept at 25±20°C with 60% relative humidity. Five seeds were placed in Whatman No.1 filter paper in Petri dishes measuring 90 mm. After placing the seeds in petri dishes, 10 mL of the PEG solution or distilled water was pipetted in to the petri dishes. Thereafter, 5 mL of distilled water was added to the 7.5%, 15%, and 25% PEG treatments everyday; the same amount of distilled water was added to the control petri dishes to keep them moist and maintain the evaporation losses. The seeds were considered germinated when the radicle (coleorhizae) measured at least 5 mm; germination percentage and other measurements were recorded after 10 days of treatment. Data were recorded on the seedlings of each cultivar. The observations were taken on germination percentage, shoot length (cm), root length (cm), fresh weight of shoot (g), fresh weight of root (g), root/shoot ratio, and seed vigor index (calculated by multiplying the sum of the root and shoot lengths by the germination percentage). The data collected were statistically analyzed by using XLSTAT 2010 software to determine significant differences among the genotypes as affected by PEG osmotic stress. A least significant difference test was applied at the 5% probability level to compare mean differences. Pearson's simple correlation coefficient between different traits at seedling stage also was computed with the software.

Table 29. Mean squares from the ANOVA for shoot length (cm; SL), root length (cm; RL), shoot fresh weight (g; SFW), root fresh weight (g; RFW), shoot dry weight (g; SDW), root dry weight (RDW), and the root:shoot ratio (R:S).

Source of variation	df	SL	RL	SFW	RFW	SDW	RDW	R:S
Genotype	11	32.98***	29.87***	0.005286	0.0027*	0.000189	0.000053	0.297**
Treatment	3	153.63***	479.45***	0.035900**	0.0442***	0.000189	0.000214*	3.415***
Genotype x treatment	33	3.05**	15.57***	0.007387	0.0025**	0.000158	0.000069	0.218**

Mean square values form the ANOVA were calculated and observed. Genotypes showed highly significant variation in shoot length, root length, and root:shoot ratio. the root and shoot fresh or dry weight could not cause significant variation in the genotypes. In the treatments and the 'genotype x treatment' interaction, the significance was similar (Table 29, p. 80). From the LSDs, SHD-42, SHD-25, and DRL-1 were significantly different among the genotypes with respect to shoot and root length (Table 30). From the correlation table, seedling vigor index was found to be highly correlated with root and shoot length. Root and shoot weights were highly correlated with their lengths (Table 31, pp. 81-82).

Table 30. Least significant differences among the genotypes for shoot length (cm, SL), root length (cm, RL), root fresh weight (g; RFW), and the root:shoot ratio (RL:SL).

Genotype	Shoot length (cm)	Root length (cm)	Root fresh weight (g)	Root:shoot ratio
LC2	14.87 ab	9.7 b	0.11 b	0.95 e
LC3	14.98 ab	8.04 cd	0.11 bc	1.33 ab
LC4	14.58 ab	9.29 bc	0.11 b	1.18 bcde
LC5	12.85 c	9.66 b	0.11 bc	1.27 abc
LC6	12.54 cd	10.00 b	0.11 bc	1.22 bc
DRL-1	11.83 d	9.16 bc	0.12 ab	1.52 a
DRL-4	12.62 cd	7.41 de	0.11 bc	1.31 abc
DRL-6	14.22 b	10.00 b	0.13 ab	1.07 cde
SHD-25	15.29 a	10.33 b	0.11 b	1.21 bcd
SHD-42	14.95 ab	12.66 a	0.15 a	1.22 bcd
NARC-09	9.75 e	6.54 e	0.08 c	1.16 bcde
DURUM-7	13.08 c	10.37 b	0.11 bc	0.96 de
LSD Value	1.003	1.414	0.028	0.256

Table 31. Pearson's correlation coefficient for shoot length (cm; SL), root length (cm; RL), root:shoot ratio (RL:SL), shoot fresh weight (g, SFW), root fresh weight (g, RFW), shoot dry weight (g, SDW), root dry weight (g, RDW), and root:shoot dry weight ratio (RW:SW).

	SL	RL	RL:SL	SFW	RFW	SDW	RDW	RW:SW
Root length								
Control	0.296444							
7.50%	0.524969							
15.50%	0.706094							
22.70%	0.646982							
Root length:shoot length ratio								
Control	–0.271280	0.837365						
7.50%	0.256590	0.954407						
15.50%	0.216458	0.841235						
22.70%	–0.124670	0.670838						
Shoot fresh weight								
Control	–0.652080	–0.06776	0.326883					
7.50%	0.050850	0.208231	0.243353					
15.50%	0.779498	0.479115	0.068941					
22.70%	0.800233	0.737985	0.188666					
Root fresh weight								
Control	0.389142	0.719547	0.480178	–0.407660				
7.50%	0.507273	0.642640	0.528976	–0.121930				
15.50%	0.711619	0.939642	0.745960	0.592305				
22.70%	0.418570	0.657584	0.460609	0.572542				

Table 31. Pearson's correlation coefficient for shoot length (cm; SL), root length (cm; RL), root:shoot ratio (RL:SL), shoot fresh weight (g, SFW), root fresh weight (g, RFW), shoot dry weight (g, SDW), root dry weight (g, RDW), and root:shoot dry weight ratio (RW:SW).

	SL	RL	RL:SL	SFW	RFW	SDW	RDW	RW:SW
Shoot dry weight								
Control	0.359071	0.769049	0.564575	–0.163900	0.579765			
7.50%	0.472504	0.360522	0.236320	–0.071750	0.102192			
15.50%	0.702091	0.274264	–0.142740	0.894353	0.400084			
22.70%	0.279932	0.276042	0.089990	0.357253	0.357536			
Root dry weight								
Control	0.290032	0.221029	0.056403	0.060100	0.048613	0.188440		
7.50%	0.381970	0.456905	0.390496	–0.192770	0.659155	–0.218360		
15.50%	0.331981	0.730418	0.718320	0.383083	0.711905	0.222157		
22.70%	–0.103580	0.236161	0.473584	–0.004170	–0.047590	–0.135380		
Root dry weight:shoot dry weight ratio								
Control	–0.514590	0.055699	0.355197	0.421415	–0.045750	–0.31213	–0.289220	
7.50%	–0.209140	–0.091050	–0.027750	–0.148560	0.184877	–0.75811	0.719706	
15.50%	–0.322810	0.348964	0.683387	–0.337010	0.264258	–0.55766	0.666709	
22.70%	–0.165510	–0.259040	–0.212630	–0.359020	–0.086160	–0.71671	–0.101230	
SVI								
Control	0.429525	0.900982	0.664442	–0.147920	0.648923	0.767162	0.341680	–0.135680410
7.50%	0.781241	0.869703	0.735728	0.226182	0.664196	0.449724	0.438831	–0.212110630
15.50%	0.750181	0.756623	0.466283	0.624931	0.642574	0.501977	0.628624	0.106637384
22.70%	0.772956	0.720521	0.171480	0.770152	0.342675	0.144443	0.188704	0.007968453

Varied genotypic response to PEG treatment is important for plant breeders, because genotypes can be screened initially and tagged at the seedling stage before extensive and expensive field tests are conducted. Water stress, due to drought, is undoubtedly the most significant abiotic factor limiting plant and also crop growth and development. Drought stress *in vitro* is physiologically related, because of the induced osmotic stress and most of the metabolic responses that it affects, which are similar to some extent to *in vivo* performance. Water deficit negatively affects seed germination and plant growth of seedlings. Our results suggest that the SHD-42, SHD-25, and DRL-1 performed well under osmotic stress regarding seed germination percentage, root and shoot length, and root and shoot weight. Tthese lines can be utilized further in a breeding program for drought tolerance.

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High-throughput SNP and functional marker-based genotyping to assist marker-based breeding activities in the Wheat Wide Crosses Program.

Awais Rasheed, M. Jamil, A.A. Napar, Alvina Gul Kazi, and A. Mujeeb-Kazi.

High-density molecular markers are powerful tools for studying genomic patterns of diversity, the relationship between individuals in populations, and marker-trait associations in mapping experiments. Similarly, functional markers, designed from the gene of interest, aid in selecting superior progeny. These two genotyping resources are currently under exploitation that will be beneficial in following three disciplines:

– Identify new loci for the traits of economic interest.
– Slect superior genotypes with superior alleles for grain quality and yield.
– Unravel patterns of linkage disequilibrium and population structure in advanced progenies derived from wheat wide crosses.

Given the mandate of wheat wide crosses to enrich the wheat gene pool by exploiting available historical genetic diversity (cultivars and landraces) and novel germplasm developed from new Triticeae genomic resource (e.g. synthetic hexaploids), the main activities in progress are:

– High-throughput, DArT-based genotyping and phenotyping led to the identification of new loci for grain weight and size in synthetic hexaploids. Based on these findings, a chromosomal region on 3D is the future target for fine mapping and subsequent gene cloning for grain size and weight (Rasheed et al. 2014; BMC Plant Biol; in press). This initiative was funded by the GRDC, Australia, and Bioversity International, Italy, under a Vavilov-Frankel Fellowship in 2013.
– We genotyped 182 synthetic hexaploids in an Illumina iSelect SNP 9K assay (Cavanagh et al. 2013; Proc Natl Acad Sci USA) and several new loci were identified for stripe rust resistance (F.C. Ogbonnaya, personal communication). This set of synthetic hexaploids is under phenotyping experiments for grain Fe, Zn, Ca, and phytate contents, which are expected to unravel new genetic loci to enhance nutritional value of wheat.
– Illumina iSelect SNP 90K genotyping for 230 historical wheat cultivars and landraces from Pakistan is expected to unravel the footsteps of wheat domestication in Pakistan and will aid trait discovery.
– We developed 210 advanced lines from crossing elite Pakistan wheat cultivars and synthetic hexaploids. These advanced lines show promising agronomic features over the years in field experiments. This germplasm set is now in progress for genotyping using an Illumina iSelect SNP 90K assay that will highlight the important genomic regions from synthetic hexaploids retained in the advanced lines and influencing abiotic stress tolerances.
– The 210 advanced bread wheat/synthetic hexaploid lines are being investigated to identify novel haplotype variations for two important drought-tolerance genes TaDREB-D1 and TaCWI-D2. Important SNPs influencing drought tolerance will be targeted to design KASP-based, allele-specific markers for future diagnostic in germplasm derived from synthetic hexaploids. This initiative is partially funded by Food Security Center, Germany, and the CIMMYT-CAAS Wheat Improvement Center, China.
– Allelic variations at 24 loci in economically important traits were identified using functional markers in historical wheat cultivars and landraces from Pakistan. The results identified several genotypes carrying combinations of superior alleles for grain quality and yield which can be important parental candidates for future wheat breeding in Pakistan.

All germplasm mentioned in the above subsection are currently being phenologically observed, under seed increase, maintained in the Wheat Wide Crosses Program working collection. Five grams of each entry will be deposited in the NARC (Islamabad) gene bank from which seed can be requested under an MTA when shipping costs to be provided.

Thinopyrum bessarabicum for wheat improvement: current status.

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Bread wheat cultivation in Pakistan and globally is under irrigated and rainfed conditions. In irrigated areas with inorganic fertilizer input, salinity build-up is a common abiotic stress that limits crop productivity causing breeders to develop

cultivars with salinity tolerance. Conventional salinity diversity is very limited, with three sources receiving recognition so far, the cultivars Chinese Spring, Kharchia 65, and Shorawaki. Improved breeding material has been cultivars Lu26S, Pasban 90, KRL 1-4, KRL 19, the unreleased, advanced derivative S-24, plus a handful of others. Even after more than two decades since its release, Pasban 90 stands as the national salt-tolerance standard in Pakistan. *Thinopyrum distichum* (2n=4x=28) is in the pedigree of this cultivar. Several reports have associated alien allelic variation as a potent means from which to incorporate salt tolerance into wheat, including *Elytrigia pontica* (a decaploid), via use of the *Phl* cytogenetic manipulation system developed from *Th. junceiforme* (a tetraploid), salt-tolerant, wheat stocks (Wang, personal communication).

Numerous, global research efforts utilizing alien diversity are limited, but on-going activities appear promising as the value of using carefully selected alien species have a distinct advantage for addressing complex traits such as salinity. Hence, diploid alien sources are a priority in wheat improvement irrespective of their gene pool location. Well recognized is the D-genome diploid *Aegilops tauschii* (2n=2x=14) of the primary gene pool (Kazi 2011), a very effective source of salinity tolerance source with enormous diversity. Another diploid, *Th. bessarabicum* (2n=2x=14, E^bE^b) of the tertiary gene pool, has demonstrated superior tolerance potential and remains under study even today, after earlier promise was shown a few decades ago. At the diploid level, another resource, *Lophopyrum elongatum*, whose cytogenetic stocks are available in bread wheat and durum wheat backgrounds, has yet to be fully exploited.

Our current progress status with *Th. bessarabicum* on genetic stocks produced and maintained through continued efforts by A. Mujeeb-Kazi, first at CIMMYT, Mexico, and now in Pakistan collaborating with the parent wide cross program in CIMMYT, Mexico, are the following:

– A 2n=8x=56, AABBDDE^{b}E^b Chinese Spring/*Th. bessarabicum* amphiploid
– A complete set of seven *Th. bessarabicum* disomic chromosome addition lines (1E^b to 7E^b)
– Amount of the above stocks after selfing of the amphiploid and the seven disomic addition lines in the 2012–13 crop cycle are

Amphiploid (2n=8x=56)	225 seed
1E^{b}E^b (2n=6x=42+2)	750 seed
2 E^{b}E^b (2n=6x=42+2)	750 seed
3 E^{b}E^b (2n=6x=42+2)	750 seed
4 E^{b}E^b (2n=6x=42+2)	750 seed
5 E^{b}E^b (2n=6x=42+2)	750 seed
6 E^{b}E^b (2n=6x=42+2)	750 seed
7 E^{b}E^b (2n=6x=42+2)	750 seed

At the start of 2000, experiments were initiated at CIMMYT, Mexico, to produce wheat/*Th. bessarabicum* homoeologous translocation lines using the amphiploid/*phph*-based strategy. A wide array of translocations were generated around in the test materials. Restoring the *PhPh* composition by backcrossing, translocation homozygotes resulted and were increased. Detection and validation of euploid products was done by fluorescent in situ hybridization and Giemsa C-banding (Kazi et al. 2011) and further studies are elucidated in this update (Table 32).

Table 32. Seven euploid derivatives from the effort involving Pakistan/CIMMYT.

Entry	Detail	Chromosome #	Seed #
WWX-1	T7DS·7DL-4J	Euploid 42	250
WWX-2	T6BS·6BL-6J	Euploid 42	250
WWX-3	T6JS·7DL	Euploid 42	250
WWX-4	T5JS-5DS·5DL	Euploid 42	250
WWX-5	T1DS·1JS	Euploid 42	250
WWX-6	T1AS·1AL-1JL	Euploid 42	250
WWX-7	T3JS·3BL	Euploid 42	250

Targeted wheat/alien chromosome translocation production. From the disomic additions produced and maintained, biotic and abiotic stress screening aspects are in place. Our focus is on yellow rust, stem rust (local race), Karnal bunt, digital imaging for seed profile, and salinity/drought/heat tolerance. Interesting characters that also are observed for wheat stock development are solid stem (group-3 chromosomes), blue aleurone (group 4), and club-shaped spike (group 5). To effect these possible exchanges, we have initiated crosses of each disomic addition line with the Chinese Spring *phph* stock. We will select derivatives in the future that will possess translocations of each *Th. bessarabicum* chromosome with its homoeologous wheat group, i.e., 1E^b with 1A or 1B, or 1D through 7E^b with 7A, 7B, or 7D.

Practicality for food security and wheat productivity. We face two major concerns regarding wheat production. These are salinity and stem rust. Addition line $5E^bE^b$ was identified to contribute, and the role of chromosome additions $3E^b$, $4E^b$, and $7E^b$ also were positive. associated Ug99 stem rust resistance to the amphiploid and some addition lines. We have several *Th. bessarabicum* chromosomes contributing resistance to these stresses. The solid-stem characteristic on group 3 also is of breeding interest because, in our efforts to maximize yield with a high 1,000-kernel weight between 55 to 65 g from the D-genome synthetic hexaploids, tiller solidity will be valuable. We have in place a long-term program that is actively exploiting the translocations from the amphiploids through *phph* manipulation and also using individual disomic addition lines for targeted group transfers.

Germplasm sharing. The germplasm from the CIMMYT Wide Cross Program has been shared with various global programs and partners. Of notable mention is the USDA–ARS, Logan, Utah, (R.C-C. Wang) and Steven Xu in North Dakota. The disomic additions also were provided to Rafiq Islam at the Waite University, Adelaide, Australia. In 2011, a student from Leicester, UK, (Pat Heslop-Harrison's group) took the seven euploid translocations from the CIMMYT program with the major objective of marker designation for each of the earlier produced homozygous translocation stocks 1160, 1164, 1168, 1172, 1176, 1180, and 1184. These lines are similar to the translocation euploids mentioned earlier as WWX1 to WWX 7.

The disomic addition lines and all translocation lines are currently the subject of extensive field trials in a saline environment at Pakka Anna in the Punjab and are being studied for various morpho-physiological traits after which seed will be freely shared globally.

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Total arabinoxylan content in flour of selected wheat cultivars.

Qurrat ul ain Afzal, Saqib Arif, Mubarik Ahmed, Zia ul Hasan, Alvina Gul Kazi, and Abdul Mujeeb-Kazi.

Arabinoxylans (AXs) are an important component of wheat having nutraceutical value and functional properties, which influence the processing and baking of wheat-based products. Arabinoxylans are generally classified as water-extractable arabinoxylan (WEAX) or water-unextractable arabinoxylan (WUAX). This study was conducted on flour of different wheat varieties of Pakistan to determine the total arabinoxylan (TOAX) content and WEAX.

The TOAX and WEAX of the eight hard white spring wheat cultivars grown in different years in various locations are summarized (Table 33A and Table 33B, p. 86). The highest TOAX level across the years was in cultivars SKD-1 (15.1–20.4 mg/g, = 17.1 mg/g) and Anmol (14.6–20.3 mg/g = 17.1 mg/g), followed by that of Imdad (15.2–18.0 mg/g = 17.1 mg/g) (Table 33A). The minimum AX contents were found in the cultivar TJ-83 (11.3-12 mg/g, =11.7 mg/g). These results also agree with those of Finlay et

Table 33A. Total arabinoxylan content in the flour of eight Pakistani hard white spring wheat cultivars grown in three locations for three crop years. The values are expressed as mg xylose equivalents/g of sample and were the average of triplicates ± SE.

Location	Year	Cultivar								Mean	CV (%)
		TD-1	Imdad	Mehran	Abadgar	Moomal	Anmol	SKD-1	TJ-83		
Nawabshah	2006	12.3±0.20	15.8±0.03	13.9±0.47	14.8±1.08	14.3±1.53	15.0±0.03	15.1±0.46	11.7±0.21	14.1	10.1
	2007	13.0±0.50	16.5±1.21	13.9±0.59	15.3±1.29	14.7±1.28	14.6±0.50	15.4±0.01	11.3±0.12	14.3	11.3
	2008	12.7±0.07	15.2±0.44	13.9±0.03	15.0±0.03	14.5±0.03	15.5±0.93	15.6±1.29	11.5±0.03	14.2	10.3
Hyderabad	2006	14.4±0.24	17.9±0.03	14.6±0.06	15.5±0.07	18.2±1.27	17.3±0.32	20.4±1.97	11.9±0.03	16.3	16.5
	2007	14.5±0.27	17.9±1.21	14.2±1.48	15.8±0.27	18.8±2.68	20.3±2.10	18.5±0.09	12.0±0.32	16.5	17.1
	2008	14.5±0.03	17.8±0.86	15.0±0.55	15.2±0.60	18.6±0.07	18.8±0.03	16.5±0.07	11.8±1.48	16.0	14.9
Dadu	2006	12.9±0.40	17.7±0.69	13.7±0.26	14.9±0.16	14.5±0.06	17.4±0.39	20.1±1.77	11.6±0.10	15.4	18.4
	2007	13.0±0.31	18.0±1.15	14.5±0.39	14.7±0.98	18.3±1.17	15.1±0.10	16.4±0.24	11.8±0.36	15.2	14.9
	2008	14.2±0.41	15.8±0.06	13.8±0.53	15.4±0.60	18.7±0.62	20.2±0.84	15.5±0.10	11.7±0.21	15.7	17.2
Mean		13.5	17.0	14.2	15.2	16.7	17.1	17.1	11.7		
CV (%)		6.5	6.6	3.1	2.4	12.7	13.1	12.1	1.8		

al. (2007), who reported that pentosans range between 1.65% and 2.08% (16.5–20.8 mg/g) in flours of various wheat genotypes. The percentage of AX in flours of various cultivars with respect to TOAX content showed only minor differences (24.02–26.07%) among the cultivars. The WEAX in cultivar TJ-83 was the lowest among all. The highest WEAX was found in Imdad (6.4±0.7 mg/g), followed by that of SKD-1 (6.3±0.8 mg/g), Moomal (6.2±1.0 mg/g), and Anmol (6.0±1.0 mg/g). The level of WEAX in flour significantly ($P < 0.01$, $r = 0.941$) corresponded to the level of TOAX in flours (Table 33B). Water-extractable arabinoxylan was the major fraction in the TOAX of meal and flour. The proportion of WEAX in TOAX in the flour was larger than in the meal. On average, around 33% of AX in flour was in the form of WEAX. The larger extraction of WEAX from flour may be due to its presence in the outside of the cell wall (Courtin and Delcour 2002). A greater level of WEAX also increased the levels of TOAX in the flour.

The results also show that a larger coefficient of variation exists among the cultivars that range between 10.1–18.4%, compared to the variation within a cultivar (1.8–13.1%) (Table 33A, p. 85). The largest variation observed was in 2006 in the cultivar Dadu (18.4%), and the minimum in Nawabshah (10.1%) also in 2006. These findings clearly indicate that TOAX is largely dependent on the varietal composition and is less influenced by the location.

Larger coefficients of variation were expressed among different cultivars, ranging from 4.3–17.5% (Table 33B). The coefficient of variation has a broader range than TOAX content in the flour. Among the different cropping environments, which include different cropping location and years, the coefficients of variation ranged from 4.7–6.0%. Variation in WEAX content in the flour is largely due to cultivar differences.

Table 33B. Water-extractable arabinoxylan content in the flour of eight Pakistani hard white spring wheat cultivars grown in three locations for three crop years. The values are expressed as mg xylose equivalents/g of sample and were the average of triplicates ± SE.

Location	Year	Cultivar								Mean	CV (%)
		TD-1	Imdad	Mehran	Abadgar	Moomal	Anmol	SKD-1	TJ-83		
Nawabshah	2006	3.7±0.30	5.7±0.03	4.1±0.49	5.2±0.27	5.1±0.70	4.9±0.03	5.5±0.12	3.3±0.21	4.7	18.7
	2007	3.7±0.24	5.9±0.59	4.4±0.20	5.1±0.60	5.1±0.44	4.7±0.19	5.5±0.01	2.9±0.09	4.7	20.8
	2008	3.7±0.03	5.5±0.06	4.3±0.03	5.1±0.03	5.1±0.03	5.3±0.79	5.5±0.42	3.1±0.03	4.7	19.2
Hyderabad	2006	4.7±0.27	7.0±0.03	5.1±0.03	5.3±0.03	7.5±0.75	6.3±0.15	7.6±0.71	3.6±0.01	5.9	24.4
	2007	5.1±0.33	7.0±0.68	5.3±0.24	5.6±0.27	6.6±0.84	7.4±0.90	6.9±0.03	3.7±0.27	6.0	20.8
	2008	4.9±0.03	7.0±0.44	5.0±0.12	5.0±0.32	7.0±0.03	6.9±0.06	6.4±0.10	3.5±0.03	5.7	22.7
Dadu	2006	3.6±0.20	7.1±0.21	4.1±0.16	5.2±0.10	5.2±0.10	6.4±0.10	7.5±0.66	3.0±0.06	5.3	31.0
	2007	3.6±0.09	6.9±0.24	5.1±0.18	5.3±0.21	6.7±0.76	5.0±0.09	6.3±0.12	3.2±0.10	5.3	25.7
	2008	4.9±0.12	5.8±0.10	4.5±0.33	4.8±0.20	7.3±0.52	7.2±0.59	5.7±0.16	3.7±0.16	5.5	23.2
Mean		4.2	6.4	4.7	5.2	6.2	6.0	6.3	3.3		
CV (%)		15.8	10.7	10.0	4.3	16.7	17.5	13.5	9.2		

Effect of variety, location, and crop year on the arabinoxylan content in wheat flour.

Qurrat ul ain Afzal, Saqib Arif, Mubarik Ahmed, Zia ul Hasan, Alvina Gul Kazi, Abdul Aziz Napar, Hadi Bux, and Abdul Mujeeb-Kazi.

The arabinoxylan (mainly endosperm arabinoxylan) of flour are known to differ in extractability due to differences in molecular structure compared to the arabinoxylan accumulated in aleurone layers (Wang et al. 2006). We wanted to determine the sources of variation in arabinoxylan present in flour in addition to meal.

An analysis of variance (ANOVA) was used to analyze the effects of cultivar, growing location, and crop year on total (TOAX), water-extractable (WEAX), and water-unextractable (WUAX) arabinoxylan content of hard white spring wheats. The ANOVA models described the variation in arabinoxylan content in flour (Tables 34, 35, and 36, p. 87). The cultivar, location, and 'cultivar × location' interaction showed a significant influence on the total arabinoxylan content of wheat flour ($P < 0.001$) (Table 34, p. 87). Crop year caused negligible variation ($F = 0.118$, $P = 0.888$). The influence of the 'cultivar × year' interaction was less significant ($P < 0.01$) compared to that of the 'cultivar × location' interaction. The 'cultivar × location × year' interaction was the least significant ($P < 0.05$) source of variation in relation to TOAX content in flour. The 'location × year' interaction

was found to have an insignificant (F = 0.834, P = 0.506) effect on the TOAX in flour.

The cultivar, location and 'cultivar × location' interaction caused significant (P < 0.001) variation in the WEAX content of flour, compared to crop year (F = 0.015, P = 0.985) and the 'location × year' interaction (F = 1.049, P = 0.384), which did not seem to make any significant influence (Table 35). The 'cultivar × year' and 'cultivar × location × year' interactions led to significant (P < 0.01) effects on the WEAX content of flour.

Cultivar and location significantly (P < 0.001) influenced WEAX (Table 36), whereas, the year showed an insignificant (F = 0.192, P = 0.826) influence. The 'cultivar × location' and 'cultivar × year' interactions also had significant (P < 0.01) effects on WEAX in flour. The 'location × year' and 'cultivar × location × year' interactions did not influence significantly (P > 0.05).

Table 34. Analysis of variance for total arabinoxylan content in the flour of eight hard white spring wheat cultivars (R^2 = 0.824 (adjusted R^2 = 0.737)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	1,162.889	71	16.379	9.500	0.000
Intercept	50,583.332	1	50,583.332	29,339.679	0.000
Cultivar	773.674	7	110.525	64.107	0.000
Location	149.524	2	74.762	43.364	0.000
Year	0.408	2	.204	0.118	0.888
Cultivar x location	74.811	14	5.344	3.099	0.000
Cultiavar x year	71.348	14	5.096	2.956	0.001
Location x year	5.748	4	1.437	0.834	0.506
Cultivar x locatiokn x year	87.375	28	3.121	1.810	0.013
Error	248.264	144	1.724		
Total	51,994.485	216			
Corrected total	1,411.153	215			

Table 35. Analysis of variance for total arabinoxylan content in the flour of eight hard white spring wheat cultivars (R^2 = 0.873 (adjusted R^2 = 0.810)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	346.622	71	4.882	13.882	0.000
Intercept	6,053.668	1	6,053.668	17,214.221	0.000
Cultivar	247.559	7	35.366	100.566	0.000
Location	48.432	2	24.216	68.861	0.000
Year	1.037 E^{-2}	2	5.185 E^{-3}	0.015	0.985
Cultivar x location	14.911	14	1.065	3.029	0.000
Cultiavar x year	13.586	14	0.970	2.759	0.001
Location x year	1.476	4	0.369	1.049	0.384
Cultivar x locatiokn x year	20.648	28	0.737	2.097	0.003
Error	50.640	144	0.352		
Total	6,450.930	216			
Corrected total	397.262	215			

Table 36. Analysis of variance for total arabinoxylan content in the flour of eight hard white spring wheat cultivars (R^2 = 0.693 (adjusted R^2 = 0.541)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	276.583	71	3.896	4.569	0.000
Intercept	21,639.018	1	21,639.018	25,380.021	0.000
Cultivar	154.484	7	22.069	25.885	0.000
Location	27.814	2	13.907	16.311	0.000
Year	0.327	2	0.164	0.192	0.826
Cultivar x location	26.741	14	1.910	2.240	0.009
Cultiavar x year	31.097	14	2.221	2.605	0.002
Location x year	2.100	4	0.525	0.616	0.652
Cultivar x locatiokn x year	34.020	28	1.215	1.425	0.093
Error	22038.375	216	0.853		
Total	399.358	215			
Corrected total	1,411.153	215			

Reference.

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Effect of pentosans on dough properties of wheat.

Saqib Arif, Qurrat ul Ain Afzal, Najmus Sahar, Mubarik Ahmed, Abid Hasnain, Alvina Gul Kazi, and Abdul Mujeeb-Kazi.

Keeping in view the importance of hard wheats and pentosans as an alternate source of dietary fiber, we studied the effects of pentosans on the farinographic properties of hard white spring wheats. The results and discussion for the effect of pentosans on each of the farinographic parameters of water absorption, dough-development time, dough stability, and mixing tolerance index are presented.

Effect of pentosans on the water absorption of wheat flour. At same absorption level, the farinograms of the control flours were compared with those of pentosans added flours of different hard white spring wheata cultivars (Fig. 21). These farinograms were developed on the water absorption of the control flours and the drifts were measured in BU. The addition of water-unextractable (WUP) and water-extractable (WEP) pentosans tend to shift the farinogram upward without change in the pattern. However, the drift varied with the change of cultivar. Furthermore, the drift was increased by increasing the level of pentosan from 1% to 2%. The flours of all cultivars showed greater shifts when supplemented with WEP.

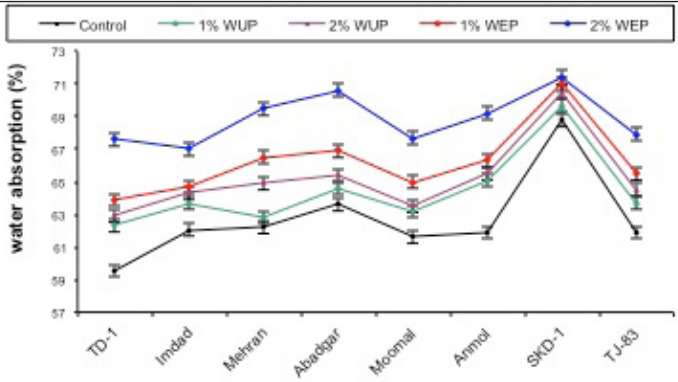

Fig 21. The water absorption of control flours and water-unextractable (WUP) and water-extractable (WEP), pentosan-supplemented flours of hard white spring wheat cultivars.

An analysis of variance determined the effects of cultivar differences, WEP, and WUP on water absorption of hard white spring wheat flour (Table 37). The results indicate that cultivar differences, WEP, and WUP contributed significantly ($P < 0.001$) in the variation of water absorption of the flour. However, WEP had a much greater influence than WUP and cultivar on the water-absorption capacity of the flour. The 'cultivar × WUP' interaction also was found to have significant influence on water absorption ($P < 0.01$) but to a much lesser magnitude compared to the individual effects of these components. The 'cultivar × WEP' interaction had an insignificant influence ($P > 0.05$) .

Table 37. Analysis of variance of water-unextractable (WUP) and water-extractable (WEP) pentosans on water absorption in the flour of eight hard white spring wheat cultivars ($R^2 = 0.911$ (adjusted $R^2 = 0.883$)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	1,377.660	39	35.325	31.686	0.000
Intercept	260,854.801	1	260,854.801	233,985.470	0.000
Cultivar	169.355	7	24.194	21.702	0.000
WUP	103.968	2	51.984	46.629	0.000
WEP	608.191	2	304.095	272.772	0.000
Cultivar x WUP	15.499	14	1.107	0.993	0.465
Cultivar x WEP	44.996	14	3.214	2.883	0.001
Error	133.780	120	1.115		
Total	686,903.840	160			
Corrected total	1,511.440	159			

Kim and D'Appolonia, (1977) confirmed the impact of pentosans on water absorption. Denli and Ercan (2000) reported that water absorption highly increased with the addition of pentosan fractions obtained from wheat and rye. Moreover, the role of pentosans in end-use quality of flour is mainly due to its higher water-absorbing capacity (Finnie et al. 2006; Du et al. 2009).

Effect of pentosans on the dough-development time of wheat flour. Pentosan-added flours took a longer time to develop optimum dough compared to the control flours (Fig. 22, p. 89). The difference in the dough-development time of the control flours and 1% WUP-added flours varied between 0.3 and 5.4 min, with the minimum and maximum differences shown by the cultivar Moomal and Imdad. Larger differences were observed in the control flours, and 2%

WUP-added flours. The minimum (0.7 min) and maximum (10.5 min) differences were exhibited in SKD-1 and Imdad, respectively. Dough-development time of WEP-added flours of all cultivars, except Abadgar and TJ-83, were longer compared to that of the control flours.

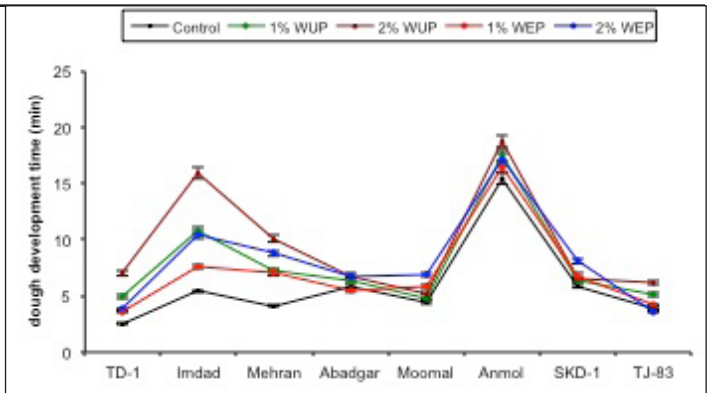

Fig 22. The dough-development times of control flours and water-unextractable (WUP) and water-extractable (WEP), pentosan-suppplemented flours of hard white spring wheat

An analysis of variance determined the effects of cultivar differences, WEP, and WUP on dough-development time in hard white spring wheat flour (Table 38). Cultivar differences, WEP, and WUP had a significant ($P < 0.001$) influence on dough-development time. We also found that the 'cultivar x WUP' interaction had a significant ($P < 0.001$) influence, but the 'cultivar x WEP' interaction did not ($P > 0.05$). Micniewicz et al. (1991) studied the effect of pentosans on dough and gluten attributes. They found a remarkable effect of pentosans on dough-development time. Pentosans have a greater capacity to absorb water compared to other flour constituents (Brennan and Cleary 2007; Rao et al. 2007). Thus, the higher amount of arabinoxylan reduced the water availability for other components like gluten and ultimately delayed the development of dough (Autio 2006).

Table 38. Analysis of variance of water-unextractable (WUP) and water-extractable (WEP) pentosans on dough-development time in the flour of eight hard white spring wheat cultivars ($R^2 = 0.897$ (adjusted $R^2 = 0.864$)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	2,895.044	39	74.232	26.894	0.000
Intercept	4,583.881	1	4,583.881	1,660.726	0.000
Cultivar	1,044.007	7	149.144	54.034	0.000
WUP	212.816	2	106.408	38.551	0.000
WEP	82.066	2	41.033	14.866	0.000
Cultivar x WUP	156.564	14	11.183	4.052	0.000
Cultivar x WEP	47.954	14	3.425	1.241	0.255
Error	331.220	120	2.760		
Total	12,737.320	160			
Corrected total	3,226.264	159			

Effect of pentosans on the dough stability of wheat flour.
The stability of WUP-added dough of all cultivars (except Anmol and Mehran) was greater than that of the control dough (Fig. 23). On the other hand, WEP-added dough of all cultivars had greater stability than that of the control dough. The difference in dough-stability time of 1% WEP-added dough and that control dough varied between 0.4 and 3.3 min. The difference increased when the control dough was compared with that of the 2% WEP-added dough and ranged between 0.5 and 8.0 min.

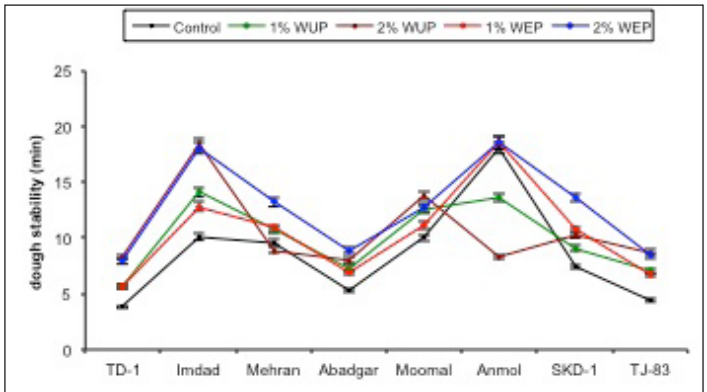

Fig 23. The dough-stabilityt times of control flours and water-unextractable (WUP) and water-extractable (WEP), pentosan-suppplemented flours of hard white spring wheat cultivars.

An analysis of variance determined the effects of cultivar, WEP, and WUP on dough stability of the hard white spring wheat flours (Table 39, p. 90). The cultivar, WEP, and WUP were found to have significant ($P < 0.001$) influence on the dough stability of wheat flour. The influence of WEP was larger than that of WUP and the cultivar. The interaction between culitvar and WUP significantly influenced the dough stability of wheat flour ($P < 0.001$). However, the 'cultivar x WEP' interaction was not a significant ($P > 0.05$) influence on dough stability. The increased stability of dough may be due to the interaction of hydroxyl groups present in hydrocolloids (Park et al. 1997; Rosell et al. 2001, 2009; Collar et al. 1999).

Effect of pentosans on the mixing-tolerance index of wheat flour. The mixing-tolerance index of control and pentosan-added dough was lower than that of the control dough (Fig. 24). However, the mixing-tolerance index value of WUP-added dough of Anmol was greater than that of the control dough.

Table 39. Analysis of variance of water-unextractable (WUP) and water-extractable (WEP) pentosans on dough stability in the flour of eight hard white spring wheat cultivars ($R^2 = 0.841$ (adjusted $R^2 = 0.789$)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	2,479.220	39	63.570	16.286	0.000
Intercept	7,708.952	1	7,708.952	1,974.924	0.000
Cultivar	547.822	7	78.260	20.049	0.000
WUP	67.286	2	33.643	8.619	0.000
WEP	231.181	2	115.590	29.613	0.000
Cultivar x WUP	411.541	14	29.396	7.531	0.000
Cultivar x WEP	71.026	14	5.073	1.300	0.217
Error	468.410	120	3.903		
Total	20,132.800	160			
Corrected total	2,947.630	159			

An analysis of variance to determine the effects of cultivar, WEP, and WUP on the mixing-tolerance index (Table 40). The influence of WEP and WUP was highly significant on dough mixing-tolerance index values ($P < 0.001$). However, the effect of WEP was greater in magnitude compared to cultivar and WUP. The interaction between variety and WUP was a less significant source of variation ($P < 0.05$). The 'cultivar x WEP' interaction did not influence significantly the mixing-tolerance index values ($P > 0.05$). The effects of individual components were far greater than the interaction effects on mixing-tolerance index.

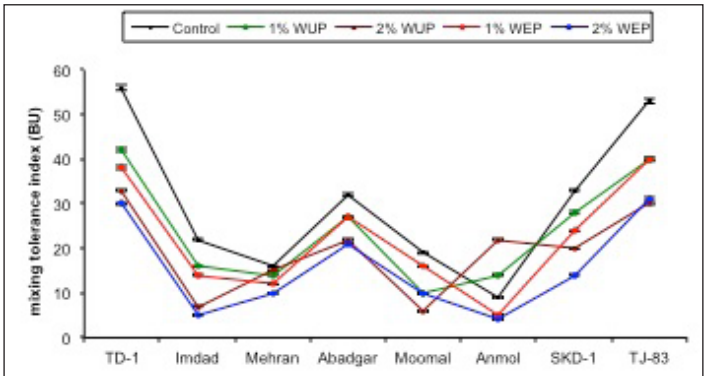

Fig 24. The mixing-tolerance index of control flours and water-unextractable (WUP) and water-extractable (WEP), pentosan-suppplemented flours of hard white spring wheat cultivars.

Table 40. Analysis of variance of water-unextractable (WUP) and water-extractable (WEP) pentosans on the mixing-tolerance index in the flour of eight hard white spring wheat cultivars ($R^2 = 0.769$ (adjusted $R^2 = 0.694$)).

Source	Type III sum of squares	df	Mean square	F	Significance
Corrected model	26,415.100	39	677.310	10.247	0.000
Intercept	16,080.100	1	16,080.100	243.269	0.000
Cultivar	4,142.300	7	591.757	8.952	0.000
WUP	1,820.333	2	910.167	13.770	0.000
WEP	3,320.333	2	1660.167	25.116	0.000
Cultivar x WUP	2,023.667	14	144.548	2.187	0.012
Cultivar x WEP	912.333	14	65.167	0.986	0.472
Error	7,932.000	120	66.100		
Total	111,260.000	160			
Corrected total	34,347.100	159			

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Relationship of dough parameters with arabinoxylan fraction and flour quality attributes.

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The relationship between water absorption and arabinoxylan fractions. We found that WA has slightly positive relationship with water-extractable arabinoxylan but does not relate with total and water unextractable arabinoxylan fractions (Table 41). Water absorption of the hard white spring wheat flours does not relate with dough parameters. The correlation coefficients of water absorption with dough-development time, dough stability, and mixing-tolerance index are 0.113, –0.086, and –0.049, respectively.

Table 41. Correlation of water absorption with arabinoxylan fractions and dough parameters.

	Total arabinoxylan	Water extractable arabinoxylan	Water unextractable arabinoxylan	Dough-development time	Dough stability	Mixing-tolerance index
Water absorption	0.194	0.235	0.140	0.113	–0.086	–0.049

The relationship between dough-development time and arabinoxylan fraction. All arabinoxylan fractions are positively related with dough-development time. However, the relationship of dough-development time is slightly greater with water-unextractable arabinoxylan ($r = 0.561$, $P < 0.05$) as compared to total ($r = 0.482$, $P > 0.05$) and water-extractable arabinoxylan ($r = 0.403$, $P > 0.05$). Biliaderis et al. (1995) recorded that water-soluble pentosans of different molecular weights imparted a significantly positive influence on dough-development time.

The relationship between dough-stability time and arabinoxylan fractions. The relationship between arabinoxylan fractions and dough-stability time was determined (Fig. 25). We found that dough stability is significantly ($P < 0.05$) and positively correlated with total arabinoxylan ($r = 0.556$), water-extractable arabinoxylan ($r = 0.502$), and water-unextractable

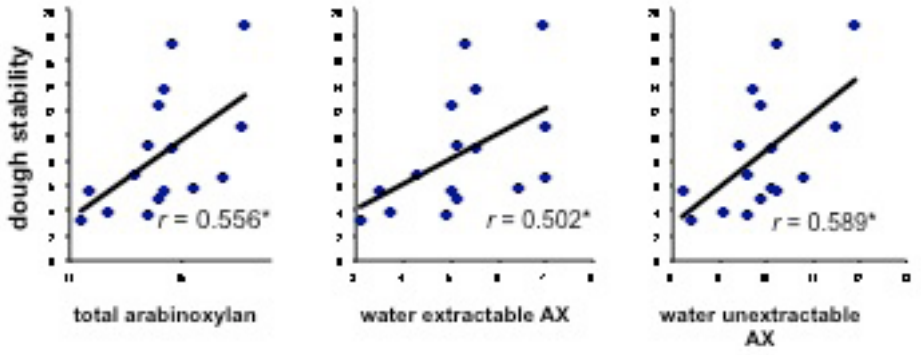

Fig. 25. The relationship between dough stability and arabinoxylan fraction.

arabinoxylan (r = 0.589). Thus, flours with higher arabinoxylan content may form dough with greater stability compared to the flours of lower arabinoxylan content. Stojceska and Ainsworth (2008) indicated that the dietary fiber significantly ($P < 0.001$) and positively influence dough stability.

The relationship between mixing-tolerance index and arabinoxylan fractions. Conversely to that of the dough-development and dough-stability times, the relationship of the mixing-tolerance index was found to be moderately negatively correlated with all arabinoxylan fractions. The correlations of mixing-tolerance index with water-unextractable arabinoxylan ($r = –0.458$, $P > 0.05$) was found to be slightly higher in magnitude than that of the water-extractable arabinoxylan ($r = –0.396$, $P > 0.05$) and total arabinoxylan ($r = –0.435$, $P > 0.05$).

The relationship between flour quality attributes and the water absorption capacity of wheat flour. The correlation coefficients between arabinoxylan and flour quality attributes are presented (Table 42). We found that water absorption did not relate with most of the flour quality attributes. Shogren et al. (1987) also found no relationship between water absorption and protein. The water absorption of flours in this study was only found to weakly positively relate with wet gluten (r = 0.316) and negatively relate with moisture (r = –0.428) contents. Adeyeye and Aye (1998) studied yam bean flour and confirmed the protein functionality in water-retention capacity of food products such as soups, dough, and baked product. The damage to starch during milling is capable of absorbing a much greater (10 times) amount of water compared to intact starch and, therefore, the amount of damaged starch is generally positively related with the water absorption of flour (Catteral 1995; Rasper and Walker 2000). In this study, all flours had a narrow range (20.9–23.1 UCD) of starch damage, because all wheats were milled by the same procedure, which possibly may be the reason that water absorption did not relate with starch damage.

Table 42. Correlation of water absorption and flour quality attributes.

	Starch damage	Falling number	Ash	Protein	Wet gluten	Dry gluten	Gluten index	Moisture
Water absorption	0.013	0.020	–0.152	0.089	0.316	–0.007	0.009	–0.428

The relationship between flour quality attributes and dough-development time. The relationship of flour quality attributes and dough-development time was determined. All wheats were milled at the same extraction rate to yield straight grade flour. The variation in ash content (0.52–0.72%) may be due to varietal differences. We found that the ash content of flour positively correlated (r = 0.30) with dough-development time. Vetrimani et al. (2005), Orth and Mander (1975), and Haridas and Rao (1991) have investigated the relationship of dough-development time with the extraction rate of flour and all reported that the higher extraction flours have longer dough-development times compared to straight-grade flours. The higher amount of bran in high-extraction flour hinders the hydration and quick development of dough (particularly gluten) resulting in a higher dough-development time. Rao et al. (1983) and Corbellini et al. (1999) also indicated that whole-meal flour has a higher dough-development time compared to that of straight-grade flour.

Dough-development time also was found to be significantly and positively correlated with falling number ($r = 0.521$, $P < 0.05$). All the flours were sound, as interpreted by a greater falling number (> 420s) and peak viscosity (950 BU). The positive relationship between falling number and dough-development time shows that the flours with greater falling number take longer for dough development. Dough-development time was weakly, but positively, corelated with protein content (r = 0.222) and gluten index (r = 0.269) but did not correlate with wet gluten (r = 0.042) and dry gluten (r = 0.041). Lin et al. (2003) observed a significant and positive relationship between protein and dough rheological properties. Cuniberti et al. (2003) recorded a positive correlation between percentage of polymeric proteins in protein and dough-development time.

The relationship between flour quality attributes and dough stability. Gluten strength is one important parameter that determines the appropriate use of wheat and is well interpreted by gluten-index values. Gelinas and McKinnon (2011) suggested that gluten index, in combination with dry gluten, is a useful test for early breeding lines. We found that dough stability is significantly ($P < 0.01$) and positively correlated with gluten index (Fig. 26, p. 93). Flours with stronger gluten may develop a more stable dough compared to weak gluten flours.

A positive correlation ($r = 0.350$, $P > 0.05$) is found between ash content and dough stability. Flours with higher ash content may form dough of greater stability. Koppel and Ingver (2010) suggest that a positive correlation between

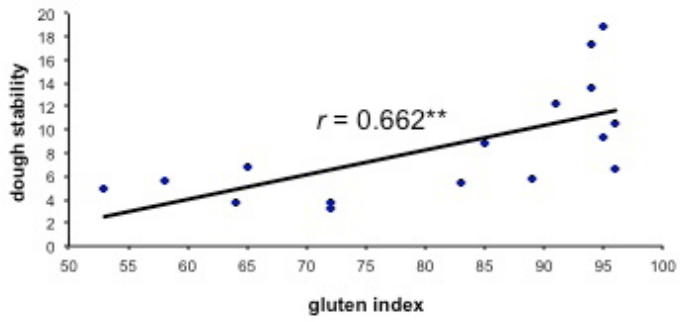

Fig. 26. The relationship between dough stability and gluten index.

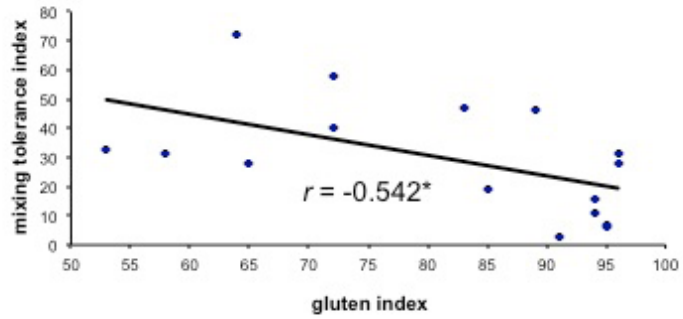

Fig. 27. The relationship between mixing-tolerance index and gluten index.

protein and dough-stability time. In this study, the protein did not correlate (r = 0.173) with dough-stability time, and also that dough-stability time exhibited no relationship with starch damage (r = 0.075), falling number (r = 0.245), wet gluten (r = –0.186), dry gluten (r = 0.004), and moisture (r = 0.044).

Relationship between flour quality attributes and mixing-tolerance index. The relationship between mixing-tolerance index and flour quality attributes was determined. The strength of gluten has a direct influence on dough properties. Gluten index is a good reflection of gluten strength, and the extent of dough tolerance after development can be seen from mixing-tolerance index values. We have found a significant but inverse relationship (r= –0.542, P < 0.05) between the mixing-tolerance and gluten indicies (Fig. 27), which indicates that stronger flour has a greater tendency to tolerate against mixing after development.

We found that the protein is negatively correlated (r = –0.321, P > 0.05) with the mixing-tolerance index. Sadeghi and Bhagya (2008) studied the effect of a mustard protein isolate fraction on pasta dough properties and indicated that the mixing-tolerance index was reduced with an increasing fortification level up to 10%. We found that the mixing-tolerance index is weakly correlated with ash (r = –0.253), dry gluten (r = –0.200), and moisture (r = 0.245), whereas it did not relate with starch damage (r = 0.077), falling number (r = 0.070), or wet gluten (r = –0.039).

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High-molecular-weight glutenin subunit variation in a spring wheat collection.

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The composition of high-molecular-weight glutenin subunits (HMW-GS) and allele frequencies in 26 Pakistani cultivars and 47 CIMMYT wheat accessions were identified. Sixteen different *Glu-1* alleles were found, three at the *Glu-A1* locus, nine at the *Glu-B1* locus, and four at the *Glu-D1* locus (Figs. 1 and 2). Those loci in the CIMMYT accessions, but not in the local cultivars, included four alleles (8, 13+19, 14+15, and 20) at *Glu-B1* and two (5+11 and 2+11) at *Glu-D1*. No Pakistani cultivars had alleles that were absent in the CIMMYT accessions (Figs. 1 and 2). These sixteen alleles at *Glu-A1*, *Glu-B1*, and *Glu-D1* loci resulted in 28 allelic HMW-GS combinations (Table 1). Of these 28 combinations in both groups, five were present only in the Pakistani cultivars (Table 1, p. 95), whereas 12 combinations were present only in CIMMYT accessions (Table 1). Ten different alleles were identified in all the Pakistani cultivars; three corresponding to the *Glu-A1* locus, five to *Glu-B1*, and two to *Glu-D1* (Fig. 1). All of the commonly found allelic variants at the *Glu-A1* locus (null, 1, and 2*) were found in the germplasm. The frequency of HMW-GS (Table 2, p. 107) and the percent partial frequency (Fig. 2) of the 2* allele were 12 and 46.15%, respectively, and were high among all the alleles at the *Glu-A1*locus. At the *Glu-B1* locus, five different HMW-GS combinations (17+18, 13+16, 7+9, 7+8, and 7) appeared in the Pakistani cultivars. Among these, subunits 7+9 and 17+18 were more frequent with a frequency and partial frequency of 9 and 34.62% (Fig. 1). Subunit 7 occurred

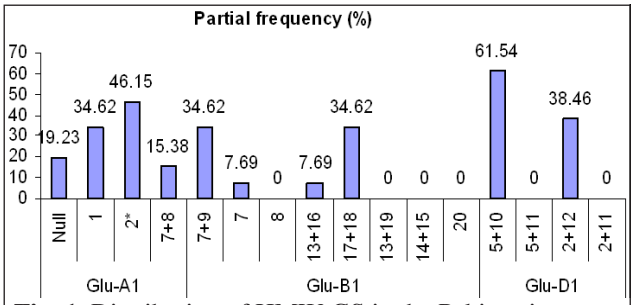

Fig. 1. Distribution of HMW-GS in the Pakistani genotypes for the *Glu-A1*, *Glu-B1*, and *Glu-D1* loci.

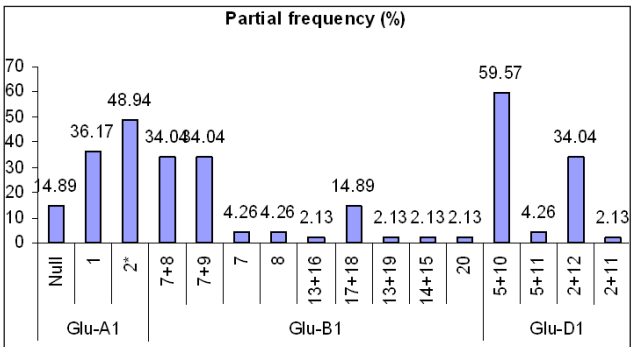

Fig. 2. Distribution of HMW-GS in the CIMMYT genotypes for the *Glu-A1*, *Glu-B1*, and *Glu-D1* loci.

Table 1. Combination of *Glu-1* alleles and quality scores in Pakistani wheat cultivars.

Glu-A1	*Glu-B1*	*Glu-D1*	Frequency	Pakistani cultivar	Quality score
1	7+8	5+10	1	Kohsar-95	10
1	13+16	5+10	1	SA-75	10
1	17+18	5+10	1	Zamindar-80	10
2*	17+18	5+10	1	Zardana-89	10
1	7+9	5+10	3	Lu-26, Punab-76, Punjab-85	9
2*	7+9	5+10	4	Karwan, Manthar, Pasina-90, Satluj-86	9
Null	17+18	5+10	2	Naeem-82, Pavon-76	8
2*	7+8,	2+12	2	Fareed-6, Shahkar-95	8
2*	17+18	2+12	4	Bulbul, Parwaz-94, Punjab-81, Punjab-96	8
2*	7	5+10	1	MH-97	8
1	13+16	2+12	1	Ufaq	8
1	7	5+10	1	Pari-73	8
1	7+9	2+12	1	Kohinoor-83	7
Null	17+18	2+12	1	SA-42	6
Null	13+16	2+12	1	Shalimar-88	6
Null	7+9	2+12	1	Blue Silver	5

Table 2. Combination of *Glu-1* alleles and quality scores in CIMMYT wheats lines and cultvars.

Glu-A1	*Glu-B1*	*Glu-D1*	Frequency	Pakistani cultivar	Quality score
1	7+8	5+10	5	Hoosam-3, KAUZ/STAR, PBW65/ROEK, SW89-5277/BOR95, Milan	10
1	17+18	5+10	2	SNI/PBW65, TE173	10
2*	17+18	5+10	3	TOBA97/BAV-92, Pastor//2*Milan/KAUZ, HUW234/LR 34	10
2*	7+8	5+10	3	PVN/YACO, F60314.76, VEE/PVN	10
1	7+9	5+10	6	NG 8201/KAUZ, RL6043/4*NAC, JUP/ZP//COC, SW91-4903/Circus, Opata//SOR, Johara-14	9
1	7+9	5+11	1	AMSEL/2*BAU	9
1	7+9	5+11	1	AMSEL/2*BAU	9
2*	7+9	5+11	1	SKAUZ	9
2*	7+9	5+10	1	Mango	9
Null	17+18	5+10	1	Crow ‘S’	8
2*	7+8	2+12	6	SHA7/VEE5, Girwill-7, Gamdow-6, Local White, BAYA ’S’, Kanchan	8
2*	17+18	2+12	1	Myna ’S’	8
2*	7	5+10	1	Attila/Pastor	8
2*	20	5+10	1	Weaver/TSC	8
2*	13+19	2+12	1	Weaver/VEEP	8
2*	7+8	2+11	1	HD29/2*Weaver	8
1	7	5+10	1	PBW343*2/Kuruku	8
Null	7+8	5+10	1	KAUZ/TSC	8
Null	7+9	5+10	0	KAUZ ’S’	7
Null	14+15	5+10	1	ESDA/SHWA	7
2*	7+9	2+12	4	SLVS/Pastor, NG8201/KAUZ/Pastor, PBW343*2/Chapio, V763.2312	7
1	8	5+10	2	KAUZ*2/MNV, Kasyon	6
Null	7+8	2+12	1	HXL8246	6
Null	7+9	2+12	2	Opata/Rayon/KAUZ, HP-1744	5

with the least frequency (2) and lease partial frequency (7.69%) (Fig. 2, p. 94). Two alleles (5+10 and 2+12) were found at the *Glu-D1* locus. Allele 5+10 had a higher frequency (16) and partial frequency (61.54%).

Sixteen HMW-GS combinations were observed in the Pakistani cultivars (Table 1, p. 95). Subunit compositions of 2*, 7+9, 5+10 and 2*, 17+18, 2+12 were the most frequent and each was observed in four of the 26 Pakistani cultivars. The second most frequent combination was 1, 7+9, 5+10 found in three of the 26 cultivars. Subunit compositions 2*, 7+8, 2+12 and N, 17+18, 5+10 were present in two cultivars. Eleven other subunit combinations had low frequencies (1) and were present in only one cultivar.

The HMW-GS quality scores for the individual cultivars ranged from 5 to 10 (Table 1). According to the quality score, Kohsar-95, SA-75, Zamindar-80, and Zardana-89 had the highest scores of 10. Seven cultivars (Lu 26, Karwan, Manthar, Pasina 90, Punjab-85, Satluj-86, and Punjab-76) had a quality score of 9. Blue Silver had the lowest score of 5.

Sixteen different alleles at the *Glu-1* locus were identified in the 47 CIMMYT accessions, three corresponding to the *Glu-A1* locus, nine to *Glu-B1*, and four to *Glu-D1* (Table 2, p. 95). At the *Glu-A1* locus, three HMW-GS (Null, 1, and 2*) were present. The frequency and partial frequency of the 2* allele were 23 and 48.94%, respectively, were among the highest of all the alleles at the *Glu-A1* locus (Fig. 2, p. 94). Subunit 1 was second most frequent with a frequency and partial frequency of 17 and 36.17%, respectively (Fig. 2). At the *Glu-B1* locus, nine different subunit combinations (17+18, 13+16, 7+9, 7+8, 7, 8, 13+19, 14+15, and 20) appeared in the CIMMYT accessions. Of these subunits, 7+8 and 7+9 were the most frequent, each with a frequency and partial frequency of 16 and 34.04%, respectively (Fig. 2). Subunits 13+16, 13+19, 14+15, and 20 occurred with the least frequency (1) and partial frequency of (2.13%) (Fig. 2). Four subunits were found at the *Glu-D1* locus (5+10, 5+11, 2+12, and 2+11). Subunits 5+10 had the highest frequency (28) and partial frequency (59.57%), and subunit combination 2+11 was the least frequent (1) and partial frequency (2.13%) (Fig. 2).

Twenty different allelic combinations of *Glu-A1*, *Glu-B1*, and *Glu-D1* were found (Table 1, p. 95). Each of the combinations, 1, 7+9, 5+10 and 2*, 7+8, 5+10, was of the highest frequency of 6 (Table 1). Combination 1, 7+8, 5+10 had the next highest frequency of 5. Fourteen different subunit combinations were the lowest in frequency at 1 and each combination was found in only one accession.

Thirteen accessions, SW89-5277/BOR95, Milan, TOBA97/BAV-92, Astor//2*Milan/KAUZ, HUW234/LR34, PVN/Yaco, SNI/PBW65, VEE/PVN, Hoosam-3, KAUZ/Star, TE173, F60314.76, and PBW65/ROEK had the maximum score of 10, indicating their use to improve bread-making quality. The second highest score (9) for HMW-GS was observed in NG-8201/KAUZ, SW91-4903/Circus, RL6043/4*NAC, OPTA//SOR JUP/ZP//COC/3, AMSEL/2*BAU, Skauz, Mango, and Johara-14. Thirteen accessions, including Crow 'S', SHA7/VEE5, Girwill-7, Gamdow-6, Local White, Baya 'S', Kamcjam, Myna 'S', Attila/Pastor, Weaver/TSC, Weaver//VEEP, HD29/2*Weaver, PBW343*2/ Kuruku, and KAUZ/TSC had a quality score of 8. Only two CIMMYT accessions, Opata/Rayon/KAUZ and HP-1744 had the lowest quality score of 5 (Table 1, p. 95).

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Phenotype-based genetic diversity in spring wheat germplasm for wheat yield improvement.

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Diverse genetic resources are necessary for adequate food production in changing environments. Germplasm is often exploited to develop improved culitvars for changing needs and challenges. Variability for economic traits in the working germplasm is very important for rewarding utilization following recombination breeding and selection. Selecting genetically diverse parents for recombination breeding in a self-pollinated species such as wheat to produce transgressive segregants has been repeatedly emphasized. Assessing the genetic diversity can also be invaluable for analyzing genetic

variability in cultivars and introgressing desirable traits from diverse germplasm into the available genetic base. A collection of 500 cultivars and breeding lines of spring bread wheat was evaluated to determine (i) the magnitude of variability in the germplasm for twelve quantitative traits, (ii) the grouping pattern of the genotypes, and (iii) identify genetically diverse and agronomically promising genotypes for exploiting in breeding programs to improve grain yield potential of wheat.

Our analysis of variance (ANOVA) revealed that the genotypes included in the study had significant variation for most of the traits. In 2008–09, spike density and chlorophyll content had no workable diversity in the germplasm. Chlorophyll content was the only trait that showed no significant variation among the genotypes in 2009–10. Spike density was significant in 2009–10. The means of all traits decreased from 2008–09 to 2009–10. The range for grain yield was 10.5–71.0 g/plant in 2008–09 and 10.3–66.8 g/plant in 2009–10. The number of kernels/plant ranged from 253 to 1,812 in 2008–09 and 246 to 1,764 in 2009–10. The minimum and maximum kernel size for the year 2008–09 was 25.6 and 68.6 g/1,000 kernels, respectively. The range in kernel size in 2009–10 was 24.7–66.4 g/1,000 kernels. The number of spikes/plant was 6.3–55.2 in 2008–09 and 6.1–53.7 in 2009–10. The range for the number of spikelets/spike was 16.7–27.2, maximum number of fertile florets/spikelet was 3–508, spike dry weight was 2.3–5.9 g, plant height was 62.1–129.4 cm, spike length was 8.1–16.8 cm, awn length was 0.0–13.6 cm, spike density was 1.5–2.2 spikelets/cm, and chlorophyll content was 36.9–65.8 in 2008–09. In 2009–10, the number of spikelets/spike was 16.2–26.5, maximum fertile florets/spikelet was 2.9–5.6, spike dry weight was 1.8–5.6 g, plant height was 60.9–126.8 cm, spike length was 7.8–16.0 cm, awn length was 0.0–13.2 cm, spike density was 1.4-4.7 spikelets/cm, and chlorophyll content was 35.5–63.2.

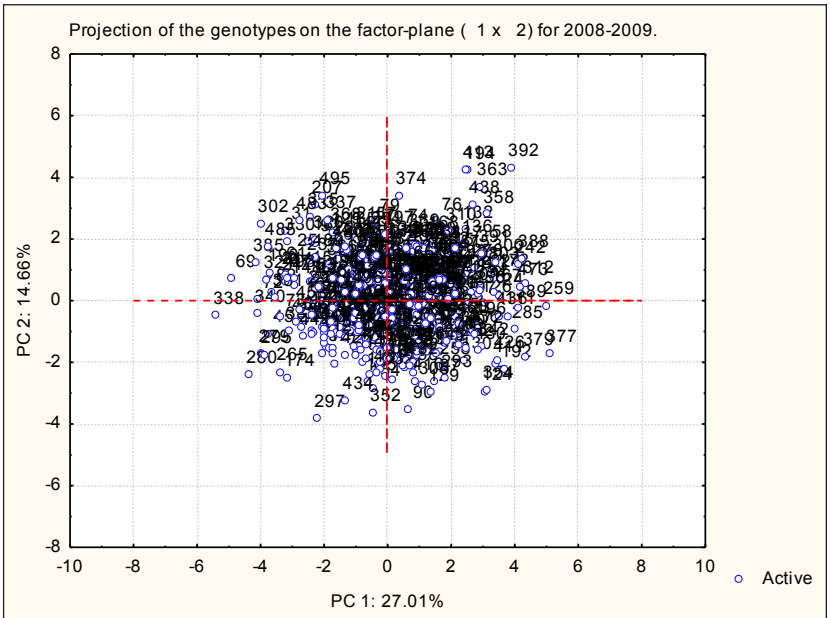

Fig. 3. Two-dimensional ordination of 500 wheat genotypes on prinicpal components PC1 and PC2 in 2008–09.

Of the 12 principal components (PCs), the first four had eigen values (latent root) > 1 (significant) in 2008–09 and 2009–10. The other eight PCs explained a nonsignificant amount of variation and were not worth interpreting. For 2008–09 and 2009–10, the first four PCs showed 62.03% and 64.47% variation, respectively, in the germplasm. The first PC accounted for 27.01% of the variance, the second for 14.66%, the third for 11.77%, and the fourth for 8.59% in 2008–09 (Fig. 3). The first PC showed 27.76% of the total variance, the second for 16.28%, the third for 11.86%, and the fourth for 8.57% in 2009–10 (Fig. 4).

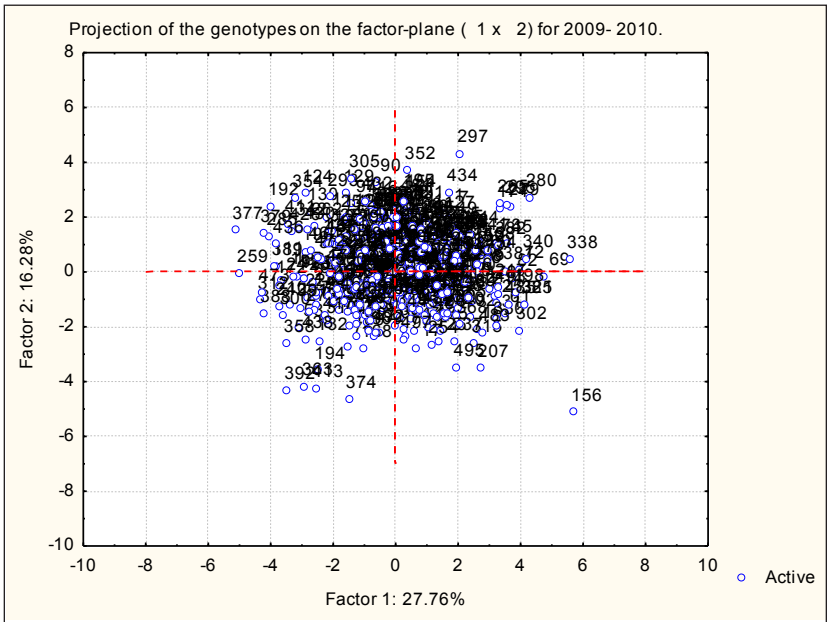

Fig. 4. Two-dimensional ordinations of 500 wheat genotypes on PC1 and PC2 in 2009–10.

The importance of a trait coefficient for each significant principal component was determined. The first PC was highly related to grain yield, number of kernels/plant, spike dry weight, and

spike length for both years, implying that PC1 is a weighted average of these four traits. The number of spikes/plant, 1,000-kerne. weight, and the number of kernels/plant was of significant importance in PC2 in 2008–09. The important traits in PC2 in 2009–10 were the number of spikes/plant, 1,000-kernel weight, number of kernels/plant, and spike density. The third PC was related to the number of spikelets/spike and PC4 to 1,000-kernel weight and the maximum number of fertile florets/spikelet in 2008–09. The significant trait in PC3 was the number of spikelets/spike and in PC4 were 1,000-kernel weight and spike length in 2009–10. The projection of traits on PC1 and PC2 revealed that the number of kernels/plant, the number of spikes/plant, and the number of spikelets/spike were positively related to grain yield in both years. Spike density was opposite grain yield and other yield contribution traits on PC1 in both years and, therefore, it had a negative correlation with all other traits. Becaise the variation in chlorophyll content wasa not significant among the genotypes, it was not projected significantly on the first two PCs by the principal component analysis. The projection pattern of the traits on first two PCs for both years indicated that the key yield-contributing traits were the number of kernels/plant, spike dry weight, and spike length. The projection of genotypes on the first two PCs was useed to identify diverse groups of parents for better transgressive segregation. The projection of genotypes on PC1 and PC2 showed a population structure in both years (Figs. 3 and 4). For 2008–09, the following hetrotic groups were identified: 192, 363, 392, 414, and 488 (Kambara-1, KAUZ//TFAU/VEE#5, V-97100, and Jauhar-78) were opposite to 174, 297, 265, and 280 (Local White, Condor 'S'/ANA75//Condor 'S'/MUS 'S', and Abadgar-93) (Fig. 3). Genotype 338 (Qafzah-21) was in contrast to 259 (Goshawk 'S'). Genotype 374 (Hibara-3) had the maximum diversity from 352 (Bolsena 'S'). Genotypes 69, 385, and 485 (Oasis AGA/3*YR, IZAZ-1, and Abadgar-93) were opposite to 124, 192, 334, and 377 (Webelli/Kambi, Kambara-1, Crow 'S'/BOW#1, and Qafzah-18) (Fig. 3). In 2009–10, the most diverse parents were 280 (BLS/KLT 'S') vs. 392 (KVZ/3/TOB/CFTN//BB/4/BLO 'S'/5/VEE#5/6/BOW 'S'/3/YDING 'S'//BB/CHA), 352 (Bolsena 'S') vs. 374 (Hubara-3), and 302 (Parula) vs. 307 (BUC 'S'/BJY 'S'/3CNDR 'S'/ANA//CNDR 'S'/MUS 'S') (Fig. 2, p. 94).

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Association mapping identifies drought-tolerance QTL on wheat chromosome 2A.

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Most of the association mapping studies so far have been reported under favorable conditions. In the previous studies, a number of QTL for agronomic traits (spike length, spikelets/spike, grains/spike, plant height, spikelet density, and 1,000-kernel weight) were identified on different chromosomes. For complex traits, such as drought tolerance and yield, the knowledge of the interaction between the marker/QTL and the environment are necessary to efficiently utilize marker-assisted selection in plant breeding. Comparing the performance of the same genotype across environments, the best-suited environment for the expression of a particular QTL, can be identified, but hundreds of markers are required for sufficient mapping resolution covering the whole genome of wheat. Therefore, targeting an individual linkage group is a quite reasonable strategy. This study identified the population structure among a collection of 108 germplasm lines, the extent of LD decay on chromosome 2A, and the association of SSR markers with drought-tolerance traits on chromosome 2A.

Association mapping analysis was performed on a panel of 108 diverse wheat accessions to dissect the genetic background of drought-adaptive traits. These genotypes were characterized with 25 SSR loci on chromosome 2A. Sixteen agronomic traits were evaluated under well-irrigated and drought-stress conditions. The population structure and kinship were inferred on the basis of 30 unlinked SSR loci covering all 21 wheat chromosomes, which enhanced the mapping strength by eliminating spurious associations.

The admixture, model-based analysis with the STRUCTURE software was used to investigate the genetic relationship among the population. An optimal number of subpopulations was identified when K was set to three, because the likelihood peaked at K = 3 in the range of 2–20 subpopulations. The number of genotypes assigned to each inferred subpopulation was 33, 37, and 36. The FST values between all subpopulations were significant ($P < 0.001$), confirming a real difference among these subpopulations and supporting the prevalence of genetic structure.

A mixed, linear model approach was used to determine marker–trait associations (MTAs) for the 16 phenotypic traits and 28 SSR loci on chromosome 2A. Subpopulations were used as covariates for association mapping analysis. A total of 10 MTAs were identified for five morphological traits under drought-stress conditions at a probability level of 0.001 with the range of 3.63 to 29.16% of the phenotypic variation (Table 3). Under well-irrigated conditions, only four MTAs were found, and the r^2 range was 3.55 to 10.04 (Table 4). The highest number of associations was observed for awn length under drought stress. Other traits that showed significant associations under drought include days-to-heading, glaucausness, shoot length, and the stress susceptibility index. Under well-irrigated conditions, significant marker trait associations were found for 1,000-kernel weight, shoot length, and coleoptile length. Nineteen SSR markers showed significant association with morphological traits, 11 (*Xcfa2121*, *Xwmc382*, *Xwmc407*, *Xgwm122*, *Xwmc445*, *Xwmc552*, *Xbarc212*, *Xgwm445*, *Xwmc445*, *Xbarc5*, and *Xgwm558*) were associated only with one trait and, therefore, can be considered as trait-specific MTAs. Markers *Xcfa2099*, *Xcfa2043*, *Xcfa2263*, and *Xgwm95* were associated with two traits, and markers *Xcfa2086*, *Xbarc124*, *Xgwm312*, and *Xgwm265* were associated with three traits.

Table 3. Association (r^2) of the SSR markers with drought-related traits under stress conditions in wheat.

Trait	QTL	Flanking marker/s	R^2 (%)	P (Q+K)
Days-to-heading	*QDth.uaf.2A.3*	*Xcfa2099*	4.35	0.0063
	QDth.uaf.2A.2	*Xcfa2121*	8.1	0.0000
Awn length	*QAl.uaf.2A.2*	*Xwmc407*	12.16	0.0000
	QAl.uaf.2A.2	*Xcfa2099*	29.16	0.0000
	QAl.uaf.2A.2	*Xcfa2263*	5.82	0.0001
Glaucausness	*QGla.uaf.2A.2*	*Xwmc445*	8.75	0.0038
	QGla.uaf.2A.2	*Xcfa2043*	5.41	0.0005
	QGla.uaf.2A.2	*Xbarc212*	5.0	0.0084
Shoot length	*QSl.uaf.2A.2*	*Xcfa2263*	6.75	0.0003
Stress-susceptibility index	*QSsi.uaf.2A.2*	*Xgwm265*	4.93	0.0031

Table 4. Association (r^2) of the SSR markers with morphological traits under normal conditions in wheat.

Trait	QTL	Flanking marker/s	r^2 (%)	P (Q+K)
1,000-kernel weight	*Qgw.uaf.2A.3*	*Xwmc455*	10.04	0.002
Shoot length	*QSl.uaf.2A.3*	*Xbarc5*	4.17	0.007
	QSl.uaf.2A.3	*Xgwm265*	4.84	0.003
Coleoptile length	*QCl.uaf.2A.1*	*Xbarc124*	4.35	0.006

Under drought stress conditions, *Xcfa2099* and *Xcfa2121* showed a significant association with number of days to heading (Table 3). Awn length, which showed the maximum number of MTAs, was associated with primers wmc382, wmc407, cfa2043, cfa2086, cfa2099, cfa2263, barc124, gwm95, gwm312, and gwm122. Only three primers, wmc 382, wmc 407, and gwm312, showed non-overlapping associations. Marker–trait associations for glacousness were found with primers wmc445, wmc552, cfa2043, cfa2086, barc212, gwm265, and gwm445. Overlapping associations for glacausness were observed only for cfa2043, cfa2086, and gwm445. Shoot length was associated with cfa2263, barc124, gwm95, and gwm312, and the stress-susceptibility index with cfa2086 and gwm265. Under favorable conditions, only six marker–trait associations were found, and shoot length showed a maximum number of three MTAs. Markers *Xbarc5*, *Xgwm265*, and *Xgwm312* showed a significant association with shoot length under well-irrigated conditions, and gwm312 was associated with shoot length under both well-irrigated and drought environments (Table 4). Coleoptile length also showed two MTAs with *Xbarc124* and *Xgwm558*. Only one MTA was found for 1,000-kernel weight with wmc445 under favorable conditions.

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Association mapping identifies yield QTL on wheat chromosome 3A.

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Association mapping, which has been widely used in human and animal genetics where large segregating populations are not possible to develop, has been validated in plants. Association mapping has many advantages over the traditional FBL-based, QTL mapping including higher QTL resolution, higher allele coverage, and readily available mapping populations in the form of natural germplasm. Initially, the presence of a population structure within the mapping population was not statistically handled, causing spurious associations, compared to FBL mapping, but the recent statistical developments, such as Q and K estimates, substantially reduced false associations due to population structure. These matrices take into account population structure and combine it to covariate in association tests. Gene mapping studies in wheat using the assoication mapping approach are still few. Most of these studies have focused on individual chromosomes, where QTL have been previously identified by linkage analysis, or on monogenic traits. Grain yield increment is the most important challenging objective faced by plant breeders. Several yield-related QTL on chromosome 3A were identified using this RICL population. Covering the whole genome of hexaploid wheat with sufficient mapping resolution requires hundreds of SSR probes, therefore, targeting individual linkage group is a reasonable strategy. Marker–trait associations for grain yield traits on chromosome 3A of hexaploid spring wheat were determined. We analyzed population structure, linkage disequilibrium, and associations of SSR markers with 12 yield-related traits.

A panel of 94 diverse hexaploid wheat accessions was used to map QTL underlying the yield-related traits on chromosome 3A. Population structure and kinships were estimated using unlinked SSR markers from all 21 chromosomes, which eliminated spurious associations and enhanced mapping strength. Analysis of variance revealed significant difference among accessions; however, the 'genotype × year' interaction was not significant for most yield-related traits.

An admixture, model-based analysis with the STRUCTURE software identified an optimal number of subpopulations when K was set at 7, because likelihood peaked at K = 7 in the range of 2–20 subpopulations. The number of genotypes assigned to each inferred subpopulation ranged from 8 to 16. The FST values between all subpopulations were significant ($P < 0.001$), confirming the real difference among these subpopulations and supporting the prevalence of genetic structure.

The unlinked markers used to detect population structure also were used to determine background LD (unlinked LD). The background LD in the genome, caused by the genetic structure, was used to set a critical value of LD for markers on chromosome 3A. The unlinked r^2 value ranged from 0.000 to 0.1303 for all unlinked loci pairs, with an average of 0.0014. The 95th percentile of the distribution of unlinked r^2 (0.015) was used as a population-specific threshold for this parameter as an evidence of LD because of linkage. The syntenic r^2 was obtained from the analysis of 23 SSRs on chromosome 3A. The value of the pairwise syntenic r^2 ranged from 0.0007 to 0.167 with an average of 0.016, significantly higher than the average of the unlinked r^2.

A decay scatterplot of the syntenic LD values of r^2 in population was made. The extent of LD on chromosome 3A was ~40 cM, with a critical value of 0.015. About 40% of the LD pairs were found with an $r^2 < 0.015$. The chromosomal region where all pairs of flanking loci were in LD, were referred to as an LD block. One LD block was observed on chromosome 3A between 37–46 cM, including markers *Xbarc45*, *Xgwm2*, *Xgwm674*, and *Xgwm30*.

We used a mixed linear model approach to determine marker–trait associations for 12 yield traits and 23 SSRs on wheat chromosome 3A. The results were similar for both years. A mixed linear model approach identified six QTL for four traits that individually accounted for 10.7–17.3% of the phenotypic variability (Table 5). Primers cfa2134 (51 cM) and gwm369 (14 cM) were significantly associated with maximum number of fertile florets/spikelet. Grain yield/plant, plant height, and spike length were significantly associated gwm155 (85 cM), wmc527 (53 cM), gwm155 (85 cM), and gwm369 (14 cM).

Table 5. Association (r^2) of SSR markers with yield traits in wheat. Map position (cM) was based on the consensus map Ta-SSR-2004; r^2 indicates the percentage of the total variation explained at the loci significant at a level of $P < 0.01$.

Trait	QTL	Flanking marker/s	r^2 (%) 2008–09	P (Q+K) 2008–09	r^2 2009–10	P (Q+K) 2009–10
Grain yield	*QGyld.uaf.3A.3*	*Xgwm155–Xwmc215*	17.3	0.0020	16.9	0.0030
	QGyld.uaf.3A.2	*Xwmc527–Xwmc269*	16.1	0.0023	15.3	0.0029
Plant height	*QPht.uaf.3A.3*	*Xgwm155–Xgwm215*	10.7	0.0093	10.7	0.0090
Spike length	*QSpl.uaf.3A.1*	*Xgwm369–Xcfd79*	16.8	0.0062	14.9	0.0013
Fertile florets/spikelet	*QMff.uaf.3A.2*	*Xgwm369–Xcfd79*	15.3	0.0070	13.6	0.0090
	QMff.uaf.3A.1	*Xcfa2134–Xwmc527*	15.4	0.0098	14.3	0.0016

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ITEMS FROM POLAND

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Pollen grain morphogenesis in Triticeae and Avena amphiploids.

R. Kosina, M. Florek, and P. Tomaszewska.

The world of plants offers a wealth of hybrid forms, especially within the grass family with wind pollination exp ression. The plant breeding system ranges between a recombinational generative reproduction and a replicative vegetative one. At first, variation is created by self-fertilization in autogamy and, secondly, by geitonogamy and cross-fertilization in allogamy (Richards 1988). The balance between auto- and allogamy depends on the floral characteristics, such as cleistogamy or chasmogamy. As early as 1945, Harlan showed in *Bromus carinatus* that such variation may be expressed on in single plant (Harlan 1945). The tribe Triticeae includes species presenting different breeding systems; e.g., from the cleistogamic *Hordeum jubatum* to the allogamic *Secale cereale*. In the genus *Avena*, *A. barbata* is nearly cleistogamic and, in *A. fatua*, 12% outcrossing has been detected (Grant 1981).

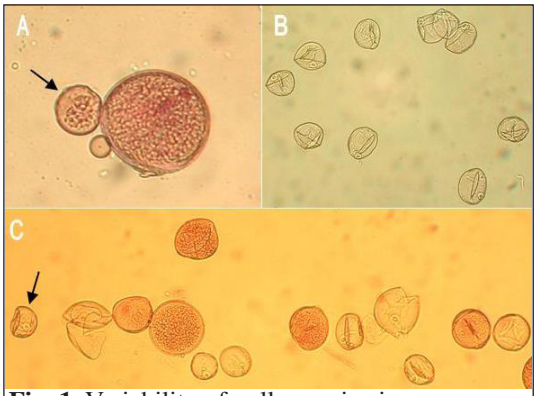

Fig. 1. Variability of pollen grains in a micrograin (arrow) in *Lophopyrum elongatum* (A), dead, empty grains in *L. elongatum* (B), and a large, unreduced, biporate (arrow) and small dead grains (C) in an '*Avena barbata* / *A. sativa* ssp. *nuda*' amphiploid.

Pollen quality is usually poor in a hybrid population but can be rapidly improved by natural polyploidization or by plant breeders after the application of colchicine. An example of such pollen variability in a vigorous plant of *Lophopyrum elongatum* produces some amount of micrograins (Fig. 1A) and dead pollen (Fig. 1B). This highly allogamic plant does not show any sign of hybridity and probably has a cryptic hybrid nature, maybe of interspecific origin. A similar pollen grain development was noted in an *Avena* amphiploid (Fig. 1C), in which a biporate grain was also detected. Kihara (1982) presented a pollen grains with two pores in the F_1 a of '*Triticum turgidum* / *Aegilops tauschii*' cross, however he did not mention it. In addition, Kihara also documented partial, unequal, and multipolar cytokineses. Pollen grains from a complex hybrid between *T. aestivum* and *L.* (*Agropyron*) *glaucum* show that multiple cytokineses and elimination of micronuclei occurred during their development (Cicin 1978). Special attention should be given to the morphogenesis of multiporate pollen grains. Such morphs were detected in Triticeae amphiploids between *S. cereale* and some *Aegilops* species (Kalinowski et al. 2001). In a single grain, many pores developed as separate units or as a complex pore formed by two or three joined together. Sometimes the pore is incompletely expressed. Li et al. (2005) presented data on pollen grain morphogenesis in a *T. aestivum–Leymus mollis* partial amphiploid. They found anomalous pollen grains having as many as 10 pores. Ma et al. (2009), in the Panicoideae, discovered that multiporate pollen grains are expressed in apomictic plants. Apomixis is often linked with high level of polyploidy (Grant 1981; Quarin et al. 2001). In the genus *Avena*, multiporate pollen grains also developed in a series of hybrids and

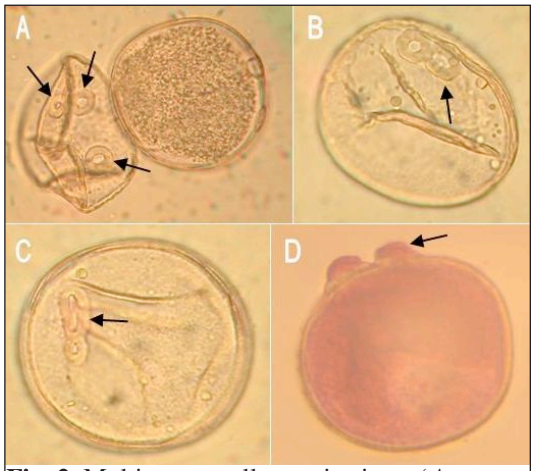

Fig. 2. Multiporate pollen grains in an '*Avena barbata* / *A. sativa* ssp. *nuda*' amphiploid; three pores form separate units (A), two pores develop as one unit (B), a complex structure of three pores (C), and simultaneous germination of a pollen grain through two pores (D).

amphiploids of high ploidy level (Fig. 2, p. 102). The development of pores is variable, but pollen germination through many pores (Fig. 2D) seems to be most important for pollen tubes competition. This competition creates a genetical status of a hybrid population, wild or cultivated. We concluded that high ploidy level, hybridity, multiporate pollen grains. and apomixis often are linked.

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Cytogenetic events in amphiploids: Triticeae versus Avena

R. Kosina, M. Florek, and K. Markowska.

Cicin (1978) showed that Triticeae amphiploids, derived from hybrids of *Triticum* and *Lophopyrum* through a colchicine treatment, have a stabilized meiosis and improved pollen quality. Young amphiploids of wheat undergo intragenomic alterations occur despite a gross genomic change (Feldman and Levy 2005), including the nonrandom elimination of coding and noncoding DNA sequences, epigenetic changes such as DNA methylation of coding and noncoding sequences, and activation of genes and retroelements. These changes diploidize meiosis and alter gene expression. Han et al. (2003) did not find gross chromosome changes that could be accompanied by the abovementioned means. However, Kosina and Heslop-Harrison (1996) detected structural changes in chromosomes in a young, trigeneric hybrid of the Triticeae. Such changes also are common in stabilized alloploid species. For instance, Leggett et al. (1994) found intergenomic translocations, mainly terminal, in the wild tetraploid oat *Avena maroccana*.

We exemplify cytogenetic behavior in two, ~50-year-old amphiploids. In a '*Triticum timopheevii* (4x) / *Aegilops umbellulata*' (2x) amphiploid (Fig. 3), an extremely rare high decondensation of anaphase-telophase chromosomes was discovered (Fig. 3A). A delayed division of telocentric chromosome (Fig. 3B), a dicentric chromosome (Fig. 3C), nondisjunction of mitotic sister chromosomes (Fig. 3D), tri- (or multi-) polar telophase (Fig. 3E), and the elimination of micronuclei (Fig. 3F) were noted cytogenetic abnormalities. Studying decondensed chromosomes of *Drosophila*, Steffensen et al. (2001) concluded that their status caused disorder in anaphase, chromosome breakage, and apoptosis. Possibly, multipolar telophases are related to this decondensation. The creation of telocentrics is associated with misdivision of the centromere. In common wheat, Vega and Feldman (1998) discovered that two doses of the *Ph1* gene distinctly increased centromeric misdivision. Both examples (Fig. 3B, C) prove that an interaction between the kinetochore and spindle microtubules is disordered. Sears and Câmara (1952) showed that in *T. aestivum* a dicentric chromosome is normally divided during root mitoses. Such a chromosome moving to the right pole is functionally normal (Fig. 3C). However,

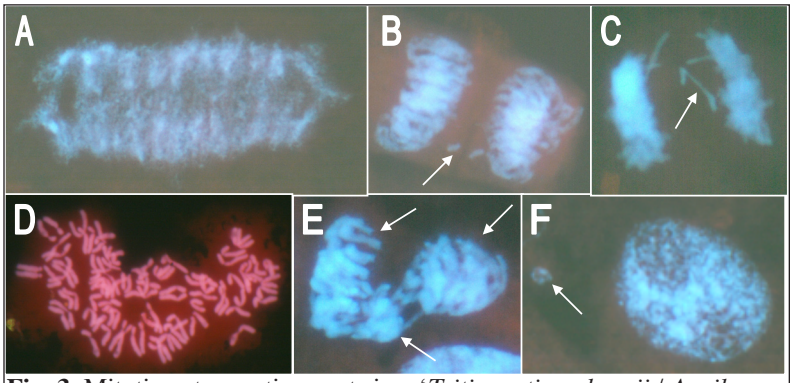

Fig. 3. Mitotic cytogenetic events in a '*Triticum timopheevii* / *Aegilops umbellulata*' amphiploid; an anaphase with highly decondensed chromosomes (A), a telophase with a delayed divided telocentric (B), a delayed dicentric chromosome (C), mitotic nondisjunction (D), tri-polar telophase with bridges (E), and a micronucleus (F).

Brasileiro-Vidal et al. (2005) reported on dicentric chromatids forming bridges in 'wheat / *Thinopyrum ponticum*' derivatives. They also found that the lack of H3 phosphorylation in a pericentric region causes dysfunction of the centromere and lagging chromosomes (Fig. 3D, p. 103). A similar cytogenetic behavior was found in an octoploid selection of an *Avena* amphiploid, '*A. barbata* (4x) / *A. sativa* ssp. *nuda*' (6x) (Fig. 4), which was manifested in the form of hypoploidy (Fig. 4A), and the presence of telocentrics (Fig. 4B), ring chromosomes (Fig. 4C), micronuclei (Fig. 4D), and bridges (Fig. 4E). In this amphiploid, the breakage-fusion-bridge cycle is active. Tang et al. (2012) showed such cytogenetic instability in somatic tissues of a wheat–rye allopolyploid and attribute the instability to young hybrid offspring. In another complex Triticeae hybrid, rings and telocentrics also were common (Kosina and Heslop-Harrison 1996). Thus, in general, phenomena that are components of cytogenetic instability in hybrids are the same among the grasses or in higher plants.

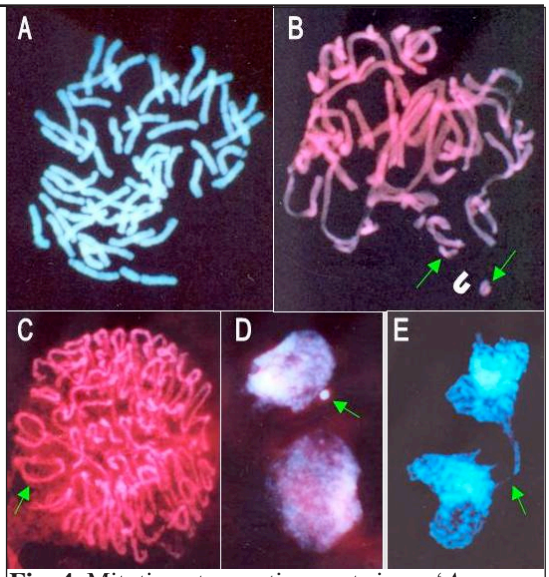

Fig. 4. Mitotic cytogenetic events in an '*Avena barbata* / *A. sativa* ssp. *nuda*' octoploid, a hypometaphase (A), a metaphase with two sister telocentrics (B), a prophase with a large ring (C), a micronucleus (D), and telophase bridges (E).

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The GISH nuclear architecture in Triticeae and Avena amphiploids.

R. Kosina, M. Florek, and K. Markowska.

Schwarzacher et al. (1989) were the first to successfully use genomic *in situ* hybridizaiton (GISH) to detect parental genomes in plant hybrids specifically a '*Secale africanum* / *Hordeum chilense*' hybrid. This research showed that parental genomes are ordered through a cell cycle, and sets of maternal and paternal chromosomes are positioned side-by-side or concentrically. This spatial arrangement of chromosomes influences gene expression. Linde-Laursen and Jensen (1991) proved that parental genomes also can be identified by a Giemsa method and/or by dimensions of chromosomes. In an '*H. vulgare* / *Psathyrostachys fragilis*' hybrid, chromosomes of *Psathyrostachys* were longer, less stained by Giemsa, and distributed outside of the *Hordeum* chromosomes. A pair of *Hordeum* SAT-chromosomes was nonrandomly arranged within the metaphase plates. In another study, two sets of parental chromosomes could be separated in very distinct sectors in a hybrid nucleus Kosina and Heslop-Harrison (1996).

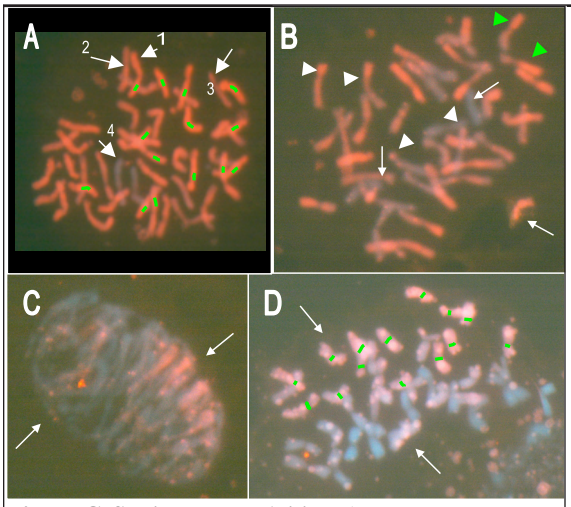

Fig. 5. GISH in root nuclei in a '*Triticum timopheevii* / *Aegilops umbellulata*' amphiploid. Genomic DNA of *Ae. umbellulata* was used as a probe. *Ae. umbellulata* hromosomes are stained green (A). Four types of chromosomes are marked by arrows, translocations by arrowheads, and one reciprocal by green arrowheads (B). A Rabl prophase with red *Ae. umbellulata* chromosomes arranged side-by-side with wheat chromosomes (C). A side-by side chromosomes arrangement with rose chromosomes of *Ae. umbellulata* marked in green.

umbellulata genomes need to be studied at an increased level of stringency (80–85%). Better discrimination of *Ae. umbellulata* chromosomes and multiple translocations between U-, A-, and G-genome chromosomes (red, weak red, and violet chromosomes) is shown (Fig. 5). The translocations are mainly terminal. Some translocations are between wheat genomes and some are of the Robertsonian type (green arrows). In a prophase Rabl arrangement (Fig. 5C) as well as at metaphase (Fig. 5D), the side-by-side separation of wheat and *Ae. umbellulata* chromosomes is distinct. Zhang et al. (1998) proved that U-genome chromosomes are homeologous to the A, B, and D genomes of Chinese Spring wheat. The B genome is close to the G genome; chromosomes 2G, 3G, 5G, and 6G are structurally similar to their Chinese Spring equivalents in the B genome (Maestra and Naranjo 1999). In addition, Devos and Gale (2000) highlighted extensive structural rearrangements in the U genome. In a '*T. aestivum* (ABD genomes) / *Ae. biuncialis* (UM genomes)' amphiploid, chromosomes of *Ae. biuncialis* are clearly discriminated (Molnár et al. 2009).

In the *Avena* amphiploid, the A genome of *A. sativa* were discriminated well (light green-yellow) by an A^sA^s-genome probe from *A. nuda*. Many were terminal intergenomic translocations and also Robertsonian type (Fig. 6). Hayasaki et al. (2000) detected many intergenomic translocations in polyploid species of *Avena*. However, Irigoyen et al. (2001) did not find such rearrangements between the genomes of *A. barbata* (AABB). The latter

Here, we present cytogenetic pictures of chromosomes prepared by GISH for two grass amphiploids. DNA in a Triticeae amphiploid, '*Triticum timopheevii* (4x, AAGG) / *Aegilops umbellulata* (2x, UU)' was detected using an *Ae. umbellulata* probe. In an *Avena* amphiploid, '*A. barbata* (4x, AABB) / *A. sativa* ssp. *nuda* (6x, AACCDD)', a probe was prepared from the diploid species *A. nuda*. Baum (1977) reports that *A. nuda* has the AA genomes. Badaeva et al. (2005) considered this species at a subspecific rank within *A. strigosa* with the A^sA^s genomes. In the Triticeae, amphiploid chromosomes of the U genome were discriminated by a light red colour with green marks (Fig. 5A), however, at a 70–75% stringency level, chromosomes of the wheat A and G genomes and the U genome are discriminated in four groups: (1) U genome, (2) a weaker red wheat genome, (3) a other weak, red wheat chromosomes, and (4) a special pair of violet chromosomes most distantly related to the U genome. The relationships between the wheat (AG) and *Ae.*

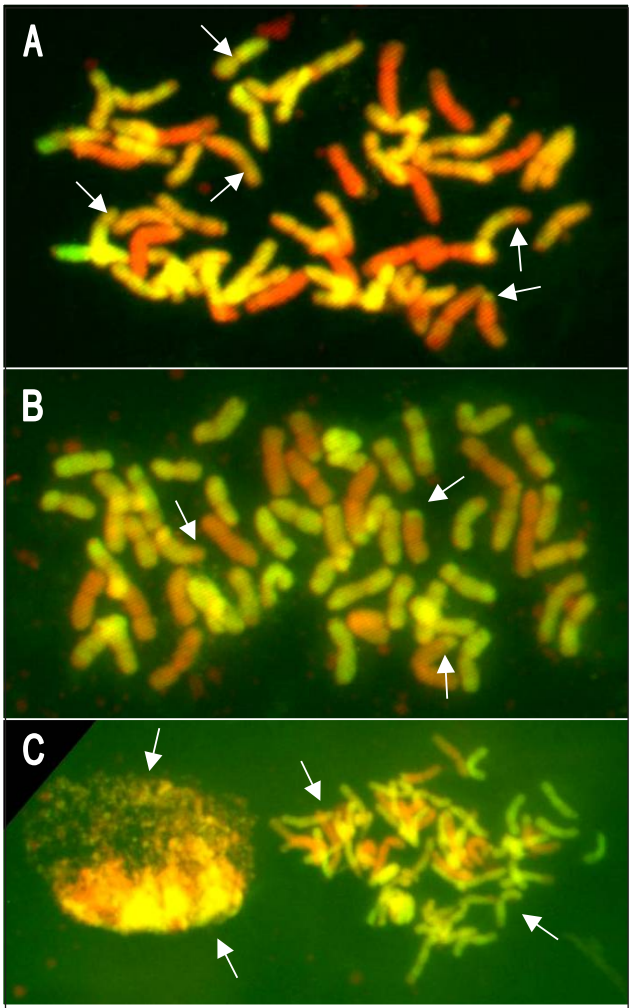

Fig. 6. GISH in the root nuclei in an '*Avena barbata* / *A. sativa* ssp. *nuda*' octoploid amphiploid. Genomic DNA from the diploid species *Avena nuda* (A^sA^s) was used as a probe to detect metaphase yellow and green chromosomes (A and B) and terminal and Robertsonian translocations (arrows). A side-by-side arrangement of chromosomes in prophase and metaphase (C).

study successfully hybridized the As120a sequence from *A. strigosa* (A^sA^s) to the A genome of *A. barbata*, but not to B genome. The selection of this octoploid from a decaploid resulted in the rejection of two genomes. Six A^s genomes in the octoploid metaphase proves high homology between the A and D genomes (Fig. 6B, p. 105). Linares et al. (1998) discovered that the sequence As120a from *A. strigosa* is absent in C genome. In our material, 14 red chromosomes were assigned to the B or C genomes. Because no translocations between the A and B genomes were found by Irigoyen et al. (2001), the red–green translocations (Fig. 6B) probably are between chromosomes of the A and C genomes. Such A–C translocations have been discovered by Leggett et al. (1994) in *A. maroccana*. Our conclusion is that chromosomes of B genome are not present in the octoploid *Avena* amphiploid. In addition, the B genome of *Avena* is inactivated earlier and does not control apoptosis (Kosina and Tomaszewska 2013). The arrangement of the parental genomes (green versus red) in the *Avena* amphiploid is side-by-side, in both prophase and metaphase nuclei (Fig. 6C).

A common pattern of intermediate inheritance in plant hybrids is probably correlated with such an arrangement of parental genomes. Both sets of parental genomes can be expressed without epigenetic restrictions. However, the spatial arrangement of parental genomes can be changed when a nucleus approaches to apoptosis, in the root as well as in the endosperm (Kosina and Tomaszewska 2013).

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Nucleolar variability in grass antipodals.

R. Kosina and P. Tomaszewska.

The clonal and mosaic nature of grass endosperm has been studied by Ivanovskaya (1983), Kosina (1992, 2007, 2009, and 2012), and Kosina and Tomaszewska (2012). Mosaics are frequent and more variable in grass hybrids and amphiploids (Kosina and Tomaszewska 2010; Kosina and Zając 2010). In the endosperm tissue, antipodals are very special cells with respect to their origin, function, and death. In some grasses, for instance in rye, antipodals are uninuclear and uninucleolar (Poddubnaja-Arnoldi and Dzhalilova 1976). Antipodal chromosomes can by polytenized in Triticale (Kaltsikes 1973), and the number of rDNA loci is not increased, as in the '*Triticum* (4x) / *Aegilops tauschii*' amphiploid (Kosina 1995). At the final stage of their activity, antipodals are apoptized, and this process in wheat varies from that in the synergids (An and You 2004). Parental genomes are differentiated in their roles during apoptosis of

endospermal nuclei in the Avena amphiploid (Kosina and Tomaszewska 2013). In an antipodal cell, many nuclei and nucleoli can appear similar (Fig. 7), but between antipodal cells, the nuclei can vary in the number and stage of the cell cycle (Fig. 7B). Nucleolar and rDNA variation in the grass endosperm has been described (Kosina 1995, 1996, 1997, and 2011a, b). The number of nucleoli is less variable in the diploid Triticeae species and more variable in polyploids. Dendrograms presenting the variation of endosperm nucleoli can be properly constructed with the use of the Canberra metric (Kosina 1997). The number of rDNA loci and nucleoli can be changed due to multipolar anaphases, which are frequent in the endosperm, and/or to loss of loci located on bridges or laggards (Kosina 1995; Kosina and Kłyk 2011). In our study, free-nuclear endosperm tissue was stained *in vivo* by acridine orange (DNA green and RNA red) and on squashed slides by complex staining (DAPI+PI) or by means of a FISH method with using rDNA probe pTa71, stained Cy3. Two types of antipodal nuclei were discovered:

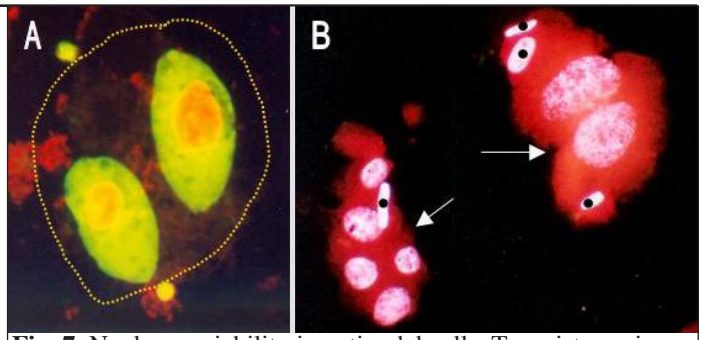

Fig. 7. Nuclear variability in antipodal cells. Two sister uni-nucleolar nuclei in one antipode of *Elymus caninus* (nucleolar RNA in orange, nuclear DNA in green) (A) and two antipodal protoplasts (red) with prophase nuclei (light blue) of different ploidy level in each, in *Avena sativa* (foreign nuclei are marked by black dots) (B).

1. A highly polyploidized antipodal nucleus has one or a few large nucleoli, for instance in *T. aestivum* and *Lophopyrum elongatum* (Fig. 8). A similar nucleolar status has been expressed in many other member of Triticeae. However, a different nucleolar and rDNA pattern was detected in Triticeae amphiploids, the antipodal nuclei have many nucleoli and many rDNA sites (Fig. 9).
2. A huge polyploidized nucleus has many, often more than 100, small nucleoli. Examples are *Avenula planicul mis*, *Lolium temulentum*, and *Briza maxima* (Fig. 10). Other members of the Avenae tribe express a similar nucleolar pattern, but also the same was noted in some species of Triticeae such as *Hordeum bulbosum* and *Elytrigia repens*.

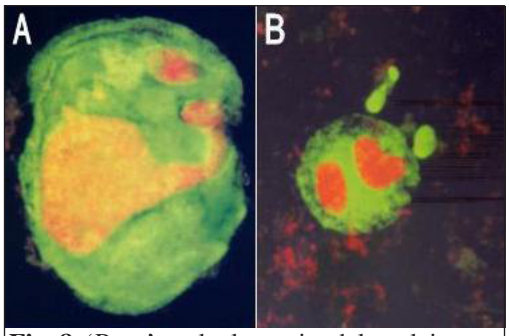

Fig. 8. 'Poor' nucleolar antipodal nuclei in *Triticum aestivum* (A) and *Lophopyrum elongatum* (B) (DNA in green, RNA in red).

Both kinds of antipodal cells are good models to study developmental, functional, and apoptotic variation.

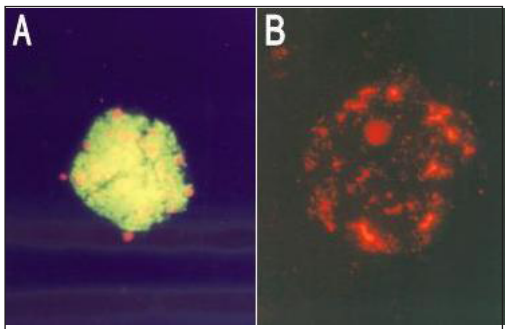

Fig. 9. Nucleolar variability in amphiploid antipodal nuclei. A multinucleolar nucleus from the cross '*Triticum turgidum* subsp. *carthlicum* / *Aegilops tauschii*' (DNA in green, RNA in red). Multiple red loci of rDNA (a pTa71 probe) in the nucleus of a '*T. turgidum* supsp. *turanicum* / *Ae. tauschii*' hybrid (B).

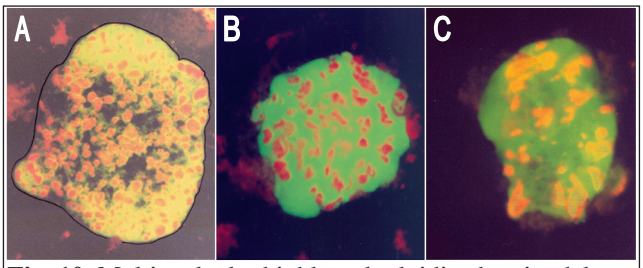

Fig. 10. Multinucleolar highly polyploidized antipodal nuclei (DNA green or yellow, RNA red or orange) in *Avenula planiculmis* (A), *Lolium temulentum* (B), and *Briza maxima* (C).

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Variability of vegetative propagation in Brachypodium distachyon.

R. Kosina and P. Tomaszewska.

Natural phenotypic variation is still of great interest, to relate it to DNA characteristics. Many studies on *Brachypodium distachyon* provide new data in this area. For instance, Tyler et al. (2014) presented variability of habit in *B. distachyon*, including a prostrate one with elongated and flexible shoots, whereas in the Kosina collection of *B. distachyon*, the longest shoots were found in an accession from Italy (ITA1, Fig. 11A). Some plants from this accession exhibited a winter behavior, not flowering in the first year of cultivation. Schwartz et al. (2010) also noted a winter habit in the species. Under moist weather conditions, these plants formed vegetative tufts (Fig. 11A), whereas blooming individuals developed several tillers with spikes. Vegetative tufted plants were cultivated through the autumn and winter in a greenhouse. They developed very long shoots (~1 m), with internodes reaching 12 cm, and sporadically

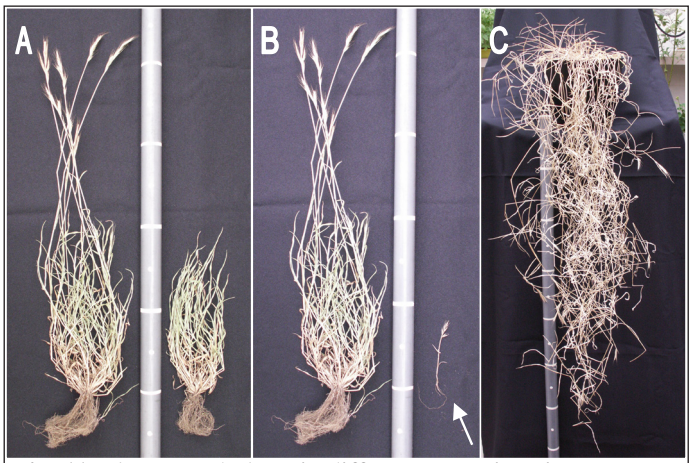

Fig. 11. Plant morphology in different accessions in *Brachypodium distachyon*; generative and vegetative habit in ITA1 (Italy) (A), two plants of various vigor and height (ITA1 on the left and PAK1 (Pakistan) on the right (B)), and plants of ITA1 presenting an excessive elongation growth in the greenhouse (C).

terminated by inflorescences. Opposite variation was noted, especially in accessions from Spain (ESP2) or Pakistan (PAK1), plants with one short (less than 10 cm) tiller terminated by a spike (Fig. 11B, p. 108). Thus, in *B. distachyon*, the variability related to vegetative versus generative potential is large. In late autumn in accession ITA1 and several others, prostrate shoots rooted and from axillary buds new tillers were produced (Fig. 12). These plants resembled perennials. Such a rooting behavior is a new characteristic in annual *Brachypodium* and can change its invasive potential in areas adjacent to cultivated fields or in pastures. Interaccessional (-populational) differences in reproductive versus vegetative effort could be studied more effectively under water stress (Aronson et al. 1993).

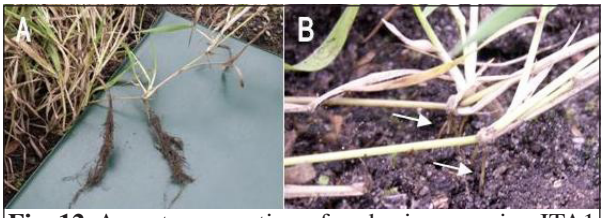

Fig. 12. An autumn rooting of nodes in accession ITA1 of *Brachypodium distachyon* from Italy.

In the perennial *B. pinnatum*, a vegetative dispersal is prevalent over generative, but Schläpfer and Fischer (1998) discovered a high clonal diversity within the population of this grass. The vegetative propagation allows *B. pinnatum* to invade effectively new disturbed areas (Buckland et al. 2001). The number of tillers created by a grass plants is under genetic control (Kebrom et al. 2013), and a gene (*tin3*) inhibiting the tiller development was discovered in *Triticum monococcum* (Kuraparthy et al. 2006). Possibly, the same genes were expressed in the uniculm bread wheat Gigas (Atsmon and Jacobs 1977) and in the dwarf form of *B. distachyon* (Fig. 11B).

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Questions about the nature of an anomalous plant in Brachypodium distachyon.

R. Kosina and P. Tomaszewska.

New types of plants can be mutational or hybrid origin. Any trait of an individual can be changed by mutation and a new phenotype is, *de facto*, only a small component of the total variation of a given taxon. In plant breeding, induced mutants are widely used to create new cultivars. Most often, the new characters are easily identified, such as size and shape of the plant or its separate organs (Allard 1960). New phenotypes created by hybridization of two parental plants are represented by the F_1 or next generations. The progeny of distant parents is often completely sterile due to many meiotic anomalies (Cicin 1978).

In the collection of *Brachypodium* maintained by R. Kosina, an extraordinary plant has been identified (Fig. 13B, p. 110). This plant exhibits extremely long and multiflowered spikelets and was found within a selection from an accession AFG1 from Afghanistan (Fig. 13A). Possible donors of such a trait could be two accessions from Morocco, MAR1 and MAR2 (Fig. 13D and E). All the mentioned accessions are within *B. distachyon*. Comparative morphological data show that traits of the new plant are closest to the characteristics of MAR1, especially those related to the spikelet (Table 1, p. 110); however, some characteristics of the plant are remarkable. In the very long spikelets composed of

more than 40 flowers, no caryopsis developed. The analysis of pollen grains showed that this plant is completely sterile (Fig. 13C). A spontaneous cross-pollination with MAR1 as a pollen donor is possible in nature, because all accessions in the collection express chasmogamic behaviour (Kosina and Tomaszewska 2012). Such a case of pollen sterility is rather impossible after an intra-specific cross-pollination. Another pollen donor that expresses long and multi-flowered spikes is *B. phoenicoides*. This species is also cultivated in the above-mentioned collection and represents strong chasmogamy and produces a lot of pollen grains. Khan and Stace (1999) crossed *B. distachyon* with *B. pinnatum*, but no seeds were obtained from the F_1 hybrid and its plants were sterile as well.

Fig. 13. Spikes of various accessions in *Brachypodium distachyon*: AFG1s, a selection from an accession AFG1 (Afghanistan) (A), a sterile hybrid found in AFG1s (B) and its sterile pollen grain (C), MAR1 from Morocco with short and long spikelets (D), and MAR2 from Morocco with long spikelets (E).

Table 1. Data on plant morphology of some accessions in *Brachypodium distachyon* presented in Fig. 13.

Character	AFG1s	AFG1s (a sterile plant)	MAR1	MAR2
Plant height (cm)	27.0	39.0	23.0	34.5
Number of tillers	3	6	4	10
Number of main tillers	2	1	4	1
Number of secondary tillers	1	5	0	9
Spikelet length (cm)	3.5	8.0	7.0	5.5
Number of spikelets/spike	1–2	1–2	1–2	1–3
Number of flowers/spikelet	16	44	27	26

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Variability of coleorhizal hairs in the Triticeae and Brachypodium.

R. Kosina and P. Tomaszewska.

The efficient growth of a seedling and its competitiveness in a population depend on successful germination of its diaspore. Many factors, including the morphology of diaspore, affect germination. Coleorhizal hairs are one of these factors. Coleorhizal hairs are components of a coleorhiza epidermis, and they are able to absorb water from capillary channels in the soil (Fig. 14B, a seed on the left having abundant hairs). The capillary potential of hairs is increased in specimens with many

Fig. 14. Germination of naked caryopses in various accessions in *Brachypodium distachyon* 48 h after imbibition. Coleorizal hair spheres and the tips of coleoptile are outlined in white. An early heading, spring accession from Iran (IRN1, A), a biennial accession from Iraq (IRQ, B), and a form with smooth glumellae (C), a facultatively biennial accession from Iraq, a form with hairy glumellae (D). All pictures were taken at the same magnification.

long hairs. When soil humidity is high, water highly condenses on them. Previously, Rost (1975) assigned the role of water absorption to the coleorhizal hairs in *Setaria lutescens*. Northam et al. (1996) documented that in *Taeniatherum caput-medusae* (Triticeae), development of coleorhizal hairs strongly depends on the germination temperature. At the end of the first 24h of germination, at 18°C, 15% to 74% of caryopses had these hairs. Bureś (2008) discovered that in a '*Triticum turgidum* subsp. *dicoccum* / *Aegilops tauschii*' amphiploid the coleorhizal hairs are expressed poorly (Fig. 15A), a trait similar to that found in a '*T. timopheevii* subsp. *timopheevii* / *Ae. umbellulata*' amphiploid (Fig. 15B). Another amphiploid, *T. kiharae* with the genomic formula AAGGDD, develops a rich sphere of the coleorhizal hairs (Fig. 15C). Germination tests showed that hairs also are variable in *T. aestivum*, from a sphere with many hairs to almost none (Fig. 16A), and this variation seems to be continuous. In *Secale cereale* (Fig. 16B), the development of the coleorhizal hairs can be described rather by a bimodal distribution with states of hairs, present versus absent. The coleorhizal hairs do not develop on the coleorhizal papilla, especially on its attachment point. The 0–1 character state for hair is also typical for *Ae. umbellulata* (Figs. 17A and 17B), and a winter form of *Brachypodium distachyon* (Fig. 17C). The 0–1 state, in fact, is rather an intermediate state towards a continuous one. The coleorhizal hairs develop quickly in accessions of the annual *B. distachyon* (Fig. 14A, p. 110); however, there is intrasample variable. In the facultatively biennial form (Fig. 14B and 14C), for smooth and hairy diaspores of accession IRQ from Iraq, coleorhizal hairs are shorter on average and in some caryopses absent. Kosina and Jaroszewicz (2007) presented a large difference between hairs in *B. distachyon* and *B. sylvaticum*; being long and abundant in the former species. The development of the coleorhizal hairs appears to be very variable. In species from the tribe Triticeae, this development is more variable. The coleorhizal hairs are shorter, less dense, and often the tip of the coleorhiza is naked. We can assume that their role in the quickly germinated seeds of cereals is not as significant as in the seeds of wild species, such as in *Brachypodium*, with slower germination and a slower seedling growth rate. The coleorhizal hairs function over many days of the seedling development.

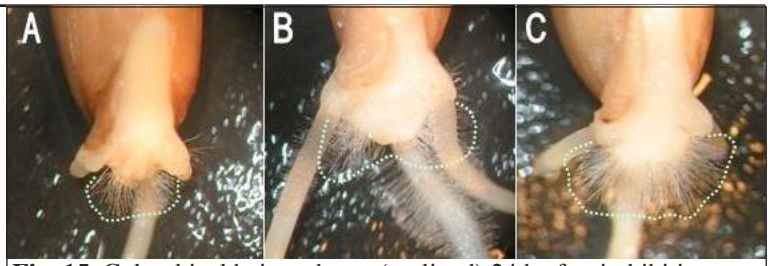

Fig. 15. Coleorhizal hairs spheres (outlined) 24 h after imbibition in the amphiploid K221-13 (*Triticum turgidum* subsp. *dicoccum* / *Aegilops tauschii*) (A); the amphiploid K217-1 (*T. timopheevii* subsp. *timopheevii* / *Ae. umbellulata*) (B), and *T. kiharae* (C). All specimens are at the same magnification.

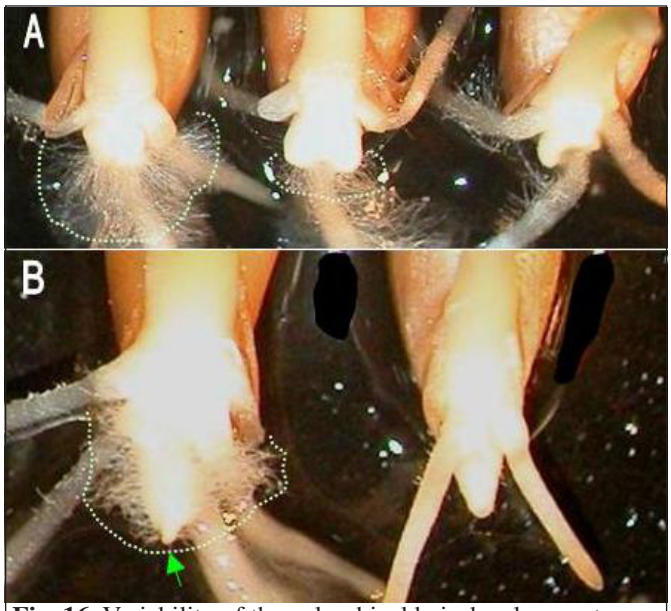

Fig. 16. Variability of the coleorhizal hair development in *Triticum aestivum* (A) and *Secale cereale* (B). The coleorhizal hair sphere is outlined. Pictures were taken 48 h after imbibition at the same magnification.

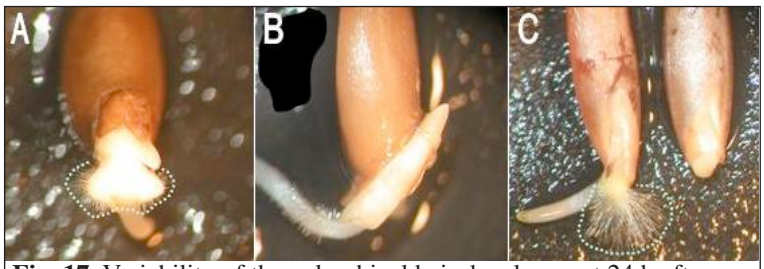

Fig. 17. Variability of the coleorhizal hair development 24 h after imbibition in *Aegilops umbellulata*, with a small coleorhizal hair sphere (A) and without hair (B); and *Brachypodium distachyon* accession ITA1 (from Italy) with a rich sphere on the left and without hair on the right (C). A, B, and C are not at the same magnification.

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Intrapopulational variation of germination in Triticeae and Brachypodium.

R. Kosina and P. Tomaszewska.

Bromus tectorum (cheatgrass) is an annual grass which is very similar with respect to its autogamic breeding system to common wheat and *Brachypodium distachyon*. Beckstaed et al. (1996) identified germination differences in cheatgrass depending on temperature. This variation appeared to be habitat dependent (interhabitat variation). A cheatgrass population growing in a more favorable habitat expressed larger phenotypic plasticity. The great variation in seed dormancy between individual plants in populations (intrapopulational variation) of four weeds was detected by Andersson and Milberg (1998); however, we do not know anything about their breeding systems.

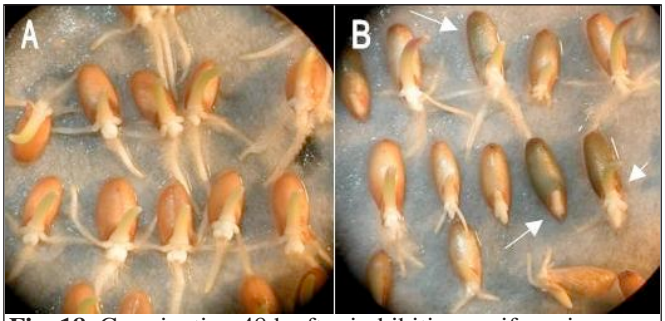

Fig. 18. Germination 48 h after imbibition, uniform in *Triticum aestivum* (A) and uneven in *Secale cereale* (B).

In our research material, germination tests show that within random samples of diaspores, a distinct difference between individuals is noted. Caryopses of common wheat germinate very quickly and uniformly (Fig. 18A). The germination behavior of *Secale cereale* is different (Fig. 18B), and at least three classes can be distinguished 48h after imbibition: 1. good germination and growth, 2. later germination and slower growth, and 3. germination only beginning. Perennial species of *Brachypodium* are situated at the other end of the germination spectrum. We present examples of *B. rupestre* and *B. pinnatum*. Their germination is very variable within a given population (Figs. 19A and 19B). Dormant diaspores, stored for 1 year, germinate later (9 days after imbibition). Growth of seedlings ranges from those with long coleoptiles and roots to those with only a little marked growth of coleoptile under the lemma (Fig. 19B, green arrow). In an annual *B. distachyon*, germination 48h after imbibition is quick in accession IRN1 (Fig. 20A). Three classes of germination, as in rye, can be distinguished. Another type of germination was observed in a facultatively biennial form of *B. distachyon* (accession IRQ from Iraq). Regardless of the type of glumellae surface, smooth or hairy, diaspore germination was delayed. A distinct imbibition of coleoptile was noted several hours after maintaining the diaspore in a watered Petri dish, however, no further development was seen during the 24h after imbibition. The diaspores of the biennial

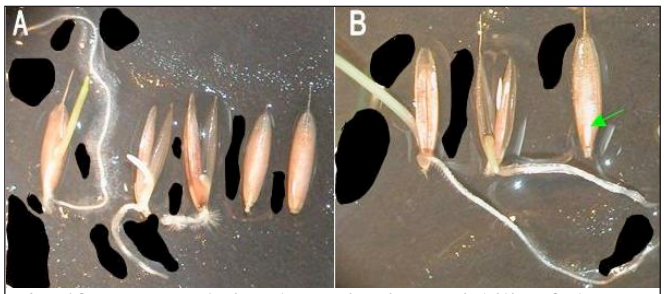

Fig. 19. Intrapopulational germination variability, 9 days after imbibition, in *Brachypodium rupestre* (A) and *B. pinnatum* (B). Coleoptile growth under the lemma is indicated by a green arrow.

Fig. 20. Intrapopulational germination variability of *Brachypodium distachyon* diaspores 48 h after imbibition. Coleorizal hair spheres and tips of coleoptile are outlined in white. Different stages of germination are shown by arrows. Early heading, spring accession IRN1 (Iran, A), biennial accession IRQ (Iraq, B), a form with smooth glumellae, and facultatively biennial accession IRQ (Iraq), C, a form with hairy glumellae. Pictures are not at the same magnification.

form are a little more dormant than those of the spring type. Forty-eight hours after imbibition, coleorhizal hairs were visible, growth of root ceased, and growth of coleoptile progresed under the lemma (Figs. 20B and 20C, see marked coleorhizal spheres and coleoptiles, p. 112).

Variation in germination is created by two main patterns of grass variability. One is associated with the grass breeding system, namely autogamy versus allogamy. The proportion of homozygotes and heterozygotes is determined by the breeding system. Heterozygous populations express obviously larger intra-populational variation in germination. The second pattern relates to annual versus perennial grasses. Our results prove that perennials express larger variation in germination. Interactions between the four above-mentioned syndromes can form the background for studying germination differences.

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Interpopulational and interspecific variation of germination in Brachypodium.

R. Kosina and P. Tomaszewska.

A germination analysis was performed for several perennial species of *Brachypodium*, *B. pinnatum* (Bp), *B. phoenicoides* (Bph), *B. rupestre* (Br), and *B. sylvaticum* (Bs), and for annual *B. distachyon* accessions ITA (Italy), TUR (Turkey), IRQ (Iraq), IRN (Iran), and AUS (Australia). The various accessions in the species were numbered (Fig. 21) and the percent germination and root growth rate was observed and recorded for successive days. In *B. distachyon*, spring, winter, and biennial biotypes were studied. The multivariate evaluation of accessions is presented (Fig. 21). The accessions of *B. distachyon* are differentiated in separate clusters on the dendrogram. The perennial species also create separate clusters (Fig. 21). The biennial forms of *B. distachyon* (IRQ) are close to perennial species *B. pinnatum* and *B. phoenicoides*. The values of average taxonomic distance presented in the dendrogram prove that interpopulational (interaccessional) variation in *B. distachyon* is greater than that in the interspecific variation. In *B. distachyon*, this variation concerns highly homozygous units, whereas in the genus, it is related to differences between highly heterozygous species. In *Brachypodium* caryopses, germination can proceed in two ways: (1) root and coleoptile growth almost simultaneous and a short dormancy in annuals and (2) root growth stopped and only coleoptile grows under lemma and highly dormant in perennials. Thus, the allocation of digested stored starch and proteins during germination is different in both groups of species. Our latest observations show that in the facultatively biennial form IRQ, selecting plants expressing short dormancy is possible. Such a trait can be quickly fixed in the population due to autogamic mating in the species. Other traits of the species also can be changed quickly under selection (Bakker et al. 2009). However, because all the accessions of *B. distachyon* in the our collection express chasmogamic flowering, some level of heterozygosity can be present in the species populations (Kosina and Tomaszewska 2012).

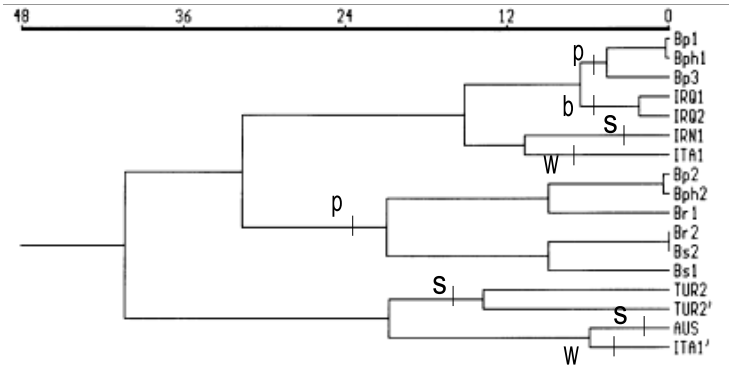

Fig. 21. Dendrogram (average taxonomic distance, UPGMA) of perennial species of the genus *Brachypodium* and accessions of *B. distachyon* described by several germination characteristics. Different accessions are marked by numbers or an apostrophe. Bp = *B. pinnatum*, Bph = *B. phoenicoides*, Br = *B. rupestre*, Bs = *B. sylvaticum*; IRQ, IRN, ITA, TUR, and AUS are accessions of *B. distachyon*; s, w, b, p are spring, winter, facultatively biennial, and perennial forms, respectively.

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A role of caryopsis tissues in germination of Brachypodium.

R. Kosina, P. Tomaszewska, and K. Kamińska.

The nucellus of the caryopsis of both annual and perennial *Brachypodium* species develops a thick epidermis. This tissue is well preserved in ripe caryopses. In perennials, the nucellus is a little thinner than in annuals (Kłyk 2005). Perennials contain more starch and aleurone protein in proportion to hemicelluloses in the nucellar epidermis. In *B. distachyon*, this proportion favors hemicelluloses. The tangential walls of epidermal cells are distinctly layered and, when observed in a polarizing microscope, are less anisotropic than pure cellulosic walls (Kamińska 2013). During germination, the nucellar epidermis is digested and the hemicelluloses are used by the developing seedling (Kosina and Kamińska 2013). The role of the aleurone layer in germination is well known. This tissue not only releases enzymes that digest starch and proteins in the endosperm but also hemicelluloses in the nucellar epidermis and, in addition, cell walls and the proteinaceous protoplast. The cell walls are isotropic in the aleurone layer, a set of aleurone grains decreases and, finally, a protoplast condenses. Starch is heavily digested before these changes. At that point, the nucellar epidermis seems to be intact (Fig. 22A). This epidermis first is digested enzymatically from the side adjacent to the aleurone layer (Fig. 22B). In the next step, the internal tangential walls disappear and adjacent aleurone cells are preserved (Fig. 22C). The nucellar epidermis becomes isotropic and the aleurone protoplasts only are remnants. The disappearance of the nucellar epidermis appears as a continuous process (Fig. 23A, B, and C) and in the lateral parts of the cross-section of caryopsis, the epidermis is most resistant to digestion. How much different is germination in annuals versus perennials in its dependence on caryopsis tissue resources? This is a question that needs further study.

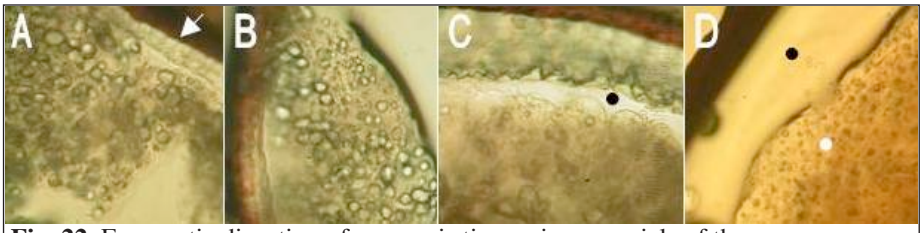

Fig. 22. Enzymatic digestion of caryopsis tissues in perennials of the genus *Brachypodium*, a dorsal part with digested starch and an intact nucellar epidermis (arrow) in *B. pinnatum* (A), digested starch in *B. pinnatum* (B), a digested nucellar epidermis and thin-walled aleurone layer with a free area (black dot) between both tissues in *B. pinnatum* (C), and highly digested starch (white dot) and an amorphous nucellar epidermis (black dot) in *B. rupestre* (D).

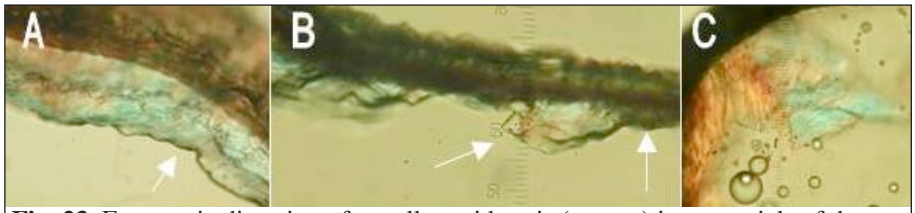

Fig. 23. Enzymatic digestion of nucellar epidermis (arrows) in perennials of the genus *Brachypodium*, *B. phoenicoides* (A), *B. phoenicoides* (B), and *B. rupestre* (C).

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Variation of winter hardiness in Brachypodium distachyon.

R. Kosina and P. Tomaszewska.

Manzaneda et al. (2012) present interesting data for *Brachypodium distachyon* about relationships between the level of polyploidy and its geographical distribution in more or less arid area in Spain. The authors concluded that polyploid cytotypes are distributed in the arid southern parts of the country. Is summer water shortage similar or comparable to that seen in the winter? What is the relationship between cold acclimation and winter water shortage? Many other questions can be posed to consider winter hardiness in *B. distachyon*. Colton-Gagnon et al. (2014) studied cold acclimation for seven, diploid accessions of *B. distachyon*. In light of Manzaneda et al. (2012) results, analyzing the winterhardiness of the species for a set of accessions of various ploidy seems to be more appropriate. Our collection is more appropriate for such a purpose, because the biotypes of *B. distachyon* represent various ploidy levels and cytogenetic stability (Jaroszewicz et al. 2012). In 2013, several accessions, from Afghanistan, Bulgaria, Italy, Iraq, and Turkey, had a prolonged vegetative period into the winter of 2013–14 (see Fig. 24). Some accessions did not bloom and some produced only few flowering shoots. The winter of 2013–14 was very mild in Wroclaw, Poland, where the collection is maintained. The lowest temperatures were recorded at the end of January, lasting nine days. Temperatures from –10°C to –14°C lasted only three days. Among the overwintering accessions, only one accession from Iraq was finally preserved. This accession is composed of two morphs, smooth and hairy glumellae. The hairy morph overwintered successfully (Fig. 24B). During the current hot and dry spring, this accession flowered and developed diaspores. In a future study, this form will be treated as a facultatively biennial biotype. Plants of the other accessions died.

Fig. 24. Variability of winterhardiness in some accessions of *Brachypodium distachyon*, a selection from accession TUR2 (Turkey, A) and an overwintered part (arrow) of an IRQ tuft (Iraq, B). A matchbox is included for comparison.

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Variability in germination in 'Triticum turgidum subsp. diccocum / Aegilops tauschii' amphiploids.

R. Kosina and M. Bureś.

Seeds of two amphiploids, K222 and K221-13, from a '*T. turgidum* subsp. *dicoccum* / *Ae. tauschii*' hybrid, were obtained from the Plant Germ-Plasm Institute in Kyoto, Japan. K222 appeared to be a highly preharvest sprouting biotype; K221-13 did not express this unfavorable trait. Some germination characteristics, such as thegrowth of main and lateral roots and the development of coleorhizal hairs, were studied for both amphiploids (Bureś 2008). K221-13 had polymorphism in both spike and grain color (dark and light). The coleorhizal hairs seem well developed in germinating dark

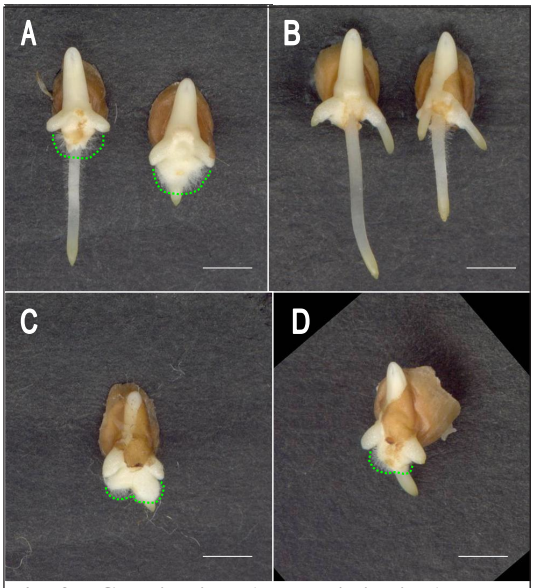

Fig. 25. Germination characteristics in the '*Triticum turgidum* subsp. *dicoccum* / *Aegilops tauschii*) hybrid K221-13, dark grains from a mother plant with a dark phenotype (A), light grains from a mother plant with a dark phenotype (B), dark grains from a mother plant with a light phenotype (C), and light grains from a mother plant with a light phenotype (D).

grains (Fig. 25A, p. 115) but not in light grains (Fig. 25B). Both types of seed developed on plants with dark spikes. The maternal influence on germination is shown (Figs. 25Cand 25D). The dark and light seeds gathered from plants with light spikes developed coleorhizal hairs, but germination in both types was slow. K222, a non preharvest sprouting form, exhibits dynamic growth of the main and lateral roots but does not develop coleorhizal hairs (Fig. 26).

Fig. 26. Germination in the preharvest sprouting '*Triticum turgidum* subsp. *dicoccum* / *Aegilops tauschii*' hybrid K222.

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Is the microstructure of palea in Brachypodium distachyon a good taxonomic tool ?

R. Kosina and P. Tomaszewska.

Microstructure of the grass palea is scarcely used in taxonomy. Ammann (1981) applied characteristics of palea in taxonomy of *Bromus hordeaceus* and *B. racemosus*. He considered both the shape and hairiness of this organ. Skowrońska (2005) performed a more detailed study regarding the variability of a tip of palea in a distinct group of *Bromus* species, *i.e.*, *B. secalinus*, *B. commutatus*, and *B. racemosus*. Many differences were observed in the morphogenesis of the upper part of palea in *B. secalinus* as well as in the *B. commutatus-racemosus* species complex. In the genus *Brachypodium*, variability of palea morphology was presented by Kłyk (2005), who discovered an original morphogenesis of hair and cilia bases.

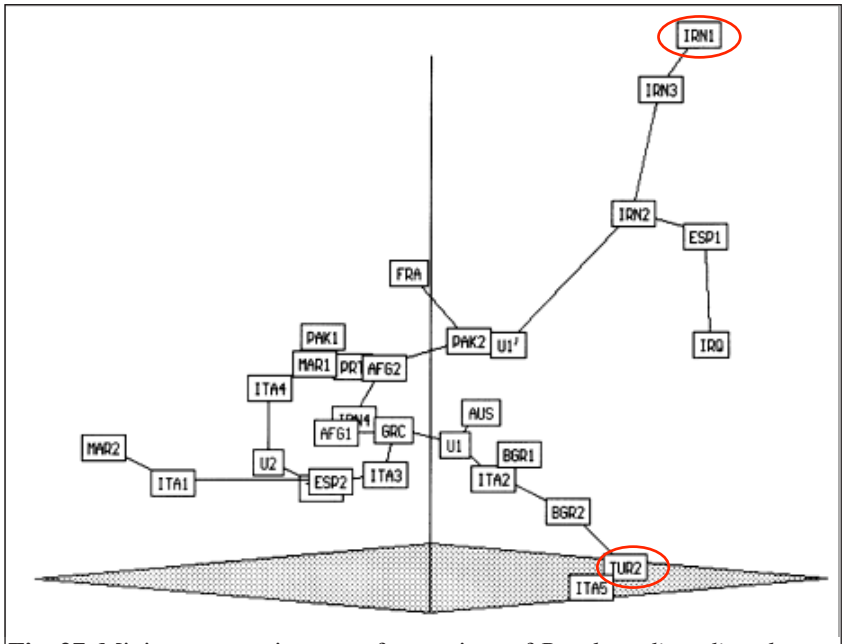

Fig. 27. Minimum spanning tree of accessions of *Brachypodium distachyon* described by traits of the palea tips. The tree was constructed after calculation of the average taxonomic distances and the use of nonmetric multidimensional scaling. Two examples of extreme accessions are circled in red and depicted in Fig. 28.

We studied variability of the tip of palea in *B. distachyon*, a model system for grasses. Twenty-nine accessions of the species were cultivated under the same soil-climatic conditions. Random samples of paleas were analyzed for seven characteristics, width and shape of tip, length of lateral cilia, distance between cilia, presence of microcilia, and the presence of hooks in the central, upper, and lower parts of the palea. The following accessions (OTU, operational taxonomic unit) were detected as extremes: IRN1 (Iran), TUR2 (Turkey), MAR2 (Morocco), ITA1 (Italy), FRA (France), and AUS (Australia). Accessions IRN1 and TUR2 are marked in a minimum spanning tree (Fig. 27) and pictured (Fig. 28). For separate traits, additional OTUs appeared as extremes: U1 (unknown origin), IRQ (Iraq), BGR2 (Bulgaria), and PAK1 (Pakistan).

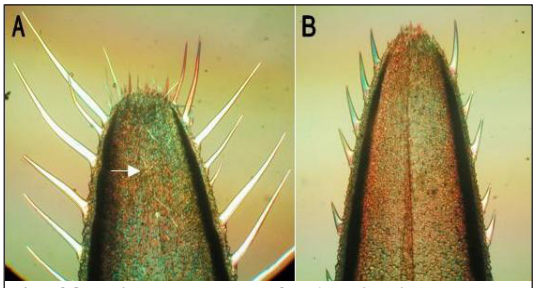

Fig. 28. Microstructure of palea tips in two extreme accessions of *Brachypodium distachyon*, IRN1 from Iran (an arrow shows short hairs on the surface of the palea) (A) and TUR2 from Turkey (B).

Differences in the morphogenesis of hair and cilia can play some role in the possibility of capturing of self and/or foreign pollen grains. When a flower is closed, the upper parts of both glumellae, haired or ciliated lemma, and the palea, stop foreign pollen grains and they fall on the stigma. If the flower expresses chasmogamy, both organs create an additional screen for pollen. We suppose that the more hairy and ciliated organs decrease the level of cross-pollination. A high level of interaccessional variation of palea microstructure can be suitable for taxonomy and to study intraspecific evolution.

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Morphometry of lodicules in Brachypodium distachyon and its application for taxonomy.

R. Kosina and P. Tomaszewska.

For a broad spectrum of Iranian grasses, Kosina (2005) discovered a trait syndrome of the stamens and lodicules that was different for auto- and allogamy. The activity of lodicules is based on metabolism of starch, calcium oxalate, and callose. In the next step of a lodicule study (Kosina 2006), a morphogenetic separateness of lodicule cushion and lodicule lobe was detected. Stomatous biotypes were found in *B. distachyon*. Kłyk (2005) described different morphs of a lodicule in the genus *Brachypodium*, and stated that *B. rupestre* and *B. sylvaticum* have them most different. Pietrzak (2007) presented a role of callose and various tissues at the base of lodicule during *B. distachyon* flowering. Some characteristics of the lodicule show that this organ is a reduced leaf. Kosina (2010) presented new traits for lodicule leafyness. Traits of the main lobe of the lodicule appeared to be the best discriminants of wheat species. *Triticum urartu* appeared to be an extreme in ordination space (Kosina 2011a). Finally, for taxonomic ordination of wheats described by lodicule characteristics, some parameters of correlation and regression were used beyond the arithmetic means (Kosina 2011b).

The lodicules of 29 accessions (OTUs, operational taxonomic units) of *B. distachyon* were described with eight characteristics. OTUs were set in an ordination space using a nonmetric multidimensional scaling. The following accessions were distinguished as extremes: GRC (Greece), ITA (Italy), ESP (Spain), IRN (Iran), and TUR (Turkey); two accessions, ITA5 and IRN4, are covered with the label IRN1 and are marked in red (Fig. 29). The early flowering, spring types are situated in the lower left part of Fig. 29 and the semiwinter, winter, or biennial types in the upper right. Such a surprising result indicates a difference between summer chasmogamic flowers versus autumn cleistogamic ones. In the first, chasmogamic flowers, large lodicules are developed (Fig. 30B, p. 118), and in the second ones the lodicules are sm aller (Fig. 30A). However, the lodicule of ITA5 also has a distinct cushion, an

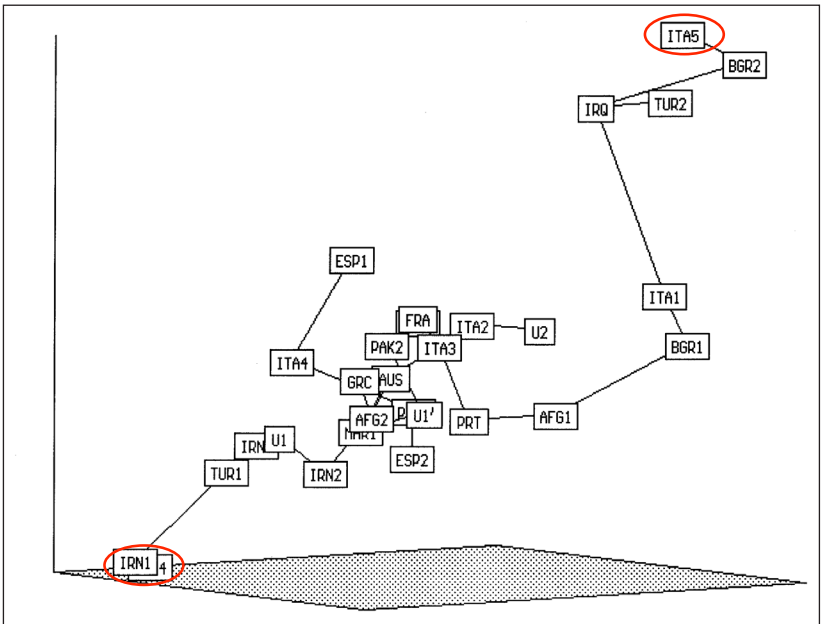

Fig. 29. Minimum spanning tree of accessions of *Brachypodium distachyon* described by traits of the lodiculae. The tree was constructed after calculation of average taxonomic distances and the use of a nonmetric multidimensional scaling method. Two examples of extreme accessions are outlined in red and depicted in Fig. 30.

organ that opens the flowers. In that case the above-mentioned conclusion can be ambiguous.

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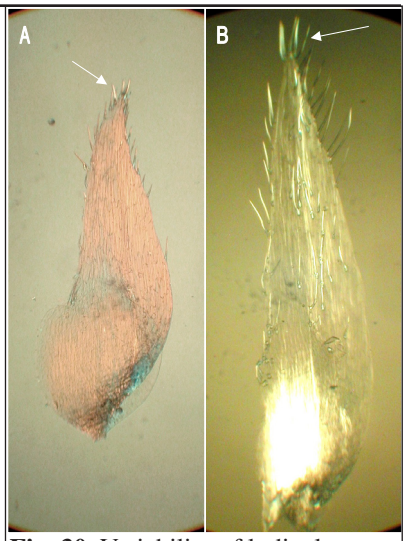

Fig. 30. Variability of lodiculae morphology in two extreme accessions of *Brachypodium distachyon*, ITA5 from Italy (A) and IRN4 from Iran (B). Arrows show short hairs on the top of the

Microstructural variability of endosperm in Triticeae versus Avena.

R. Kosina, P. Tomaszewska, and M. Florek

Kosina (2012) showed a clonal development of a starchy-aleurone endosperm in caryopses of *Thinopyrum distichum*. The last cytokineses are known to be tangential to the surface of the previous embryo sac. In the center of the caryopsis, cells are large and often polyploidized, while in the outer layers, cells are smaller and lack or are less polyploidized. Such a developmental pattern is often expressed in the form of mosaics, which have been observed in the endosperm tissue (Kosina and Tomaszewska 2010, Kosina and Zając 2010). These mosaics are related to various components of caryopsis structure. The somatic crossing-over are a process leading to a 'sister mosaic'. Developmental irregularities were noted in pure species but relatively more often in the progeny of various hybrids. In the hybrids, endosperm development is less balanced and exhibits some original properties (Kosina et al. 2013a, b). Such a hybrid endosperm has a domainant structure. Here we present some new data related to some Triticeae members and from the genus *Avena*. The aleurone cells can apparently be maintained at the basic level of polyploidy (3n). Such a level is characteristic for a young endosperm of any plant progeny (see Fig. 31A, here for *Leymus racemosus*, a pure species). The excess of assimilates can be located either in aleurone grains or in hemicellulosic

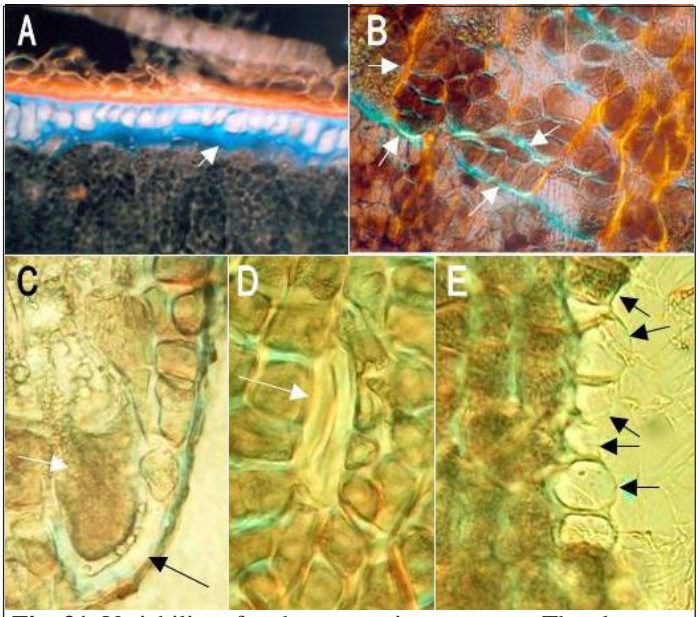

Fig. 31. Variability of endosperm microstructure. The aleurone layer in cross-section of caryopsis *Leymus racemosus*, thick hemicellulosic cell walls show blue natural fluorescence (arrow) (A) and the aleurone layer domains in a '*Triticum aestivum* subsp. *orientale* / *Aegilops tauschii*' amphiploid, domains are bordered by thick walls (arrows) seen under a polarizing microscope (B). The aleurone layer developmental events in the amphiploid '*Avena barbata* / *A. sativa* ssp. *nuda*' identified using a polarizing microscope, arrows show a polyploid cell filled by an aleurone protoplast and enclosed by thick hemicellulosic walls (C), an aleurone polyploid empty cell with thick hemicellulosic walls (D), and an aleurone layer at the edge of a domain, formed by thin-walled aleurone cells (arrows) (E).

cell walls (see blue walls of small aleurone cells in Fig. 31A, p. 118). In a '*Triticum turgidum* subsp. *turanicum* / *Aegilops tauschii*' amphiploid, in an aerial view of the aleurone layer, some distinct sectors enclosed by thick cell walls can be noted, these sectors are domains in the aleurone layer. In the *Avena* amphiploid, a highly polyploid aleurone cell (Fig. 31C, p. 118) with an abundant matrix of aleurone grains and a very thick hemicellulosic wall was detected. This case is evidence that amphiploid assimilates are located in both the protoplast and cell wall. A similar development in the form of a clone of polyploid aleurone cells was documented in wheat/*Th. distichum* amphiploids (Kosina and Tomaszewska 2012). The second case (Fig. 31D) shows that assimilates are located only in cell walls. The third case (Fig. 31E) presents unique development at the edge of the aleurone layer domain, cells have thinner walls and finally disappear. On the right of this disappearing domain in the endosperm exists a free space that can be occupied by ingrowths of starchy or aleurone tissue or by nucellar epidermis. The above-mentioned data prove that in members of different grass tribes, development of the caryopsis tissues is similar. The development of fruit is an evolutionary conservative process and, therefore, is useful in many procedures in genetics and taxonomy.

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Architecture of transfer tissues and endosperm cavity in the caryopsis crease – Triticeae and Avena cases.

R. Kosina, M. Florek, A. Grabińska, A. Koźlik, and K. Markowska.

Kosina et al. (2012) demonstrated that size and shape of nucellar projection and adjacent to it an endosperm cavity is intra- and interspecifically variable in the genus *Triticum*. The nucellar projection in *T. kiharae* and *T. fungicidum* developed as a U- or V-shaped structure, respectively (Kosina and Bureś (2011). Kosina and Tomaszewska (2012) documented in wheat/*Thinopyrum distichum* amphiploids that a very irregular narrow endosperm cavity penetrated deeply into endosperm tissue. Kosina et al. (2013a) proved in a Triticeae amphiploid that demethylation of DNA changes the shape of nucellar projection. The development of this transfer structure is correlated with a number of xylem vessels neighboring the pigment strand. The endosperm cavity in the amphiploid varies from that in the parental species. Relationships within a set of a transfer complex in caryopsis are recently presented by Kosina (2014).

The above citations reveal that the cavity and adjacent transfer complex composed of phloem and xylem bundles, pigment strands, plus a nucellar projection are difficult to present in the form of ideograms (Fig. 32). In a '*T. timpoheevii* subsp. *timopheevii* / *Aegilops umbellulata*' amphiploid, the nucellar projection and endosperm cavity complex is horizontal (Fig. 32B, blue rectangle), whereas this structure is more or less vertical in the parental species. Undoubtedly, the size of any structure depends on size of caryopsis. The shape of the pigment strand

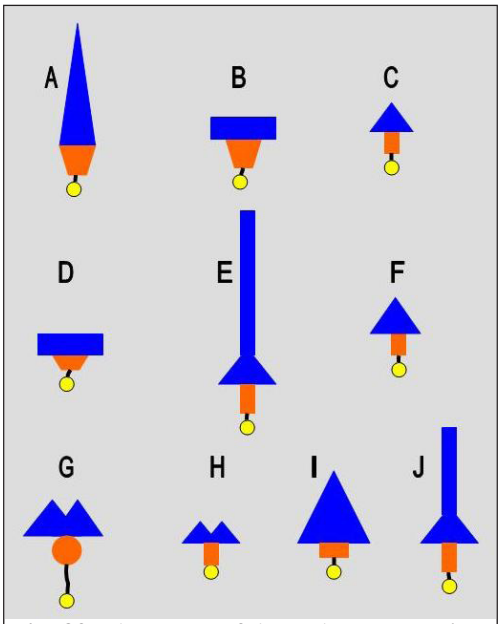

Fig. 32. Ideograms of the endosperm cavity and transfer tissues in the caryopsis of some Triticeae and *Avena* members (endosperm cavity + nucellar projection in blue, pigment strand in orange, xylem bundle in yellow). *Triticum timopheevii* subsp. *timopheevii* (A), a '*T. timopheevii* subsp. *timopheevii* / *Aegilops umbellulata* amphiploid (B), *Ae. umbellulata* (C), *A. barbata* (D), an '*A. barbata* / *A. sativa* ssp. *nuda*' amphiploid (E), *A. sativa* ssp. *nuda* (F), *A. brevis* (G), *A. hirtula* (H), and *A. strigosa* (I and J).

also is different in the depicted taxa. In the genus *Avena* (Fig. 32 D–J, p. 119), some additional shapes of the nucellar projection + endosperm cavity were detected (Fig. 32E and J). Ideograms (Fig. 32D, E, and F) prove that in an *Avena* amphiploid a change in the shape of nucellar projection + endosperm cavity structure occurs compared to the parental species. In *Avena* species, M-shaped endosperm cavities were noted (Fig. 32G and H). Xylem vessels can develop near the pigment strand (Fig. 32H) or at some distance (Fig. 32G). This difference could mostly affect the development of endosperm tissue.

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AGRICULTURAL RESEARCH INSTITUTE FOR THE SOUTH-EAST REGIONS (ARISER)
Department of Genetics, Laboratory of Genetics and Cytology, 7 Toulaikov St., Saratov, 410010, Russian Federation.

The influence of alien genetic materials for grain productivity and bread-making qualities in NILs of spring bread wheat.

S.N. Sibikeev and A.E. Druzhin.

We have obtained sets of spring bread wheat NILs carrying alien Lr-genes at the Genetics and Cytology Laboratory at ARISER. These NILs have the following genetic material: *Lr19+Lr9*, *Lr19+Lr24*, *Lr19+Lr25*, *Lr19+Lr26*, *Lr19+Lr37*, and wheat–*Thinopyrum intermedium* substitution 6Agi (6D) and wheat–*Thinopyrum elongatum* substitution 3Age (3B). These sets of NILs have the *Lr* genes from *T. turgidum* subsps. *dicoccum* and *dicoccoides*. The vegetative period in 2013 was very wet and moderate leaf rust epidemics were observed. In these conditions, grains yield of the NILs carrying *Lr19+Lr9*, *Lr19+Lr24*, *Lr19+Lr25*, *Lr19+Lr26*, and *Lr19+Lr37* and the NILs with *Lr* genes from *T. turgidum* subsp. *dicoccum* were similar to those of other cultivars and lines, but the NILs with *Lr* genes from *T. turgidum* subsp. *dicoccoides* and the 3Age (3B) and 6Agi (6D) substitutions significantly higher at 2.89, 2.96, and 3.22 t/ha, respectively. For complex bread-making qualities, the NILs with *Lr19+Lr25* and *Lr19+Lr37* were the best. All the NILs were excellent for gluten content and strength. For flour strength (W), the minimum value was 196 (cultivar L503) and the maximum was 667 (L2032 (*Lr19+Lr24*)). As a whole, the presence of alien genetic material in the NILs has not worsened bread-making qualities and was estimated as good and excellent.

The genetic control of leaf rust resistance in the new spring bread wheat introgression lines.

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New spring bread wheat introgression lines resistant to leaf rust have been produced by the Laboratory of Genetics and Cytology. The resistance has been transferred from *T. turgidum* subsps. *dicoccum* (k7507) and *dicoccoides* (k46216) and *T. kiharae*. During the 2011–13 seasons, the infection type to leaf rust of these lines was 0;–1. The genetic analysis has shown that the resistance transferred from *T. turgidum* subsp. *dicoccum* (k7507) and *T. kiharae* is determined by one dominant gene, but the resistance from *T. turgidum* subsp. *dicoccoides* (k46216) is controlled by two dominant, complementary genes. At present, BC_2 and BC_3 have been obtained with the spring bread wheat cultivars Saratovskaya 68, Saratovskaya 70, and Dobrynya.

The features of inheritance of T7DL-7Ae#1L-7Ae#1S translocations with Lr29 in Saratov-bred spring bread wheat cultivars.

S.N. Sibikeev and A.E. Druzhin.

During the 2005, 2007, 2008, and 2013 growing seasons, the high efficiency of the *Lr29* gene to populations of *Puccinia triticina* was shown. This gene is effective to *P. triticina* pathotypes virulent to *Lr19* (pp19). The infection type (IT) of *Lr29* was 11+. A NIL of Thatcher *Lr29* (TH Lr29) has been crossed with cultivars Saratovskaya 68 (S68) and Saratovskaya 70 (S70) (both cultivars do not have any *Lr* genes), and also with cultivars L503 and Dobrynya (DOBR) (both cultivars have *Lr19*). After inoculation with populations of *P. triticina* with high pp19 concentrations, segregating F_2 populations of the following were screened: BC_1 S68/TH *Lr29*, BC_2 S68/TH *Lr29*, BC_1 S70/TH *Lr29*, BC_2 S70/TH *Lr29*, BC_1 L503/TH *Lr29*, BC_2 L503/TH *Lr29*, BC_1 DOBR/TH *Lr29*, and BC_2 DOBR/TH *Lr29*. The *Lr29* gene is inherited in a monogenic dominant manner in the combinations with cultivars Saratovskaya 68 and Saratovskaya 70. An excess of susceptible plants was observed in the crosses with L503 and Dobrynya, and the ratio of resistant to susceptible plants not fit a 3R:1S ratio, indicating partial suppression of *Lr29* by *Lr19*. This conclusion agrees with earlier studies. However, earlier reports of the suppression of *Lr29* by *Lr19* were after inoculation by population or pathotypes of *P. triticina* not virulent to gene *Lr19* and observed ITs characteristic for *Lr19*. In our case, after inoculation with pp19, we observed that *Lr19*, or unknown genes in the translocations, reduce the protective action of *Lr29* and increase the number of susceptible plants; the IT of resistant plants is 11+.

The analysis of structure productivity of spring bread wheat introgression lines of the Laboratory of Genetics and Cytology, ARISER.

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The Laboratory of Genetics and Cytology, ARISER, produced a set of introgression lines for increasing the genetic variability of spring bread wheat. These introgression lines were obtained from crosses between bread wheat and various related donor species from the primary, secondary, and tertiary gene pools. To successfully work with these lines, characterization, both cytogenetically and genetically, is important. However, the definitive agronomical value of these lines can be found during prebreeding research including the analysis of productivity structure. Preliminary analysis of the introgression lines in spring bread wheat has shown that *Thinopyrum intermedium* chromosome 6Agi increases plant height, spike length, and number of spikelets, and lodging resistance is high. In the future, we will expand this research.

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Response of wheat seedlings interacting with glycosylated flagellins of the plant endophyte bacterium Azospirillum irakense KBC1.

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Plants grow and develop in an environment formed and densely populated by bacteria. However, plants exhibit homeostasis, restraining bacterial colonization of their inner tissues. Flagellin, a structural protein that forms the flagellar filament of motile microorganisms, is a bacterial molecule triggering a cascade of biochemical-defense reactions in plants. The interaction of bacterial flagellins with specific plant receptors leads to a considerable increase in the intracellular concentration of hydrogen peroxide and decreases the level of metabolism and the growth rate (Chinchilla et al. 2007). One factor of bacterial evolution necessary for the successful colonization of macroorganisms is the method of overcoming the immune system of plants. An example of such a mechanism is flagellin glycosylation, which reduces the probability that flagellin will be recognized by receptors.

We investigated the effect of flagellin from the growth-promoting rhizobacteria *Azospirillum irakense*, strain KBC1, on seedlings of soft spring wheat cultivar Saratovskaya 29. This endophyte bacterium was isolated from rice (*Orysa sativa* L.) roots (Khammas et al. 1989). Earlier, we showed that the polar flagellum flagellin of *Az. irakense* KBC1 is a glycoprotein and the residues of rhamnose, mannose, and galactose are present in the carbohydrate fragments of its flagellin at a 3:1:2 ratio, which is the same ratio as that found to exist between these sugars in the KBC1 O-specific polysaccharide (Fedonenko et al. 2004).

When 3-day-old wheat seedlings were treated with a bacterial flagellin solution (10.0 μg/mL), root length and root dry weight were inhibited considerably, −65% and −55%, respectively, and the mitotic index of the root meristem cells decreased twofold. When the seedlings were treated with different flagellin concentrations (0.01, 0.1, and 1.0 μg/mL), no statistically significant differences in the mitotic index compared with the control plants were observed. The morphometric parameters changed slightly; the root dry weight decreased by 9% and 15% for the 0.1 and 1.0 μg/mL solutions, respectively. For the glycosylated flagellin of the *Az. irakense* KBC1 polar flagellum, 10.0 μg/mL (~10^{-7} M) was found to inhibit plant growth, which is a concentration two orders of magnitude higher than the concentrations of nonglycosylated flagellins inhibitory to the growth of *Arabidopsis* (Chinchilla et al. 2007). One can speculate that the glycosylation of *Azospirillum* flagellins is one of the most important traits necessary for the successful colonization by *Azospirillum* of plants, including their inner tissues.

In summary, this study is the first to detect responses in the innate immune system of wheat to treatment with a bacterial flagellin, indicating the presence of receptors that recognize microbe-associated molecular patterns. The present results may be useful in understanding the molecular mechanisms of plant-microbe interactions and also in choosing plant microsymbionts and in developing bacteria-based fertilizers in agrobiotechnology.

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Specific action of bacterial lipopolysaccharide on the embryogenic ability of wheat calli in in vitro culture.

A comparative study on the effect of lipopolysaccharide (LPS) of the associative, plant-growth-promoting bacterial strains *Azospirillum brasilense* Sp245 and enterobacteria *Escherichia coli* K12 on the morphology of somatic calli of spring wheat was conducted *in vitro*. For this purpose, we used a genetic model including two near-isogenic lines of the wheat cultivar Saratovskaya 29 that differed in the *RhtB1c* gene and had contrasting embryogenic capacity. Calli were obtained on Linsmaier-Skoog medium with 2 mg/L of 2,4-dichlorophenoxyacetic acid (2,4-D) from immature (14-day old) wheat germ. In the experimental treatments, the standard medium, after being autoclaved, received 10 μg/mL of LPS, isolated from the bacterial outer membrane. The resulting calli were transplanted on a regeneration medium of the same composition without 2,4-D, but containing kinetin and indoleacetic acid in the amount 0.5 mg/L.

In preliminary studies, we found that LPS bacteria *A. brasilense* Sp245 in a concentration of 10 μg/mL stimulated the secondary processes of differentiation and regeneration capacity of wheat callus cells, thus increasing the efficiency of this genotype's low embryogenic potential (Tkachenko et al. 2012; 2013). We confirmed that the introduction of LPS *A. brasilense* Sp245 in to the medium increased calli formation with effecting meristematic activity and the regenerative capacity of cultured tissues. The introduction of bacterial LPS *E. coli* K12 to the nutrient medium did not cause similar effects. Yield of morphogenic calli and regenerated plants in the presence of the LPS did not differ from those of the control.

Based on our data, the LPS of the associative bacterium *A. brasilense* Sp245 has physiological activity against wheat callus cells unlike the LPS from *E. coli* K12. We note that these results are consistent with those obtained earlier when LPS and the bacteria *A. brasilense* Sp245 and *E. coli* K12 were exposed to the root system of wheat seedlings in *in vivo* experiments (Evseeva et al. 2011). Perhaps this difference is determined by the specificity of the mechanisms of action of LPS associative bacteria.

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ITEMS FROM UKRAINE

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Monitoring the phytosanitary state of winter bread wheat fields and grain yield depending on sowing date.

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Global climatic changes are increasing medium and maximum air and soil temperatures and the frequency of extreme atmospheric phenomenon. Climate change impacts the growth and development of agricultural crops, among them winter wheat. Thus, determining the sowing date of winter wheat will be condusive for improving the phytosanitary state of winter wheat fields and increasing the grain yield.

These investigations were conducted in a nine-corse rotation stationary field at the laboratory for Plant Production and Cultivar Investigations of the Plant Production Institute nd. a. V.Ya. Yuriev (Eastern Forest-Steppe of Ukraine) during 2006–13. The soil was a typical medium-humus black earth soil on loess with up to 5.4% humus in the plowing layer. Winter bread wheat was sown during three periods: early optimal (10–14 September), optimal (19–25 September), and admissible late (29 September–5 October). The sowing rate of winter wheat on black fallow was 4.5–5.0 x 10^6 viable seeds/ha and 5.0–5.5 x 10^6 viable seeds/ha after dried peas. Nutrition was humus, 6.7 t/ha of crop rotation area, and $N_{(30–60)}$ $P_{(30–60)}$ $K_{(30–60)}$ + N_{30} (additional fertilizing by root feeding at the spring tillering stage) + N_{30} (root feeding at ear stage). Agrotechniques were general use. The degree of damage in the plants by intrastalk pests and the intensity of root rot development was studied using conventional methods (Omelyuta 1986).

Results. For over 40 years (2006, 07, 08, and 12 for yield capacity in 2007, 08, 09, and 13, respectively), we assessed that the damage by root rots (*Helminthosporium*/*Fusarium*) was low on average. During autumn tillering (the second stage of organogenesis of winter wheat according to F.M. Koupermann), the spread of root rots ranged between 0.8–3.9% and the intensity of disease development was 0.2–1.4% (on black fallow); spread and development of root rots did not exceed 2.5–0.8 %, after peas as a forecrop (Table 1). The occurence of harmful flies in winter wheat fields on different forecrops was very similar. At the early optimal sowing date, shoot damage caused by fly larvae was 6.2% on black fallow and 5.2% after peas.

Table 1. The phytosanitary state of winter bread wheat at the autumn tillering stage depending on sowing date, averaged over the years 2006–13.

Index	Forecrop					
	Black fallow			Dried peas		
	Early	Optimal	Late	Early	Optimal	Late
Number of plants/m^2	510	480	570	450	490	550
Total tillering	4.6	3.4	1.1	3.9	3.1	1.5
Number of tillers/m^2	2,330	1,640	640	1,790	1,500	810
Root rots, % spread	3.10	3.90	0.80	2.30	2.50	0.07
Root rots, % development	0.9	1.4	0.2	0.7	0.6	0.8
Tiller damage by fly larvae (total)	6.20	2.50	0.00	5.20	3.40	0.02
Tiller damage by *Oscinella* spp. larvae	2.8	1.3	0.0	2.1	1.9	0.0
Tiller damage by *Mayetiola destructor* larvae	0.70	0.20	0.00	0.20	0.07	0.00
Tiller damage by *Phorbia securis* larvae	2.7	0.7	0.0	2.9	1.4	0.0
Number of tillers undamaged by Diptera larvae/m^2	2,190	1,600	640	1,690	1,450	810

At the optimal sowing date, we observed less shoot damage by fly larvae compared with that on black fallow (2.5 times less) and after peas (1.5 times less). During autumn in winter wheat fields, the specific composition included *Oscinella* spp. and *Phorbia securis* Tiensum. We recorded the greatest quantity from 10–14 September, i.e., at the begining of the optimal sowing date. Tiller damage by *Oscinella* larvae was 2.8% on black fallow and 2.1% after peas. Tiller damage by *P. securis* larvae was 2.7% pm black fallow and 2.9% after peas. Tiller damage by *Oscinella* larvae was 53.6% less on black fallow and damage by *P. securis* larvae was 71.1% less (on black fallow) and 51.7% less (after peas) for plants sown at the optimal time compared to those sown at the early optimal time. Solitary damage to plants by *Mayetiola destructor* Say was observed. Shoot damage by *M. destructor* larvae was not greater than 0.7% at the optimal sowing dates on both forecrops. At the late sowing date, larvae of the various Diptera were not observed.

During spring tillering, the spread and development of root rots in winter wheat fields following peas was much less than those fields with a black fallow forecrop (Table 2). The lowest indexes for spread and development of root rots were 3.5% and 1.5% after peas and 5.9% and 2.8% on black fallow, respectively. We observed a higher degree of spread of root rots (3.2x greater on black fallow and 2.8x greater after peas) and intensity of disease (3.0x greater on black fallow and 2.9x greater after peas) for winter wheat sown at the optimal dates compared with sowning at the late date. During the spring, *Opomyza florum* F. was the dominate fly in winter wheat fields. Tiller damage by *O. florum* larvae at the optimal sowing date was 17.4–19.3% on black fallow and 21.0–23.2% after peas. The effectiveness of the late sowing date was 48.7% on black fallow and 44.8% after peas compared with the early optimal sowing date (Table 3, p. 126).

Table 2. The phytosanitary state of winter bread wheat at the spring tillering stage depending on sowing date, averaged over the years 2006–13.

Index	Forecrop					
	Black fallow			Dried peas		
	Early	Optimal	Late	Early	Optimal	Late
Number of plants/m^2	490	480	530	430	440	500
Total tillering	3.6	3.3	3.0	3.4	3.0	2.7
Number of tillers/m^2	1,740	1,580	1,670	1,480	1,340	1,360
Root rots, % spread	12.0	18.8	5.9	9.6	9.7	3.5
Root rots, % development	5.6	8.3	2.8	4.3	3.7	1.5
Tiller damaged by fly larvae (total)	30.0	24.9	22.7	34.7	31.3	25.0
Tiller damaed by *Oscinella* spp. larvae	4.0	1.5	1.6	4.7	1.8	1.7
Tiller damage by *Mayetiola destructor* larvae	3.3	3.1	2.3	3.1	3.9	4.9
Tiller damage by *Opomyza florum* larvae	19.3	17.4	9.9	23.2	21.0	12.8
Tiller damage by *Chaetocnema aridula* larvae	0.6	0.1	1.5	0.3	0.5	1.0
Tiller damage by *Chaetocnema hortensis* larvae	2.7	2.8	7.4	3.3	4.2	4.7
Number of tillers undamaged by intrastalk larvae/m^2	1,250	1,180	1,360	980	940	1,070

At spring tillering, *M. destructor* larvae caused 3.3% tiller damage on black fallow and 3.9% tiller damage after peas at the optimal sowing dates (Table 2). However, tiller damage by *M. destructor* larvae in fields sown at the late date on black fallow was 30.3% less compared to that at the early optimal date, but was 36.7% greater after peas. Tiller damage by *Oscinella* larvae in the wheat fields after both forecrops at the early optimal sowing date ranged between 4.0–4.7%. A shift in sowing date led to a reduction in tiller damage by *Oscinella* larvae on black fallow and after peas was 2.7% and 2.8% less, respectively. Less tiller damage was caused by *Leptohylemyia coarctata* Fll. Larvae were observed between 0.1–1.5% on black fallow and between 0.3–1. % after peas (an increase in damage was observed at the late sowing date). Less tiller damage by *Chaetocnema aridula* Gyll. and *Ch. hortensis* Geoffr. was observed at the early sowing date; 2.7% on black fallow and 3.3% after peas. Winter wheat sown at the late date was damaged by stem flea larvae to a higher degree on black fallow (63.5%) than after peas (29.8%) compared to plants sown at the early optimal date. In general, shifting the sowing dates for winter wheat from optimal to late led to reduction in total tiller damage by fly larvae from 30.0% to 22.7% on black fallow and from 34.7% to 25.0% after peas. Thus, in autumn, regulating the sowing date of winter wheat may improve the phytosanitary state of winter wheat fields without chemical protection in autumn.

A sowing date for winter wheat and an index for tillering ability influence the density of stems. During autumn, the number tillers/m^2 was 2.6–3.6 times greater on black fallow and 1.8–2.2 times greater after peas for plants sown at the optimal dates compared to those sown at the late date. As a result, undamaged tillers on black fallow were 94.0–98.0% and 94.0–97.0% after peas (from the total number of tillers) during autumn tillering at the optimal sowing dates. At the spring tillering stage, tillers not damaged by intrastalk pests was 72.0–75.0% on black fallow and 66.0–70.0% after peas (from the total number of tillers). At the late sowing date, 100% of the tillers on winter wheat were undamaged by fly larvae for both forecrops during autum; 81.0% of the tillers were not damaged by intrastalk larvae on black fallow and 79.0% after peas at during spring. Despite these results, the grain yield of winter wheat sown at the optimal dates was 6.12–6.40 t/ha on black fallow and 6.16–6.28 t/ha after peas compared with that sown at the late date, 5.70 t/ha on black fallow and 5.86 t/ha after peas (Table 3). The increase in grain yield of winter wheat sown at the optimal dates was 0.42 t/ha on black fallow and 0.30–0.42 t/ha after peas compared to the late sowing date.

Table 3. The effecitveness of sowing date (%) on the grain yield of winter bread wheat (t/ha), averaged over the years 2006–13.

Index	Season	Forecrop					
		Black fallow			Dried peas		
		Early	Optimal	Late	Early	Optimal	Late
Root rots, % development	autumn	—	—	—	—	—	—
	spring	—	—	66.3	—	59.5	65.1
Tiller damaed by *Oscinella* spp. larvae	autumn	—	53.6	100	—	—	100
	spring	—	62.5	60.0	—	61.7	63.8
Tiller damage by *Mayetiola destructor* larvae	autumn	—	71.4	100.0	—	—	—
	spring	—	—	30.3	36.7	—	—
Tiller damage by *Phorbia securis* larvae	autumn	—	74.1	100.0	—	51.7	100.0
Tiller damage by *Opomyza florum* larvae	spring	—	—	48.7	—	—	44.8
Tiller damage by *Leptohylemyia coarctata* larvae	spring	60.0	93.3	—	70.0	50.0	—
Tiller damage by *Chaetocnema aridula* and Ch. *hortensis* larvae	spring	63.5	62.2	—	29.8	—	—
Total number of tillers	autumn	—	59.7	100.0	—	34.6	100.0
	spring	—	17.0	24.3	—	—	27.9
Grain yield (t/ha)	summer	6.12	6.40	5.70	6.28	6.16	5.86

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ITEMS FROM THE UNITED STATES OF AMERICA

KANSAS

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Winter cover crops for the Great Plains.

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Little information exists concerning the appropriate cover crop to grow during the winter in the Great Plains. Therefore, this study compared legume and non-legume winter cover crops grown for 3 years (2009–10, 2010–11, and 2011–12) at two locations in Kansas: Manhattan, in the northeastern part of the state, and Hutchinson, in the south-central part of the state. Six cover crops were studied, which included three legumes or alfalfa (*Medicago sativa* L.), Austrian winter pea (*Pisum sativum* var. *arvense* Poir.), and red clover (*Trifolium pratense* L.), and three non-legumes, which were triticale (*X Triticosecale*; *Triticum* x *Secale*), winter oats (*Avena sativa* L.), and winter wheat. There were four replications. The cover crops were planted at times that they might be used in a corn (*Zea mays* L.) or a forage sorghum (*Sorghum bicolor* (L.) Moench) rotation. However, the cover crops were not in rotation with these crops, but were planted at times to match corn and forage sorghum harvest times and sampled for dry matter at times to match corn and forage sorghum planting times. Table 1 gives the average dry matter of the four replications.

Cover crops grown in a forage-sorghum rotation had a higher dry weight than cover crops grown in a corn rotation (Table 1), which was probably due to the fact that the cover crops in a forage sorghum rotation had more time to grow in the spring, because forage sorghum is planted about three weeks after corn. Cold temperatures resulted in killing of the legumes, especially during the winter of 2011–12, when there was no dry matter production from the legumes at either location (Table 1). Winter oats also was winter killed at Manhattan during the winter of 2011–12. Triticale and winter wheat were the only cover crops that did not die during the winter at either location during all three years of the study. The results indicated that non-legume winter cover crops are better adapted to Kansas than legume winter cover crops and that triticale and winter wheat should be grown because they do not winter kill.

Table 1. Dry matter (kg/ha) of six winter cover crops grown at two locations in Kansas for three years ([1] Cover crops harvested before time of planting of corn, [2] cover crops harvested before time of planting forage sorghum, and [3] winter killed

Location	Year of harvest	Rotation	Alfalfa	Winter pea	Red clover	Triticale	Winter oats	Winter wheat
Manhattan	2010	Corn [1]	1,763	865	2,074	1,969	1,813	2,569
		Forage sorghum [2]	7,150	3,800	8,050	12,488	8,800	7,138
	2011	Corn	— [3]	1,561	—	654	836	2,118
		Forage sorghum	913	1,251	771	3,303	2,674	2,519
	2012	Corn	—	—	—	1670	—	1,119
		Forage sorghum	—	—	—	3,916	—	2,291
Hutchinson	2010	Corn	1,181	1,443	858	1,769	1,611	1,236
		Forage sorghum	1,421	2,594	1,375	2,995	3,106	2,171
	2011	Corn	—	696	—	935	910	1,120
		Forage sorghum	1,083	1,074	1,153	3,124	2,364	3,888
	2012	Corn	—	—	—	1,491	1,475	829
		Forage sorghum	—	—	—	2,313	2,470	1,271

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KANSAS STATE UNIVERSITY
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Notice of release of KS14WGRC61 Fusarium head blight-resistant wheat germplasm.

Bernd Friebe, William W. Bockus, Joey Cainong, Duane L. Wilson, W. John Raupp, and Bikram S. Gill; Peidu Chen, Nanjing Agricultural University, Cytogenetics Institute, Nanjing, Jiangsu, PR China; Lili Qi, USDA–ARS, Fargo, ND; Jesse Poland and Robert L. Bowden, USDA–ARS, Manhattan, KS; and Alan K. Fritz, Department of Agronomy, Kansas State University

The Agricultural Research Service, the U.S. Department of Agriculture, and the Kansas Agricultural Experiment Station announce the release of KS14WGRC61, a hard red winter wheat germplasm resistant to Fusarium head blight, caused by the fungus *Fusarium graminearum* Schwabe.

KS14WGRC61 is derived from the cross 'TA5655/TA3809*2//Everest (TA9121)*2', where TA5655 is a wheat–*Elymus tsuksusiensis* Honda Robertsonian translocation TW·1E^{ts}#1S and TA3809 is a Chinese Spring stock homozygous for the *ph1* mutant allele. KS14WGRC61 is homozygous for the distal wheat–*E. tsuksuiensis* recombinant chromosome TWL·WS-1E^{ts}#1S consisting of the complete long arm and most of the short arm of a wheat chromosome and a distal segment drived from 1E^{ts}#1S. The 1E^{ts}#1S segment has a gene that confers type-2 resistance to Fusarium head blight. The TWL·WS-1E^{ts}#1S stock is a novel source of Fusarium head blight resistance and may be useful in wheat improvement.

Small quantities of seed (3 grams) are available upon written request. We request that the appropriate source be given when this germplasm contributes to the development of a new cultivar. Seed stocks are maintained by the Wheat Genetics Resource Center, Kansas State University, Manhattan.

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MINNESOTA

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Wheat leaf rust caused by Puccinia triticina in the United States in 2013.

J.A. Kolmer and M.E. Hughes.

Summary. Wheat leaf rust (*Puccinia triticina*) was widely distributed across the U.S. from the Great Plains to the east coast but was generally found at low levels. Cool spring weather in the Great Plains and eastern states delayed small grain development, planting and field work. In late May, wheat leaf rust was at atypically low levels for the time of year, particularly in the southern and central Great Plains. Inoculum levels from Texas into the central and northern Great Plains were low, due to cooler spring temperatures, dry conditions, and the application of fungicides. Races with virulence to both *Lr39*/*Lr41* that is present in many hard red winter wheat cultivars grown from Texas to Kansas, and *Lr21* that is in many hard red spring wheat cultivars, were present in Texas and Minnesota. Races with virulence to *Lr3ka*, *Lr11*, *Lr26*, and *Lr18* were most common in the soft red winter wheat areas of the southeastern states and Ohio Valley. In the hard red wheat area of the southern and northern Great Plains, races with virulence to *Lr24*, *Lr17*, *Lr21*, and *Lr39*/*Lr41* were the most common.

Estimated losses in wheat due to leaf rust of 1–2% occurred in North Carolina, South Carolina, Mississippi, Missouri, Wisconsin, Illinois, Indiana, and Lousiana with trace level of losses in other states.

Texas. Wheat leaf rust severity was high in plots (up to 80S) at Pearsall and uniform in the lower canopy of plots at Uvalde in south Texas in early February. Leaf rust continued to develop at Uvalde and susceptible cultivars at Feekes 4–5 growth stage had high leaf rust severity by late February. Leaf rust was at trace levels and was uniformly distributed through the spreader rows in plots at Castroville in south central Texas in early February and continued to develop in the spreader rows and lower to mid-canopy of the cultivar TAM 110 reaching 50S in early March. By mid-April, high levels of leaf rust were observed in plots at Castroville. Generally, leaf rust was at low levels in commercial fields in the state due to cool spring temperatures, dry conditions, and the application of fungicides.

Oklahoma. Low levels of wheat leaf rust were found on the winter wheat cultivar Overley (boot to head emergence) near Devol in south-central Oklahoma the second week of April. This was the first cereal rust report in Oklahoma in 2013. No leaf rust was found in plots and fields (at boot stage) in central Oklahoma on 26 April. By the second week of May, there appeared to be very little wheat leaf rust in the state. Leaf rust was found in plots at Perkins (5–20S) and Stillwater in north-central Oklahoma the fourth week of May. Drought and late season freezes severely impacted wheat

production in the panhandle in 2013. Trace amounts of wheat leaf rust were found in north-central Oklahoma on 5 June. Generally, wheat leaf was at atypically low levels in the state in 2013.

Kansas. A single wheat leaf rust pustule was found in Stafford County in south-central Kansas the second week of May. This was the only report of wheat leaf rust in in the state by the second week of May. Wheat in southwestern Kansas suffered from drought and freeze damage, whereas wheat in south-central and central Kansas was in better condition due to some much needed rain. By late May, there were only a few reports of wheat leaf rust in state. Trace amounts of wheat leaf rust were found in susceptible plots of Winterhawk in Saline County in central Kansas. On 31 May, trace amounts of wheat leaf rust were found in plots in Reno County in south-central Kansas. Trace amounts of wheat leaf rust were found in fields in south-central Kansas, and plots in north-central and northeastern Kansas in early June. Susceptible cultivars such as Overley (*Lr39*/*Lr41*), Jagger (*Lr17*), Jackpot (*Lr39*/*Lr41*), and Fuller (*Lr17*, *Lr39*/*Lr41*) had higher severities but incidence was low. Trace amounts of leaf were observed on the cultivars Everest (*Lr1*, *Lr14a*), Armour (*Lr39*/*Lr41*) and Cedar (*Lr14a*, *Lr37*). No rust was reported in Ellis, Rush, Ness, Lane, and Russell Counties in central and west-central Kanas where the wheat was in very poor condition due to drought.

Nebraska. Wheat leaf rust had not yet been reported in the state by 30 May. A hot-spot of wheat leaf rust was found in plots at Lincoln in southeastern Nebraska on 7 June. The lower leaves had 40% rust severity and higher, whereas the flag leaves had only trace amounts. Wheat in the plots was at flowering to milk stage. This was the first report of wheat leaf rust in the state in 2013. Wheat leaf rust development increased rapidly in mid-late June in winter wheat plots and surrounding fields at Mead and Lincoln in southeastern Nebraska. Flag leaves of susceptible lines had high severities and the rust was widespread in the fields. Leaf rust also was observed in fields in south-central Nebraska where wheat was mostly in dough growth stages.

Iowa. Trace amounts of wheat leaf rust were reported in a field in Lee County in extreme southeastern Iowa on 8 June.

Louisiana. Low levels of wheat leaf rust were found in plots at Baton Rouge in southeastern Louisiana in early March. High levels of leaf rust were found in plots in south-central and southwestern Louisiana on 2 April. Rains and morning dews in late March created conditions conducive for further development. Wheat leaf rust was found in cultlivar and fungicide tests around the state in 2013.

Mississippi. Low levels of leaf rust were found in three counties in the Delta area in late March. Leaf rust was confirmed in six counties scattered across the state by mid-April and, by 20 May, leaf rust had been found in 10 counties across the state.

Arkansas. Low levels of leaf rust were found in plots at Kibler in northwestern Arkansas on 17 May. The first report of wheat leaf rust in the state was at low levels in plots at Rohwer in southeastern Arkansas on 10 May. Generally, wheat leaf rust appeared just before crop maturity and caused little damage.

Missouri. Wheat leaf rust was found in plots in Johnson, Pettis, and Boone Counties in west-central and central Missouri in early June. Severities ranged from trace to 20% and incidence from trace up to 40%. Trace levels also were found in fields in Lincoln and Marion Counties in northeastern Missouri.

Georgia. Wheat leaf rust was at very low levels in the state in 2013, likely due to the widespread use of fungicides to control stripe rust.

North Carolina. Leaf rust disease pressure was moderately severe in the Kinston and Plymouth plots in eastern North Carolina in 2013. The leaf rust arrived early in the plots and severely attacked the Saluda (*Lr11*) border rows. Other lines and cultivars in the plots were not as severely impacted as Saluda. Leaf rust also was found in plots at Clayton and Lake Wheeler in east-central North Carolina. Many commercial fields were sprayed with fungicides to reduce leaf rust losses. Wheat leaf rust was generally at low levels in commercial wheat fields, below average levels for the state.

Virginia. Low levels of leaf rust were found in plots at Painter in eastern Virginia in mid-May. Relatively higher incidences were found on susceptible cultivars, such as Massey, as well as cultivars with *Lr9*. Lower leaf rust incidence was found on cultivars with *Lr24* and much lower incidence on cultivars with *Lr26*. No rusts were found on visits to the plots at Blackstone (southern Virginia) and Holland (northeastern Virginia) in mid-May. Wheat leaf rust was found in plots at Blacksburg in western Virginia in late May. Leaf rust was severe on susceptible lines in plots at Warsaw in eastern

Virginia on 11 June. A few weeks earlier only trace amounts of wheat leaf rust were found in the plots.

South Dakota. Very low levels of leaf rust were found in fields in Douglas and Buffalo County in central and south central South Dakota, respectively, in late June. On 10 July, low levels of leaf rust were found in a winter wheat field in Clark County in northeastern South Dakota. Leaf rust was readily found in the southern half of the state at levels from trace to 40% infection in research plots in early July, however, it was difficult to find in commercial fields possibly due to fungicide applications. Wheat ranged form soft dough to dough stage. Wheat leaf rust was difficult to find in northern South Dakota even in research plots. It appeared many of the commercial fields were treated with fungicides. Generally, leaf rust was found at trace levels in fields with some fields having moderate levels.

North Dakota. Trace amounts of wheat leaf rust were found in Baart-Wolfe spreader rows and spring wheat entries in nurseries at Carrington in east-central North Dakota on 11 July. Low levels of wheat leaf rust were found on lower leaves in plots at Casselton in eastern North Dakota on 16 July. There was some flecking on flag leaves. Wheat leaf rust development increased in plots of Decade and other susceptible cultivars in plots maintained by Ducks Unlimited in the Dakotas by mid-July. High levels of infection were noted at Napoleon in south-central North Dakota. Wheat leaf rust was present at low levels in plots in central North Dakota and at trace levels in north-central North Dakota in late July. Plots of Faller wheat (*Lr21*) in northwestern North Dakota had large uredinia although at low severity. The leaf rust races with virulence to *Lr21* are now well established in the Great Plains, as these races also were found in plots of Faller and Glenn wheat in Castroville, Texas, earlier in 2013. In northeastern North Dakota, wheat leaf rust was present at trace levels in plots of susceptible wheat cultivars.

Minnesota. Trace levels of wheat leaf rust were found in winter wheat plots in southeastern Minnesota on 14 June. The infections were highly localized and not distributed throughout the plots. A single pustule of wheat leaf rust was found on a hard red winter wheat line in a nursery in northwestern Minnesota on 26 June. Low levels of wheat leaf rust were found on Baart in plots at Lamberton in southwestern Minnesota in early July. Wheat leaf rust was present at moderate to high levels in plots in west-central Minnesota the last week of July. Trace levels of leaf rust were found in wheat fields in the same area that had been sprayed with fungicide. In northwestern Minnesota, wheat leaf rust was present at trace levels in plots of susceptible wheat cultivars.

Wisconsin. Very low levels of wheat leaf rust were found on winter wheat in plots at Janesville in south-central Wisconsin on 20 June. Wheat leaf rust was widespread in soft red winter wheat plots at Arlington in south-central Wisconsin in early July. Flag leaf severities ranged from 10–50%. Wheat was at dough stage. Low levels of wheat leaf rust were found in fields in eastern and northeastern Wisconsin in early July.

Michigan. Wheat leaf rust was found in plots at Mason in central Michigan in mid-June. High levels of wheat leaf rust were found in Sanilac County in the thumb region of Michigan in early July. Leaf rust likely was present throughout the state by early July.

Ohio, Indiana, and Illinois. Wheat leaf rust at low levels was readily found in winter wheat fields across the northern halves of these states in late June. One field in Shelby County in west-central Ohio had higher leaf rust severities. Wheat was generally at hard dough stage.

New York. The first report of wheat leaf rust in the state was made at Brockport in northwestern New York on 5 June. The rust was found on a single leaf of an unknown cultivar in a commercial field. The wheat was a number of days past flowering and rainy, cool conditions continued in the area. Low levels of wheat leaf rust were observed on winter wheat in central and western New York the fourth week of June.

Washington. Wheat leaf rust was found at lower than typical levels in plots at Mt. Vernon in northwestern Washington but was not found in eastern Washington and northern Idaho in 2013.

Ontario, Canada. Trace amounts of wheat leaf rust were found in winter wheat plots at Ridgetown in southwestern Ontario (about an hour east of Detroit) on 21 June.

The number and frequency of virulence phenotypes of *Puccinia triticina* found in 2013 in the U.S. can be found in Table 1 (pp. 132-133), Table 2 (p. 134), Table 3 (pp. 135-136), and Table 4 (p. 137).

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2011 identified by virulence to 19 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3a*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, Lr39/*Lr41* and *Lr42*.

Pheno-type	Virulences	AL, AR, GA, LA, MS, NC, SC, TN, VA		NY		IL, IN, MI, eastern MO, OH, WI		OK, TX		CO, IA, KS, west-ern MO, NE		MN, ND, SD		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBBD	39/41	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
CCPSB	3,26,3ka,17,30,B,10,14a	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
FBPSB	2c,3,3ka,17,30,B,10,14a	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
FCPLB	2c,3,26,3ka,17,30,B	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.2
KFBJG	2a,2c,3,24,26,10,14a,28	0	0	0	0	1	1.2	0	0	1	1.1	0	0	2	0.4
LBBGG	1,10,28	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
MBDSB	1,3,17,B,10,14a	0	0	0	0	0	0	1	1.4	0	0	1	0.9	2	0.4
MBDSD	1,3,17,B,10,14a,39/41	0	0	0	0	0	0	5	7.2	6	6.5	13	11.5	24	4.9
MBPSB	1,3,3ka,17,30,B,10,14a	0	0	0	0	1	1.2	7	10.1	0	0	4	3.5	12	2.4
MBPSD	1,3,3ka,17,30,B,10,14a,39/41	2	1.6	0	0	0	0	1	1.4	1	1.1	1	0.9	5	1.0
MBTNB	1,3,3ka,11,17,30,B,14a	28	22.8	0	0	42	49.4	1	1.4	5	5.4	1	0.9	77	15.7
MBTSB	1,3,3ka,11,17,30,B,10,14a	4	3.3	0	0	1	1.2	0	0	3	3.2	0	0	8	1.6
MCDSB	1,3,26,17,B,10,14a	0	0	0	0	0	0	1	1.4	0	0	0	0	1	0.2
MCDSD	1,3,26,17,B,10,14a,39/41	0	0	0	0	1	1.2	0	0	1	1.1	2	1.8	4	0.8
MCPSD	1,3,26,3ka,17,30,B,10,14a,39/41	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.2
MCRHG	1,3,26,3ka,11,30,10,18,28	0	0	2	28.6	0	0	0	0	0	0	0	0	2	0.4
MCSQB	1,3,26,3ka,11,17,B,10	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2
MCTNB	1,3,26,3ka,11,17,30,B,14a	20	16.3	0	0	7	8.2	2	2.9	2	2.2	0	0	31	6.3
MCTQB	1,3,26,3ka,11,17,30,B,10	0	0	0	0	1	1.2	0	0	0	0	0	0	1	0.2
MCTSB	1,3,26,3ka,11,17,30,B,10,14a	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2
MDPSB	1,3,24,3ka,17,30,B,10,14a	0	0	0	0	0	0	2	2.9	0	0	0	0	2	0.4
MFBSB	1,3,24,26,B,10,14a	0	0	0	0	0	0	1	1.4	0	0	0	0	1	0.2
MFDSB	1,3,24,26,17,B,10,14a	0	0	0	0	0	0	0	0	0	0	2	1.8	2	0.4
MFNSB	1,3,24,26,3ka,17,B,10,14a	0	0	0	0	0	0	2	2.9	1	1.1	4	3.5	7	1.4
MFNSD	1,3,24,26,3ka,17,B,10,14a,39/41	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.2
MFPSB	1,3,24,26,3ka,17,30,B,10,14a	2	1.6	0	0	0	0	9	13.0	4	4.3	5	4.4	20	4.1
MFQHG	1,3,24,26,3ka,11,10,18,28	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2
MHDNB	1,3,16,26,17,B,14a	1	0.8	0	0	1	1.2	0	0	1	1.1	0	0	3	0.6
MHDSB	1,3,16,26,17,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.2
MJBJG	1,3,16,24,10,14a,28	0	0	0	0	0	0	0	0	2	2.2	0	0	2	0.4
MJPSB	1,3,16,24,3ka,17,30,B,10,14a	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
MLDSD	1,3,9,17,B,10,14a,39/41	0	0	2	28.6	0	0	2	2.9	1	1.1	0	0	5	1.0
MLPSD	1,3,9,3ka,17,30,B,10,14a,39/41	0	0	0	0	0	0	1	1.4	7	7.5	1	0.9	9	1.8
MMPSD	1,3,9,26,3ka,17,30,B,10,14a,39/41	0	0	0	0	0	0	1	1.4	0	0	1	0.9	2	0.4
NBBRG	1,2c,B,10,18,28	0	0	0	0	1	1.2	0	0	0	0	1	0.9	2	0.4
PBDBG	1,2c,3,17,28	0	0	0	0	0	0	1	1.4	0	0	0	0	1	0.2
PBDGG	1,2c,3,17,10,28	0	0	0	0	0	0	3	4.3	0	0	2	1.8	5	1.0
PBDGJ	1,2c,3,17,10,28,39/41	0	0	0	0	0	0	2	2.9	0	0	4	3.5	6	1.2
PBDQJ	1,2c,3,17,B,10,28,39/41	0	0	0	0	0	0	0	0	3	3.2	3	2.7	6	1.2
PCDGJ	1,2c,3,26,17,10,28,39/41	0	0	0	0	0	0	3	4.3	0	0	0	0	3	0.6
PCLQG	1,2c,3,26,3ka,B,10,28	0	0	1	14.3	0	0	0	0	0	0	0	0	1	0.2
SBDGG	1,2a,2c,17,10,28	2	1.6	2	28.6	0	0	2	2.9	3	3.2	0	0	9	1.8
TBBBJ	1,2a,2c,3,28,39/41	0	0	0	0	1	1.2	0	0	1	1.1	0	0	2	0.4
TBBGJ	1,2a,2c,3,10,28,39/41	0	0	0	0	2	2.4	4	5.8	8	8.6	10	8.8	24	4.9
TBBGS	1,2a,2c,3,10,21,28,39/41	0	0	0	0	0	0	1	1.4	0	0	10	8.8	11	2.2
TBBJG	1,2a,2c,3,10,14a,28	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	22	17.9	0	0	4	4.7	0	0	2	2.2	2	1.8	30	6.1
TCBJG	1,2a,2c,3,26,10,14a,28	0	0	0	0	0	0	0	0	0	0	2	1.8	2	0.4
TCDSB	1,2a,2c,3,26,17,B,10,14a	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2011 identified by virulence to 19 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1, Lr2a, Lr2c, Lr3a, Lr9, Lr16, Lr24, Lr26, Lr3ka, Lr11, Lr17, Lr30, LrB, Lr10, Lr14a, Lr18, Lr21, Lr28,* Lr39/*Lr41* and *Lr42*.

Pheno-type	Virulences	AL, AR, GA, LA, MS, NC, SC, TN, VA		NY		IL, IN, MI, eastern MO, OH, WI		OK, TX		CO, IA, KS, west-ern MO, NE		MN, ND, SD		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%
TCGJG	1,2a,2c,3,26,11,10,14a,28	3	2.4	0	0	0	0	0	0	0	0	0	0	3	0.6
TCJSB	1,2a,2c,3,26,11,17,B,10,14a	4	3.3	0	0	0	0	0	0	1	1.1	2	1.8	7	1.4
TCQJG	1,2a,2c,3,26,3ka,11,10,14a,28	0	0	0	0	0	0	0	0	0	0	3	2.7	3	0.6
TCRFG	1,2a,2c,3,26,3ka,11,30,14a,18,28	0	0	0	0	1	1.2	0	0	0	0	0	0	1	0.2
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a, 18,28	16	13.0	0	0	9	10.6	0	0	2	2.2	0	0	27	5.5
TCTSB	1,2a,2c,3,26,3ka,11,17,30,B,10, 14a	2	1.6	0	0	2	2.4	0	0	0	0	0	0	4	0.8
TDBGJ	1,2a,2c,3,24,10,28,39/41	0	0	0	0	1	1.2	1	1.4	2	2.2	3	2.7	7	1.4
TDBGQ	1,2a,2c,3,24,10,21,28	0	0	0	0	0	0	0	0	0	0	4	3.5	4	0.8
TDBJG	1,2a,2c,3,24,10,14a,28	0	0	0	0	0	0	1	1.4	1	1.1	2	1.8	4	0.8
TDBJJ	1,2a,2c,3,24,10,14a,28,39/41	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.2
TDBJQ	1,2a,2c,3,24,10,14a,21,28	0	0	0	0	0	0	3	4.3	0	0	2	1.8	5	1.0
TDBSB	1,2a,2c,3,24,B,10,14a	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2
TDGJG	1,2a,2c,3,24,11,10,14a,28	0	0	0	0	1	1.2	0	0	0	0	0	0	1	0.2
TDPSB	1,2a,2c,3,24,3ka,17,30,B,10,14a	0	0	0	0	0	0	1	1.4	0	0	1	0.9	2	0.4
TFBGJ	1,2a,2c,3,24,26,10,28,39/41	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
TFBJQ	1,2a,2c,3,24,26,10,14a,21,28	0	0	0	0	0	0	0	0	1	1.1	0	0	1	0.2
TFKDB	1,2a,2c,3,24,26,11,17,30,14a	0	0	0	0	2	2.4	0	0	0	0	0	0	2	0.4
TFKNB	1,2a,2c,3,24,26,11,17,30,B,14a	0	0	0	0	1	1.2	0	0	0	0	0	0	1	0.2
TFPSB	1,2a,2c,3,24,26,3ka,17,30,B,10, 14a	1	0.8	0	0	1	1.2	0	0	0	0	0	0	2	0.4
TJBJG	1,2a,2c,3,16,24,10,14a,28	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.2
TBRFG	1,2a,2c,3,3ka,11,30,14a,18,28	2	1.6	0	0	0	0	0	0	1	1.1	0	0	3	0.6
TNBGJ	1,2a,2c,3,9,24,10,28,39/41	0	0	0	0	1	1.2	5	7.2	17	18.3	16	14.2	39	8.0
TNBJJ	1,2a,2c,3,9,24,10,14a,28,39/41	2	1.6	0	0	1	1.2	5	7.2	6	6.5	2	1.8	16	3.3
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,14a, 28,39/41	4	3.3	0	0	0	0	0	0	0	0	0	0	4	0.8
TPBGJ	1,2a,2c,3,9,24,26,10,28,39/41	0	0	0	0	0	0	1	1.4	2	2.2	3	2.7	6	1.2
TPBJJ	1,2a,2c,3,9,24,26,10,14a,28,39/41	0	0	0	0	0	0	0	0	2	2.2	0	0	2	0.4
TPRJJ	1,2a,2c,3,9,24,26,3ka,11,30,10, 14a,28,39/41	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.2
Total		123		7		85		69		93		113		490	

The 2013 wheat leaf rust observation map can be found at: http://www.ars.usda.gov/Main/docs.htm?docid=9757 (Fig. 1).

Lr gene postulations of current soft red winter, hard red winter, and hard red spring wheat cultivars are available in a searchable database at:

http://160.94.131.160/fmi/iwp/cgi?-db=Lr%20gene%20postulations&-loadframes

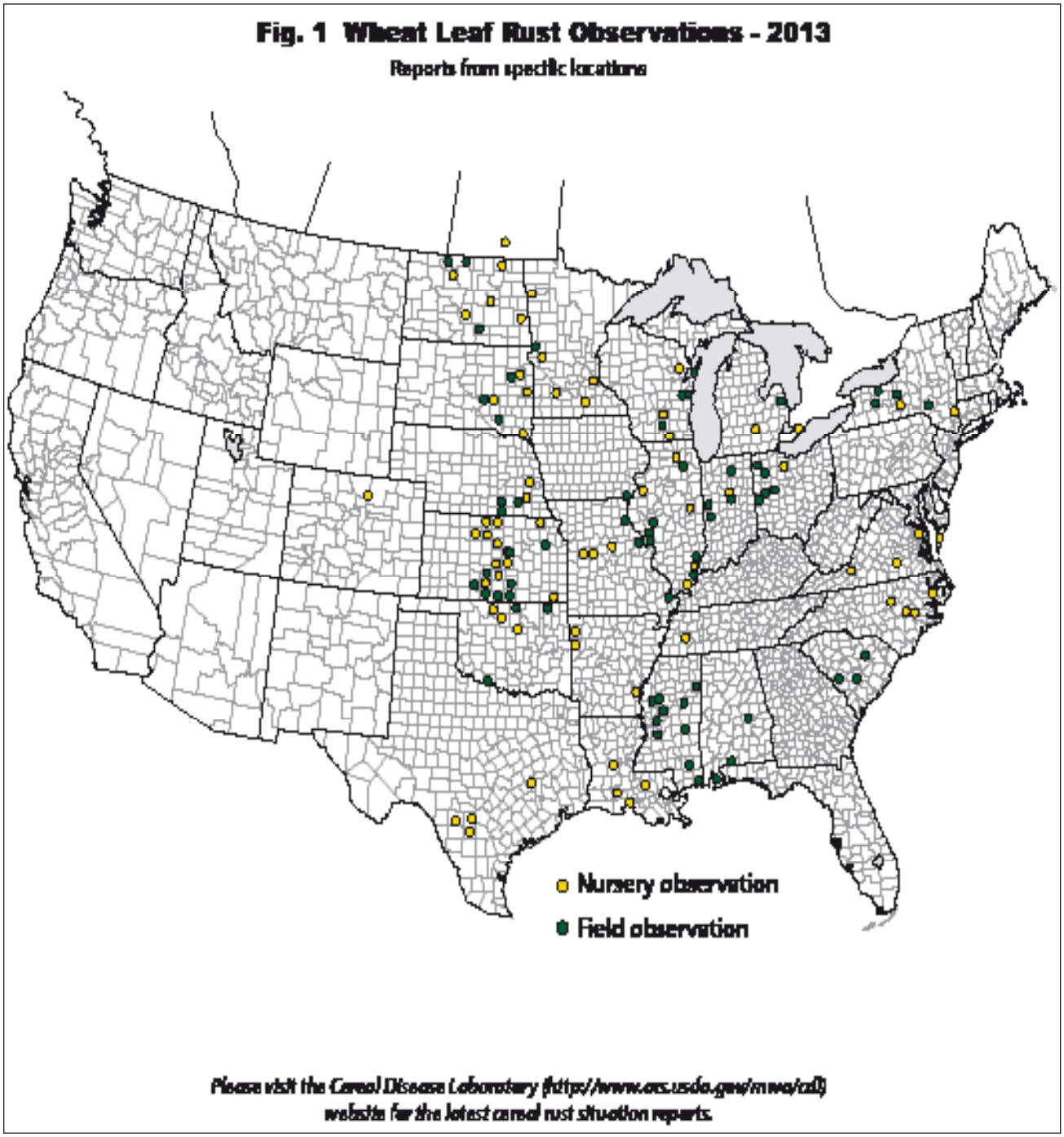

Table 2. Number and frequency (%) of isolates of *Puccinia triticina* in the United States in 2013 virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance gene	AL, AR, GA, LA, MS, NC, SC, TN, VA		NY		IL, IN, MI, eastern MO, OH, WI		OK, TX		CO, IA, KS, western MO, NE		MN, ND, SD		Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	123	100.0	7	100.0	84	98.8	69	100.0	89	95.7	112	99.1	484	98.8
Lr2a	63	51.2	2	28.6	30	35.3	24	34.8	51	54.8	64	56.6	234	47.8
Lr2c	63	51.2	3	42.9	31	36.5	33	47.8	55	59.1	75	66.4	260	53.1
Lr3	121	98.4	5	71.4	84	98.8	67	97.1	88	94.6	112	99.1	477	97.3
Lr9	7	5.7	2	28.6	2	2.4	15	21.7	35	37.6	23	20.4	84	17.1
Lr16	1	0.8	0	0.0	1	1.2	0	0.0	4	4.3	2	1.8	8	1.6
Lr24	12	9.8	0	0.0	9	10.6	31	44.9	41	44.1	47	41.6	140	28.6
Lr26	54	43.9	3	42.9	27	31.8	20	29.0	20	21.5	28	24.8	152	31.0
Lr3ka	107	87.0	3	42.9	69	81.2	27	39.1	31	33.3	26	23.0	263	53.7
Lr11	110	89.4	2	28.6	72	84.7	3	4.3	16	17.2	8	7.1	211	43.1
Lr17	70	56.9	4	57.1	61	71.8	47	68.1	42	45.2	51	45.1	275	56.1
Lr30	105	85.4	2	28.6	72	84.7	25	36.2	30	32.3	18	15.9	252	51.4
LrB	69	56.1	3	42.9	59	69.4	37	53.6	39	41.9	46	40.7	253	51.6
Lr10	72	58.5	7	100.0	30	35.3	65	94.2	82	88.2	111	98.2	367	74.9
Lr14a	119	96.7	2	28.6	78	91.8	46	66.7	54	58.1	56	49.6	355	72.4
Lr18	41	33.3	2	28.6	15	17.6	0	0.0	5	5.4	3	2.7	66	13.5
Lr21	0	0.0	0	0.0	1	1.2	4	5.8	1	1.1	16	14.2	22	4.5
Lr28	54	43.9	5	71.4	25	29.4	32	46.4	56	60.2	71	62.8	243	49.6
Lr39/Lr41	9	7.3	2	28.6	7	8.2	32	46.4	59	63.4	72	63.7	181	36.9
Lr42	0	0.0	0.0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Total	123		7		85		69		93		113		490	

Table 3. Estimated losses in winter wheat due to rust in 2013 (T = trace, less than 1% loss statewide; — no state estimates available; and * = preliminary 2013 Kansas wheat disease loss estimate).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
AL	270	69.0	18,630	0.0	0.0	T	T	2.0	380
AZ	10	99.5	800	—	—	—	—	—	—
AR	615	62.0	38,130	0.0	0	0.0	0	T	T
CA	340	83.3	27,200	0.0	0	0.0	0	2.0	555
CO	1,640	27.3	44,280	0.0	0	0.0	0	0.0	0
DE	78	68.0	5,304	—	—	—	—	T	T
FL	19	59.0	1,121	—	—	—	—	—	—
GA	350	60.0	21,000	0.0	0	T	T	3.0	649
ID	720	82.1	61,920	0.0	0	0.0	0	1.0	625
IL	830	67.0	55,610	0.0	0	1.0	562	3.0	1,720
IN	440	73.0	32,120	T	T	1.0	324	1.0	324
IA	21	52.0	1,092	0.0	0	T	T	0.0	0
KS *	8,400	38.0	319,200	0.0	0	T	T	T	T
KY	610	75.0	45,750	0.0	0	T	T	0.0	0
LA	250	58.0	14,500	0.0	0	1.0	146	3.0	448
MD	260	67.0	17,420	—	—	—	—	—	—
MI	600	75.0	45,000	T	T	T	T	T	T
MN	27	56.7	1,161	0.0	0	T	T	0.0	0
MS	385	58.0	22,330	T	T	1.0	226	3.0	69
MO	1,000	56.0	56,000	0.0	0	2.0	1,143	T	T
MT	1,900	38.9	81,700	0.0	0	0.0	0	3.0	2,527
NE	1,130	35.0	39,550	0.0	0	T	T	T	T
NV	11	86.8	990	—	—	—	—	—	—

Table 3. Estimated losses in winter wheat due to rust in 2013 (T = trace, less than 1% loss statewide; — no state estimates available; and * = preliminary 2013 Kansas wheat disease loss estimate).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
NJ	29	54.0	1,566	—	—	—	—	—	—
NM	70	44.0	3,080	—	—	—	—	—	—
NY	115	68.0	7,820	0.0	0	T	T	0.0	0
NC	920	57.0	52,440	0.0	0	2.0	1,070	T	T
ND	205	44.9	8,815	T	T	T	T	0.0	0
OH	665	70.0	46,550	T	T	T	T	T	T
OK	3,400	31.0	105,400	0.0	0	0.0	0	T	T
OR	780	62.1	48,360	0.0	0	0.0	0	2.0	987
PA	160	68.0	10,880	—	—	—	—	—	—
SC	255	54.0	13,770	0.0	0	1.0	139	T	T
SD	670	42.2	26,130	T	T	T	T	T	T
TN	540	71.0	38,340	0.0	0	T	T	2.0	T
TX	2,250	29.0	65,250	—	—	—	—	—	—
UT	110	44.5	4,840	—	—	—	—	—	—
VA	275	62.0	17,050	—	—	—	—	—	—
WA	1,660	66.9	114,540	0.0	0	T	T	1.0	1,157
WV	7	52.0	364	—	—	—	—	—	—
WI	265	58.0	15,370	T	T	2.0	314	2.0	314
WY	120	24.0	2,880	—	—	—	—	—	—
U.S. % loss				T		0.3		0.7	
U.S. total	32,402	47.4	1,534,253		T		3,924		10,378

. **SOUTH DAKOTA**

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Fine mapping and metabolic and physiological characterization of the glume glaucousness inhibitor locus Iw3 derived from wild wheat.

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Cuticular wax constitutes the outermost layer of plant skin and its composition greatly impacts plant appearance and plant-environment interaction. Epicuticular wax in the upper part of adult wheat plants can form the glaucousness, which associates with drought tolerance. We characterized the glume-specific, glaucousness inhibitor *Iw3* by fine mapping and physiological and molecular approaches. *Iw3* inhibits glaucousness formation by altering wax composition. Compared to the wild type, *Iw3* eliminates β-diketone, reduces primary alcohols by 47%, but increases aldehyde 400-fold and alkanes fivefold, which leads to a 30% reduction of total glume wax load. Loss of glaucousness increased cuticle permeability, suggesting an important role in drought sensitivity. Genetically, the glaucousness-inhibiting effect of *Iw3* is partially dominant in a dosage-dependent manner. We localized the *Iw3* locus within a 0.13-cM interval delimited by marker loci *Xpsp3000* and *XWL3096*. Of the 53 wax genes assayed, we detected transcription changes in nine genes by *Iw3*, down-

Table 4. Estimated losses in spring and durum wheat due to rust in 2013 (T = trace, — = no state estimate available, N/A = data not available, * U.S. total does not includestates for which loss or production data is not available).

SPRING WHEAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
CA	N/A	N/A	N/A	0.0	0	0.0	0	T	T
CO	9	82.0	738	0.0	0	0.0	0	0.0	0
ID	510	77.0	39,270	0.0	0	0.0	0	5.0	2,067
MN	1,160	57.0	66,120	0.0	0	T	T	0.0	0
MT	2,850	37.0	105,450	0.0	0	0.0	0	3.0	3,261
ND	5,060	46.0	232,760	0.0	0	T	T	0.0	0
NV	3	75.0	225	—	—	—	—	—	—
NY	N/A	N/A	N/A	0.0	0	T	T	0.0	0
OR	88	63.0	5,544	0.0	0	T	T	2.0	1,046
SD	1,165	44.0	51,260	T	T	T	T	T	T
UT	14	48.0	672	—	—	—	—	—	—
WA	495	60.0	29,700	T	T	T	T	T	T
U.S. % loss				T		T		1.2	
U.S. total *	11,354	46.8	531,739		T		T		6,374
DURUM WHEAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
AZ	79	102.0	8,058	—	—	—	—	—	—
CA	67	100.0	6,700	0.0	0	0.0	0	T	T
ID	11	62.0	682	0.0	0	0.0	0	0.0	0
MT	490	34.0	16,660	0.0	0	0.0	0	0.0	0
ND	770	38.0	29,260	0.0	0	T	T	0.0	0
OR	N/A	N/A	N/A	0.0	0	0.0	0	0.0	0
SD	4	42.0	168	0.0	0	0.0	0	0.0	0
U.S. % loss				0.0		T		T	
U.S. total *	1,421	43.3	61,528		0		T		T

regulation of Cer4-1 and up-regulation of other five Cer4 and three KCS2 homologs. All these results provided initial insight into the *Iw3*-mediated regulation of wax metabolism and paved the way for an in-depth characterization of the *Iw3* locus and the glaucousness-related β-diketone pathway.

W3 is a new wax locus that is essential for biosynthesis of β-diketone, development of glaucousness, and reduction of cuticle permeability in common wheat.

Zhengzhi Zhang, Wenjie Wei, Huilan Zhu, Ghana S. Challa, and Wanlong Li; Caili Bi (Department of Biology, Hebei Normal University, Shijiazhuang, Hebei 050024, PR China); and Harold N. Trick (Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA).

The cuticle plays important roles in plant development, growth, and defense against biotic and abiotic attacks. Different from the model plants, cuticles of adult wheat and barley plants are rich in hentriacontane-14,16-dione and its hydroxy isoforms (also known as β-diketone), but their biosynthetic pathway largely remains unknown. We identified a novel wax mutant in the wheat cultivar Bobwhite. The mutation is not allelic to the known wax gene loci *W1* and *W2*, and is designated as *W3*. Genetic analysis localized *W3* on chromosome arm 2BS. The *w3* mutation reduced by 99.0% β-diketones, which account for 63.3% of the total wax load, but increased the hydroxy-β-diketones to β-diketone ratio

11-fold, suggesting differential roles of *W3* in β-diketone biosynthesis and its hydroxylation. Loss of β-diketones caused failure to form glaucousness and a significant increase in cuticle permeability in terms of water loss and chlorophyll efflux in the *w3* mutant. Transcription of 23 cuticle genes from five functional categories was altered in the *w3* mutant; 19 down-regulated and four up-regulated, suggesting a possibility that *W3* encodes a transcription regulator coordinating expression of cuticle genes. Biosynthesis of β-diketones in wheat and their implications in glaucousness formation and drought and heat tolerance were discussed.

Fine mapping of shattering locus Br2 revealed local chromosomal structure differentiation between the two lineages of Aegilops tauschii.

Zhengzhi Zhang, Huilan Zhu, and Wanlong Li, and Bikram S. Gill (Wheat Genetics Resource Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA).

Chromosome inversions often accompany population differentiation and capture local adaptation during speciation. *Aegilops tauschii*, the D-genome donor species of hexaploid wheat, consist of two genetically isolated lineages, L1 and L2, but little is known about the genetic mechanisms underlying the population split in this diploid species. During fine-mapping of shattering gene *Br2* using a large F_2 population derived from a cross between *Ae. tauschii* accessions TA1604 (an L1 accession) and AL8/78 (an L2 accession), we found contrasting patterns of crossover distribution in the *Br2* interval and neighboring regions despite the high, local gene synteny with *Brachypodium distachyon* and rice. *Br2* is localized in an 0.08-cM interval, and 13 marker loci formed a block, where single-crossover was completely suppressed, but a double crossover was enriched with a recombination rate of ~11 cM/Mb. In a neighboring region, no double crossover was recovered, but the single-crossover rate reached 24 cM/Mb, much higher than the genome-wide average. This result suggests a tentative inversion polymorphism between the parental lines in the *Br2* region. Genotyping using the markers from the *Br2* region divided a collection of 55 randomly sampled *Ae. tauschii* accessions into two major groups, and they are largely isolated in genetics. The two groups correspond to the lineages L1 and L2 based on their geographic distribution patterns. This data provides first line of evidence that inversion may underlie the evolution of *Ae. tauschii* lineages.

The chloroplast view of the evolution of polyploid wheat.

Huilan Zhu, Junwei Wang, Ghana S. Challa, Zhengzhi Zhang, and Wanlong Li, and Piotr Gornicki (Department of Molecular Genetics and Cell Biology, University of Chicago, 920 E 58th St, Chicago, IL 60637, USA) and Bikram S. Gill (Wheat Genetics Resource Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA).

Polyploid wheats comprise four species: *Triticum turgidum* (AABB genomes) and *T. aestivum* (AABBDD) in the emmer lineage, and *T. timopheevii* (AAGG) and *T. zhukovskyi* ($AAGGA^mA^m$) in the timopheevi lineage. Genetic relationships between chloroplast genomes were studied to trace the evolutionary history of the species. Twenty-five chloroplast genomes were sequenced, and 1,127 plant accessions were genotyped, representing 13 *Triticum* and *Aegilops* species. *Aegilops speltoides* (SS genome) diverged prior to the divergence of *T. urartu* (AA), *Ae. tauschii* (DD), and *Aegilops* species of the Sitopsis section. *Aegilops speltoides* forms a monophyletic clade with the polyploid emmer and timopheevi wheats, which originated within the last 0.7 and 0.4 million years, respectively. The geographical distribution of chloroplast haplotypes of the wild tetraploid wheats, as well as of, illustrates the possible geographic origin of the emmer lineage in the southern Levant and the timopheevi lineage in northern Iraq. *Aegilops speltoides* is the closest relative of the diploid donor of the chloroplast (cytoplasm), as well as the B and G genomes to the timopheevi and emmer lineages. Chloroplast haplotypes were often shared by species or subspecies within major lineages and between the lineages, indicating their contribution in introgression to the evolution and domestication of polyploid wheats.

VIRGINIA

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2013 wheat production in the Commonwealth of Virginia.

Growing conditions. Most small grain was seeded timely in the autumn of 2012 due to cooperative weather conditions (Figs. 1 and 2). By mid-October, 22% of wheat and 72% of barley was planted, which was ahead of the five-year average for both crops. Early November brought hurricane Sandy and the associated rains that left some flooded areas and killed wheat and barley in low spots in fields in some areas. These rains delayed planting of the final wheat acres, but by November 25, 77% of the crop was seeded, which was still 8% ahead of the long term average. In most of the Commonwealth, December was relatively mild and dry until rain showers occurred at the very end of the month. January was mostly dry but cold in most areas, which delayed tillering of small grain in many areas.On 30 January, 66% of the small grain crop was rated good, 22% fair, and only 8% excellent. A large portion of February and March was unseasonably cold, but the wheat crop was still rated as 65% good at the end of March. By 15 April, warm weather, 14° above normal for some areas, along with rain showers accelerated development of the small grain crop. However, cooler temperatures returned quickly, and the month as a whole was significantly cooler than the long term average. By 30 April, only 23% of the wheat crop had headed, compared with 85% the previous year. Rainy weather occurred throughout wheat and barley flowering and created conditions that were conducive to development of fusarium head blight in many areas of eastern Virginia. Growers also reported significant infestations of Stagonospora leaf and glume blotch. In many areas, preharvest sprouting of grain also was an issue due to frequent rains occurring during the harvest season.

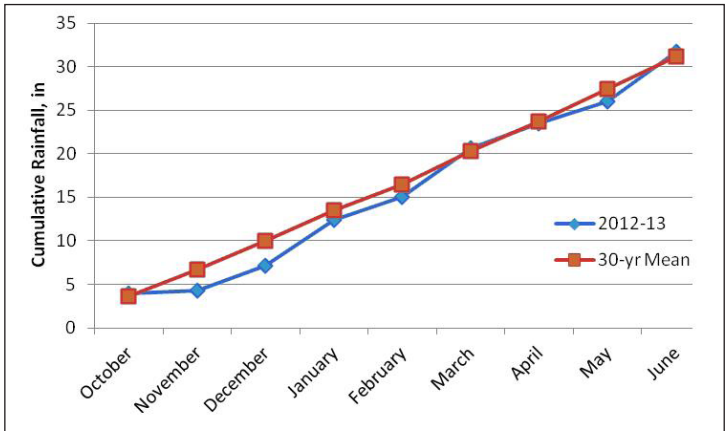

Fig. 1. The 2012–13 and 30-yr mean cumulative growing season precipitation for Virginia.

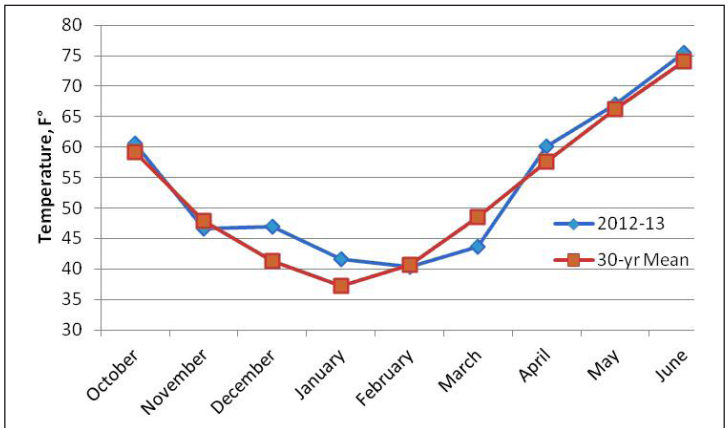

Fig. 2. Growing season monthly average temperature, 2012–13 and 30-yr mean for Virginia.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service, in the spring of 2013 there were 275,000 acres (111,289 ha) of wheat harvested in the state of Virginia. The average yield was 62 bu/A (4,166 kg/ha), down 3 bu/A (202 kg/ha) from 2012. In 2013, Virginia saw a 9% increase in wheat production with 17.6 x 10^6 bushels (383,540 metric ton) of wheat being produced in the state.

Disease incidence and severity. Entries in Virginia's 2013 state wheat variety trials were rated (0 = no infection to 9 = severe infection) for disease severity at four diverse locations. The 101 entries in the 2013 trial had mean powdery mildew (*Blumeria graminis*) ratings that varied from 0 to 6 in Virginia's southwestern region (Montgomery Co.) and from 0 to 4 on the Eastern Shore (Accomack Co.). Barley/cereal yellow dwarf virus infection was moderate at Blackstone, VA, in the Southern Piedmont with ratings ranging from 1 to 5. Fusarium head blight (*Fusarium graminearum*) was widespread across the Commonwealth and severe in several regions. At Warsaw, VA, in Richmond County, entries in the state wheat trial received disease index (accounts for incidence and severity) values ranging from 0 to 9%. Glume blotch also was prevalent in the Warsaw trial with ratings ranging from 1 to 4. Leaf rust (*Puccinia triticina*) was prevalent in many regions and was severe at the southwestern test site where susceptible lines had ratings ranging from 5 to 9. Race surveys conducted by Dr. James Kolmer of the USDA–ARS Cereal Disease Lab on 29 isolates from three regions in Virginia identified nine races of leaf rust and only race MCTNB was common at two locations (Accomack and Montgomery counties). Five additional races (MCTSB, MFPSB, MFQHG, SBDGG, and TNRJJ) were identified on the Eastern Shore, and three other races (TBRKG, TCGJG, and TCRKG) were identified at Warsaw. Stripe rust (*Puccinia striiformis*) was prevalent and moderately severe in the trial at Blacksburg, VA. Rust samples were sent to Dr. Xianming Chen at USDA-ARS in Pullman, WA, for race identifications. Three races were identified, including PSTv-37 (virulence for genes *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, *Yr27*, *Yr43*, *Yr44*, *YrTr1*, and *YrExp2*), race PSTv-52 (virulence for *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, *Yr27*, *Yr43*, *Yr44*, and *YrExp2*), and race PSTv-53 (virulence for *Yr1*, *Yr6*, *YrSP*, and *YrTye*).

State cultivar tests. In the 2012–13 tests, there were a total of 101 entries planted in seven environments across Virginia (http://www.grains.cses.vt.edu/). The test included 58 soft red winter (SRW) wheat cultivars and 43 experimental lines. No-till tests and tests planted after corn were conducted at Warsaw and Holland, VA. Mean grain yields varied from 45 bu/ac (3,024 kg/ha) at Holland, VA, in the Tidewater region to 93 bu/ac (6,249 kg/ha) at Orange, VA, in the northern Piedmont, and the mean yield over six locations was 79 bu/ac (5,308 kg/ha). Commercial cultivars USG 3404, USG 3013, USG 3612, USG 3523, AgriMAXX 434, SY Harrison, SY 474, Steyer Hunker, and Pioneer Brands 25R40, 26R10, and 26R41 all produced yields (85–89 bu/ac, 5,711–5,980 kg/ha) that were significantly higher than that of the overall trial average. Average grain yields among the 101 entries ranged from 62.0 bu/ac (4,166 kg/ha) for the long-term check cultivar Massey to 91 bu/ac (6,114 kg/ha) for experimental line VA10W-21. Test weight means among six locations varied from 51.6 lb/bu (66.4 kg/hl) at Blackstone, VA, in the southern Piedmont, to 59.3 lb/bu (76.3 kg/hl) at Orange, VA. Average test weights of the 101 entries over five environments ranged from 51.5 lb/bu (66.3 kg/hl) to 58.3 lb/bu (75.0 kg/hl), with an overall trial average of 55.9 lb/bu (71.9 kg/hl).

Mapping studies on Fusarium head blight resistance (FHB) in the SRW wheat cultivars Roane and Jamestown were conducted using data from field and greenhouse experiments. Preliminary results identified a putative QTL on chromosome 1B of Jamestown that is associated with resistance to FHB. The QTL accounted for 12.7% to 13.3% of the phenotypic variation in deoxynivalenol (DON) toxin accumulation and 26.1% of the phenotypic variation in FHB severity. The most diagnostic marker for the QTL on chromosome 1B is *Xwmc500.6* located 7.2 cM from the QTL peak and flanked by markers *Xwmc500.7* and *Xgwm273.2* (28.2 cM interval). Similarly, preliminary results from first year field data in another FHB-mapping study involving the SRW wheat cultivar Tribute indicate the presence of putative QTL associated with FHB incidence on chromosomes 2D, 3BSc, and 5D; QTL for FHB severity on chromosomes 2A, 2D, 3BSc, 5A, and 5D; and QTL for DON content on chromosome 2A.

Table 1. Virginia Wheat Yield Contest results. The 2013 contest was conducted statewide and the results can be found in the table below. Congratulations to our winners!

Place	Grower	Farm	County	Variety	Yield (bu/acre)
1	Robert Hinton	Cedar Plains Farm	Westmoreland	USG 3251	98.0
2	Ronnie Russell	Corbin Hill Farm	Middlesex	Pioneer 26R15	94.2

Release of soft red winter wheat cultivar 72014415.

The SRW wheat cultivar **72014415**, formerly designated VA07W-415, was developed and released in March 2013 by the Virginia Agricultural Experiment Station. The cultivar was derived from the cross 'VA98W-895/GA881130LE5//

VA98W-627'. Cultivar 72014415 is a broadly adapted, high-yielding, full-season, medium-height, semidwarf (gene *Rht2*) wheat. Plant color of 72014415 is blue green; at maturity it has creamy, white-colored, strap-shaped spikes with short tip awns, and yellow-colored straw. In the southern SRW wheat region, head emergence of 72014415 (106 days) is about 1 day later than USG 3555. In the eastern SRW wheat region, head emergence of 72014415 (131 days) is about 1 day later than that of Branson and 1 day earlier than Shirley. Average mature plant height of cultivar 72014415 has varied from 35 to 38 inches (89–97 cm) and is similar to that of Pioneer Brand 25R15. On average, straw strength (0 = erect to 9 = completely lodged) of cultivar 72014415 (0.5–3.6) is good, being most similar to that of Chesapeake (0.9–3.7) and better than that of 5187J (1.9–4.5). Winter kill (0 = none to 9 = complete) of cultivar 72014415 (0.9) in the 2010 Uniform Eastern SRW Wheat Nursery was most similar to those of check cultivars Bess (0.6) and Shirley (1.2). In Virginia's State Variety Trials (2010–12), cultivar 72014415 had a mean grain yield (88 bu/ac, 5,913 kg/ha) that was similar to those of the highest yielding cultivars Shirley and Featherstone Brand VA258. Over the same period, cultivar 72014415 had a mean test weight (59.5 lb/bu, 76.6 kg/hl) that was significantly higher than those of Shirley and USG 3555. Cultivar 72014415 is resistant to Hessian fly (*Mayetiola destructor* (Say)) biotypes B, C, D, O, and L, and possesses gene *H13*. The cultivar also has the *Lr37*/*Yr17*/*Sr38* gene complex that governs resistance to leaf rust, stripe rust, and stem rust.

Release of soft red winter wheat cultivar Featherstone 73.

The SRW wheat cultivar **Featherstone 73**, formerly designated VA09W-73, was developed and released in March 2013 by the Virginia Agricultural Experimental Station. The cultivar was derived from the cross '38158 (PI 19052)/VA99W-188//Tribute (PI 632689)'. Featherstone 73 is a broadly adapted, high-yielding, full-season, medium-height, semidwarf (gene *Rht2*) wheat. Plant stem and spike color of Featherstone 73 is blue, and spikes are strap shaped with short tip awns. In the eastern SRW wheat region, head emergence of Featherstone 73 (116 days) was most similar to that of Branson, and 2 days earlier than Shirley. Average mature plant height of Featherstone 73 has varied from 33 to 36 inches (84–91 cm) and is similar in height to that of Branson. Straw strength (0 = erect to 9 = completely lodged) of Featherstone 73 (0.9–3.6) is good being most similar to that of USG 3555 (0.8–4.0) and better than that of Featherstone VA258 (2.8–4.8). In the Uniform Eastern SRW Wheat Nursery, winter hardiness and spring freeze tolerance (0 = no injury to 9 = severe injury) of Featherstone 73 (1.2 and 0.4) were similar to those (1.1–1.4 and 0.2–0.5) of check cultivars Bess, Branson, and Shirley. Featherstone 73 ranked second over locations for grain yield (77.1 bu/ac, 5,180 kg/ha) among 35 entries evaluated at 25 locations in the 2012 Uniform Eastern SRW Wheat Nursery. Average test weight of Featherstone 73 (60.2 lb/bu, 77.5 kg/hl) was most similar to that of the check cultivar Bess and significantly ($P < 0.05$) higher than those of Branson and Shirley. Featherstone 73 expresses moderate to high levels of resistance to diseases prevalent in the SRW wheat region including leaf and stripe rusts, powdery mildew, leaf and glume blotches, Fusarium head blight, and barley yellow dwarf virus.

Release of soft white winter wheat cultivar MCIA Venus.

The soft white winter wheat cultivar **MCIA Venus**, formerly designated VA09W-188WS, was developed and released in March 2013 by the Virginia Agricultural Experiment Station. The cultivar was derived from the cross 'Pioneer Brand 25W60 (PI 607579)//Pioneer Brand 25W33 (PI 599197)/VAN98W-170WS'. MCIA Venus is a broadly adapted, high-yielding, early heading, medium-height, semidwarf (gene *Rht2*) wheat. At maturity, the cultivar has yellow-colored straw and spikes with the latter being slightly recurved, tapering in shape, and awned. In the northeastern soft winter wheat regions of the U.S. and Ontario, Canada, average head emergence of MCIA Venus (139–157 days) was 2 to 4 days earlier than that of Caledonia and 4 to 7 days earlier than Superior. Average mature plant height of MCIA Venus has varied from 36 to 41 inches (91–104 cm). MCIA Venus is most similar in height to Featherstone Brand VA258, 2 to 3 inches taller than Branson, and 3 to 5 inches shorter than Superior. Straw strength (0 = erect to 9 = completely lodged) of MCIA Venus (3.2–3.7) is moderate, most similar to those of SS 520 (3.1–4.5) and USG 3555 (2.0–4.0). In the Uniform Eastern Soft White Winter Wheat Nursery, winter hardiness (0–100% survival) of MCIA Venus (93–97%) was similar to those of northern check cultivars. MCIA Venus was evaluated at five locations (Michigan, New York, Virginia, and Ontario, Canada) in the 2012 Uniform Eastern Soft White Winter Wheat Nursery and had a mean grain yield of 77 bu/ac (5,174 kg/ha) over locations. MCIA Venus also was evaluated in this nursery in 2011 at seven locations (Indiana, Ohio, Michigan, New York, Virginia, and Ontario) and ranked second for grain yield (80 bu/ac, 5375 kg/ha). In these two nursery years, average test weights of MCIA Venus were 57.1 and 57.4 lb/bu (73.5–73.9 kg/hl) and similar to or significantly ($P < 0.05$) higher than those of Caledonia. MCIA Venus expresses moderate to high levels of resistance to diseases preva-

lent in the eastern soft white winter wheat region, including leaf and stripe rusts, powdery mildew, Septoria tritici leaf blotch, Fusarium head blight, barley yellow dwarf virus, wheat soil-borne mosaic virus, and Hessian fly.

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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 durum wheat.

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Breeding celiac-safe wheat cultivars: a future market class of wheat.

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The gluten-induced disorders dubbed the 'gluten syndrome' collectively affect >7.5% of the U.S. population. So far, the only known therapy for gluten syndrome is a life-long adherence to an abstinence diet, which is difficult to follow, and shown to have an adverse influence on the diversity of gut microbiota in consumers making them vulnerable to a number of disorders including colon cancer. It has been demonstrated repeatedly that strict adherence to gluten-free diet result in an upward shift in the body mass index (BMI) of the consumers, predisposing them to many other disorders. Extensive efforts put into the analysis of a wide range of wheat genotypes, including diploid einkorn; tetraploid emmer; and hexaploid common wheat accessions, landraces, and old/new cultivars at best resulted in the identification of lines with reduced-toxicity. None of the wheats (including einkorn, Khorasan, or Kamut), barley, and rye genotypes are free of gliadins and, thus, cannot be considered celiac-safe for common use by all celiac patients. The present technology does not allow healthcare providers to make recommendations to the patients that they only have sensitivity for a specific group of gluten proteins and, thus, can consume a specific wheat variety/product lacking certain gluten protein(s)/epitope(s). Moreover, research on alternative sources of gluten-free grains, including cereals (such as rice, sorghum, oats, and maize) and pseudocereals (such as tef, quinoa, and buckwheat) revealed that certain varieties of maize, oats,

quinoa, and buckwheat induce immune reactions in susceptible individuals. On the other hand, with rice, there is a risk of increasing the glycemic index of the consumers and exposure to arsenic. In addition, cases of allergenicity to rice grain-storage proteins (other than prolamins and glutelins) were reported throughout the world, thus it is not an ideal choice for consumption by celiac patients. So far, sorghum and tef are the two noncontroversial choices, but sorghum is predominantly used as animal feed, thus more research is needed on its end-uses to introduce it in human diet, whereas tef, due to morphological similarities with wheat grains, is the fear of contamination. Furthermore, because wheat is a primary source of dietary fiber, protein, vitamins, antioxidative compounds, and mineral elements, the World Health Organization recommends eating bread several times a day, and a number of countries (depending upon the national food habits) recommend consuming 250–350 g of bread per day.

In summary, developing potential alternatives of a gluten-free diet by modifying the composition of wheat grain to make them less prone to inducing the most common of dietary disorders is imperative. Also evident from the above description is that no natural product makes a perfect dietary solution for celiac patients. Thus, this trait is an obvious candidate for genetic engineering.

Our research showed that it is possible to obtain wheat genotypes completely devoid of immunogenic prolamins while retaining their baking properties by silencing the wheat *DEMETER* (*DME*) homoeologues (Fig. 1). The DME genes are responsible for transcriptional activation of genes encoding gliadins and the low-molecular-weight glutenins (LMWgs) in the developing wheat endosperm. But, so far, after screening ~400 transformants expressing hairpin or artificial micro-RNAs targeting wheat *DME* homoeologues, one genotype showing 85.6% suppression in *DME* transcript abundance and up to 76.4% reduction in the amount of immunogenic prolamins could be identified. This low frequency of desired transformants can be attributed to the unpredictability of both the number and site of transgene integration(s) using the current transformation procedures, which has a consequential effect on the transcription level of the transgene.

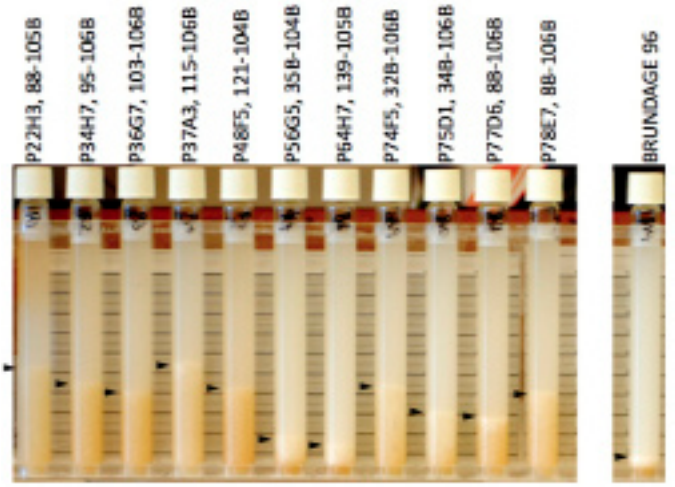

Fig. 1. Results of the SDS (sodium dodecyl sulfate) sedimentation test performed on a set of 11 T_2 transformants (whole-grain flour) and the wild-type control Brundage 96 as a preliminary test for grain quality. Because Brundage 96 is a soft white winter wheat, it showed a low sedimentation value as expected. Some of the transformants developed in Brundage 96 background showed high sedimentation values comparable to the hard wheat cultivars (generally used for bread making). Thus, suggesting that the changes in composition of grain-storage proteins resulted in a shift of market class from soft to hard in these transformants.

In view of the technical difficulties associated with current transformation procedures, we used a TILLING (Targeting Induced Local Lesions In Genomes) procedure to identify knockout or knockdown mutants in the wheat *DME* homoeologues. Screening of hexaploid wheat cultivar Express and tetraploid cultivar Kronos wheat TILLING populations for mutations in *DME* homoeologues resulted in identification of 191 mutants in the Express and 77 mutants in the Kronos background. These single mutants identified in DME homoeologues showed specific eliminations and/or reductions in the amount of prolamins. However, developing celiac-safe wheat genotypes requires pyramiding single mutations to obtain double mutations in the Kronos and triple mutations in the Express backgrounds. The nonsense mutations and splice-site variants in individual *DME* homoeologues with quantifiable effects on prolamin composition/content showed adverse effects on pollen viability and germination, imposing difficulties in pyramiding the effects of individual mutants in a single genotype. In view of these difficulties, an alternative approach employing a chimeric-hairpin construct capable of producing multiple interfering RNAs corresponding with the transcripts of the prolamin super-family genes was undertaken. This approach required aligning the sequences of the wheat gliadins (α/β-, γ- and ω-types) and LMWgs available in the public domain. The alignment results allowed identification of the five consensus sequences each representing a prolamin gene family, which were fused together to obtain the arms of the chimeric-hairpin. The chimeric-hairpin construct was used for wheat transformation of embryogenic-microspore and scutellar calli in the cultivars Louise, Hollis, WPB926, Farnum, Brundage 96, and Simon. The transformants showed sizable amount of reductions in the content of immunogenic

prolamins very similar to the transformants expressing *DME* hairpin or amiRNA constructs, which showed reductions and specific eliminations to variable degrees in the grain prolamin content. A compensatory increased in the amount of high-molecular-weight glutenins also was observed in some cases, which is a desirable characteristic for maintaining the end-use quality of the genotypes. Because none of the wheat transformants showed complete elimination of immunogenic prolamins, these genotypes with reduced gluten content are currently being crossed with an aim of pyramiding their effects on prolamin content or composition into a single wheat genotype.

We are currently using a site-directed procedure to achieve complete silencing of *DME* genes in the developing wheat endosperm to avoid the negative consequences of introducing point mutations in *DME* genes and obtain wheat genotypes showing complete elimination of immunogenic prolamins. To achieve this objective, we are attaching an engineered DNA binding domain of the *Xanthomons* transcription activator-like effector (TALE) to a universal *Arabidopsis* ethylene-responsive element binding factor-associated Amphiphilic Repression (EAR) domain that allows transcriptional suppression of the targeted gene(s). This DME-specific, TALE repressor will be introgressed in to the wheat genome via homologous recombination. In this procedure, the selected wheat transformants will be used as explant donors for retransformation with the expectation of a complete silencing of *DME* homoeologues. We are working in parallel on an alternative method of delivering recombinant TALEs in the plant cell using the type-III secretion system of *X. translucens*. This method does not require integration of foreign DNA in the plant genome to make desired genetic-modifications. Thus, this approach is expected to be the method of choice in future plant breeding efforts.

As a small number of celiac patients also were reported to show sensitivity to the HMW glutenins, we undertook another approach, which involves detoxification of gluten proteins by ectopic expression of gluten detoxifying enzymes (glutenases). For this purpose, a combination of a glutamine-specific, barley endoprotease B2 (EP-B2) and a post-proline cleaving prolyl endopeptidase from *Flavobacterium meningosepticum* (Fm-PEP) were selected and expressed in wheat endosperm. Wheat transformants showing sizable amount of reduction in Pro/Gln-rich peptides under simulated gastro-intestinal conditions were obtained. Because we intend to use wheat grains expressing glutenases as an ingredient of the daily bakery products, it is ideal to have thermostable enzymes that retain activity at and over 90°C. In order to achieve this objective, a site saturation mutagenesis approach was followed. The amino acid substitutions at residues 412, 413, 414, and 415 increased thermostability of Fm-PEP from 60°C to 90°C, while maintaining its catalytic properties under simulated gastro-intestinal conditions. Similarly, in view of increasing thermostability of EP-B2, a structure-based site directed mutagenesis approach was adapted and an increase in thermostability by 4°C was reported. The observed increase in the thermostability of EP-B2 is not substantial, but this pilot study demonstrated a possibility of obtaining thermostable variant of both Fm-PEP and EP-B2.

The solutions undertaken in the present research are based on developing wheat plants by genetic transformation. It is important to point out that most transgenic crops currently in use have been generated for the benefit of the producer, whereas crops that would lack immunogenic gluten proteins would benefit the consumer and the celiac populations in particular. They are thus acceptable to both regulatory authorities and the general public. Because these wheat transformants are developed in view of a medical purpose, they are exempt from labeling restriction in the State of Washington.

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National Small Grains Collection activities.

H.E. Bockelman, Agronomist and Curator.

Recent PI Assignments in Triticum, X Triticosecale, Aegilops, and Secale.

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 (PVPO) or insufficient inventories.** Accessions registered in the *Journal of Plant Registrations* are available by contacting the developers. Some accessions require agreement with the Standard Material Transfer Agreement of the IT PGRFA in order to receive seed. No PI assignments were made in *Aegilops* in the past year.

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
667743 PVPO	*Triticum aestivum* subsp. *aestivum*	Antero	United States	Colorado
667744	*Triticum aestivum* subsp. *aestivum*	ARS-Selbu	United States	Washington
667767 PVPO	*Triticum aestivum* subsp. *aestivum*	SY 007	United States	Iowa
667768 PVPO	*Triticum aestivum* subsp. *aestivum*	SY 474	United States	Iowa
667769 PVPO	*Triticum aestivum* subsp. *aestivum*	SY Steelhead	United States	Iowa
667770 PVPO	*Triticum aestivum* subsp. *aestivum*	SY Razor	United States	Iowa
667771 PVPO	*Triticum aestivum* subsp. *aestivum*	Carberry	Canada	Alberta
667772 PVPO	*Triticum aestivum* subsp. *aestivum*	SY Rowyn	United States	Iowa
668090	*Triticum aestivum* subsp. *aestivum*	SY Clearstone 2CL	United States	Montana
668099 PVPO	*Triticum aestivum* subsp. *aestivum*	Elgin-ND	United States	North Dakota
668100 PVPO	*Triticum turgidum* subsp. *durum*	Silver	United States	Montana
668130	*Triticum aestivum* subsp. *aestivum*	Bila od Dukovan	Czech Republic	
668131	*Triticum aestivum* subsp. *aestivum*	Arida	Slovakia	
668132	*Triticum aestivum* subsp. *aestivum*	Ratborska Heineho Teverson	Czechoslovakia	
668133	*Triticum aestivum* subsp. *aestivum*	Seladon	Czech Republic	
668134	*Triticum aestivum* subsp. *aestivum*	Kostomlatska Sametka	Czech Republic	
668135	*Triticum aestivum* subsp. *aestivum*	Moravska Hneda	Czech Republic	
668136	*Triticum aestivum* subsp. *aestivum*	Presivka Cerveny Oujezd	Czech Republic	
668137	*Triticum aestivum* subsp. *aestivum*	Rokycanska Sametka	Czech Republic	
668138	*Triticum aestivum* subsp. *aestivum*	Sandomierka	Poland	
668139	*Triticum aestivum* subsp. *aestivum*	Sandomierka	Czech Republic	
668140	*Triticum aestivum* subsp. *aestivum*	Sklienka	Slovakia	
668141	*Triticum aestivum* subsp. *aestivum*	Vouska z Tremosnice	Czech Republic	
668142	*Triticum aestivum* subsp. *aestivum*	Barbara	Slovakia	
668143	*Triticum aestivum* subsp. *spelta*		Kromeriz	Czech Republic
668144	*Triticum aestivum* subsp. *aestivum*	Rada	Slovakia	

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
668145	*Triticum aestivum* subsp. *aestivum*	Sana	Slovakia	
668146	*Triticum aestivum* subsp. *aestivum*	Solida	Slovakia	
668147	*Triticum monococcum* subsp. *monococcum*	Kromeriz	Czechoslovakia	
668148	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668149	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668150	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668151	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668152	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668153	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668154	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668155	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668156	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668157	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668158	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668159	*Triticum aestivum* subsp. *aestivum*	Krajova-Myjavska Pahorkatina	Slovakia	
668160	*Triticum aestivum* subsp. *aestivum*	Krajova-Myjavska Pahorkatina	Slovakia	
668161	*Triticum aestivum* subsp. *aestivum*	Krajova-Myjavska Pahorkatina	Slovakia	
668162	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668163	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668164	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668165	*Triticum aestivum* subsp. *aestivum*	Male Karpaty	Slovakia	
668166	*Triticum aestivum* subsp. *aestivum*	Biele Karpaty	Slovakia	
668167	*Triticum aestivum* subsp. *aestivum*	Alana	Czech Republic	
668168	*Triticum turgidum* subsp. *durum*	Vendur	Slovakia	
668169	*Triticum aestivum* subsp. *compactum*	Jezka Hladka	Czechoslovakia	
668170	*Triticum aestivum* subsp. *compactum*	Jezka Modra Hladka	Czechoslovakia	
668171	*Triticum aestivum* subsp. *spelta*	Svetla	Czechoslovakia	
668172	*Triticum aestivum* subsp. *spelta*	Tmava	Czechoslovakia	
668173	*Triticum aestivum* subsp. *spelta*	Uhrineves	Czechoslovakia	
668174	*Triticum aestivum* subsp. *spelta*	Uhrineves	Czechoslovakia	
668175	*Triticum aestivum* subsp. *aestivum*	Bety	Czech Republic	
668176	*Triticum aestivum* subsp. *aestivum*	Malvina	Slovakia	
668177	*Triticum aestivum* subsp. *aestivum*	Solara	Slovakia	
668178	*Triticum aestivum* subsp. *aestivum*	Sarka	Czech Republic	
668179	*Triticum aestivum* subsp. *aestivum*	Pavlina	Czech Republic	
668180	*Triticum aestivum* subsp. *aestivum*	Niagara	Czech Republic	
668181	*Triticum aestivum* subsp. *aestivum*	Vlasta	Czech Republic	
668182	*Triticum aestivum* subsp. *aestivum*	Banquet	Czech Republic	
668183	*Triticum aestivum* subsp. *aestivum*	Sulamit	Czech Republic	
668184	*Triticum aestivum* subsp. *aestivum*	Svitava	Czech Republic	
668185	*Triticum aestivum* subsp. *aestivum*	Klea	Slovakia	
668186	*Triticum monococcum* subsp. *monococcum*	Tabor	Czech Republic	
668187	*Triticum aestivum* subsp. *aestivum*	Venistar	Slovakia	
668188	*Triticum aestivum* subsp. *aestivum*	Mladka	Czech Republic	

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
668189	*Triticum aestivum* subsp. *aestivum*	Rheia	Czech Republic	
668190	*Triticum aestivum* subsp. *aestivum*	Meritto	Czech Republic	
668191	*Triticum aestivum* subsp. *aestivum*	Malyska	Slovakia	
668192	*Triticum aestivum* subsp. *aestivum*	Eva	Slovakia	
668193	*Triticum aestivum* subsp. *aestivum*	Vanda	Slovakia	
668194	*Triticum aestivum* subsp. *aestivum*	Balada	Czech Republic	
668195	*Triticum aestivum* subsp. *aestivum*	Zerda	Slovakia	
668196	*Triticum aestivum* subsp. *aestivum*	Velta	Slovakia	
668197	*Triticum aestivum* subsp. *aestivum*	Barroko	Czech Republic	
668198	*Triticum aestivum* subsp. *aestivum*	Evelina	Czech Republic	
668199	*Triticum aestivum* subsp. *aestivum*	Simila	Czech Republic	
668200	*Triticum aestivum* subsp. *aestivum*	Etela	Czech Republic	
668201	*Triticum aestivum* subsp. *aestivum*	Ines	Czech Republic	
668202	*Triticum aestivum* subsp. *aestivum*	Raduza	Czech Republic	
668203	*Triticum aestivum* subsp. *aestivum*	Penalta	Czech Republic	
668204	*Triticum aestivum* subsp. *aestivum*	Bohemia	Czech Republic	
668205	*Triticum aestivum* subsp. *aestivum*	Sakura	Czech Republic	
668206	*Triticum aestivum* subsp. *aestivum*	Verita	Slovakia	
668207	*Triticum aestivum* subsp. *aestivum*	Bonita	Slovakia	
668208	*Triticum aestivum* subsp. *aestivum*	Petrana	Slovakia	
668209	*Triticum aestivum* subsp. *aestivum*	Federer	Czech Republic	
668210	*Triticum aestivum* subsp. *aestivum*	Secese	Czech Republic	
668211	*Triticum aestivum* subsp. *aestivum*	Silueta	Czech Republic	
668212	*Triticum aestivum* subsp. *aestivum*	Sarlota	Slovakia	
668213	*Triticum aestivum* subsp. *aestivum*	Stanislava	Slovakia	
668214	*Triticum aestivum* subsp. *aestivum*	Genoveva	Slovakia	
668215	*Triticum aestivum* subsp. *aestivum*	Veldava	Slovakia	
668216	*Triticum aestivum* subsp. *aestivum*	Markola	Slovakia	
668217	*Triticum aestivum* subsp. *aestivum*	Pavlina	Slovakia	
668218	*Triticum aestivum* subsp. *aestivum*	Viador	Slovakia	
668219	*Triticum aestivum* subsp. *aestivum*	Ignis	Slovakia	
668220	*Triticum aestivum* subsp. *aestivum*	Axis	Slovakia	
668221	*Triticum aestivum* subsp. *aestivum*	Armelis	Slovakia	
668222	*Triticum aestivum* subsp. *aestivum*	Bardotka	Czech Republic	
668223	*Triticum aestivum* subsp. *aestivum*	Bazilika	Czech Republic	
668224	*Triticum aestivum* subsp. *aestivum*	Bosorka	Czech Republic	
668225	*Triticum aestivum* subsp. *aestivum*	Bona Dea	Slovakia	
668226	*Triticum aestivum* subsp. *aestivum*	IS Karpatia	Slovakia	
668227	*Triticum turgidum* subsp. *durum*	IS Pentadur	Slovakia	
668228	*Triticum aestivum* subsp. *aestivum*	Nikol	Czech Republic	
668229	*Triticum aestivum* subsp. *aestivum*	Bodycek	Czech Republic	
668230	*Triticum aestivum* subsp. *aestivum*	Elly	Czech Republic	
668231	*Triticum aestivum* subsp. *aestivum*	Jindra	Czech Republic	
668232	*Triticum aestivum* subsp. *aestivum*	RW Nadal	Czech Republic	
668233	*Triticum aestivum* subsp. *aestivum*	Auburn	Slovakia	
668234	*Triticum aestivum* subsp. *aestivum*	Kostomlatska Sametka	Czech Republic	
668235	*Triticum aestivum* subsp. *aestivum*	Presivka Cerveny Oujezd	Czech Republic	

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
668236	*Triticum aestivum* subsp. *aestivum*	Terrasol Krajova	Czechoslovakia	
668237	*Triticum turgidum* subsp. *dicoccon*	Durka	Czechoslovakia	
668238	*Triticum turgidum* subsp. *dicoccon*	Malov	Czechoslovakia	
668239	*Triticum turgidum* subsp. *dicoccon*	Toman	Czechoslovakia	
668240	*Triticum turgidum* subsp. *dicoccon*	Stevak	Czechoslovakia	
668241	*Triticum turgidum* subsp. *dicoccon*	Krajova-Stara Huta	Czechoslovakia	
668242	*Triticum turgidum* subsp. *dicoccon*	Krajova-Horny Tis-ovnik	Czechoslovakia	
668243	*Triticum turgidum* subsp. *dicoccon*	Mittak	Czechoslovakia	
668244	*Triticum turgidum* subsp. *dicoccon*	Krajova-Vrbovce	Czechoslovakia	
668245	*Triticum aestivum* subsp. *aestivum*	Leguan	Czech Republic	
668246	*Triticum aestivum* subsp. *aestivum*	Aranka	Czech Republic	
668247	*Triticum aestivum* subsp. *aestivum*	Postoloprtska Presivka 61	Czechoslovakia	
668248	*Triticum turgidum* subsp. *dicoccon*	Rudico	Czech Republic	
668249	*Triticum aestivum* subsp. *compactum*	Jezka Hladka	Czechoslovakia	
668250	*Triticum aestivum* subsp. *spelta*	01C0200981	Czechoslovakia	
668251	*Triticum aestivum* subsp. *aestivum*	Galan	Czech Republic	
668252	*Triticum aestivum* subsp. *aestivum*	Zuzana	Czech Republic	
668253	*Triticum aestivum* subsp. *aestivum*	Granny	Czech Republic	
668254	*Triticum aestivum* subsp. *aestivum*	Sirael	Czech Republic	
668255	*Triticum aestivum* subsp. *aestivum*	Septima	Czech Republic	
668256	*Triticum aestivum* subsp. *aestivum*	Séance	Czech Republic	
668257	*Triticum aestivum* subsp. *aestivum*	Tercie	Czech Republic	
668363 PVPO	*Triticum aestivum* subsp. *aestivum*	SY 311	United States	Iowa
668364 PVPO	*Triticum aestivum* subsp. *aestivum*	SY Vaca	United States	Iowa
668559	*Triticum aestivum* subsp. *aestivum*	Fhb1NIL75	United States	Kansas
668560	*Triticum aestivum* subsp. *aestivum*	Fhb1NIL78	United States	Kansas
668561	*Triticum aestivum* subsp. *aestivum*	Fhb1NIL80	United States	Kansas
668562	*Triticum aestivum* subsp. *aestivum*	Fhb1NIL90	United States	Kansas
668563	*Triticum aestivum* subsp. *aestivum*	Fhb1NIL98	United States	Kansas
668564 PVPO	*Triticum aestivum* subsp. *aestivum*	Cowboy	United States	Colorado
668572 PVPO	*Triticum aestivum* subsp. *aestivum*	1863	United States	Kansas
668573 PVPO	*X Triticosecale spp*.	Fredro	Poland	Leszno
669385	*Triticum aestivum* subsp. *aestivum*	NC09BGTUM15	United States	North Carolina
669386	*Triticum aestivum* subsp. *aestivum*	NC09BGTS16	United States	North Carolina
669387	*X Triticosecale spp*.	AN38	Mexico	Coahuila
669388	*X Triticosecale spp*.	Anpelon	Mexico	Coahuila
669441 PVPO	*Triticum aestivum* subsp. *aestivum*	LCS Mint	United States	Colorado
669443	*Triticum aestivum* subsp. *aestivum*	Zak ERA8	United States	Washington
669450	*Triticum aestivum* subsp. *aestivum*	REA 98-01	United States	Washington
669451	*Triticum aestivum* subsp. *aestivum*	REA 98-02	United States	Washington
669452	*Triticum aestivum* subsp. *aestivum*	REA 98-03	United States	Washington
669453	*Triticum aestivum* subsp. *aestivum*	REA 98-04	United States	Washington
669454	*Triticum aestivum* subsp. *aestivum*	REA 98-05	United States	Washington
669455	*Triticum aestivum* subsp. *aestivum*	REA 98-06	United States	Washington
669456	*Triticum aestivum* subsp. *aestivum*	REA 98-09	United States	Washington
669457	*Triticum aestivum* subsp. *aestivum*	REA 98-12	United States	Washington

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
669458	*Triticum aestivum* subsp. *aestivum*	REA 98-13	United States	Washington
669459	*Triticum aestivum* subsp. *aestivum*	REA 98-14	United States	Washington
669460	*Triticum aestivum* subsp. *aestivum*	REA 98-15	United States	Washington
669461	*Triticum aestivum* subsp. *aestivum*	REA 98-16	United States	Washington
669462	*Triticum aestivum* subsp. *aestivum*	REA 98-30	United States	Washington
669463	*Triticum aestivum* subsp. *aestivum*	REA 98-31	United States	Washington
669464	*Triticum aestivum* subsp. *aestivum*	REA 98-33	United States	Washington
669465	*Triticum aestivum* subsp. *aestivum*	REA 98-34	United States	Washington
669466	*Triticum aestivum* subsp. *aestivum*	REA 98-35	United States	Washington
669467	*Triticum aestivum* subsp. *aestivum*	REA 98-36	United States	Washington
669468	*Triticum aestivum* subsp. *aestivum*	REA 98-38	United States	Washington
669469	*Triticum aestivum* subsp. *aestivum*	REA 98-39	United States	Washington
669470	*Triticum aestivum* subsp. *aestivum*	REA 98-40	United States	Washington
669471	*Triticum aestivum* subsp. *aestivum*	REA 98-41	United States	Washington
669472	*Triticum aestivum* subsp. *aestivum*	REA 98-43	United States	Washington
669473	*Triticum aestivum* subsp. *aestivum*	REA 98-44	United States	Washington
669474	*Triticum aestivum* subsp. *aestivum*	REA 98-45	United States	Washington
669475	*Triticum aestivum* subsp. *aestivum*	REA 98-46	United States	Washington
669476	*Triticum aestivum* subsp. *aestivum*	REA 98-47	United States	Washington
669477	*Triticum aestivum* subsp. *aestivum*	REA 98-48	United States	Washington
669478	*Triticum aestivum* subsp. *aestivum*	PT771	Canada	Alberta
669490 PVPO	*Triticum aestivum* subsp. *aestivum*	Keldin	Canada	Ontario
669491 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-4059CLP	United States	Illinois
669569 PVPO	*Triticum aestivum* subsp. *aestivum*	Ladd	United States	Oregon
669570 PVPO	*Triticum aestivum* subsp. *aestivum*	Kaseberg	United States	Oregon
669571 PVPO	*Triticum aestivum* subsp. *aestivum*	72014415	United States	Virginia
669572 PVPO	*Triticum aestivum* subsp. *aestivum*	Featherstone 73	United States	Virginia
669573 PVPO	*Triticum aestivum* subsp. *aestivum*	Southern Harvest 3200	United States	Virginia
669574 PVPO	*Triticum aestivum* subsp. *aestivum*	LCS Wizard	United States	Virginia
669575 PVPO	*Triticum aestivum* subsp. *aestivum*	MCIA Venus	United States	Virginia
669817	*Triticum aestivum* subsp. *aestivum*	KY06C-11-3-10	United States	Kentucky
669998 PVPO	*Triticum aestivum* subsp. *aestivum*	WB-1081CL+	United States	Illinois
669999 PVPO	*Triticum turgidum* subsp. *durum*	Tiburon	United States	Arizona
670000 PVPO	*Triticum turgidum* subsp. *durum*	Helios	United States	Arizona
670015	*Triticum aestivum* subsp. *aestivum*	CDL001	United States	Minnesota
670019	*Triticum aestivum* subsp. *aestivum*	OK05312	United States	Oklahoma
670035 PVPO	*Triticum aestivum* subsp. *aestivum*	25W31	United States	Iowa
670036 PVPO	*Triticum aestivum* subsp. *aestivum*	WB9576	United States	Illinois
670037 PVPO	*Triticum aestivum* subsp. *aestivum*	WB9518	United States	Illinois
670038 PVPO	*Triticum aestivum* subsp. *aestivum*	Puma	United States	Washington
670039 PVPO	*Triticum turgidum* subsp. *durum*	Carpio	United States	North Dakota
670040 PVPO	*Triticum turgidum* subsp. *durum*	Miwok	United States	California
670041 PVPO	*X Triticosecale spp*.	Traction	Canada	Ontario
670115	*Secale cereal*	ER1-Chason	United States	Oklahoma
670156 PVPO	*Triticum aestivum* subsp. *aestivum*	Colter	United States	Montana
670157 PVPO	*Triticum aestivum* subsp. *aestivum*	Warhorse	United States	Montana
670158 PVPO	*Triticum aestivum* subsp. *aestivum*	WB3768	United States	Montana
670159	*Triticum turgidum* subsp. *durum*	SBEIIa-SBEIIb A	United States	California

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
670160	*Triticum turgidum* subsp. *durum*	SBEIIa-SBEIIb AB	United States	California
670161	*Triticum turgidum* subsp. *durum*	SBEIIa-SBEIIb B	United States	California
670170 PVPO	*Triticum aestivum* subsp. *aestivum*	Oakley CL	United States	Kansas
670447	*Triticum aestivum* subsp. *aestivum*	1315	Turkey	Tokat
670448	*Triticum aestivum* subsp. *aestivum*	IWA8611237	Iran	Khorasan
670449	*Triticum aestivum* subsp. *aestivum*	Mahmoudi	Tunisia	Bizerte
670450	*Triticum aestivum* subsp. *aestivum*	ELS 6404-84-1	Ethiopia	Harer
670451	*Triticum aestivum* subsp. *aestivum*	141	China	Jiangsu
670452	*Triticum aestivum* subsp. *aestivum*	Menceki	Turkey	Urfa
670453	*Triticum aestivum* subsp. *aestivum*	Karisik	Turkey	Burdur
670454	*Triticum turgidum* subsp. *durum*	5514	Turkey	Kastamonu
670455	*Triticum turgidum* subsp. *durum*	Katha	India	Rajasthan
670456	*Triticum turgidum* subsp. *durum*	10198	Ethiopia	Harer
670457	*Triticum turgidum* subsp. *durum*	125	Iran	
670462	*Triticum aestivum* subsp. *aestivum*	NE05548	United States	Nebraska
670475 PVPO	*Triticum aestivum* subsp. *aestivum*	A020128P1	United States	Iowa
670476 PVPO	*Triticum aestivum* subsp. *aestivum*	A020167A1	United States	Iowa
670477 PVPO	*Triticum aestivum* subsp. *aestivum*	W01007212	United States	Iowa
670478 PVPO	*Triticum aestivum* subsp. *aestivum*	W010425E1	United States	Iowa
671855	*Triticum aestivum* subsp. *aestivum*	Egan	United States	Montana
671896 PVPO	*Triticum aestivum* subsp. *aestivum*	Sprinter	United States	Washington
671897 PVPO	*X Triticosecale spp*.	Southern States Trical 1414	United States	North Carolina

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2013–14 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 12Th International Wheat Genetics Symposium held in Yokohama, Japan, is available on 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.

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Morphological and Physiological Traits

At the end of the introductory paragraph add:
A summary of trait genotypes and markers used in the Canadian wheat breeding program is given in {11044}.

1. Gross Morphology: Spike characteristics

5. Anthocyanin Pigmentation

5.3. Red/purple coleoptiles.

After the introductory sentence add:
In chromosome substitution lines of wild emmer to common wheat, both the 7AS and 7AL derivatives had red coleoptiles, placing *Rc-A1* in the centromeric region {10974}.

5.5. Purple grain/pericarp

Continue the first paragraph:
A purple line PC was obtained from a cross of the nonpurple Line 821 (a 7S(7B) substitution from *Ae. speltoides*) and Line 102/00, a chromosome 2A introgression from *T. timopheevii* {10946}. Purple-grained accessions are unknown in both *Ae. speltoides* and *T. timopheevii*.

8. Blue Aleurone

NEW Brittle Culm

Three independent mutants with brittle tissues were obtained as EMS-induced mutants in *T. monococcum* subsp. *monococcum* accession PAU 14087 {11002}. The mutations likely affected cellulose synthesis and involved all tissues {11002}.

brc1 {11002}. 1AL {11002}. **dv:** *T. monococcum* subsp. *monococcum* mutant *brc1* {11002}.
ma: *Xwmc470-1A* – 3.9 cM – *brc1* – 2.1 cM – *Xgwm135-1A* {11002}.

brc2 {11002}. 3AL {11002}. **dv:** *T. monococcum* subsp. *monococcum* mutant *brc2* {11002}.
ma: *Xcfa2170-3A* – 2.9 cM – *brc2* – 0.8 cM – *Xcfd62-3A* {11002}.

brc3 {11002}. 6AS {11002}. **dv:** *T. monococcum* subsp. *monococcum* mutant *brc3* {11002}.
ma: *Xbarc37-6A* – 1.9 cM – *brc3* – 10.3 cM – *Xbarc113-6A* {11002}.

9. Brittle Rachis

After the introductory sentence add:
In chromosome substitution lines of wild emmer to common wheat, the 3AS derivative was more brittle than the 3BS derivative {10974}.

11. Cadmium Uptake

11.1. Low cadmium uptake

***Cdu1*.** **tv:** Brigade {11044}; CDC Desire {11044}; CDC Verona {11044}; CDC Vivid {11044}; Enterprise {11044}; Eurostar {11044}; Napoleon {11044}; Transend {11044}; Strongfield {11044}.

13. Cleistogamous Flowering

Delete 'in durums' from the heading and begin the section with the following:
Cleisogamy in barley is controlled by the *Cly1* gene, which encodes an AP2 protein. The *Cly1* and *cly1* alleles differ by a single nucleotide within the miR172 binding site. Three wheat homologues of *Cly1*, *i.e., TaAP-2A*, *TaAp-2B*, and *TaAp-2D*, were located in the terminal bins of chromosomes 2AL, 2BL, and 2DL, respectively, in Chinese Spring and Shinchunaga {11013}.

Cleistogamous flowering in durums
Present data.

16. Crossability with Rye and *Hordeum* and *Aegilops* spp.

16.1. Common wheat

Kr1. **ma:** Mapped to a 2.0-cM region flanked by *Xw5145-5B* and *CA1500122*/*Xw9340-5B* {10922}.

A second gene in 5BL distal to the *Ph1* locus and flanked by *Oshypl* and *Os09g36440*, but including *Xgwm371-5B*, affected the temperature sensitivity of seed set in *Kr1* genotypes in wide crosses {10922}.

17. Dormancy (Seed)

17.1. Vivipary

Vp-A1g [[11047}]. *Vp-1Ab* {11047}. **v:** Kayansona {11047}; Sonalika {11047}; Yaqui 50 {11047}; Yecora Rojo 76 {11047}.
c: GenBank Gu385899 {11047}.

Vp-A1h [{11047}]. *Vp-1Ad* {11047}. **v:** Attila {11047}; Glenlea {11047}; Tanori F71 {11047}.
c: GenBank Gu385901 {11047}.

Vp-A1i [{11047}]. *Vp-1Af* {11047}. **v:** Debeira {11047}; Kancahn {11047}; Rayon F89 {11047}.
c: GenBank Gu385903 {11047}.

Vp-1Be {10998}. **v:** Fulingkemai {10999}; Hongmangchun {10998}; Wangshuibai {10999}.

Vp-1Bf {10998}. **v:** Wanxanbaimaizi {10998}.

Vp-B1g {11000}. **v:** HD2939 {11000}; Pavon 76 {11000}; Sonora 64 {11000}.
c: GenBank GU385904 {11000}.

17.2. Pre-harvest sprouting

QTL

Association mapping of 198 winter wheat genotypes detected eight QTL on seven chromosomes, 1BS, 2BS, 2BL, 2DS, 4AL, 6DL, 7BS, and 7DS {10959}.

18. Ear Emergence

19. Earliness per se

Add at end of section:

Cutler / AC Barrie: Three QTL were mapped on chromosomes 1B (*QEps.dms-1B.1* and *QEps.dms-1B.2*) and 5B (*QEps.dms5B*) {11039}.

NEW Flag Leaf Width

Two NILs in the backgrounds of Mianyang 99-323 and PH691 possessing *Fhb5* in a *Xbarc303-5A – Xbarc100-5A* interval from Wangshuibai spanning the centromere had a narrow-leaf phenotype. *QFlw.nau-5A*, redesignated as *TaFLW1*, was mapped to a 0.2-cM region, *Xwmc492-5A – Xwmc752-5A*: bin 5AL12-0.37-0.57, and was separated from *Fhb5*: bin 5AS3-C-0.75 {10934}.

40. Height

40.1. Reduced Height : GA-insensitive

Rht-A1a. 4A {10923}, 4AL {11017}.
ma: *Xwmc48-4AS* – 2 cM – *Xgwm610-4A* – 1 cM – *Rht-A1* – 2 cM – *Xgpw4545-4AL* {11017}.

Add to existing note:

A functional *Rht-A1a* allele is expressed at a similar level to its orthologues {10923}.

Rht-B1c. **ma:** Allele-specific markers were designed from the gene sequence {10923}.
c: The *Rht-B1c* transcript carries a 90-bp, in-frame insertion within the region encoding the conserved N-terminal DELLA domain plus two SNPs upstream of the insertion. A much larger insertion occurs in the g-DNA {10923}.

Rht-B1d. **c:** Has the same point mutations as in *Rht-B1b*, there is likely to be another mutation outside the coding region {10923}.

Rht-B1e. **v:** Karlik 1 PI 504549 {10924}, Polukarlikovaya 49 and 11 derivatives {10924}.
ma: A PCR marker distinguishes this allele from *Rht-B1a* and *Rht-B1b* {10923}.
c: A stop codon occurs three codons upstream of the *Rht-B1b* mutation {10923}.

Rht-D1. **bin:** 4AL10-0.82-1.00 {11017}.

Immediately following the *Rht-D1d* entry, and before present footnote, insert:
Rht-D1b, *Rht-D1c*, and *Rht-D1d* are identical across the coding region, but *Rht-D1c* has a four-fold increase in copy number relative to *Rht-D1b*; *Rht-D1d* has a reduced copy number relative to *Rht-D1c* {10923,11016}.

40.2. Reduced Height : GA-sensitive
Rht11 {718}. See *Rht-B1e*.

42. Hybrid Weakness
42.1. Hybrid necrosis
Ne2m. **v:** After Manitou {939}add: 'HD2329 {10985}.'

Genotype lists in: add: '10985.'

65. Response to Vernalization
Vrn-B1b. **v:** Ciano 67 {10991}; Polo {10991}; Yaktana 54 {10991}.

Vrn-B1d [{10977,10978}]. Referred to as *Vrn-B1c* in {10977,10978}, *Vrn-B1*^{S} {10977}.
v: Albidum 43 {10991}; Albidum 29 {10991}. Garnet {10991}; Lutescens 62 {10991}; McMurachy {10991}; Saraovskaya 29 {10977,10991}. Six cultivars {10977}; 25 cultivars {10978}.
c: GeneBank HQ593668 {10977}, HQ130482 {10978}. Relative to *Vrn-B1a* (= *Vrn-B1*^{DM}, *Vrn-B1d* has a deletion of 0.8 kb and duplication of 0.4 kb in intron 1 {10977}.

Vrn-D1
List the current *Vrn-D1a* as a continuation under *Vrn-D1*.
To the following note, change the ending to '….Ushio Komugi relative to Vrn-D1 {10202}.
Add note: Nine, spring-habit *Ae. tauschii* accessions from Pakistan and Afghanistan shared a 5,437-bp deletion in the first intron of *Vrn1-D*^{t}*1*; the deletion resulted in a more abundant WFT transcript {10958}. Wheat lines identified as having genotype *vrn-A1*, *vrn-B1*, *Vrn-D1*, *vrn-2*, *vrn-3* were subdivided into spring and facultative types based on a 110-day, nonvernalization flowering test. Relative to *Vrn-D1a*, *Vrn-D1b* has a SNP located 161 bp upstream from the ATG initiation site; cytidylic acid is replaced by aenylic acid. The SNP is in the CArG box, a recognition site for MADS-box proteins {10996}. In qRT-PCR analyses, expression of *Vrn-D1b* was reduced relative to *Vrn-D1a* {10996}. A molecular marker was developed to distinguish the alleles {10996}.

Vrn-D1a {10996}. *Vrn-D1* {1398}. Spring habit.
v: Shimai 12 {10996}; Yumai 7 {10996}; Yumai 18 {10996}; Yangmai 3 {10996}; Yangmai 18 {10996}.

Vrn-D1b {10996}. *Vrn-D1* {10996}. Facultative habit.
v: Jimai 26 {10996}; Kenong 199 {10996}; Shi 4185 {10996}; Shi-91-5093 {10996}; J5265 {10996}.
c: GenBank JQ406528 {10996}.

vrn-D1. **c:** GenBank AY616457 {10996}.

Following the gene lists continue the paragraph starting 'Allelic variations…..{773}: *Vrn-1*, *Vrn-2*, *Vrn-4*, and *Vrn-4* alleles in Indian wheats based on markers are postulated in {10986}.

Following **69. Segregation Distortion**

NEW. Short Roots

A 'very short root' phenotype was produced by heterozygous genotypes from selected crosses between Chinese Spring and certain synthetics. The *Vsr1* locus was localized to a 3.8-cM interval on chromosome 5DL {11014}.

Vsr1 {11014}. 5DL {11014}.
ma: *Xwmc765-5D* – 7.7 cM – *Vsr1* – 1.1 cm – *Xbarc144-5D* {11014}; *Xwmc765-5D* – 1.9 cM – *XWL938* – 3.3 cM – *XWL2506* – 3.3 cM – *Vsr1* – 0.5 cM – *XWL954* – 0.5 cM – *Xbarc144-5D* {11014}.

Vsr1a. **v:** Chinese Spring {11014}.
Vsr1b. **v:** TA4152-71 {11014}.

Proteins

80. Proteins

80.1. Grain protein content

Move the first paragraph and insert below gene *Pro2*.

Gpc-B1b. Add synonym '... NAM-B1 {10995}.'
i: Yecora Rojo NIL PI 638740 {10138}.
v: As II {10995}; Burnside {11044}; Diamant {10995}; Glencross {11044}; Glupro {10138}; Lilian {11044}; Prins {10995}; Somerset {11044}; Stanley {10995}, *T. aestivum* subsp. *spelta* Altgold {10995}.
tv: *T. turgidum* subsp. *dicoccoides* FA-15 {10138}.

This allele was relatively frequent in Scandinavian and Finnish common wheats, landraces, and spelts {10995}.

80.2. Enzymes

80.2.34. Polyphenol oxidase

Ppo-A1. **ma:** *Xcfa2058-2A* – 0.4 cM – *Ppo-A2* – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – *Ppo-A1* – 11.0 cM – *Xwmc181-2A* {10931}.
Ppo-A1f. **v:** Penawawa {10931}.
Ppo-A1h {10931}. **v:** Louise {10931}.
c: GenBank JN632506 {10931}.

Ppo-D1. **ma:** *Xcfd62-2D* – 0.2 cM – *Ppo-D2* – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – *Ppo-D1* – 0.9 cM – *Xbarc349-2D* {10931}.
Ppo-D1a. **v:** Louise {10931}.

Ppo-A2 {10930}. *PPO-A2* {10931}. 2AL {10930}.
ma: *Xcfa2058-2A* – 0.4 cM – *Ppo-A2* – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – *Ppo-A1* – 11.0 cM – *Xwmc181-2A* {10931}.
Ppo-A2a {10930}. **v:** Alpowa {10930}.
c: GenBank HQ228148 {10930}.
Ppo-A2b {10930}. **v:** Panawawa {10931}.
c: GenBank HQ 228149 {10930}.
Ppo-A2c {10931}. **v:** Louise {10931}.
c: JN632507 {10931}.

Ppo-B2 {10930}. *PPO-B2* {10930}. 2B {10930}.
ma: *Xiwa175*/*Xiwa4866-2* – 0.7 cM – *Ppo-B2* – 2.3 cM – *Xiwa7593-2B* {10931}.
Ppo-B2a {10930}. **v:** Penawawa {10931}.
c: GenBank HQ228150 {10930}.
Ppo-B2b {10930}. **v:** Alpowa {10930}.
c: GenBank HQ228151 {10930}.

Ppo-B2c {10931}. **v:** Louise {1211}.
c: GenBank JN632508 {10930}.

Ppo-D2 {10930}. *PPO-D2* {10930}. 2DL {10930}.
ma: *Xcfd62-2D* – 0.2 cM – *Ppo-D2* – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – *Ppo-D1* – 0.9 cM – *Xbarc349-2D* {10931}.

Ppo-D2a {10930}. **v:** Louise {10931}.
c: GenBank HQ228152 {10931}.

Ppo-D2b {10930}. **v:** Penawawa {10930}.
c: HQ228153 {10930}.

80.5.5. Salt soluble globulins

80.5.6. Waxy proteins

Wx-A1

Wx-A1a. **v:** Bao Hua {10989}.
tv: Langdon {10989}.

Wx-A1i {10989}. **v:** KU9259 {10989}.

Wx-A1j {10989}. **v:** M1 {10989}.

After *Wx-A1j* add note:
Functional markers for *Wx-A1c*, *Wx-A1d*, *Wc-A1e*, and *Wx-A1i* were developed from DNA sequences {10990}.

Pathogenic Disease/Pest Reaction

83. Reaction to *Blumeria graminis* DC.

83.1. Designated genes for resistance

Pm24

Pm24a [{571}]. *Pm24* {571}. **bin:** 1DS5-0.70-1.00.
ma: In the present listing modify '– *Pm24* –' to '– *Pm24*/*Xgwm1291-1D* –' and add reference to {10109,10957}.

Pm24b {10994}. 1DS {10994}. **bin:** 1DS1-0.59-1.00.
v: Baihulu {10994}.
ma: *Xgwm789*/*Xgwm603-1D* – 2.4 cM – *Pm24b* – 3.6 cM – *Xbarc229-1D* {10994}.

Pm47. **bin:** Correct to: 7BS1-0.27-1.00.
ma: Change to: *Xgpw2119-7B* – 7.5 cM – *BE606897* – 1.7 cM – *Pm47* – 3.6 cM – *Xgwm46-7A* {M10912}.

Pm48 [{M1215}]. *Pm46* {M1215}. 5DS {M1215}.
bin: 5DS1. **v:** Tobasco {M1215}.
ma: *Xgwm205-5D* – 17.6 cM – *Pm47* – 1.3 cM – *Xmp510* (*BE498794*) – 1.8 cM – *Xcfd81-5D* {M1215}.

Pm49 {10938,[{10937}]}. *Ml5323* {10937}. 2BS {10937}.
bin: 2BS3-0.84-1.00. **tv:** *T. turgidum* subsp. *dicoccum* MG5323 {10937}.
ma: *Xcau516-2B* – 7.2 cM – *Pm48* – 4.1 cM – *XCA695634* {10937}.

Pm50 {10942}. 2AL {10942}. **bin:** C-2AL1-0.85.
v: K2 TRI 29907 {10942}. **tv:** *T. turgidum* subsp. *dicoccum* M129 {10942}
ma: *Xgwm294-2A* – 2.9 cM – *Pm50* {10942}.
K2 is a backcross derivative of German winter wheat cultivar Alcedeo with *T. turgidum* subsp. *dicoccum* accession M129 as donor of mildew resistance {10942}.

Pm51 {11026}. Putative *Th. ponticum* derivative. *PmCH86* {11026}.
2BL {11026}. **bin:** 2BL6-0.89-1.00. **v:** CH7086 {11026}.
ma: *Xwmc332-2B* – 4.7 cM – *Pm51* – 1.4 cM – *BQ246670* {11026}.

Pm52 {11029}. *MlLX99* {11028,11029}. **bin:** 2BL2-0.35-0.50.
v: Liangxing 99 {11028,11029}.
ma: *Xcfd73-2B* – 5.3 cM – *Xwmc441-2B* – 0.2 cM – *XBE604758* – *Pm52* – 2.9 cM – *Xgwm120-2B* {11028}; *XBE604758* – 5.5 cM – *Xics34* – *Pm52* – 0.8 cM – *Xics30* – six additional *ics* markers – *Xgwm120* {11029}.

Pm53 {11045}. Derived from *Ae. speltoides*. *PmNC-S16* {11045}.
5BL {11045}. **v:** NC09BGTS16, PI669386 = 'Saluda*3 / TAU829' {11045}.
al: *Ae. speltoides* TAU829 {11045}.
ma: *Xwmc759*/*Xgwm499-5B*/*IWA6024* – 0.7 cM – *Pm53* – *IWA2454* – 5.9 cM – *Xgwm408-5B* {11045}.

83.2. Suppressors of *Pm*

In the introductort paragraph insert ', and 11025}' following reference 491, that is '{401, and 11025}'.

83.3. Temporarily designated genes for resistance to *Blumeria graminis*

MlIw170 {10921}. 2BS. **bin:** 2BS3-0.84-1.00.
tv: *T. turgidum* subsp. *dicoccoides* IW170 {10921}.
ma: *XcauG2* – 0.6 cM – *MlIw170*/*Xcau516*/*Xcfd238-2B* – 2.15 cM – *XcauG8*/*BF201235*/*Xwmc243-2B* {10921}. *Iw1* – 18.77 cM – *MlIw170* {10921}.
This gene is located in the same region as *Pm26* {M1201}.

MLNCD1 {11004}. 7DS {11004}. **bin:** 7DS4-0.61-1.00 {11004}.
v: NC96BGD1 PI 597348 {11004} = 'Saluda*3 / TA2570' {11004}.
ma: *Xgwm635-7D* – 5.5 & 8.3 cM – *MlNCD1* – 16.2 & 13.6 cM – *Xgpw328-7D* {11004}.

PmAS846 {10926}. 5BL {10926}. **bin:** 5BL14-0.75-0.76.
v: N9134 {10926}; N9738 {10927}.
tv: *T. turdigum* subsp. *dicoccoides* AS846 {10926}.
ma: *XMAG2498-5B* – 1.3 cM – *Pm36*/*XBJ261635* – 1.1 cM – *PmAS846* – 1.3 cM – *XFCP1-5B* {10927}.

PmTm4 {10961}. 7BL {10961}. **bin:** 7BL10-0.78-1.00.
v: Tangmai 4 {10961}.
ma: *Xgwm611-7B* – 7.0 cM – *PmTm4* – 14.6 cM – *Xest92* – 2.9 cM – *Xbarc1073*/*Xbarc82-7B* {10961}.

Pmx {11009}. Recessive. 2AL {11009}. **bin:** 2AL1-0.58-1.00.
v: Xiaohongpi {11009}.
ma: *Xhbg327-2A* – 0.6 cM – *Pmx*/*Xsts-bcd1231* – 8.9 cM – *XresPm4*/*Xgpw4456-2A* {11009}.

This gene and close markers showed distorted segregation ratios and some discrepancy of markers relative to *Pm4* alleles {11009}.

Add at end of section:
A normally inherited resistance to powdery mildew in wheat–*Th. intermedium* translocation line 08-723 (T?B–?S^{t}·6AL) was reported in {11035}.

83.4. QTL for resistance to *Blumeria graminis*

AGS 2000 (*Pm3a+Pm8*) / Pioneer 26R61 (*Pm8*). *QSuSuPm.uga-1AS* (*SuPm8*) with an inhibitory effect on powdery mildew response was located at or near *Pm3a*. *QPm.uga-7AL* from Pioneer 26R61, flanked by *Xcfa2257-7A* and *Xwmc525-7A,* was in the region of the *Pm1* locus, even though the test culture was virulent for known *Pm1* alleles {11025}.

SHA3/CBRD (S) / Naxos (R): RIL population: A major QTL on chromosome 1AS accounted for 35% of the phenotypic variation; other QTL from Naxos were on 2DL, 2BL and 7AL. Although 'SHA3/CBRD' possessed a *Pm3* haplotype but no known *Pm3* allele, there was no evidence that the *Pm3* allele suppressed *Pm8*, which appeared to be effective in Norway {10934}.

Reaction to *Colletrichum cereale*

Rcc1 {10939}.	5AL {10939}.	
	v:	Chinese Spring {10939}; Norin 4 {10939}; Shinchunaga {10939}.
	ma:	*Xbarc165-5A* – 1.2 cM – *Rcc1* – 12.8 cM – *Xgwm671-5A* – 0.7 cM – *Xwmc415-5A* {10939}.
***rcc1*.**	**v:**	Hope {10939}.

Susceptibility to this non-pathogen of common wheat is rare, with only one susceptible genotype being documented. A few susceptible tetraploid genotypes were identified {10939}.

86. Reaction to *Diuraphis noxia* (Mordvilko)

***Dn6*.**	7D.	
Dn626580 {10981}.	7DS {10981}.	**v:** PI 626580 {10981}.
	ma:	*Dn626580* – 1.8 cM – *Xbarc214-7D* – 3.2 cM – *Xgwm473-7D* – 3.2 cM – *Xgwm473-7D* {10981}.

87. Reaction to *Fusarium* spp.

87.1. Disease: Fusarium head scab, scab

***Fhb5*.**

At end of entry add:

Closely linked in coupling with *Qflw.nau-5A* for narrow leaf width, but recombination is reported in {11041}.

To the alphabetical list of crosses insert:

Alve (S) / Line 685 R: DH population: QTL on chromosomes 4D (*Rht-D1*), 3BS, 5A, and 2BL {10972}. Two resistance QTL were needed to counteract the negative effect of the *Rht-D1b* semidwarfing allele {10972}.

Baishanyuehuang (R) / Jagger (S): RIL population: Four genes/QTL derived from the resistant parent included *Fhb1* (R^2 = 0.16), *Qfhb.hwwg-3BSc* (R^2 = 0.09), *Qfhb.hwwg-3A* (R^2 = 0.05-0.08), and *Qfhb.hwwg-5A* (R^2 = 0.05 in one trial) {10950}.

Sumai 3 (R) / Y1193-6 (S): RIL population: Three resistance QTL on chromosomes 3BS, 6BL, and 2DS with R^2 values of 0.26, 0.11, and 0.19, respectively; the last was derived from Y1193-6 {11001}.

Treho (S) / Heyne (MR): RIL population: Three QTL from Heyne, *Qfhb.hwwwg-3AS* (R^2 up to 0.18), *Qfhb.hwwg-4DL* (R^2 = 0.14-0.23), and *Qfhb.hwwg-4AL* (R^2 up to 0.18) {11005}.

VA00W-38 (mod. R) / Pioneer 26R46 (S): RIL population: Consistent QTL from VA00W-38 detected on chromosomes 1BL, 2A, 2DL, 5B, 6A, and 7A explained 6.5-21.3% of the phenotypic variation; one QTL from 24R46 was identified on chromosome 7A {11022}. Major QTL on 2DL, 6A, and 5B decreased FHB index, Fusarium damaged kernels, and DON, respectively {11022}.

Tetraploid wheat

T. turgidum subsp. *dicoccum* line Td161 crossed to three durum parents: small-effect QTL were detected on chromosomes 3B, 4B, 6A, 6B, and 7B; all except the 6A QTL were located at previously known positions {10993}.

87.2. Disease: Crown rot caused by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species.

Sunco / Macon: RIL population: QTL were located in chromosomes 2B, 3B, 4B, and 4D. *Qcrs.wsu-3BL* from Macon and flanked by *Xgwm247-3B* and *Xgwm299-3B* was the most effective {10932}.

Sunco / Otis: RIL population: QTL were located in chromosmes 2B, 3B, 4B, and 7A. *Qcrs.wsu-3BL* from Otis was the most effective {10932}.

88. Reaction to *Heterodera avenae* Woll.

89. Reaction to *Magnaporthe grisea* (Herbert) Barr

Rmg6 {10948}. 1DS {10948}. **v:** Chinese Spring {10948}; Norin 4 {10948}; Shin-Chunaga {10948}.
ma: *Xwmc432-1D* – 9.6 cM – *Rmg6* – 6.6 cM – *Xwmc222-1D* {10948}.
Rmg6 and a second gene with a weaker effect conferred resistance to a selected '*Triticum* x *Lolium*' isolate {10948}.

Rmg7 {11046}. **tv:** *T. turgidum* subsp. *dicoccum* KU112 {11046}; KU120 {11046}; KU1222 {11046}.

RmgTd(t) {10949}. 7BL {10949}. **tv:** *T. turgidum* subsp. *dicoccoides* KU109 {10949}.
ma: *Xhbg338-7B* – 10.5 cM – *Rmg7* {10949}.
RmgTd(t) was detected with a white culture of an *Avena* pathogen isolate backcrossed to a wheat isolate. Avirulence to *RmgTd(t)* was completely associated with white color of the pathogen isolate {10949}. The white color appeared as a mutant variant during backcrossing.

90. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

H13. **v:** AGS 2010 {11008}; AGS 2026 PI 658065 {11008}; Oglethorpe PI 657986 {11008}.

H33 {10954}. 3AS {10954}. **v:** Line 97211 {10954}.
tv: PI 134942 {10954}.
ma: *Xgwm218-3A* – 10 &7 cM – *H33* – 28 &25 cM – *Xhbg-3A* {10954}.

H34 {11018}. *Qhf.hwwg-6B* {11018}. 6BS {11018}.
v: Clark {11018}.
ma: Flanked by *Xsnp921-6B* and *Xsnp2745-6B* within a 4.5-cM region, $R^2 = 0.38$-0.42 {11018}.

HR61 {11008}. 6AL {11008}. **bin:** 6AL8-0.90-1.00 {11008}.
v: 26R61 PI 612153 {11008}.
ma: Mapped as a QTL ($R^2 = 0.63$) flanked by *Xgwm427-6A* and *wPt-731936* {11008}.

Insert after temporary designations:

Qhf-hwwg-1A {11018}. 1AS {11018}. **v:** Clark H34 {11018}.
ma: Closely linked to *Xwgm33-1A* {11018}; Located within a 6-cM region flanked by *Xwgm33-1A* and *Xsnp5150-6B*, $R^2 = 0.1$ {11018}.

Add to comment at end of section:

Haplotype analysis was used to postulate *Ae. tauschii*-derived genes *H13*, *H22*, *H23*, *H26*, and *H32* in a set of synthetic wheat lines {10983}.

91. Reaction to *Meloidogyne* spp.

92. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

Stb2. Add: ', 1BS {10976}'.

ma: Following the present information add: According to {10976} *Stb2* is neither on 3BS nor linked with *Xgwm389-3B*. *Xwmc406-1B* – 6.0 cM – *Stb2* – 5.0 cM – *Xbarc008-1B* {10976}.

QTL:

Solitar (R) / Mazurka (S): DH population: Resistance under field conditions was associated with QTL on chromosomes 5A, 6D and 7D, which accounted for 20% of the genotypic variation; all three were derived from Solitar, but there was no evidence that *Stb6* and *Stb11*, also present in Solitar, were involved {10984}.

Steele-ND (R) / ND735 (S): RIL population: A consistent QTL ($R^2 = 0.1$) for seedling resistance flanked by DArT markers *XwPt-7101* and *X377410* was mapped to chromosome 5BL in the region of *Stb1* {10992}. Two other QTL on chromosomes 1D and 7A were detected in single experiments {10992}.

93. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

93.1. Genes for resistance

QTL:

93.2. Sensitivity to SNB toxins (necrotrophic effectors)

Snn1. Add: **v:** M-6 {10960}.

Snn3. Add: **v:** BG220 {10960}.

Snn5 {10925}. 4BL {10925}. **bin:** 4BL-6 0.85-1.00.
tv: *T. turgidum* subsp. *carthlicum* PI 94749 {10925}.
ma: *Xbarc163*/*Xcfd-4B* – 13.3 cM – *Snn5* – 2.8 cM – *Xwmc349-4B* {10925}.

snn5. **tv:** LP749-29 {10925}.

Host sensitivity genes in U.S. southern winter wheats are listed in {1241}.

XX. Reaction to *Puccinia coronata* var. *hordei*

Cr1 {10956}. 5DL {10956}. **v:** Chris CItr 14108 {10956}.
ma: *Xwmc41.2-5D* – 11.3 cM – *Cr1* – 16.8 cM – *Xgdm63-5DL* {10956}.

9*5*. Reaction to *Puccinia graminis* Pers.

Sr9. *Sr9h* {11010}. *SrWeb* {10858}. 2BL {10858,11010}.
v: RL6203 {11010}.
v2: Gabo 56 CI 14035 *Sr11* {11010}; Gabo CI 12795 *Sr11* {11010}; Timstein CI 12347 *Sr11* {11010}. Webster RL6201 *Sr30* {10858}.
ma: *Xgwm47-2B* – 1.4 cM – *SrWeb* – 12.5 cM – *Xwmc332-2B* {10858}.

Sr33. **dv:** *Ae. tauschii* PI 603225 {11012}.
ma: *Xwmc432-1D* – 0.3 cM – *Xwmc336-1D* – 1.0 cM – *Sr33* – 4.2 cM – *Xwmc222*/*Xcfa2158-1D* {11012}. Flanked by *BE405778* and *BE499711* within a 1-cM region {10987}.
c: *Sr33* encodes a CC-NBS-LRR protein and is orthologous to *Sr31*, *Sr50*, and the barley powdery mildew locus *Mla* {10987}.

Sr35. **c:** *Sr35* is a CC-NBS-LRR gene {10988}.

Sr39. 2B {651} = T2SL–2SS#2·2SL#2 {11037}.
Add at end of section:
Further lines with shortened segments are described in {11037} along with tightly linked co-dominant STS markers.

Sr42. **ma:** *Xcfd49-6D* – 5.5 cM – *Xbarc183-6D* – 0.5 cM – *Sr42*/*FSD_RSA* – 11.8 cM – *Xbarc301-6D*; *Xcfd6D* – 5.9 cM – *Sr42* – 46.9 cM – *Xcfd13-6D* {10952}.
Add note:
The likelihood that *Sr42* is the same as *SrTmp* and *SrSha7* (see below) is discussed in {11035} where Blouk#1, Coni#1, Niini#1, Phunye#1, Ripper, and Tinkio1 were shown to carry a gene, or closely linked genes, on chromosome 6DS. If they are the same, this list would be enlarged to include Digalu, Gambo, Koshan 09, and Morvarid {11035}. Nearest markers are *Xbarc183-6D* and *Xcfd49-6D* but not in consistent order {11035}.

Sr44 {389}. Changes and new entry as follows:
Derived from *Th. intermedium*.
T7DS–7J#1L·7J#S 7J#1L {389}. **v:** Line 86.187 TA5657 {939}; Several T7A–7J#1L translocations {0089}.
T7DL·7J#1S {11011}. **v:** TA5657 {11011}.
7J#2, 7J#2S. **su:** Group-7 alien substitution lines with 7J#1 and 7J#1S {939}.
ad: TAF2 = L1 {169}.

Sr53. **ma:** Closest markers: *BE443102*/*Mbo1* and *BE442600*/*Mse1* {10789}.

Sr54. **ma:** *Xcfd-283-2D* – 8.1 cM – *Sr54*/linkage block of 18 markers – 15.8 cM – *Xwmc167-2D* {10816}.
The possibility of a large alien linkage block was supported by the fact that many of the associated markers were null {10816}.

Sr58 {10965}. 1BL {10965}. **su:** Lalbahadur (Pavon1B) (GID 519245) {10965}.
v: *Lr46* Deletion Mutant 109 (GID 5349718) {10965}; *Lr46* Deletion Mutant 111 (GID 5349716) {10965}.

SrTA1662 {11012}. 1DS {11012}. **dv:** *Ae. tauschii* TA1662 {11012}.
ma: *Xwmc432-1D* – 4.4 cM – *SrTA1662* – 4.4 cM – *Xwmc222-1D* {11012}.

SrTmp. Add note:
The possibility of this gene being present in a number of South African cultivars, including Betta = Klein Impacto, is discussed in {10941}.

SrWeb. Delete current listing as this gene is now named *Sr9h*.

Sr10171 {10936}. 7DS {10936}. **v:** Genetic stock to be designated {10936}.
dv: *Ae. tauschii* TA10171 {10936}.
ma: *Sr10171* – 0.9 cM – *Xgdm88*/*Xwmc827-7D* – 1.9 cM – *Xcfd30-7D* {10936}.

Sr10187 {10936}. 6DS {10936}. **v:** Genetic stock to be designated {10936}.
dv: *Ae. tauschii* TA10187 {10936}.
ma: *Xcfd49-6D* – 1.9 cM – *Sr10177* – 13.6 cM – *Xbarc173-6D* {10936}.

QTL:
Avocet S / Pavon 76: RIL population of lines lacking *Sr26*: Five QTL, *QSr.cim-3B* (*Sr2*), *QSr.cim-1B* (*Lr46*/*Yr29*/*Pm39* region), and *QSr.cim-3D* ($R^2 = 0.2$) from Pavon 76; *QSr.cim-4B* and *QSr.cim-5A* from Avocet S {10975}.

Carberry (Resistant in Canada) / AC Cadillac (Resistant in Canada and Kenya): DH population: QTL effective in Kenya were located in chromosomes 2B, 5B, 7B, and 7D, those effective in Canada were on 3B (*Sr2*), 5A, and 5B; those effective in Kenya and Canada were on 4B and 6D (*Sr42*); both parents had *Lr34*/*Sr51* {11040}.

PBW343 (S) / Muu (I): RIL population: Four consistent QTL were identified, *QSr.cim-2BS, QSr.cim-3BS* (*Sr2*), and *Sr.cim-7AS* from Muu, and *QSr.cim-5BL* from PBW343 {11019}.

96. Reaction to *Puccinia striiformis* Westend.

96.1. Designated genes for resistance to stripe rust

Yr17. **v:** Jagger {10973}.

Yr29. **v:** Quaiu 3 *Yr30* {10943}.

Yr36. **v:** Burnside {11044}; Glencross {11044}; Lilian {11044}; Somerset {11044}.

Yr30. **v:** Quaiu 3 *Yr29* {10943}.

Yr31. **ma:** Add: It is mentioned in {10928} that *Yr31* maps between *Lr13* and *Lr23*.

Yr45. **v:** Add: PI 660056 {11024}.

Yr48 {10705}. Adult-plant resistance. 5AL {10705}.
bin: 5AL23-0.87-1.00.
v: UC1110 (MR) / PI 610750 (MR): RIL4 GSTR 13504 {10705}; RIL 167 GSTR 13618 {10705}.
ma: Co-segregated with *Vrn2*, *Be495011*, *Xcfa2149-5AL*, *Xgpw2181a-5AL*, *Xwmc74-5AL*, and *Xwmc410-5AL* {10705}. *Xwmc727-5AL* – 4.4 cM – *Yr48* – 0.3 cM – *Xwms291-5AL* {10705}.
PI 610750 = 'Synthetic 205 (Croc 1 / *Ae. tauschii*) / Kauz)' {10705}.

Yr50. **ma:** Change the first map value from 6.9 to 8.0.
Add note:
The genetic distance between *Yr50* and *Yr62* was estimated to be 27.1 ± 8.6 cM {11023}.

Yr51. Update by addition of second gene **v2:** AUS 27858 Yr57.

Yr53. **bin:** 2BL3-0-0.35.

Yr54 {10944}. Adult-plant resistance. 2DL {10944}.
v: *Yr54* RIL GID6032209 {10944}; *Yr54* RIL GID6032334 {10944}.
v2: Quaiu 3 *Yr29 Yr30* {10943,10944}.
ma: *Yr54* – 0.4 cM – *Xgwm301-2D* {10944}.
Yr54 could be the same as *Qyr.tam-2D* in Alcedo {10945}.

Yr55 {10953}. 2DL {10953}. **v2:** Frelon *Yr17* AUS 38882 {10953}.
ma: *Xmag4089-2D* – 11.4 cM – *Yr55* – 8.4 cM – *Xmag3385-2D* {10953}.

Yr56 {10955}. *Qyr.sun-2A* {10955}. 2AS {10955}.
bin: Tentatively 2AS5-0.78-1.00 {10955}.
tv: AUS 91575 {10955}; Wollaroi (AUS 99174) {10955}.
ma: *Xbarc212-2A* – 3.7 cM – *Xbarc124-2A* – 2.1 cM – *Xsun167-2A* – 5.7cM – *Yr56* – 7.6 cM – *Xsun168-2A* – 5.0 cM – *Xsun169 2A* – 8.0 cM – *Xgwm512-2A* {10955}.
Wollaroi has additional APR resistance QTL {10955}.

Yr57 {10963}. 3BS {10963}. **bin:** 3BS8-0.78-1.00.
v: AUS 91463 {10963}. **v2:** AUS 27858 *Yr51* {10963}.
ma: *Xsts3B-15* – 4 9 cM – *Yr57* – 2.0 cM – *Xgwm389*/*Xcfp140*/*Xmag2095-3B* {10963}; *Yr57* – *Yr4*, 5.2 ± 1.3 cM {10963}.

Yr58 {10964}. 3BL {10964}. **bin:** 3BL7-0.63-1.00.
v: Sonora W195 AUS 19292 {10964}.
ma: *100016328/123392* – 4.6 cM – *Yr58* – 3.9 cM – *1121669/3023704* {10964}.

Yr59 {10966}. Adult-plant resistance. 7BL {10966}. **bin:** 7BL-0.86-1.00.
v1: PI 660061, 'Avocet S / PI 178759' F4-158{10967}.
v2: PI 178759 {10966}.
ma: *Xwmc557-7B* – 2.2 cM – *Xwgp5175* – 2.1 cM – *Yr59* – 1.1 cM – *Xbarc32* – 0.5 cM – *Xbarc182-7B* {10966}.
Yr59 can be detected in high temperature seedling tests (10966,10967}. *Yr59* is a highly effective HTAP resistance gene. Crosses with lines possessing *Yr39*, *Yr52*, or *YrZH84* previously reported on chromosome 7BL segregated, indicating that they are at different loci. However, the allelism test data are based on F_2 phenotypes only. The linkage order of these genes is (proximal) *Yr39* – 31.2 cM – *Yr52* – 5.4 cM – *YrPI178759* – 6.0 cM – *YrZH84* (distal).

Yr60 {10968}. 4AL {10968}.
v: 'Avocet*3 // Lalbmono1B*4 / Pavon', GID 5934039 {10968}; Lal Bahadur (GID 177343) {10968}.
ma: *Yr60/Xwmc776-4A* – 0.51 cM – *Xwmc313/Xwmc219-4A* {10968}.

Yr61 {10970}. 7AS {10970}. *Yrdp34* {10970}.
v: Pindong 34 {10970}.
ma: *Xwgp5765b* – 3.9 cM – *Yr61*– 1.9 cM – *Xwp5467* – 12.5 cM – *Xcfa2174* {10970}.

Yr62 {11023}. Adult-plant resistance. **bin:** 4BL5-0.86-1.00).
4BL {11023}. **v:** PI 192252 {11023}; PI 660060 = 'Avocet S / PI 192252' F4-103{11024 }.
ma: *IWA3611-4B* – 0.8 cM – *IWA4041-4B* – 0.8 cM – *IWA2171-4B* – 0.7 cM – *IWA99-4B* – 1.0 cM – *IWA1923-4B* – 1.2 cM – *Xgwm251-4B* – 3.3 cM – *Yr62* – 2.0 cM – *Xgwm192-4B* – 0.6 cM – *Xgwm495-4B* – 0.7 cM – *Xgwm513-4B* {11023}.
The genetic distance between *Yr62* and *Yr50* was estimated to be 27.1 ± 8.6 cM {11023}.

Yr63 {11027}. 7BS {11027}. **bin:** 7BS1-0.27-1.00.
v: AUS 27955 {11027}.
ma: *IWB33120* – 0.9 cM – *Yr63* – 1.5 cM – *IWB52844* – 10.5 cM – *Xwmc606-7B* {11027}.

Yr64 {11030}. 1BS {11030}. **bin:** 1BS9-0.84-1.00.
v: PI 660064 = 'Avocet S / PI 331260' {10967}.
tv: PI 331260 {11030}.
ma: *Xbarc8-1B* – 0.6 cM – *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 3.5 cM – *Yr64* – 2.0 cM – *Xgdm33-1B* – 5.0 cM – *Xgwm498-1B* – 3.9 cM – *Xcfd59-1B* – 0.4 cM – *Xgwm273-1B* – 3.9 cM – *Xgwm18-1B* – 2.6 cM – *Xbarc137-1B* – centromere {11030}.

Yr65 {11030}. 1BS {11030}. **bin:** 1BS10-0.5-centromere.
v: 'AvS / PI 480016' F_7-12 {11030}. **tv:** PI 480016 {11030}.
ma: *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 5.5 cM – *Xgdm33-1B* – 4.6 cM – *Xgwm498-1B* – 3.5 cM – *Xbarc187-1B* – 2.8 cM – *Xgwm273-1B* – 3.7 cM – *Xgwm18-1B* – 1.2 cM – *Yr65* – 2.1 cM – *Xgwm11-1B* – 2.1 cM – *Xbarc137-1B* – centromere {11030}.

Yr66 {11032}. *YrVL1* {11032}. 3DS {11032}. **bin:** 3DS6-0.55-1.00.
v1: AGG91584WHEA = MSP4543.1 {11032}.
v2: VL892 = AGG91586WHEA *Yr67* {11032}.
ma: *IWB47165* – 3.1 cM – *Yr66* – 2.9 cM – *IWB18087/IWB56281* {11032}.

Yr67 {11032}. *YrVL2* {11032}; *YrC591* {11033}. 7BL {11032,11033}. **bin:** 7BL10-0.78-1.00.
v1: AGG91585WHEA = MSP4543.4 {11032}; C306 {11032}; C591 {11032;11033}.
v2: VL892 = AGG91586WHEA *Yr66* {11032}.
ma: *Xbarc182-7BL* – 5.2 cM – *IWB62475*/*IWB37096* – 1.1 cM – *Yr67* – 0.6 cM – *IWB71995* {11032}; *Xbarc32-7BL* – 2.2 cM – *Xcfa2040-7B* – 8.0 cM – *Yr67* – 11.7 cM – *SC-P35M48* {11033}.

96.2. Temporarily designated genes for resistance to stripe rust

YrAvS {11007}. **v:** Avocet R {11007}; Avocet S {11007}.
This designation was used to describe an assumed resistance gene in both Avocet R and Avocet S, the latter being the genetic background of the Avocet S near-isogenic lines. Av S NILs with *Yr7*, *Yr7*, and *Yr9*, as well as Avocet R, were susceptible to the variant of Pst race 6 E0 {11007}.

YrH9020 {10979}. Derived from *Psathyrostachys huashanica*. 2DS {10979}.
v: H9020-1-6-8-3 {10979}.
ma: *Xgwm102-2D* – 3.8 cM – *Xgwm455-2D* – 5.8 cM – *YrH9020* – 4.4 cM – *Xgwm261-2D* – 2.3 cM – *Xwmc503-2D* – 0.6 cM – *Xcfd53-2D* {10979}.

YrKK {11034}. Adult-plant resistance. 2BS {11034}.
bin: 2BS-1. **v:** Kenya Kuku {11034}.
ma: *Xgwm148-2BS* – 3.2 cM – *YrKK* – 1.8 cM – *Xwmc474-3B* {11034}.
Resistance conferred by *YrKK* at the adult stage approached immunity. A slight effect was observed on seedling response {11034}.

96.3. Stripe rust QTL

In cross 'Avocet / Attila', correct spelling to 'Avocet'

Avocet (S) / Chapio (I): F_6 RIL population: In Mexico, QTL were located in chromosomes 2BS (*Yr31*), 3BS (*Yr30*), and 7DS (*Yr18*); only the last two were effective in 2009. In China, QTL were located in chromosomes 3BS, 5BL, and 7DS. A 3DS QTL was effective in Mexico in 2009 and in China in 2013 {11020}.

Avocet (S) / Pastor (I): RIL population: QTL mapped on 1BL (*Yr29*), 2BS (*Yr31*), 5A, 6B, and 7AL plus minor QTL on 1AL, 1B, 3A, 3B, 4D, 6A, 7AS, and 7AL {10928}.

Claire / Lemhi: DH population: Four QTL for APR: *Qyr.niab-2D.1* (at or near *Yr16*, R^2 = 0.1-0.25), *Qyr.niab2DL.2* (R^2 = 0.14-0.32), *Qyr.niab-2BL*, and *Qyr.niab-7B* (R^2 = 0.11-0.13) {10962}. An unknown seedling resistance gene was located in chromosome 3BL {10962}.

Jagger (MR) / 2174 (MS): RIL population: *Qyr.osu-2A* (*Yr17*) and *QYR.osu-5A* (in *Xgwm156-5A* – centromere region) from Jagger and *Yr18* from 2174 (but only in tests in China) {10973}.

Yr16DH70 (Cappelle Desprez / 2*Palmiet Selection) / Palmiet: DH population: One major-effect QTL, *Qyr.ufs-2A*, and three less effective QTL in 2D (possibly *Yr16*), 5B, and 6D were from Yr16DH70, and a minor effect QTL on 4B was from Palmiet {10933}.

UC1110 (MR) / PI 61070 (MR): RIL population: Four QTL for APR: two, *Qyr.ucw-3BS*, peaking at *Xgwm533.1*, R^2 = 0.22, and *Qyr.ucw-2BS*, R^2=0.05 from UC1110, and *Yr48* and *Qyr.ucw-2AS*, R^2 = 0.02, from PI 61070 {10705}.

92.Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr3a. **v:** Sinvalocho MA {10929}.

Lr3c. **v2:** CI 13227 {11021}.

Lr12. 4BL {10951}.
bin: 4BL5-0.86-1.00.
ma: *Xgwm251-4B* – 0.9 cM – *Lr12* – 1.9 cM – *Xgwm149-4B* {10951}.

Lr14. Lr14a.
bin: 7BL10-0.78-1.00.
tv: Add: Arcangelo {11015}; Bicre {11015}; Creso {11015}; Colosseo {11015}; Italo {11015}; Plinio {11015}.
ma: Add: *Xwmc10*/*Xgwm344*/*wPt1085-7B* – 1.1 cM – *wPt4038-HRM* – 0.1 cM – *Lr14a* – 1.0 cM – *wPt4140-HRM* {11015}.

Lr14b. **v2:** CI 13227 *Lr68* {10817}.

Add note: Most accessions with *Lr14b*, including the Tc NILs probably carry APR gene *Lr68* {10817}, which could be the same as *QLr.osu-7BL* {10817}.

Lr23. **v2:** Pastor *Lr46* {10928}.

Lr35. 2B {651} = T2SL–2SS#2·2SL#2 {11037}.
i: RL 6082 = 'Thatcher*7/RL 5711' {11037}.

Add note: Lines with shortened alien segments bearing *Lr35* are described in {10741}.

Lr42. **v2:** Quaiu 3 *Lr46* {10943}.

Lr46.
v: Siete Cerros {10817}.
v2: CI 13227 *Lr3c* {M12013}; Quaiu 3 *Lr42* {10943}. Parula *Lr3b Lr13 Lr14b Lr34 Lr68* {10817}. Frontana *Lr13 Lr14b Lr34 Lr68* {10817}.

Lr68 {10817}. Adult-plant resistance. 7BL {10817}.
v2: Parula *Lr3b Lr13 Lr14b Lr34 Lr46* {10817}. Frontana *Lr13 Lr14b Lr34 Lr46* {10817}. Arula 1 *Lr14b* CIMMYT GID 1847450 {10817}; Arula 2 *Lr14b* CIMMYT GID 1847422 {10817}. Rayon F89 *Lr14b* {10817}; Weebill *Lr14b* {10817}.
ma: *Xwmc232-2B* – 0.2 cM – *Xcfa2257-2B* – 1.1 cM – *Cs7BLNLRR* – 0.3 cM – *Psy1-1* – 0.5 cM – *Lr68* – 0.6 cM – *Xgwm146-2B* {10817}. Gamma-irradiation-induced deletion stocks of Arula 1 lacked *Lr68* but had *Lr14b* showing that the two genes are located at different closely linked loci {10817}.

Lr71.
bin: Markers flanking *Lr71* mapped to 1BS10-0.5-cent and 1BL6-cent-0.32.
v2: *T. aestivum* subsp. *spelta* cv. Altgold Rotkorn *Lr65* {10911}.

Lr72 {10947}. 7BS {10947}. **tv:** Altar C84 GID 30374 {10947}; Atil C2000 GID 6719128 {10947}.
ma: *Lr72* – 5.0 cM – *Xwmc606-7B* {10947}.

Lr73 {10969}. 2BS {10969}. 2BS {10969}.
v: Morocco {10969}; Several Australian cultivars {10969}.
ma: *wPt8760* – 4 cM – *Lr73* – 1.4 cM – *wPt8235* {10969}.

Lr74 {11031}. Adult-plant resistance. 3BL {11031}.
bin: 3BL7-0.63-1.00. **v1:** AGG91583WHEA = BT-Schomburgk Selection {11031}.
ma: *GBS2256311* – 3.9 cM – *Lr74* – 2.5 cM – *IWB69699*/*IWB20762* – 2.5 cM – *GBS2325308* {11031}.

LrBi16 {11042}. 7BL {11042}. **v**: Bimai 16 {11042}
ma: *Zcfa2257-7B* – 2.8 cM – *LrBi16* – 2.9 cM – *Xgwm344-7B* {11042}.

Bimai 16 also carries *Lr26* and *LrZH84* {11042}.

LrFun {11038}. 7BL {11038}. **bin:** 7BL-10.
v: Fundulea 90 {11038}. **ma:** *Xgwm344-7B* – 4.4 cM – *LrFun* – 5.7 cM – *Xwmc70-7B* {11038}.

LrGam6 {10929}. 2BL {10929}. **v2:** Sinvalocho MA *Lr3 LrSV1 LrSV2* {10929}.
ma: *Xbarc-2B* – 0.6 cM – *Xgwm382-2B* – 0.6 cM – *LrGam6* – 17.9 cM – *Xgwm528-2B* {10929}.

LrNJ97 {11043 2BL {11043}. **v:** Neijiang 977671 {11043}.
ma: *Xwmc317-2B* – 4.2 cM – *LrNJ97* – 2.2 cM – *Xbarc159-2B* – 2.3 cM – *Xwmc356-2B* {11043}.

LrSV1 {10929}. Adult-plant resistance. 2DS {10929}.
v2: Sinvalocho MA *Lr3 LrGam6 LrSV2* {10929}.
ma: *Xgwm296-2D* – 1.4 cM – *LrSV1* – 7.1 cM – *Xgwm261-2D* {10929}.

LrSV2 {10929}. Adult-plant resistance. 3BS {10929}.
v2: Sinvalocho MA *Lr3 LrGam6 LrSV1* {10929}.
ma: *Xgwm389-3b* – 3.0 cM – *LrSV2*/*Xgwm533-3B* – 4.2 cM – *Xgwm49-3B* {10929}.

LrZh84. **v:** Add: Guizhou 98-18 {11042};Tian 95HF2 {M1215}; Xinong 1183-4 {11042}.

Complex genotypes:
Insert the following alphabetically with the existing file:

Estanzuela Benteveo	*Lr13 Lr26 Lr34* {10980}
Estanzuela Pelon	*Lr1 Lr17a Lr26 Lr34* {10980}
Estanzuela Tarariras	*Lr3bg Lr13 Lr34* {10980}
INIA Boyero	*Lr13 Lr26 Lr3*4 {10980}
INIA Churrinche	*Lr10 Lr24* {10980}
INIA Tero	*Lr17a Lr24* {10980}

97.2. Suppressor of genes for resistance to *P. triticina*
97.3. QTL for reaction to *P. triticina*
To the paragraph beginning with 'QTL' add: However, Thatcher backcross derivatives of CI 13227 appeared to have *Lr3c* and *Lr46* {11021}.
Avocet / Pastor: RIL population: QTL mapped on 1BL (*Lr46*), 2BS, 5A, 6B, and 7BL plus minor QTL on 1B, 2A, and 2D {10928}.

99. Reaction to *Sitodiplosis mosellana* (Gehin)

***Sm1*.** **v:** Glencross {11044}; Goodeye {11044}.

103. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Bt11 {10997}. **v:** PI 554119, 'Elgin / PI 166910' {10997}.

Bt12 {10997}. **v:** PI 119333 {10997}.

Bt13 {10997}. **v:** Thule III, PI 181463 {10997}.

Bt14 {10997}. **tv:** Doubbi CI 13711 {10997}.

Bt15 {10997}. **tv:** Carleton CI 12064 {10997}.

Btp {10997}. **v:** PI 173437 {10997}.

QTL

Trintella / Piko: DH population: One major gene in the chromosome 1BS centromere region, nearest marker *Xgwm273-1B* {11003}. Smaller QTL effects were detected on chromosomes 7A, 7B, and 5B in different years.

105. Reaction to *Ustilago tritici* (Pers.) Rostrup

Ut5 {10940}. *Ut-Fore* {10940}. **v:** Foremost {10940}. 5BL {10940}.
ma: *Xgpw5029* – 2.8 cM – *Ut5* – 1.3 cM – *Xbarc232-5b* {10940}.
Race T10 was used for analysis {10940}.

107. Reaction to Wheat Streak Mosaic Virus

Wsm1. **v:** CA741 {10971}; KS03HW12 {11006}; Mace {11006}.

Wsm2. **ma:** Add: *Xbarc87-3B* – 4.4 cM – *Wsm2* – 3.9 cM – *Xbarc102-3B* {10982}.
Add note: Allele *Xbarc102-3B219* was the best predictor for *Wsm2* {10982}.

Wsm3. 7B, TBS·7S#3L {10775}. **v:** KS12WGGRC59 TA5624 {10775}.
Wsm3 was also effective against *Triticum* mosaic virus at 18°C {10775}.

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VI. 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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IX. VOLUME 61 MANUSCRIPT GUIDELINES.

The required format for Volume 61 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 44–60 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Use Microsoft Word™ or send an RTF file that can be converted. Please include a separate jpg, gif, 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 61 will be electronic PDF either by email or through download from the Kansas State University Research Exchange (K-REx) (https://krex.k-state.edu/dspace/browse?value=Raupp%2C+W.+J.&type=author).

The *Annual Wheat Newsletter* will continue to be available (Vol. 37–60) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.