

# ANNUAL WHEAT NEWSLETTER

Volume 64



Contribution no. 19-040-B from the Kansas Agricultural Experiment Station,  
Kansas State University, Manhattan.

# **ANNUAL WHEAT NEWSLETTER**

Volume 64

Edited by W. John Raupp Jr., 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, and the Kansas Wheat Innovation Center, 1990 Kimball Avenue, Manhattan, KS 66502.

1 September, 2018.

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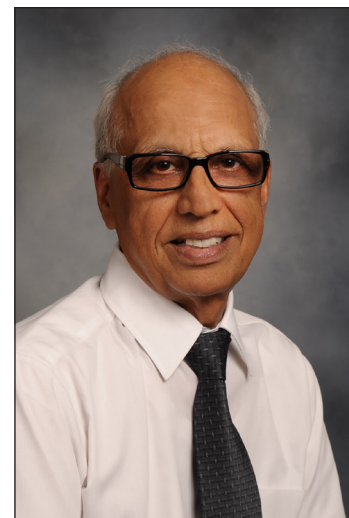
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## IN DEDICATION TO

**DR. BIKRAM S. GILL**

Bikram S. Gill retired from Kansas State University and the Wheat Genetics Resource Center on 16 June, 2018.

Bikram Gill was born on 31 October 1943, in the small village of Dhudike, District Moga, Punjab, India. He was the fifth of 10 children. His parents were farmers. Bikram was always very interested in education and worked hard on his homework, graduating from high school in 1957 first in his class. Bikram studied at DM College at Moga as a premed student from 1959 to 1961, and then went on to earn his B.S. degree at Khalsa College, Amritsar, in 1963, followed by a B.S. Honors and an M.S. Honors degrees in 1966 from Punjab University, Chandigarh, where he became interested in botany. Bikram lectured premed students at GHG Khalsa College, Gurusar Sudhar, from 1966 to 1968. In 1968, he was admitted to Brigham Young University. In the laboratory of Howard Stutz at Brigham Young, Bikram developed a chromosome staining technique for cereals. Bikram then began graduate work at the University of California, Davis, with Charlie Rick in 1969. His Ph.D. thesis was on the cytogenetics of tertiary aneuploids with unusual transmission characteristics in tomato.



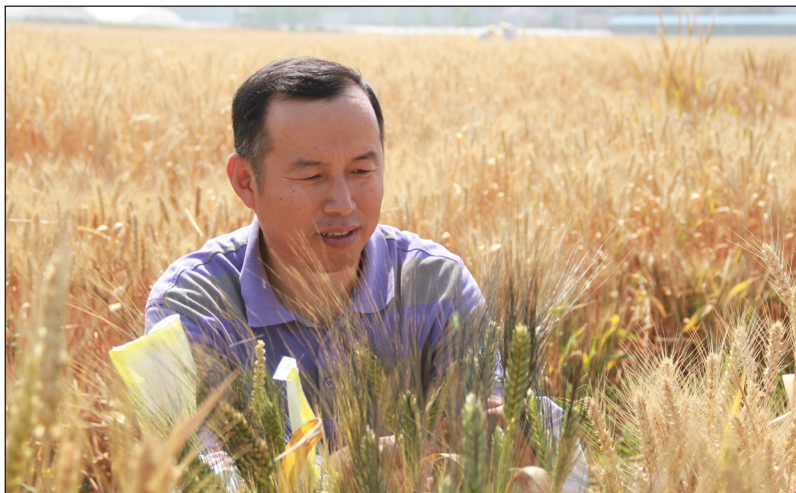
After graduating from UC Davis, Bikram moved to the University of Missouri. At Missouri, Bikram had the opportunity to work with the late Ernie Sears and Gordon Kimber, creating the first C-banded karyotypes of wheat and rye chromosomes. A year later, he was with Giles Waines at the University of California, Riverside. At Riverside, Bikram met Lennart Johnson, who introduced him to the world of genetic resources. In October 1977, Bikram hired as an assistant professor to work on sugarcane genetics and breeding at the University of Florida, Belle Glade. In 1979, he was hired by Kansas State University as a wheat cytogeneticist and, nearly five decades later, Bikram has won more than \$20 million in extramural grants to support his research, including significant funding from the Kansas Wheat Commission and the USDA for establishing the Wheat Genetics Resource Center, a gene bank at Kansas State University, and wheat genetics research, the McKnight Foundation for Fusarium head blight research, and the National Science Foundation and USDA for wheat genome sequencing.

Bikram is the author or coauthor of more than 375 refereed journal publications, 250 abstracts, 20 book chapters, and 55 newsletter items. He has contributed papers to more than 60 conference proceedings and partnered in the release of 67 germplasm lines. He has presented more than 225 lectures both nationally and internationally. He is the co-author of Chromosome Biology. Volume 37 of Plant Breeding Reviews is dedicated to Bikram Gill's career. A complete list of publications of Bikram Gill is available at <http://www.k-state.edu/wgrc/Publications/pubstoc.html>.

**PROF. JIANJUN LIU**

Prof. Jianjun Liu, a famous wheat breeder, born 20 March, 1963, in Rongcheng, Shandong, PR China, and is now working in Crop Research Institute Shandong Academy of Agricultural Sciences, PR China.

After receiving his B.S. degree in Agronomy from Laiyang Agricultural College in 1986, he has been engaged in wheat genetics and breeding in the Crop Research Institute of Shandong Academy of Agricultural Sciences. He received an M.S. degree in Crop Genetics and Breeding from the Chinese Academy of Agricultural Sciences, Beijing, in 2000. Since 1986, he has been the director of research group of wheat genetics and breeding.



Jianjun Liu trained many graduate students and wheat breeders, collaborated with many scientists, and published over 100 research papers regarding wheat breeding theory and technology. Moreover, he has made great breakthroughs in the interaction between wheat quality and high yield, super high yield and wide adaptability, and bred seven groundbreaking wheat cultivars, including Jinan 17, Jimai 19, and Jimai 22. Among these cultivars, Jinan 17 is the first high-quality bread wheat planted in China with an area of more than 666,667 ha annually, breaking the tradition that Chinese bread wheat is totally dependent on imports. Jimai 22 has been the most grown cultivar in China for 9 years with more than 10,500 kg/ha at 84 locations in different ecological areas, creating a high yield record of 11,849 kg/ha under a two crop/year system in Tengzhou, Shandong Province. This cultivar has now been popularized for 17,300,000 ha.

So far, the cultivars that Jianjun Liu has bred have been grown in China on more than 29,500,000 ha, for a wheat yield increase of approximately 20,000,000,000 kg, making a great contribution to the protection of national food security. For his outstanding achievements, he was awarded National Scientific and Technological Progress Award four times, and was rated as the Outstanding National Agricultural Scientific Research Personnel, the outstanding National Agricultural Scientific and Technological Personnel in the Grain Production, the National Candidates for 100 million Talents Project of the New Century, and the outstanding alumni of the International Maize and Wheat Improvement Center (CIMMYT). He also won the Chinese Agricultural Excellence Award in 2015, the National “May 1” Labor Medal in 2016 and National Innovation Award in 2017. His wife, Luju Liu, has retired, while his daughter Rui Liu, is studying for a Ph.D. at UC Riverside.

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**II. 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<sub>1</sub> 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.



**III. CONTRIBUTIONS****ITEMS FROM AUSTRALIA****WESTERN AUSTRALIA GRAINS RESEARCH & INNOVATION DIRECTORATE  
Department of Primary Industries and Regional Development, PO Box 483, 75 York  
Road, Northam WA 6401, Australia.**

Darshan Sharma, Rosemary Smith, Mario D'Antuono, Sharmin Rahman, and Shahajahan Miyan.

***Wheat genetics project evaluated cultivars on sodic dispersive soils in Western Australia.***

Wheat is the most predominant crop grown in Western Australia, occupying about  $4.5 \times 10^6$  hectares, which is more than 50% of the planted area in this Mediterranean type of environment. Average yield is about 2 t/ha, but yield variability is high, both over time and space.

Sodic, magnesic, and dispersive soils, irrespective of salinity level, constitute a major constraint to wheat yield. A 5-year GRDC co-invested national project was set up in 2015 with national leadership at University of Adelaide and partners in Western Australia, Queensland, Victoria, and New South Wales. This item reports on some elements researched in Western Australia.

As a starting step, pertinent germplasm, including released cultivars, international germplasm from FIGS (Focused Identification of Germplasm Strategy) nurseries obtained through ICARDA or the Australian Grains Genebank (AGG), and backcross derivatives carrying sodium exclusion genes (*Nax-1* and *Nax-2*) were tested for three seasons commencing in 2015.

Three types of sites were used for the field trials: sodic but nonsaline, sodic saline, and nonsodic nonsaline. All sodic sites had a high pH at depth. Sites were located in the low rainfall (325 mm annual average) and medium rainfall (475 mm annual average) zones. All trials were replicated four times, and sowing was done close to opening rains (late May–early June). Data were collected on a large number of plant traits (growth, development, yield, yield components, and nutrient uptake) and soil characteristics (pH, EC, dispersion, and EM38).

A multi-environment analysis is in progress. Results from the MET analysis in conjunction with lab data is being used to inform crossing block, but yield data per se forms useful information for growers in the immediate season.

Cultivars Hydra, Scepter, and Zen were often among top performers in the Western Australian subset over 2015–17 (Smith et al. 2018). Data has been presented to growers using PV values (production values) expressed as the difference from a common check. The common check in this case is the cultivar Mace, which is by far the most predominant cultivar in Australia. Scepter and Hydra were generally good under late-sown conditions.

**Reference.**

Smith R, Sharma D, D'Antuono M, Rahman S, and Miyan S. 2017. Wheat Variety Yield Performance on Sodic Dispersive and Saline Soil over three year period in Broomehill and Merredin. GRDC Research Updates 2018. Perth. <http://www.giwa.org.au/2018researchupdates>. 5 pp.

**ITEMS FROM BRAZIL****BRAZILIAN AGRICULTURAL RESEARCH CORPORATION — EMBRAPA  
Rodovia BR 285, km 294, Caixa Postal 451, Passo Fundo, RS, Brazil.*****Performance of wheat cultivars in the state of Rio Grande do Sul, Brazil, 2016.***

Ricardo Lima de Castro, Eduardo Caierão, Márcio Só e Silva, and Pedro Luiz Scheeren (Embrapa Trigo, Passo Fundo, Rio Grande do Sul, Brazil), and Marcelo de Carli Toigo and Rogério Ferreira Aires (DDPA/SEAPI. C.P. 20, 95.200-970 Vacaria, Rio Grande do Sul, Brazil).

The Brazilian Commission of Wheat and Triticale Research (BCWTR) annually conducts the State Test of Wheat Cultivars in Rio Grande do Sul state (STWC-RS), with the aim to support the indications of cultivars. This work evaluated wheat cultivar grain yield performance of STWC-RS in 2016. The grain yield of 29 wheat cultivars (Ametista, BRS 327, BRS 331, BRS Marcante, BRS Parrudo, BRS Reponete, Campeiro, CD 1104, CD 1440, CD 1805, Esporão, Jadeíte 11, LG Oro, LG Prisma, Marfim, ORS 1401, ORS Vintecinco, Quartzo, TBIO Iguaçu, TBIO Itaipu, TBIO Mestre, TBIO Noble, TBIO Pioneiro, TBIO Sintonia, TBIO Sinuelo, TBIO Sossego, TBIO Tibagi, TBIO Toruk, and Topazio) was studied in 14 environments (Coxilha, Cruz Alta, Não-Me-Toque, and Passo Fundo – season 1; Passo Fundo – season 2; Sertão and Vacaria – season 1; Vacaria – season 2; and Augusto Pestana, Eldorado do Sul, Ijuí, Santo Augusto, São Borja, and Três de Maio in Rio Grande do Sul in 2016). 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 about 330 plants/m<sup>2</sup>. Grain yield data (kg/ha) were subjected to individual analysis of variance (for each environment) and to grouped analysis of variance (for all environments). The grouped analysis of variance employed 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 an ability to respond positively to improvement of favorable environments. The general average of STWC-RS in 2016 was 5,499 kg/ha, the highest general average in the trial's history. The experiment conducted in season 1 in Passo Fundo had the highest wheat grain yield average; 6,796 kg/ha. The maximum wheat grain yield was 7,932 kg/ha in Não-Me-Toque (cultivar TBIO Toruk). The cultivars Quartzo, BRS Reponete, TBIO Toruk, ORS Vintecinco, and BRS 327 had adaptability and stability in favorable environments (environments with an average wheat grain yield higher than the general average). Cultivars TBIO Itaipu, BRS Reponete, Quartzo, TBIO Sinuelo, and TBIO Iguaçu cultivars had adaptability and stability in unfavorable environments (environments with an average wheat grain yield lower than the general average). In general, averaged over all environments, cultivars BRS Reponete (6,138 kg/ha), Quartzo (6,025 kg/ha), TBIO Itaipu (5,939 kg/ha), TBIO Sinuelo (5,817 kg/ha), and ORS Vintecinco (5,861 kg/ha) came closest to the ideal cultivar.

**Reference.**

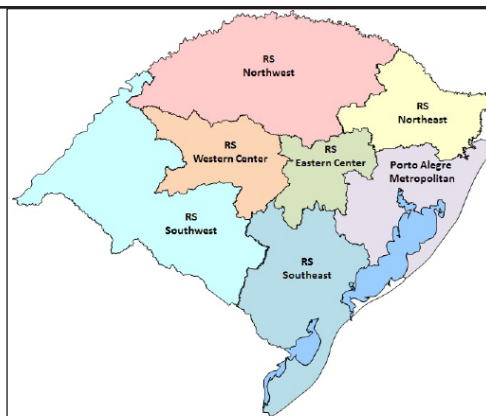
Carneiro PCS. 1998. New methodologies for analyzing the stability and adaptability of behavior. Viçosa: UFV, 1998. Ph.D. Thesis (Genetics and Breeding), Post Graduate Program in Genetics and Breeding. Federal University of Viçosa, 1998. 168p.

***Wheat crop in the state of Rio Grande do Sul, Brazil, 2016.***

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

Rio Grande do Sul state is one of the main wheat-producing states in Brazil. This study analyzed the wheat crop in Rio Grande do Sul in 2016. In 2016, Rio Grande do Sul harvested 778,486 ha of wheat (35.9 % of the total area harvested in Brazil), producing 2,541,889 tons of wheat (37.2% of the Brazilian production) with an average of grain yield of 3,265 kg/ha (110 kg/ha above the Brazilian average of 3,155 kg/ha). Among the geographical mesoregions of Rio Grande do Sul (Fig. 1, p. 6), the RS Northwest mesoregion harvested the largest wheat area, 617,066 ha (79.3% of the cropped area in the state) and had the largest production, 2,041,670 tons of grain (80.3% of the state production) (Table 1, p. 6). How-

ever, the average grain yield obtained in this mesoregion was the second highest of the state, 3,309 kg/ha (44 kg/ha above the state average) (Table 1). The RS Northeast mesoregion harvested 42,885 ha of wheat (5.5% of the cropped area in the state), produced 155,394 tons of wheat grain (6.1% of the state production), and had the highest average grain yield in the state (3,624 kg/ha, 359 kg/ha above the state average) (Table 1). The wheat crop in Rio Grande do Sul in 2016 had favorable weather conditions, with low temperatures in the winter and no late frost in the spring. Consequently, the average wheat grain yield in 2016 was the highest in the history of the Rio Grande do Sul state. Comparing the wheat crop data with the results of the State Test of Wheat Cultivars in the state of Rio Grande do Sul (STWC-RS) in 2016, we observed that the average wheat grain yield of commercial crops was 2,234 kg/ha below that of the average of STWC-RS (5,499 kg/ha).



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

### Reference.

IBGE. 2018. Sistema IBGE de Recuperação Automática - SIDRA. Available at: <<https://sidra.ibge.gov.br/tabela/5457>>. Accessed 23 March, 2018. Note: Aggregated database of studies and research conducted by IBGE.

### *A history of wheat cultivars released by Embrapa in 45 years of research.*

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

Genetic breeding of wheat in Brazil truly began in 1919, when the Ministério da Agricultura, Pecuária e Abastecimento (Ministry of Agriculture, Livestock, and Food), created experimental stations in Alfredo Chaves, RS (now Veranópolis, RS) and Ponta Grossa, PR. The station in Veranópolis, later incorporated in the Department of Agriculture of the State of Rio Grande do Sul (now the Fundação Estadual de Pesquisa Agropecuária – Fepagro (State Crop and Livestock Research Foundation)), was the site where genetic breeding first began in Brazil. These activities were led by the researcher Carlos Gaier. The first strategies were selections of wheat genotypes within local (colonial) cultivars and, soon after, in 1926, the creation of the first hybrids. Crosses between the cultivars Polyssú (Beckman 1954) and Alfredo Chaves resulted in important cultivars at the beginning of the century in Brazil (Sousa 2004). Almost simultaneously, in 1937, the Instituto Agronômico de Campinas (IAC, Campinas Agronomical Institute) also carried out its first crosses with wheat. These two institutions, allied with the other Organizações Estaduais de Pesquisa Agropecuária (OEPAS, or State Crop and Livestock Research Organizations), contributed to the genetic breeding of Brazilian wheat in various aspects, but mainly through developing the genetic base. Some cultivars developed in the first half of the last century are used as sources of resistance to biotic and abiotic stresses in current hybridizations. In this respect, even now, the institutions cited above are either protagonists or partners of other breeders in the continuing work of developing new wheat cultivars in Brazil.

In the 1970s, scientific research in wheat developed significantly with the creation of research centers by agricultural cooperatives in the state of Rio Grande do Sul (CEP/Fecotrigo, currently CCGL TEC) and in the state of Paraná (Ocepar, currently Coodetec), responsible for generating dozens of wheat cultivars of economic importance. Examples of this were the cultivars CEP 24 (in Rio Grande do Sul) and CD 104 (in Paraná). Moreover, in that decade there was the creation of the Instituto Agronômico do Paraná–IAPAR (Agronomical Institute of Parana) and expansion of the work of the IAC. More than 70 wheat cultivars have already been released by IAPAR and IAC, which also shows their importance in the development of wheat in Brazil. In 1974, the Empresa Brasileira de Pesquisa Agropecuária–Embrapa

**Table 1.** Area harvested, production, and average of grain yield of wheat in each of the mesoregions (see Fig. 1) of the state of Rio Grande do Sul, Brazil, in 2016 (Source: IBGE. 2018).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	617,066	79.3	2,041,670	80.3	3,309
RS Northeast	42,885	5.5	155,394	6.1	3,624
RS Western Center	51,687	6.6	167,953	6.6	3,249
RS Eastern Center	11,325	1.5	27,943	1.1	2,467
Porto Alegre Metropolitan	2,100	0.3	5,160	0.2	2,457
RS Southwest	46,503	6.0	127,599	5.0	2,744
RS Southeast	6,920	0.9	16,170	0.6	2,337
Rio Grande do Sul State	778,486	100.0	2,541,889	100.0	3,265

(Brazilian Crop and Livestock Research Company) was created (Sousa 1998), a milestone in crop and livestock scientific research in the country, which resulted in significant advances in agriculture, particularly in the grain yields of many crops and, especially, of wheat. The creation of private companies for wheat breeding, such as OR Sementes (in 1989), Biotrigo Genética Ltda (in 2008), and DNA Melhoramento Vegetal (also in 2008), among others, came to consolidate the system of genetic research of the cereal crop in Brazil in recent decades.

The Embrapa genetic breeding program for wheat also began in 1974, together with creation of the Centro Nacional de Pesquisa de Trigo (National Wheat Research Center), located in Passo Fundo, RS. Initially, the program was based on germplasm incorporated from the Instituto de Pesquisas e Experimentação Agropecuárias do Sul-IPEAS (Southern Crop and Livestock Research and Experimentation Institute), which later would carry out its own hybridization program (Sousa 2004). The first wheat cultivar from Embrapa, CNT 1, was released in 1975 (Sousa 1998).

Embrapa, as a research institution, is a coordinator of the national project of genetic breeding of the cereal crop in the Embrapa Trigo (CNPT) unit, located in Passo Fundo, RS. However, because the variability in climatic and soil conditions within the regions suitable for growing wheat is quite large, other units contribute to the genetic breeding of wheat to overcome specific problems of the region where they are located, and they operate as branches of the research effort of Embrapa Trigo. Three Embrapa units stand out in this role of collaboration in the national wheat project: the Embrapa Soja–CNPSO (Embrapa Soybean) unit, located in Londrina, PR, responsible for the release of cultivars adapted to the northeast of this state; the Centro de Pesquisa Agropecuária do Cerrado unit – CPAC (Crop and Livestock Research Center of the Cerrado), located in Brasília, DF, responsible for indication of cultivars of the dryland and irrigated regime for the Brazilian cerrado (tropical savanna); and the Centro de Pesquisa Agropecuária Oeste unit – CPAO (West Crop and Livestock Research Center), located in Dourados, MS, charged with indicating cultivars for that region.

Quite often, Embrapa wheat breeders are asked for information with regard to year of release, cross, pre-commercial name, and region for which the wheat cultivars released were indicated. Among those requesting this information include the technical assistance sector, the academic sector connected with the agricultural areas, and the wheat segment itself connected with the company. Part of this information may be easily accessed, especially through folders distributed at the time of launching the cultivars and in some publications of the Comissão Brasileira de Pesquisa de Trigo e Triticale (Brazilian Wheat and Triticale Research Commission). However, a significant part of this information is not available (or at least is not easily accessed), and no organized document gathers the historical information of release of wheat cultivars of Embrapa in Brazil from the time of its creation. All the wheat genetic breeding institutions, whether public or private, have made their contribution to the agronomic and qualitative development of the cereal crop in Brazil. This study is an historical survey of all the wheat cultivars released by Embrapa, compiling the main information for identification, and their contribution to wheat development in Brazil.

The historical survey of the wheat cultivars indicated for growing in Brazil from 1974 to 2018 was based on guiding bibliographical documents. Publications arising from research meetings of the Comissão Brasileira de Pesquisa de Trigo e Triticale were consulted (Comissão 2004 a, b, and c; 2005 a and b; 2006; 2007; 2008; 2009; 2010; 2011; 2012) and books from different authors connected with the breeding programs (Sousa 1998, 2003, 2004), folders, audio-visual material, and annual research reports. Technical documents filed in other Embrapa units were solicited. Retired Embrapa researchers also were consulted to complement and systematize the information. The following information was gathered together for each cultivar indicated: year of release, commercial name, pre-commercial line name, cross, Embrapa unit responsible for introduction of the cultivar, and situation of the cultivar at the Serviço Nacional de Proteção de Cultivares (National Cultivar Protection Service) (if the cultivar is protected or not).

The wheat cultivars were grouped according to the Embrapa unit in which they were generated and then by the year of release. Divergent information related to the same cultivar was checked in detail for the purpose of consistency of the document. The cultivars protected by the Ministério da Agricultura, Pecuária e Abastecimento (MAPA) were identified by accessing the site <http://extranet.agricultura.gov.br/php/snpc>.

From 1974 to 2018, Embrapa introduced 120 wheat cultivars for planting (Table 2, p. 8). The largest number of introductions were made by CNPT (81 releases). The CPAC, CNPSO, and CPAO units introduced 16, 14, and 9 cultivars, respectively. The proportion of these releases is explained through two reasons. The first is that the CNPT, being the national leader of the wheat genetic breeding project of Embrapa and, consequently, has the national mandate for development of the crop, with the greatest technical and physical structure available among the units. The second, though not less important, refers to the fact that most of the wheat-growing area in Brazil is located in the states of Rio Grande

**Table 2.** Number of wheat cultivars released by Embrapa, classified by decade of release and unit responsible for introducing the cultivar. Embrapa: Passo Fundo, RS, Brazil, 2018.

Embrapa Unit	Decade					
	1970–80	1980–90	1990–2000	2000–10	2010–18	Total
Centro Nacional de Pesquisa de Trigo (CNPT)	14	20	17	20	10	81
Centro de Pesquisa Agropecuária do Cerrado (CPAC)	1	5	6	2	2	16
Centro Nacional de Pesquisa de Soja (CNPSO)	—	—	—	9	5	14
Centro de Pesquisa Agropecuária Oeste (CPAO)	—	6	3	—	—	9
Total	15	31	26	31	17	120

do Sul, Santa Catarina, and Paraná. The crops developed by the CNPT are indicated for these states, especially in relation to adaptation and reaction to the main biotic and abiotic stresses.

Using decades since the creation of Embrapa, the 1980s and the first decade of the 21st century were those that exhibited the greatest number of cultivars indicated for planting, regardless of the unit from which they were released (31 releases). In the past eight years (2010–18), 10 new wheat cultivars were released, almost exclusively by the CNPT. All cultivars from CNPT (Tables 3 (p. 9) and 4 (p. 10)), from CPAC (Table 5, p. 11), from CNPSO (Table 6, p. 11), and from CPAO (Table 7, p. 12) are given.

Cultivars from CNPT went through four steps before receiving their commercial name. From 1975 to 1977, they were called 'CNT' (Table 3, p. 9), from 1979 to 1991, 'Trigo BR' (Tables 3 (p. 9) and 4 (p. 10)), and from 1992 to 1996, 'Embrapa' (Table 5, p. 11). With the advent of the Cultivar Protection Law (Lei de Proteção de Cultivares) in 1997, all cultivars were called "BRS" (Table 4). These name changes occurred through the years due to legal and strategic modifications of the company. The first decade of releases by the CNPT was highly influenced by the germplasm coming from the now extinct Instituto Agrônomo do Sul (IAS), located in Pelotas, RS, present in almost all the cultivars indicated in this period (Table 3). From 1986 to 2002, the germplasm used for generation of the new cultivars was highly varied and from different origins.

In 2002, Embrapa Trigo established a partnership with the Fundação Pró-Sementes de Apoio à Pesquisa (Pro-Seeds Research Support Foundation), with the goal of adapting to the need for a greater experimental network for determining the Value for Cultivation and Use (VCU) trials of its lines for purposes of protection. The Foundation cited was responsible for bringing about the experimental network of the lines that originated in that unit. In return, the producers connected with the institution were given priority in acquisition of the basic seed of the new cultivars for commercialization. In this period of the partnership, 19 cultivars were indicated for planting (in chronological order): BRS Angico, BRS Figueira, BRS Timbaúva, BRS Buriti, BRS Camboatá, BRS Guabijú, BRS Louro, BRS Umbú, BRS Camboim, BRS Canela, BRS Guatambu, BRS Tarumã, BRS Guamirim, BRS 276, BRS 277, BRS 327, BRS 328, BRS 331, and BRS 374 (Table 4, p. 10). As a marketing strategy, most were given names of trees, and only at the end of the partnership were they designated with numbers in series. The partnership between Embrapa Trigo and the Fundação Pró-Sementes de Apoio à Pesquisa ended in 2006. In spite of that, until 2012, cultivars originating from the partnership were still indicated because the lines had already been included in the Annual Work Plans at the time the contract was terminated.

Of the 81 cultivars released by Embrapa Trigo in the 40 years of research, some became the most planted cultivars in the state of Rio Grande do Sul, especially CNT 10 (1982), CNT 8 (1985–87), Trigo BR 23 (1990–94), Embrapa 16 (1995–98), BRS 49 (2000), BRS 179 (2002–03) (Sousa 2004), and BRS Guamirim (2009). The cultivar BRS 179, for example, was notable for its increased level of grain yield and tolerance to *Fusarium* head blight, and is used today in hybridizations for FHB resistance. For its part, the cultivar BRS Guamirim established a different plant size parameter at the time of its release. Of low stature and very early cycle, BRS Guamirim exhibited broad adaptation to all the wheat-growing regions of Brazil, with a rapid rise in planted area. The situation for BRS Tarumã is noteworthy (2004, Table 4, p. 10), with a dual-purpose profile, despite not appearing in official seed production statistics. This cultivar exhibits characteristics different from conventional wheat, is adapted to crop-livestock integration, with tolerance to animal trampling, high tillering capacity, and the capacity for creating new shoots when subjected to grazing. In the 10 years after its release, the official seed volume produced was never significant, although it is increasing. However, estimates in Rio Grande do Sul indicate approximately 10% of the area is planted to BRS Tarumã, especially in the dairy cattle regions. One factor that explains the absence in the official statistics is the fact that this cultivar is being used more by small producers, who save seed. In 2012 and 2013, Embrapa Trigo indicated that the cultivars BRS Parrudo and BRS Marcante

**Table 3.** Wheat cultivars released by Embrapa - Centro Nacional de Pesquisa de Trigo (CNPT) in the 1970s and 1980s, name of the pre-commercial line, and cross. Embrapa: Passo Fundo, RS, Brazil, 2018 (\* The mass of the lines PF 79765, PF 79767, PF 79780, PF 79782, and PF 7979 are not phenotypically distinguishable).

Year	Cultivar	Line	Cross
1975	CNT 1	PF 70225	PF 11-1000-62/BH 1146
1975	CNT 2	PEL 14049-68	IAS 16/Norin 26
1975	CNT 3	PF 70194	IAS 20/IAS 46
1976	CNT 4	PEL 13014-65	Lerma 50/3/IAS 31//IAS 20/Reliance
1976	CNT 5	PF 6946	IAS 46/BH 546
1976	CNT 6	PF 69162	IAS 20/IAS 50
1976	CNT 7	PF 70546	IAS 51//IAS 20/ND 81
1976	CNT 8	PEL-SL-1268-69	IAS 20/ND 81
1977	CNT 9	PEL 72016	IAS 46/IAS 49//IAS 46/Tokai 66
1977	CNT 10	PEL 72018	IAS 46/IAS 49//IAS 46/Tokai 66
1979	Trigo BR 1	PF 70402	IAS 20/IAS 50
1979	Trigo BR 2	PF 7158	IAS 50/4/IAS 46/3/Vilela Sol*4//Egypt101/Timstein
1979	Trigo BR 3	PF 72518	IAS 50/4/IAS 46/3/Vilela Sol*4//Egypt101/Timstein
1979	Trigo BR 4	PF 73226	IAS 20*3/Sinvalocho Gama
1980	Trigo BR 5	PF 74354	IAS 59//IAS 52/Gasta
1980	Trigo BR 6	PEL 73538	IAS 20/Toropi
1981	Trigo BR 7	PF 72206	IAS 20/Toropi
1983	Trigo BR 8	PF 75171	IAS 20/Toropi // PF 70100
1985	Trigo BR 13	PF 782027	IAS 51//IAS 20/ND 81, CNT 7 Sel
1985	Trigo BR 14	Multilinha*	IAS 63/Alondra Sib//Gaboto/Lagoa Vermelha
1985	Trigo BR 15	PF 79300	IAS 54*2/Tokai 80//PF 69193
1986	Trigo BR 16-Rio Verde	PF 79678	PF 70402/Alondra Sib//PAT72160/Alondra Sib
1986	Trigo BR 19	PF 79502	CNT 1/CNT 10
1987	Trigo BR 20-Guató	PF 81189	BH 1146*3/Alondra Sib
1987	Trigo BR 21-Nhandeva	PF 79475	Cajeme 71/PF 70553
1987	Trigo BR 22	PF 7942	PF 81130/CNT 10
1987	Trigo BR 23	PF 8215	Corre Caminos/Alondra Sib /3/IAS54-20/Cotiporã//CNT 8
1988	Trigo BR 24	PF 8150	IAS 58*2/Eagle
1988	Trigo BR 25	PF 81230	BH 1146*3/Alondra Sib
1988	Trigo BR 27	PF 80271	RC 7201/BR 2
1988	Trigo BR 28	PF 81330	IAS 55/PF 70553
1988	Trigo BR 32	PF 82345	IAS 60/Indus//IAS62/3/AlondraSib/4/IAS 59
1989	Trigo BR 34	PF 839204	Alvarez 110/2*IAS 54/6/Toropi /4/TZPP/Sonora 64//Napo /3/Ciano/5/PF 6968
1989	Trigo BR 35	PF 83144	IAC 5*2/3/CNT7*3/Londrina//IAC5/Hadden

were characterized by qualitative stability and bread improver profile. Cultivar BRS Parrudo has an innovative plant ideotype, combining lodging resistance, upright leaves, high vigor in initial development, and excellent resistance to the main biotic stresses of wheat. Cultivar BRS Marcante, for its part, stands out through high grain yield, without impairing flour/gluten strength, a combination difficult to find in wheat breeding. Of the 81 cultivars indicated for planting by Embrapa Trigo, 34 are protected (MAPA 2018, Table 4, p. 10).

In spite of the effort already made in the Brazilian cerrado for development of wheat cultivars for irrigated and dryland regimes, both by Embrapa and other breeders, the area occupied in the region is not yet significant compared with traditional areas of southern Brazil. Since 1974, 16 wheat cultivars have been released for this region, of which only BRS 207, BRS 254, and BRS 264 are protected in MAPA (Table 5, p. 11). Currently, the CPAC concentrates its efforts on development of wheat cultivars for irrigated areas, with BRS 254 and BRS 264 standing out for high grain yield potential, a trait indispensable for disputing the space under irrigation pivots versus vegetable crops. For several years,

**Table 4.** Wheat cultivars released by Embrapa – Centro Nacional de Pesquisa de Trigo (CNPT) from 1990 to present, name of the pre-commercial line, and cross. Embrapa: Passo Fundo, RS, Brazil, 2018 (<sup>P</sup> = cultivar protected in the National Cultivar Protection Service (MAPA); <sup>EP</sup> = cultivar in the process of obtaining protection in MAPA).

Year	Cultivar	Line	Cross
1990	Trigo BR 36-Ianomami	PF 84588	Jupateco 73*3/Amigo
1990	Trigo BR 37	PF 84431	Mazoe/F13279//Pelado Marau
1990	Trigo BR 38	PF 83348	IAS 55*4/Agent//IAS 55*4/CI 14123
1991	Trigo BR 42-Nambiquara	PF 85634	Jupateco 73*6//Lagoa Vermelha*5/Agatha
1991	Trigo BR 43	PF 853031	PF 833007/Jacuí
1992	Embrapa 15	PF 85137	CNT 10/BR 5//PF 75172/Tifton 72-59 Sel
1992	Embrapa 16	PF 86238	Hulha Negra/CNT 7//Amigo/CNT 7
1993	Embrapa 24	PF 87128	Tifton 72-59 Sel/PF79763/3/Nobeoka Bozu/3*Londrina//B7908
1994	Embrapa 27	PF 869107	PF 83743/5/PF 83182/4/CNT 10*4//Lagoa Vermelha*5/Agatha /3/Londrina*4/Agent//Londrina*3/Nyu Bai
1995	Embrapa 40	PF 84316	PF 7650/NS 18-78//CNT 8/PF 7577
1996	Embrapa 52 <sup>P</sup>	PF 86242	Hulha Negra/CNT 7//Amigo/CNT 7
1996	BRS 49 <sup>P</sup>	PF 90120	BR 35/PF 83619//PF 858/PF 8550
1997	BRS 119 <sup>P</sup>	PF 9198	PF 82252/BR 35//Iapar 17/PF 8550
1997	BRS 120 <sup>P</sup>	PF 91205	PF 83899/PF 813//F27141
1999	BRS 176 <sup>P</sup>	PF 86247	Hulha Negra/CNT 7//Amigo/CNT 7
1999	BRS 177 <sup>P</sup>	PF 92093	PF 83899/PF 813//F27141
1999	BRS 179 <sup>P</sup>	PF 92140	BR 35/PF 8596/3/PF 772003*2/PF 813//PF 83899
2000	BRS 192 <sup>P</sup>	PF 93167	PF 869114/PF 8722
2000	BRS 194 <sup>P</sup>	PF 92231	CEP 14/BR 23//CEP 17
2002	BRS 209 <sup>P</sup>	PF 940384	Jupateco 73/Embrapa 16
2002	BRS Angico <sup>P</sup>	PF 960198	PF 87107/2*IAC 13
2002	BRS Figueira <sup>P</sup>	PF 950262	Coker 762*2/CNT 8
2002	BRS Timbaúva <sup>P</sup>	PF 950419	BR 32/PF 869120
2003	BRS 234 <sup>P</sup>	PF 950407	BR 35//Embrapa 27/Buck Ombu/3/PF 87511
2003	BRS Buriti <sup>P</sup>	PF 950400	Embrapa 27/Klein Orion
2003	BRS Camboatá <sup>P</sup>	PF 970151	PF 93232 Sel 14
2003	BRS Guabijú <sup>P</sup>	PF 970141	PF 86743/BR 23
2003	BRS Louro <sup>P</sup>	PF 970128	PF 869114/BR 23
2003	BRS Umbu <sup>P</sup>	PF 960243	Century/BR 35
2004	BRS Camboim <sup>P</sup>	PF 980144	Embrapa 27*4/K. Cartucho//PF 869114/BR 23
2004	BRS Canela <sup>P</sup>	PF 979064	BRS 120PF 91204*2//Anahuac 75
2004	BRS Guatambu <sup>P</sup>	PF 970285	Amigo/2*BR 23
2004	BRS Tarumã <sup>P</sup>	PF 970343	Century/BR 35
2005	BRS Guamirim <sup>P</sup>	PF 990407	Embrapa 27/Buck Nandu//PF 93159
2008	BRS 276	PF 980537	Embrapa 27*3/Klein H3247 a 33400PF 93218
2008	BRS 277	PF 990423	OR 1/Coker 97.33
2009	BRS 296 <sup>P</sup>	PF 990283	PF 93232/Cook*4/VPM1
2010	BRS 327 <sup>P</sup>	PF 030027	CEP 24 Sel/BRS 194
2012	BRS 328 <sup>P</sup>	PF 023186-C=A	Klein H 3394 a 3110/PF 990744
2012	BRS 331 <sup>P</sup>	PF 015733-C	PF 99602/WT 98109
2012	BRS 374 <sup>P</sup>	PF 040310	PF 88618/Coker 80.33//Frontana/Karl
2012	BRS Parrudo <sup>P</sup>	PF 070478	WT 98109/TB 0001
2013	BRS Marcante <sup>P</sup>	PF 080310	PF 980533/PF 970227//BRS Guamirim
2016	BRS Guaraim <sup>P</sup>	PF 080769	(Embrapa 27/Buck Nandu//PF 93159) Sel
2016	BRS Pastoreio <sup>P</sup>	PF 010066	Coker 80:33/BRS 194
2017	BRS Primaz	PF 110046	PF 980241/PF 980560
2017	BRS Belajoia	PF 101088	PF 001237/PF 980560

the cultivar Trigo BR 33-Guará was the most planted in Goiás and the Distrito Federal, mainly because of its agronomic characteristics and resistance to lodging under irrigation (Sousa 2004). Due to cooperative efforts with the CNPT, some lines (designated PF) resulted in cultivars indicated for dryland growing in Central Brazil, such as CNT 7, Trigo BR 8,

**Table 5.** Wheat cultivars released by Embrapa in the CPAC units from 1974 to 2018. Year of release, name of pre-commercial line, and cross. Embrapa: Passo Fundo, RS, Brazil, 2018 (<sup>P</sup> = Cultivar protected in the National Cultivar Protection Service (MAPA)).

Year	Cultivar	Line	Cross
1978	Moncho BSB	—	Wren/Gaboto//Kalyansona/Blue Bird, Moncho Sib
1983	Trigo BR 9 – Cerrados	R 30469-77	BH 1146/IRN 595-71
1983	Trigo BR 10 – Formosa	R 30147-77	D6301/Nainari 60//Weique/Red Mace/3/Ciano*2//Chris, Alondra 4546 Sel
1985	Trigo BR 12 – Aruanã	—	Bucky/Maya 74 Sib/4/Blue Bird//HD 832-5-5-Olesen/3/Ciano/ Penjamo
1988	Trigo BR 26 – São Gotardo	CPAC 831243	Kavkaz/Buho Sib//Kalyasona/Blue Bird, Veery Sib
1989	Trigo BR 33 – Guará	CPAC 841222	Buckbuck Sib/Bluejay Sib
1991	Trigo BR 39 – Paraúna	CPAC 841244	Dove Sib/Pewee Sib
1993	Embrapa 21	CPAC 86133	PAT 10/Alondra Sib//Veery 5
1993	Embrapa 22	CPAC 841153	Veery Sib/3/KLTO Sib/PAT 19//Mochis/Jup. 73
1995	Embrapa 41	CPAC 88118	PF 813/Polo 1
1995	Embrapa 42	CPAC 88130	LAP 689/MS 7936
1999	BRS 207 <sup>P</sup>	CPAC 91086	Seri 82/PF 813
2005	BRS 254 <sup>P</sup>	PF 973047	Embrapa 22*3/Anahuac 75
2005	BRS 264 <sup>P</sup>	CPAC 98222	Buck Buck/Chiroca//Tui
2014	BRS 404 <sup>P</sup>	PF 100660	WT 99172/MGS 1 - Aliança
2016	BRS 394 <sup>P</sup>	CPAC 0544	Embrapa 22/CM 106793

Trigo BR 16-Rio Verde, Trigo BR 24, and Trigo BR 25 (Sousa 2004). As of 2012, a specific program, began in Uberaba by the creation of a Tropical Wheat Research Station, was connected with Embrapa Trigo for developing wheat cultivars for dryland conditions. The program has its own structure in Minas Gerais, from which promising results are expected through the aggregation of developed germplasm with additional multidisciplinary actions and through cultivars that exhibit greater adaptation to the growing system in the region.

Embrapa Soja (CNPSo) has a fundamental role as the research body connected with the national project of wheat breeding coordinated by Embrapa Trigo. From its activities, 14 wheat cultivars have been developed since 2000, all under the protection of MAPA (Table 6). Practically all the cultivars originating from this unit were derived from WT lines developed in Londrina and adapted to the main problems of the northwest region of Paraná, the important wheat production area of the state. Cultivars BRS 208 and BRS 220 may be highlighted and, more recently, BRS Tangará and BRS Pardela. All the cultivars were developed by Embrapa Soja, except for BRS 193 and BRS 208, resulted from a partnership with the Fundação Meridional de Apoio à Pesquisa (Meridional Research Support Foundation), in a manner similar to that of the partnership between Embrapa Trigo and the Fundação Pró-Sementes in Rio Grande do Sul. Nevertheless, in contrast with what occurred in RS, the partnership of Embrapa Soja with the Fundação Meridional still exists, and three other cultivars were released in recent years: BRS Gaivota, BRS Galha Azul, and BRS Sabiá. The germplasm

**Table 6.** Wheat cultivars released by Embrapa in the CNPSo units from 1974 to 2018. Year of release, name of pre-commercial line, and cross. Embrapa: Passo Fundo, RS, Brazil, 2018 (<sup>P</sup> = Cultivar protected in the National Cultivar Protection Service – MAPA).

Year	Cultivar	Line	Cross
2000	BRS 193 <sup>P</sup>	PF 95068	Anahuac 75/PF 869100
2001	BRS 208 <sup>P</sup>	WT 96053	CPAC 89119/3/BR 23//CEP 19/PF 85490
2002	BRS 210 <sup>P</sup>	WT 96061	CPAC 89119/3/BR 23//CEP 19/PF 85490
2003	BRS 220 <sup>P</sup>	WT 98109	Embrapa 16/TB 108
2004	BRS 229 <sup>P</sup>	WT 96168	Embrapa 27*3//BR 35/Buck Poncho
2005	BRS 248 <sup>P</sup>	WT 99207	PAT 7392/PF 89232
2005	BRS 249 <sup>P</sup>	WT 00124	Embrapa 16/Anahuac 75
2007	BRS Pardela <sup>P</sup>	WT 02094	Trigo BR 18/PF 9099
2007	BRS Tangará <sup>P</sup>	PF 003295-A/B	BR 23*2/PF 940382
2011	BRS Gaivota <sup>P</sup>	WT 05106	PF 940301/PF 940395
2012	BRS Galha Azul <sup>P</sup>	WT 07105	Jupateco F <sub>2</sub> /Embrapa 16//BRS Camboatá/LR 37
2013	BRS Sabiá <sup>P</sup>	WT 08111	BRS 210/PF 980583
2014	BRS Graúna <sup>P</sup>	WT 10008	LD 975/WT 01121
2016	BRS Sanhaço <sup>P</sup>	WT 11167	BRS 220/BRS 210



used in the genetic makeup of the cultivars from Embrapa Soja is quite varied, Mexican (Anahuac 75 and Jupateco F3), Argentinian (Buck Poncho), and lines and cultivars from Embrapa and from other breeders, such as Fundacep (CEP) were used.

Another research branch of wheat breeding, Embrapa is the Centro de Pesquisa Agropecuária Oeste, is located in Dourados, MS. From there, nine wheat cultivars have been released since 1984 (Table 7). Nevertheless, since 1992, no other cultivars have been developed. The program lost strength because of the small demand for wheat in Mato Grosso do Sul and the surrounding region. Of all the CPAO cultivars, Trigo BR 18–Terena is the most important, and it is even internationally relevant. Developed for dryland in 1986, Trigo BR18–Terena is still the reference for growing under the dryland cultivation for the entire region of Mato Grosso do Sul, Goiás, and Minas Gerais, because of its tolerance to heat and low water availability, quality characteristics, and good plant architecture. Although its origin is unknown, the cultivare is still highly used in crosses in breeding programs. Because of the time since release, none of the cultivars from CPAO are protected, originating mainly in lines from Mato Grosso do Sul (MS lines).

**Table 7.** Wheat cultivars released by Embrapa in the CPAO units from 1974 to 2018. Year of release, name of pre-commercial line, and cross. Embrapa: Passo Fundo, RS, Brazil, 2018.

Year	Cultivar	Line	Cross
1984	Trigo BR 11 - Guarani	MS 7810	Bluebird//Tobari 66/8156
1986	Trigo BR 17 - Caiuá	MS 7878	Tezanos Pinto Prec//IRN 46/Ciano/3/II-64-27
1986	Trigo BR 18 - Terena	PF 781148	Unknown cross
1988	Trigo BR 29 - Javaé	MS 8166	Siskin Sib/Pavon Sib
1988	Trigo BR 30 - Cadiuéu	MS 81128	Ciano/8156//Tobari/Ciano/4/NO/3/II-12300//Lerma Rojo 64/8156/5/Pavon Sib
1988	Trigo BR 31 - Miriti	Veery 1	Kavkaz/Buho//Kalyansona//BB, Giennson 81
1991	Trigo BR 40 - Tuiúca	MS 208-84	Anahuac 7/Huacamayo Sib
1991	Trigo BR 41 - Ofaié	GD 833	BH 1146*6/Alondra Sib

Information of all the wheat cultivars released by Embrapa from 1974 to 2018, together with the year of release, the name of the pre-commercial line, the cross, and other information, will be useful for the production, academic, and research purposes. It addition, this is an important historical document of the work already performed by Embrapa in the genetic breeding of wheat in Brazil.

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## ITEMS FROM GERMANY

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### *Adult yellow rust resistances from genetic resources of spring wheat from the IPK genebank.*

Two DH populations of genetic resources of spring wheat from the IPK genebank (Population 1: ‘TRI 11082 (GDR-variety HATRI) / TRI 5645 (from Iran, collected 1952-54)’, 107 DH lines; population 2: ‘TRI 10703 (from Greece) / TRI 5310 (cultivar EUREKE from France)’, 159 DH-lines) were grown in the field at IPK in 2016. A naturally occurring yellow rust infection was scored on a scale of 1 to 7 at anthesis. Yellow rust resistance was segregating in both populations. The genotyping of both populations with the 15k ILLUMINA chip from TraitGenetics GmbH, Gatersleben, resulted in 3,877 polymorphic SNPs for population 1 and 3,906 polymorphic SNPs for population 2. In each population, one single sharp peak for yellow rust resistance could be mapped in a QTL scan using interval mapping (SIM) by the software package Genestat16. In population 1, the yellow rust resistance mapped to chromosome 2DS at 47 cM and came from parent TRI 11082. The yellow rust resistance of population 2 was derived from parent TRI 5310 and mapped on chromosome 5AL at 128 cM. We assume that, in both cases, the main adult-stage resistance genes are causing the resistance reaction. Possible candidates, based on map position, are *Yr16* for population 1 and *Yr48* or *Yr34* for population 2, but it also is possible that novel genes were detected. The significant physical interval for the genomic region on chromosome 2DS comprises 2.6 Mb, containing 62 predicted genes of which 23 genes are supported by cDNAs or ESTs. On chromosome 5AL, the significant interval of 6.6 Mb comprises 104 predicted genes of which 49 genes are supported by cDNAs or ESTs. Our results support the use of genetic resources as source of novel alleles and/or genes for resistances to biotic stress.

***Genome-wide association study of calcium accumulation in grains of European wheat cultivars.***

Mineral concentrations in cereals are important for human health, especially for people who depend mainly on consuming a cereal diet. We carried out a genome-wide association study (GWAS) of calcium concentration in wheat grains using a European wheat diversity panel of 353 cultivars (339 winter wheats (WW) plus 14 spring wheats (SW)) and phenotypic data based on two field seasons. High genotyping densities of SNP markers were obtained from the application of the 90k iSELECT ILLUMINA chip and a 35k Affymetrix chip. Inductively coupled plasma optical emission spectrometry (ICP-OES) was used to measure the calcium concentrations of the wheat grains. Best linear unbiased estimates (BLUEs) for calcium concentration were calculated across the seasons and ranged from 288.20 to 647.50  $\mu\text{g/g}$  DW among the cultivars, with a mean of 438.102  $\mu\text{g/g}$  DW, and a heritability of 0.73. A total of 485 SNP marker–trait associations (MTAs) were detected in data obtained from grain cultivated in both of the two seasons and BLUE values by considering associations with a  $-\log_{10}(P\text{-value}) \geq 3.0$ . Among these SNP markers, we detected 276 markers with a positive allele effect and 209 markers with a negative allele effect. These MTAs were found on all chromosomes except chromosomes 3D, 4B, and 4D. The most significant association was located on chromosome 5A (114.5 cM) and was linked to a gene encoding cation/sugar symporter activity as a potential candidate gene. Additionally, a number of candidate genes for the uptake or transport of calcium were located near significantly associated SNPs. This analysis highlights a number of genomic regions and candidate genes for further analysis, as well as the challenges faced when mapping environmentally variable traits in genetically highly diverse variety panels. The research demonstrates the feasibility of the GWAS approach for illuminating the genetic architecture of calcium-concentration in wheat grains and for identifying putative candidate genes underlying this trait.

***Genome-wide association mapping and prediction of adult stage *Septoria tritici* blotch infection in European winter wheat using high density marker arrays.***

*Septoria tritici* blotch (STB), caused by ascomycete fungus *Mycosphaerella graminicola*, is a devastating foliar disease of wheat. As a result of STB infection, leaves are unable to provide sufficient photosynthetic assimilates at grain filling, which may lead to substantial yield losses. With improved agronomic management practices, exploiting the quantitative genetic resistance is proposed as the most durable strategy to control the STB spread. In this study, we dissected the genetic basis of STB infection in an elite European wheat panel comprising 371 cultivars based on state-of-the-art high density 35,000 and 90,000 SNP marker arrays. The phenotypic data collected at the adult stage in replicated field trials suggest that a large, significant, and heritable genetic variance exists for STB infection. The broad sense heritability of 0.78 is indicative of a strong genetic control and warrants the detection of underlying genetic loci. The GWAS performed on individual marker arrays and on marker loci combined from both arrays propose a highly quantitative nature of STB infection with potential associations on chromosomes 1A, 1B, 2D, 4A, 5A, 6A, 6D, 7A, and 7B. Genome-wide association studies reveal that increasing the marker density captures additional markers with increased genotypic variance. A local linkage disequilibrium (LD) analysis and study of LD markers points towards corresponding genes with a possible role in disease resistance. The potential of genomic selection (GS) assessed via two genomic prediction (GP) models accounting for additive effects and additive plus epistatic interactions among the loci suggest the possibility of GS to improve STB resistance. Moreover, GP results indicate that the higher order epistatic interactions are not pervasive and that both marker platforms are equally efficient for GP of STB infection. Our results provide further understanding of the quantitative genetic nature of STB infection, resource for marker-assisted breeding and highlight the potential of GS for improved STB resistance.

***Genome-wide association mapping for yield related traits under drought stress in spring wheat.***

Food demand is increasing with an increasing world population. Bread wheat is one of the most important crops worldwide facing drought stress, which affects yield negatively. Increasing crop production is the primary objective for breeding programs. Under nonstressful conditions, using chemical desiccant is one technique to simulate drought. A panel of 111 spring wheat cultivars and landraces genotyped with 11,195 SNP markers was used to identify MTAs related to a variety of traits. The panel was subjected to artificial drought stress by spraying the plants with 0.5% KI 14 days after anthesis. A genome-wide association analysis revealed 391 significant MTAs involving different agronomical and morphological traits, and mapped to 19 of the 21 wheat chromosomes. A total of 97 of the MTAs were involved in 1,000-kernel weight as an important yield related trait under control and stress conditions, where six controlling loci mapped to chromosomes 1B (74 cM), 2A (149 cM), 3A (90 and 161 cM), 6A (84 cM), and 7A (73 cM).

***Genome-wide association mapping for drought stress tolerance in winter wheat.***

The future productivity of wheat will be of the utmost importance for global food security, because it is the most widely grown crop worldwide. Drought and water deficiency are major yield limiting factors throughout the world in this crop, causing losses up to 80% of the total yield. Our primary aim was to identify loci that influence drought tolerance at the seedling stage of a winter wheat population, consisting of 266 accessions, through association mapping and determine the role of these loci. The root length (RL), coleoptile length (Cl), shoot length (Sl), and root/shoot length ratio (RSR) of ten seedlings per genotype under drought stress (12 % PEG 6000) and a control treatment (distilled water) were measured. A tolerance index (TI) was defined for RL, Cl, Sl, and RSR as the ratio between the mean trait value obtained under stress and the corresponding trait value under control. A genome-wide association analysis used the wheat 90K Illumina iSelect SNP array that consisted of 81,587 SNPs. Seventeen molecular markers were related to coleoptile length TI (1 on chromosome 1A, 1 on 2D, 2 on 3B, 8 on 4A, 1 on 4B, 2 on 6A, and 2 on 7A); 14 related to shoot length TI (1 on 2B, 5 on 4A, 1 on 4B, 1 on 5B, and 6 on 7B); 17 to root length TI (1 on 1A, 3 on 3B, 1 on 4B, 1 on 5A, 5 on 6A, 2 on 6B, and 2 on 7B); and 13 root/shoot ratio TI (1 on 1A, 3 on 2B, 3 on 4A, and 6 on 7B). Molecular markers associated to more than one trait were also identified, nine were associated to root/shoot ratio TI and shoot length TI (6 on 7B and 3 on 4A). Markers linked to the loci obtained through this project could then be used for marker-assisted selection in wheat breeding programs and be a source of drought tolerance in new genotypes.

***QTL analysis of germination and termite tolerance under water scarce conditions in durum wheat.***

An experiment was conducted to locate QTL regarding germination and termite tolerance in durum wheat in 2016–17 where QTL linked to germination were found on chromosomes 5A and 6B, QTL linked to germination under drought were found on chromosome 6B, QTL linked to relative germination were located on chromosomes 2A and 4B, and QTL linked to termite tolerance were found on chromosome 5B. Continuing that experiment to locate stable loci linked to germination and termite tolerance in field conditions, the same biparental durum wheat population, consisting of 114 recombinant inbred durum wheat lines was grown at NIAB, Pakistan, in 2017–18, at the same location where the population was grown in 2016–17. The population was developed from a cross between a drought tolerant parent Omrabi (O5) and a heat and salt tolerant cultivar Belikh 2 (B2). The cross was made at ICARDA, Syria, and the population was mapped with 265 markers at IPK-Gatersleben. The population was grown from seeds of 2016–17 harvest on 23 November, 2017, in 2-m rows with a 9 inch distance between ~5 g seed/line. One replicate was included in the control and two replicates under drought. Irrigation was applied 15 days after sowing to the control, but the drought plots were not watered. Germination data were observed 1 month after planting. Termite attack happened naturally in the drought replicates due to drought. Data for termite tolerance (TT) were recorded on 1 February, 2018, using a visual scale of 0–4, where 0 = no damaged/infected plants, 0.5 = 12.5% damaged/infected plants, 1.0 = 25% damaged/infected plants, 1.5 = 37.5% damaged/infected plants, 2.0 = 50% damaged/infected plants, 2.5 = 67.5% damaged/infected plants, 3.0 = 75% damaged/infected plants, 3.5 = 88.5% damaged/infected plants and 4.0 = 100% damaged/infected plants.

Mean germination of the control (Gr) was  $95.99 \pm 3.71$ , where the maximum and minimum values were 80 and 100%, respectively. Mean germination under drought (GrD) was  $91.24 \pm 5.56$ , with minimum and maximum values of 70 and 100%, respectively. Maximum relative germination (RGr) was 100%, whereas minimum RGr was 73.68% (mean value of  $95.11 \pm 5.29$ ). Mean TT value ranged between 0 and 3, where the mean value was  $1.11 \pm 0.59$ . QTL were detected using QTL cartographer v. 2.5, where a QTL was declared significant at an LOD > 1.5 and highly significant at an LOD > 3.0. Analysis of the observed data revealed a total of 20 QTL for the four traits of which three were highly significant.

A total of four QTL was discovered for Gr including two highly significant QTL. The highly significant QTL for Gr were observed on chromosome 1B where the confidence interval lie between 13.0–24.4 cM (LOD = 3.61) and 27.3–36.9 cM (LOD = 5.19); and the closest associated markers were *Xgwm752* and *Xbarc8*, both of which were donated by B2 and the variation explained by each QTL was 18%. The third QTL for Gr was located on chromosome 3A (LOD = 2.13 and interval between 85.0–104.7 cM) associated with marker *Xbarc356*, and another QTL was located on chromosome 6A (LOD = 2.96 and interval between 115.5–130.2 cM) with marker *Xgwm4915*. The variance explained by the former was 9%, whereas the variance explained by the latter was 14%.

Five QTL linked to GrD were located on chromosomes 3B (2 QTL) and 5B (3 QTL). The QTL intervals on chromosome 3B were 8.3–17.7 cM and 18.9–43.1 cM, and the closest markers associated were *Xgwm285* ( $R^2 = 7\%$  contributed by O5) and *Xgwm376* ( $R^2 = 8\%$  contributed by O5). The LOD for QTL on chromosome 3B was 2.4 and 1.5

for the former and the latter, respectively. The QTL intervals on chromosome 5B were 194.7–217.2 cM (LOD = 2.49), 223.9–230.8 cM (LOD = 2.83), and 255.9–266.1 cM (LOD = 1.94), and the closest associated markers were *Xbarc266* ( $R^2 = 8\%$ ), *Xbarc59* ( $R^2 = 8\%$ ), and *Xgwm790* ( $R^2 = 6\%$ ), respectively. All these QTL were provided by parent B2. The QTL linked to RGr were exactly the same as that of GrD except that for an additional QTL on chromosome 6A between 37.5–56.3 cM with an LOD score of 1.8, where the closest marker associated was *Xgwm4608* and the variation explained was 6%.

Five QTL (including one highly significant QTL) for TT were located on chromosomes 1B, 3B, 4B, 5A, and 7B. The QTL on chromosome 1B lies between 144.2 and 154.6 cM with a LOD score of 1.93, and the closest marker associated was *Xwmc548* provided by B2 and the variation explained was 6%. The QTL on chromosome 3B lies between 146.1 and 191 cM with a LOD score of 1.63, where the closest marker associated was *Xgwm247* provided by B2 and the variation explained was 6%. The QTL on chromosome 4B lies between 44 and 60.7 cM with a LOD score of 1.69, where the closest marker associated was *Xgwm495* provided by B2 and the variation explained was 5%. The QTL on chromosome 5A lies between 330.6 and 340.6 cM with a LOD score of 4.54, where the closest marker associated was *Xbarc261* provided by O5 and the variation explained was 15%. Finally, the QTL on chromosome 7B lies between 206.3 and 226.3 cM with a LOD score of 2.66, and the closest marker associated was *Xbarc276* provided by O5 and the variation explained was 9%.

When compared to the previous year, the results did not match, indicating a strong environmental factor influencing these traits. For example, in 2016–17, QTL for Gr were observed on chromosomes 5A and 6B and in 2017–18 they are observed on chromosomes 1B, 3B, and 6A. Similarly, GrD QTL in 2016–17 were observed on chromosomes 4B, 5B, and 7A, whereas in 2017–18, they were found on chromosomes 3B and 5B. The only chromosome match (5B) was for GrD QTL across two years, but the concerned QTL are not located in vicinity of each other. Likewise, RGr QTL across two years do not match. In the case of TT, QTL in 2016–17 were located on chromosomes 4A, 5B, and 7B, whereas in the 2017–18 season, they were located on chromosomes 1B, 3B, 4B, 5A, and 7B. Again, we find a chromosome match (7B) for TT QTL across two seasons. The TT QTL on chromosome 7B in 2016–17 and 2017–18, however, lie within a distance of 25 cM. Thus, this area of chromosome 7B may carry stable QTL for TT.

### ***Grain yield potential in wheat: the relationship between fruiting efficiency, spike weight at anthesis, and grain weight.***

Based on the projected cereal demand, in the coming years wheat production must be increased approximately 60%. This challenge could be reached from an increase of yield potential, because of good evidence that increasing yield potential often also leads to larger farmers' yield. In this sense, it has been suggested that yield potential could be further improved by increasing the fruiting efficiency (FE). However, some phenotypic studies showed a negative relationship between FE and yield-related traits, such as spike weight at anthesis (SWA) or grain weight (GW). Our aims were to (i) establish marker–trait associations (MTAs) and the genetic basis associated to such traits through a genome-wide association study and (ii) determine phenotypic and genetic relationships and the possible presence of a trade-off among them. Three field experiments were conducted at the Faculty of Agriculture and Forestry Sciences, La Plata, Argentina (LP), and the Julio Hirschhorn Experimental Station, Los Hornos, Argentina (LH), in split-plot designs. The wheat population used consisted of 96 winter wheat accessions sampled from 20 different countries genotyped using a 15K Infinium SNP array. Marker-trait associations were identified using a mixed linear model correcting for population stratification by using a kinship matrix among pairs of accessions. The false discovery rate (FDR) of the  $q$  value = 0.05 was used to correct for multiple comparisons. Thus, only markers that had  $\log_{10}(P) > \text{FDR}$  were considered significant markers. Fruiting efficiency showed a clear and negative phenotypic relation with SWA, yielding Pearson correlation coefficients ranging from  $-0.64$  to  $-0.72$  across the experiments. However, a wide range of variation in FE also was observed for each value of SWA. For example, for values greater than average in SWA (0.50 g) a range of FE from 29.78 to 106.08 grains/g was observed depending on the experiment analyzed. By contrast, we noticed that, except for experiment 1 at LP, when GW was plotted against FE, no negative relationship was observed for any other combination of location and experiment. For the entire dataset, four MTAs on chromosomes 2A (163 cM), 2D (100 cM), 4D (57 cM), and 5A (141 cM) were identified as significantly associated with FE. In addition, two genomic regions associated with SWA were distributed on chromosomes 2A (15 cM) and 6A (85 cM), whereas four MTAs associated to GW were detected on chromosomes 2A (48 cM), 2B (145 cM), 5D (205 cM), and 7A (43 cM). Our results showed that, at the molecular level, no overlapping occurred between significant genomic regions for FE, SWA, and GW, suggesting that these traits are determined by independent genetic factors. The independent genetic regulation found is valuable, because it means that the improvement in

each of the traits associated with the yield potential can be accomplished without a corresponding decrease in the others, so that overall yield can be increased.

### ***Tolerance to Fusarium head blight elicited by phytohormones in wheat.***

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is a very important wheat disease causing remarkable economical damage in Argentina. Because only a few resistance sources are available, we tested synthetic hexaploids as a donor for FHB resistance several years ago. Several lines showed induced resistance against FHB after a phytohormone treatment. In this study, two novel lines (L and M) and a commercial cultivar (ACA 315) were tested in two different localities (La Plata and Tres Arroyos) during three years. A split-plot design was used in order to compare the responses to the following hormone treatments: salicylic acid, jasmonic acid, gibberellic acid, a solution with a strain of *Pseudomonas fluorescens*, or water (control), which were sprayed at anthesis. Twenty-four hours later, half of the plots of each pretreatment of each genotype were inoculated. Spikes were harvested manually, and the number of total grain, damaged kernels, and 1,000-kernel weight were recorded. Pretreatment with gibberellic acid increased the total grain in lines L, M, and ACA315 with and without inoculation with *F. graminearum* compared to the controls and the rest of the treatments. Jasmonic acid induced fewer damaged kernels in lines L and M. The commercial cultivar did not show any differences between treatments. The treatment with *P. fluorescens* induced the highest levels of tolerance in both experimental lines with the lower values of damaged kernels and with a higher 1,000-kernel weight. These results were similar in both localities in the last two years. The elicitation of SAR in the experimental lines increased the tolerance to FHB.

### ***Characterization of the resistance to Pyrenophora sp. in Argentinian wheat cultivars.***

Tan spot (*Pyrenophora tritici-repentis* (Died.) Drechs. (anamorph *Drechslera tritici-repentis* (Died.) Shoem.)) is one of the most important wheat diseases. *Pyrenophora teres* Drechs. (anamorph *Drechslera teres* Sacc. Shoemaker) is a barley pathogen, but some studies conclude that it also may attack wheat. Our objectives were to determine the presence of the pathogen *P. teres* in the wheat crop and characterize the resistance to *P. teres* and *P. tritici-repentis* in Argentinian commercial wheat cultivars. The experiments were carried out at the Experimental Station J. Hirschhorn, Faculty of Agriculture and Forestry Sciences, UNLP, Argentina, during 2016, using a split-split-plot design with two replications. The main plots were two environments (pots and field), and subplots were an isolate of *P. tritici-repentis* (LH) and two isolates of *P. teres* (Pt1 and Pt2). Sub-subplots were 30 Argentinian wheat cultivars. Severity was evaluated at the adult stage (GS49), and data were analyzed by ANOVA. All genotypes were affected by both *Drechslera* species. The average severity in the field (27.1%) was significantly higher than that on the pots (18.5%). The isolates caused similar severity values, Pt1 (21.5%), LH (22.8%), and Pt2 (24.1%). The 30 cultivars showed high variability in severity, ranging between 6.1% and 41.1%. The following limits were established based on LSD ( $p < 0.05$ ): 0–15% severity, resistant cultivars (R); 15–30%, moderately resistant (MR); 30–45%, moderately susceptible (MS); and more than 45% for cultivars, susceptible (S). Among the three isolates and in the two environments tested, ten cultivars behaved as R or MR. Seven cultivars were classified as R or MR to the three isolates only in the pot experiments. Seven cultivars showed S or MS in both environments against at least one isolate. In conclusion, our results suggest the possibility that *P. teres* also may affect wheat cultivars, in addition to barley crops, producing symptoms similar to those of tan spot. At the same time, several wheat cultivars were susceptible to the isolates inoculated, suggesting the need to continue improving local cultivars, which implies the search of genotypes with resistance genes and its use in future breeding programs.

### ***Genotypic variability and effect of fungal diseases on nitrogen dynamics and grain yield in a spring wheat collection.***

Accumulation and redistribution of nitrogen (N) are important processes determining grain yield and grain quality in wheat and could be affected by foliar fungal pathogens such as leaf rust (*Puccinia triticina* Eriks) and tan spot (*Pyrenophora tritici-repentis* (Died.) Drechs., anamorph *Drechsleratritici-repentis* (Died.) Shoem.), main biotic threats that affect wheat production in Argentina and many production areas in the world. Our aim was to evaluate the effects of foliar fungal pathogens on N dynamics and grain yield in a spring wheat panel. Field experiments were carried out in 2016 at the Experimental Station J. Hirschhorn, Faculty of Agriculture and Forestry Sciences, National University of La Plata, Argentina. The experimental design was a split-plot with two replications. The main plots were with (F) and with-

out fungicide (WF). Subplots were a population of 110 wheat genotypes provided by IPK Gatersleben, Germany. The area under disease progress curve, grain yield, and parameters associated with N dynamics (N remobilization (NREM), N post-anthesis absorption (NPA), percent protein in grain (%P), and N stored in grain), were calculated. The 'Genotype × treatment' interaction showed highly significant differences for all traits ( $P < 0.001$ ). The area under disease progress curve ranged from 5,338 to 1,594 in the WF treatment, and from 3,516 to 1,153 in the F treatment, showing an average increase of 33% in the WF treatments with respect to the F treatments. Grain yield fluctuated from 10,823 to 2,195 kg/ha in F and between 7,165 to 1,380 kg/ha in WF, showing an average reduction of 39% in WF treatments with respect to F. In general terms, NREM was reduced by 43% in the WF treatments with respect to that of the F treatments, and ranged from 18.59 to 1.08 g/m<sup>2</sup> (F) and between 11.91 to 0.2 g/m<sup>2</sup> in the WF treatments. The NPA fluctuated between 15.10 to 1.31 g/m<sup>2</sup> for F and from 11.25 to 0.76 g/m<sup>2</sup> for WF, showing a general reduction of 48% in WF compared to the F treatments. For %P, the WF treatments reduced this variable 10% compared to that of the F treatments, whereas the genotypic variation was from 15.48 to 7.84 for F and 13.76 to 7.50 for the WF treatments. The N stored in grain varied from 28.41 to 4.25 g/m<sup>2</sup> for F and from 17.23 to 2.25 g/m<sup>2</sup> for WF, showing a general reduction of 46% in the WF treatments with respect to F. The studied traits will be molecularly located.

### ***Five years of evaluation of 750 bread wheat landraces at Gorgan University.***

This investigation was in 2004 from IPK-Gatersleben, Germany, and continued in Iran until now at Gorgan University. In 2005, 140 Iranian wheat accessions from different parts of Iran, mainly Alborz and Zagros Ranges, received from the IPK-Gatersleben genebank were assessed for genetic diversity based on 12 morphological traits. They also were tested for drought stress tolerance at grain filling based on a chemical desiccation approach in two field experiments in 2005 and 2006 at IPK-Gatersleben. The genetic diversity of these materials also was tested applying 70 locus-specific SSR primers. In Iran, the work has not only been extended but has broadened to other aspects, such as allelic variation for vernalization requirement and bread-making quality. By incorporating 450 accessions from other surrounding countries, such as Iraq, Syria, Turkey, Afghanistan, India, Pakistan, Nepal, Azerbaijan, and Tajikistan, and nearly all Iranian modern durum and bread wheat cultivars, the number of accessions has increased to about 750. These materials have been evaluated in five years (2011–16) in the experimental field of Gorgan University. In 2015, a collection of spike samples of all of these materials was prepared and preserved. Currently, the genotypes are being evaluated for drought and salinity stresses tolerance at seedling stage via hydroponic and PEG cultures, respectively. The plan for next year is to evaluate all of these materials for salinity in a field experiment.

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## ITEMS FROM INDIA

### ICAR-INDIAN INSTITUTE OF WHEAT AND BARLEY RESEARCH Karnal – 132001, Haryana, India.

#### *Yield gaps, resource use patterns, and technical efficiency in Indian wheat farms – tracking from highly vulnerable production regions.*

R. Sendhil, Anuj Kumar, Satyavir Singh, Surendra Singh, and G.P. Singh.

India, being a subtropical country, is highly prone to the impact of climate change. The anticipated changes will have a significant impact on crop production, because yield is highly linked with the weather. This study is an attempt to analyse yield gaps, resource use patterns, and technical efficiency in Madhya Pradesh, a state preclassified as a highly vulnerable region in India by Sendhil et al. (2018, 2017). Primary data on socio-economic and farm particulars were collected from 200 respondents in 2017 across two districts of Madhya Pradesh, i.e., Rewa and Chhatarpur, through a structured pre-tested interview schedule. Secondary data on area, production, and yield for wheat, and climate variables for the selected two districts have been collected for the past 30 years (1985–86 to 2014–15). Yield gaps were quantified utilizing methodology developed by International Rice Research Institute, Philippines. Apart from conventional tools, Data Envelopment Analysis (DEA) was used to estimate the technical efficiency of resource use in the wheat production. A step-wise regression (two stages) approach was used to identify the crop growth stages sensitive to climate change (Sendhil et al. 2016). At the first stage, agro-meteorological variables (temperature, rainfall, relative humidity, and wind speed) were disaggregated into weekly averages spanning from November to April for each crop season from 1985–86 to 2014–15 and regressed (step-wise) against the yield by including the intercept term so as to track the exact sensitive weeks and to avoid a multi-collinearity problem. In the next stage, all the significant agro-meteorological variables obtained from the first phase were collectively regressed against the yield without intercept assuming that there was no external influence on crop yield apart from the variables selected in stage 1, without considering any endogenous physical input variable as well as exogenous price variable (Karn 2014).

Our findings indicated that the share of wheat acreage in total operational holdings was 89.30% in Rewa and 59.10% in the Chhatarpur districts of Madhya Pradesh, representing the importance of crop in the region. Yield gap I, i.e., the experimental yield or farmers' potential yield, was found to be negative in Chhatarpur (–940 kg/ha or –19%) and yield gap II was highest in Chhatarpur (2,112 kg/ha or 74.7%). Conventional wisdom and theory says that yield gap I was negative and, among other things, should be attributed to difference in management and adaptation strategies. Analysis of the resource use pattern indicated that significant differences exist in the use of resources between Rewa and Chhatarpur. Seeds were used above the recommended dose by 28.38% in Rewa and 40.84% in Chhatarpur. The DEA showed that wheat growers are technically efficient to the tune of 89.30%. The analysis pointed out that 10.70% of inputs (seeds, fertilizer, irrigation, plant protection chemicals, and manure/bio-fertilizers) could be reduced to produce the same level of output. Furthermore, we found that a majority of the respondents fall under 91–100% efficiency (132 farmers or 66%). Around 40 (20%) of the wheat growers were technically inefficient by 32%, indicating the scope for rational use of resources. The difference in technical efficiency among farmers is attributed to socio-economic characteristics, such as experience in farming and their knowledge of the recommended dose of inputs/package of practices coupled with the

adoption of strategies for adaptation to climate change. Step-wise regression facilitated the identification of the sensitive stages in wheat production. In Rewa, relative humidity (week 12, 22, 23, and 24) and rainfall (week 9) were found to be sensitive stages, whereas in Chattarpur, temperature (week 8) and relative humidity (week 8, 13, and 16) were identified as sensitive weeks during crop growth. Weather during late tillering to late jointing stage, flowering to milking stage, and grain hardening to ripening stage was found to be more sensitive in affecting the crop yield.

Climate change has affected the crop phenology to a larger extent and, hence, crop advisories need to be released at each sensitive stage that affects productivity. An increase in the maximum temperature at crown root initiation requires irrigation to cool off the microenvironment. Zero tillage, a resource conservation agriculture technology, has to be adopted on a larger scale where micro-environment temperature shoots-up consistently (Kumar et al. 2017, 2018). Furthermore, adjusting sowing dates based on the seasonal anomalies will counter the sensitivity during the initial crop growth stage (Francisco and Silva 2009). Clearly, smart climate farming practices and adaptation strategies assume significance to manage the yield sensitivity in wheat arising out of climate change.

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## ITEMS FROM MEXICO

### NATIONAL INSTITUTE FOR FORESTRY, AGRICULTURE, AND LIVESTOCK RESEARCH (INIFAP-CIRNO), CAMPO EXPERIMENTAL NORMAN E. BORLAUG

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

#### *Evaluation of agronomic traits of durum wheats at three sowing dates with two and three complementary irrigations during the 2007–08 crop season.*

José Luis Félix-Fuentes, Guillermo Fuentes-Dávila, Pedro Figueroa-López, Ivón Alejandra Rosas-Jáuregui, Víctor Valenzuela-Herrera, and Gabriela Chávez-Villalba.

**Abstract.** Grain yield, test weight, days-to-flowering, days-to-physiological maturity, plant height, b pigment value, and grain protein of seven durum wheat genotypes were determined during the season 2007–08 at the Norman E. Borlaug Experimental Station in the Yaqui Valley, at three sowing dates (15 and 30 November, and 15 December, 2007), with two and three complementary irrigations (CI). Experimental plots had four beds with two 5-m rows and a seed density of 100 kg/ha and used a randomized complete block design with three replications. The ANOVA was performed using the SAS System for Windows 9.0 and mean comparison with Tukey's test ( $\alpha=0.01$ ). The agronomic management followed the recommendations of INIFAP for the region. With two CI, Júpare C2001 had the highest grain yield (6.1 t/ha) at the first sowing date, whereas with three CI, 'MUSK\_1//ACO89/FNFOOT\_2/4/MUSK\_4/3/PLATA\_3//CREX/ALLA/5/OLUS\*2/ILBOR//PATKA\_7/YAZI\_1' showed 7.6 at this date. Line 'SOOTY\_9/RASCON\_37//CAMAYO' had an overall yield above 6.0 t/ha at the different sowing dates with both two and three CI. Júpare C2001 showed the highest average test weight (84.2 kg/hl). The earliest genotype in the study, under two and three CI, was 'CS/TH.CU//GLEN/3/GEN/4/MYNA/VUL/5/2\*DON87/6/2\*BUSCA\_3' with 112 (2 CI) and 113 (3 CI) days. Line 'SULA/AAZ\_5//CHEN/ALTAR84/3/AJAIA\_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA\_13/4/ARMENT//SRN\_3/NIGRIS\_4/3/CANE-LO\_9.1' showed the highest average grain protein value with two and three CI (15.3% and 14.2%), and the highest b pigment values (28.9 with two CI and 28.3 with three). The shortest genotype was 'SOOTY\_9/RASCON\_37//CAMAYO' with an average of 75.5 and 81.1 cm, with two and three CI, respectively.

**Introduction.** Wheat is the second most important cereal in Mexico, with an average per capita annual consumption of 57.4 kg. Durum wheat represents 59.79% of the wheat production in the country, and Mexico has become the third world exporter of this product. In contrast, Mexico imported  $3.3 \times 10^6$  tons of the bread wheat from the U.S. in 2016–17 (Noltemeyer 2017). Durum wheat in Mexico is cultivated primarily in the northwestern region, whereas bread is scattered in 17 states throughout the country (SIAP 2018a). The area with durum wheat has increased in the last few years, reaching more than 250,000 ha; the state of Sonora being the main producer (SIAP 2018b), and where the highest grain yields have been obtained. Therefore, wheat breeding programs in the country are focused on generating promising lines that can meet the expectations of the producers. Our objective was to evaluate several durum wheat genotypes for grain yield, test weight, days-to-flowering, days-to-physiological maturity, plant height, and grain protein at three sowing dates with two and CI.

**Materials and methods.** The study was carried out during the 2007–08 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, located in block 910 in the Yaqui Valley, Sonora, Mexico, at 27°22'04.64" latitude north and 109°55'28.26" longitude west, 37 masl, with warm climate (BW (h)) and extreme heat according to Koppen’s classification modified by García (1988), in a heavy clay soil. Seven different durum wheat genotypes (Table 1) were used to establish the trial at three sowing dates (15 and 30 November and 15 December, 2017), with two and three CI. We evaluated for grain yield, test weight, days-to-flowering, days-to-physiological maturity, plant height, and grain protein. Experimental plots consisted of four beds with two 5-m rows with a seed density of 100 kg/ha, under a randomized complete block design with three replications. The ANOVA was performed using the SAS System for Windows 9.0 and mean comparison with Tukey’s test ( $\alpha=0.01$ ). The agronomic management followed the recommendations of INIFAP for the region (Figueroa-López et al. 2011).

**Table 1.** Wheat genotypes evaluated during the 2007–08 crop season in the Yaqui Valley, Sonora, Mexico.

Genotype	Selection history
JUPARE C2001	CD91Y636-1Y-040M-030Y-1M-0Y-0B-1Y-0B
SOMAT_4/INTER_8	CDSS95B00181S-0M-1Y-0B-1Y-0B-0Y-0B-14EY-0Y
CS/TH.CU//GLEN/3/GEN/4/MYNA /VUL/5/2*DON87/6/2* BUSCA_3	CDSS95B00803M-D-0M-1Y-0B-3Y-0B-0Y-0B-15EY-0Y
SCRIP_1//DIPPER_2/BUSHEN_3/4/ ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	CDSS02Y00381S-0Y-0M-19Y-0Y
SULA/AAZ_5//CHEN/ALTAR84/3/AJAIA_12/F3LOCAL(SEL. ETHIO.135.85)//PLATA_13/4/ARMENT//SRN_3/NIGRIS_4/3/ CANELO_9	CDSS02Y00390S-0Y-0M-8Y-0Y
MUSK_1//ACO89/FNFOOT_2/4/MUSK_4/3/ PLATA_3//CREX/ ALLA/5/OLUS*2/ILBOR//PATKA_7/YAZI_1	CDSS02Y00786T-0TOPB-0Y-0M-2Y-0Y
SOOTY_9/RASCON_37//CAMAYO	CGSS02Y00004S-2F1-6Y-0B-1Y-0B

**Results.** The grain yield range at the 15 November sowing date with two CI within genotypes was 5.2–6.1 t/ha, with an average of 5.7, and 6.6–7.6, with a 7.0 average, for three CI (Fig 1A, p. 24). The grain yield range at the 30 November sowing date with two CI within genotypes was 5.2–5.4 t/ha, with an average of 5.3, and 6.1–6.6, with a 6.4 average, for three CI (Fig 1B, p. 24). Grain yield range at the 15 December sowing date with two CI within genotypes was 4.4–5.3 t/ha, with an average of 4.9, and 5.2–6.0, with a 5.5 average, for three CI (Fig 1C, p. 24). The grain yield range at the 15 November sowing date with two and three CI within genotypes was 5.9–6.8 t/ha, with an average of 6.3; at 30 November 30, it was 5.6–6.0 t/ha, with an average of 5.8; and at 15 December, it was 4.8–5.7 t/ha, with an average of 5.2 (Fig 1D, p. 24). Grain yield at the different sowing dates with two CI was quite variable within genotypes; Júpare C2001 (genotype 1) showed the highest grain yield with 6.1 t/ha at the first sowing date. With three irrigations, ‘MUSK\_1//ACO89/FNFOOT\_2/4/MUSK\_4/3/PLATA\_3//CREX/ALLA/5/OLUS\*2/ILBOR//PATKA\_7/YAZI\_1’ (genotype 6) showed the highest grain yield with 7.6 t/ha at the first and 6.6 at the second; however, it showed the lowest yield with both irrigations (4.4 and 5.2, respectively) at the third sowing date. ‘SOOTY\_9/RASCON\_37//CAMAYO’ (genotype 7) showed good grain yield stability with three CI, because the yield was > 6.0 t/ha across the sowing dates; but when irrigations are reduced, the yield may up to 1.2 t/ha lower. The overall yield of this line at the different sowing dates with two and three CI surpassed 6.0 t/ha.

Júpare C2001 showed the highest test weight in all sowing dates with two and three CI, with an overall average of 84.2 kg/hl; followed by those of ‘MUSK\_1//ACO89/FNFOOT\_2/4/MUSK\_4/3/PLATA\_3//CREX/ALLA/5/OLUS\*2/ILBOR//PATKA\_7/YAZI\_1’ (83.6 kg/hl) and ‘SULA/AAZ\_5//CHEN/ALTAR84/3/AJAIA\_12/ F3LOCAL(SEL. ETHIO.135.85)//PLATA\_13/4/ARMENT//SRN\_3/NIGRIS\_4/3/ CANELO\_9’ (83.4 kg/hl). This variable indicates the minimum grain density required for sale, which varies according the place of commercialization. Fernández (2013) reported that test weight is primarily a genetic trait, but the lack of appropriate nutrition may affect it.

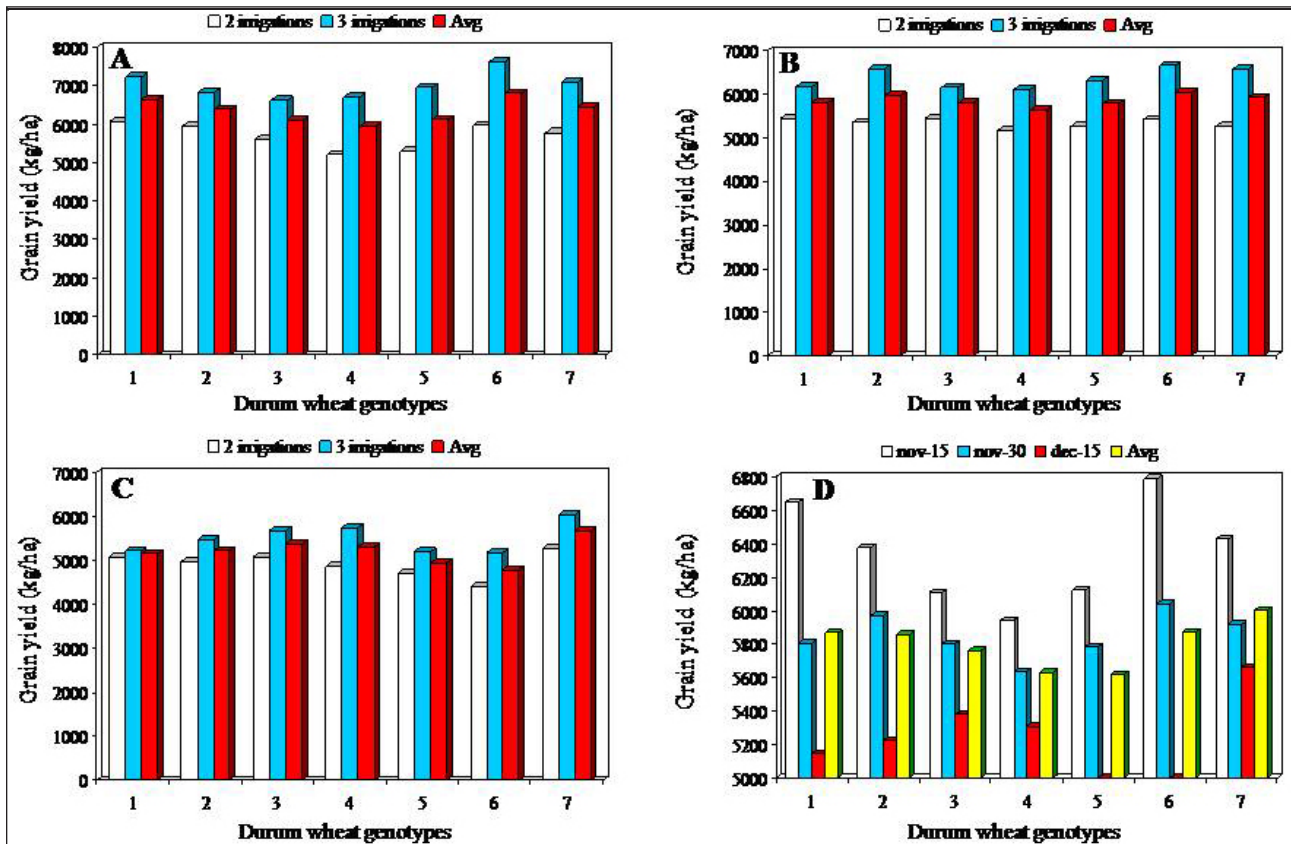


Fig. 1. Grain yield of seven durum wheat genotypes in the Yaqui Valley, Sonora, Mexico, during the 2007–08 crop season with two and three complementary irrigations. A. sowing date 15 November; B. sowing date 30 November; C. sowing data 15 December, 2007; and D. average grain yield obtained with two and three irrigations within the sowing dates.

Significant differences were observed among genotypes for days-to-flowering. Genotype 4, ‘SCRIP\_1//DIPPER\_2/BUSHEN\_3/4/ARMENT//SRN\_3/NIGRIS\_4/3/CANELO\_9.1’ showed the greatest average in the number of days-to-flowering when two and three CI were applied; the range was 82.0–90.6 and 80.0–90.6 days for two and three CI, respectively, within the three sowing dates (Fig. 2). In general, little variation was in the number of days-to-flowering in the remainder of the genotypes. For physiological maturity, the earliest genotype, which occurred at the 15 December sowing date under two and three CI, was ‘CS/TH.CU//GLEN/3/GEN/4/MYNA/VUL/5/2\*DON87/6/2\* BUSCA\_3’ with 112 and 113 days, respectively. The latest was ‘SCRIP\_1//DIPPER\_2/BUSHEN\_3/4/ ARMENT//SRN\_3/NIGRIS\_4/3/CANELO\_9.1’ from the 15 November sowing date with 129 and 132 days to maturity under two and three CI, respectively.

The highest average of grain protein value obtained (15.3%) from the three sowing dates with two CI was the genotype ‘SULA/AZ\_5//CHEN/ALTAR84/3/AJAIA\_12 / F3LOCAL(SEL. ETHIO.135.85)//PLATA\_13/4/ARMENT//SRN\_3/NIGRIS\_4/3/CANELO\_9.1’; also having the highest average with three CI (14.2%). For average pigment content in semolina at the different sowing dates with two and three CI, ‘SULA/AZ\_5//...’, ‘SCRIP\_1//DIPPER\_2//...’, and

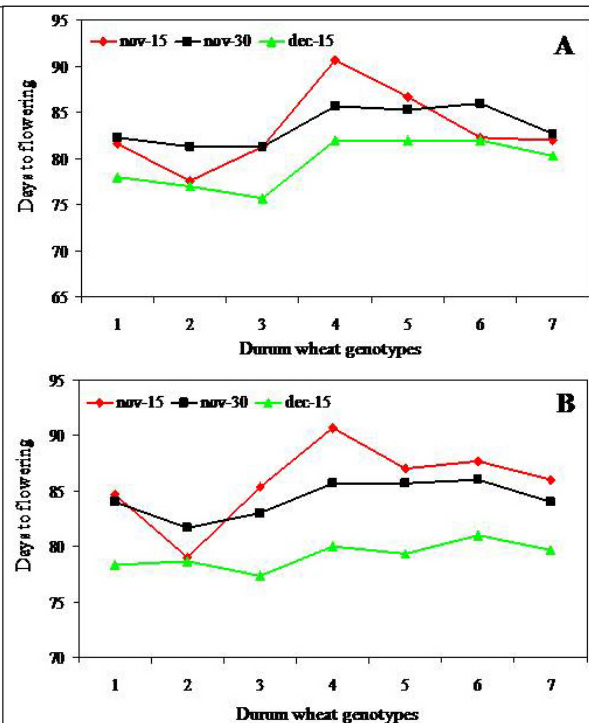


Fig. 2. Days-to-flowering of seven durum wheat genotypes in the Yaqui Valley, Sonora, Mexico, with two (A) and three (B) complementary irrigations at three sowing dates during the 2007–08 crop season.

‘MUSK\_1//ACO89...’ had values of 28.9, 28.9, and 28.4, and 28.3, 28.1, and 27.5 in the minolta scale, respectively. ‘SOOTY\_9/RASCON\_37//CAMAYO’ was the shortest genotype with a range of 68–80 cm with two CI and 78–85 cm with three, whereas ‘SCRIP\_1//DIPPER\_2/...’ was 86–98 cm and 91–96 cm with two and three CI, respectively, and was the tallest.

**Conclusions.** The best sowing date for the durum wheat genotypes evaluated in this study was between 15–30 November. Up to 30% grain yield reduction in some genotypes was observed if sowing was on 15 December. All genotypes performed better with three CI. Genotype ‘SOOTY\_9/RASCON\_37//CAMAYO’ surpassed an average grain yield of 6.0 t/ha at the different sowing dates with three CI.

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### *Evaluating advanced bread wheat lines for Karnal bunt resistance in the field during the 2012–2013 crop season.*

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**Abstract.** We evaluated 1,176 advanced bread wheat lines for resistance to Karnal bunt during the 2012–13 crop season. Planting dates were 15 and 22 November, 2012, using 8 g of seed for each 0.7-m row in a bed with two rows. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage, in 5 heads/line. Harvesting was done manually, and the percentage of infection was determined by counting healthy and infected grains. The range of the percentage of infection of the advanced lines at the first planting date was 0.0–92.1%, with an average of 30.4%, and 0.0–76.8% at the second, with an average of 17.8%. The range of the average percentage of infection was 0.28–69.8% with an average of 24.1%. Lines with the lowest average percentage of infection were ‘VILLAJUAREZF2009/5/BABAX/LR42//BABAX\*2/4/SNI/TRAP#1/3/KAUZ\*2/TRAP//KAUZ’ with 0.28%, ‘PFAU/MILAN/3/BABAX/LR42//BABAX/4/KA/NAC//TRCH’ with 0.49%, ‘WHEAR/VIVITSI//WHEAR/3/PANDORA’ with 1.04%, ‘WHEAR/VIVITSI//WHEAR/3/BECARD’ with 1.14%, ‘ATTILA/4/WEAVER/TSC//WEAVER/3/WEAVER/5/PAU-RAQUE #1’ with 1.86%, and ‘FRET2\*2/KIRITATI//KIRITATI/2\*TRCH/3/WBLL1\*2/BRAMBLING’ with 2.0%. The highest percentages were lines ‘QUAIU/BECARD//BECARD’ with 63.9%, ‘KIRITATI/HUW234+LR34/PRINIA/3/BAJ#1’ with 64.4%, ‘ND643/2\*WBLL1//VILLAJUAREZ F2009’ with 65.6%, ‘QUAIU#2\*2/TINKIO#1’ with 66.4%, and ‘TACUPETOF2001\*2/BRAMBLING//WHEAR/SOKOLL’ with 69.9%. Ten lines fell into the 0.1–2.5% infection category, 44 within 2.6–5.0%, 114 within 5.1–10.0%, 665 within 10.1–30.0%, and 343 with greater than 30.0% infection. The average of the three highest levels of infection of the susceptible check was 100%.



**Fig. 3.** Wheat grains partially infected with *Tilletia indica* in a spike.

**Introduction.** Karnal bunt of wheat, caused by *Tilletia indica*, occurs on bread wheat (Mitra 1931), durum wheat, and triticale (*X Triticosecale*) (Agarwal et al. 1977). This disease 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), the Republic of South Africa (Crous et al. 2001), and apparently in Afghanistan (CIMMYT 2011). In general, the fungus partially affects some grains in a plant (Bedi et al. 1949) (Fig. 3), and in some occasions they are totally destroyed. Although the fungus may penetrate the embryo, it does not necessarily cause damage (Chona et al. 1961; Mitra 1935). Partially infected grains may give rise to healthy plants, although it is reported that the percentage of germination decreases depending on the level of seed infection (Bansal et al. 1984; Rai and Singh 1978; Singh 1980) and that severely affected seed lose viability or show abnormal germination (Rai and Singh 1978). Fuentes-Dávila et al. (2013) indicates that seed with the greatest infection, but with the embryo intact, produce the highest number of tillers. Control of this pathogen is difficult because teliospores are resistant to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1985, 1988). Chemical control is accomplished by applying fungicides during flowering (Fuentes-Dávila et al. 2005, 2016; Salazar-Huerta et al. 1997); however, this measure is not feasible when quarantines do not allow tolerance levels for seed production (SARH 1987). The use of resistant wheat cultivars is the best control method, and it also would reduce the possibility of introducing the disease into Karnal bunt-free areas. Since the 1940s, several species of *Triticum* have been evaluated for resistance to Karnal bunt (Bedi et al. 1949; Singh et al. 1986; 1988). Bread wheat is the species most affected by the disease and, under artificial inoculation, some lines may show more than 50% infected grain (Fuentes-Dávila et al. 1992, 1993). Therefore, continued evaluation of the new advanced lines and wheat cultivars is important. Our objective was to evaluate the reaction of 1,176 advanced bread wheat lines for resistance to *T. indica* in the field.

**Materials and methods.** We evaluated, 1,176 advanced bread wheat lines for resistance to Karnal bunt during the autumn–winter 2012–13, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, located in block 910 in the Yaqui Valley, Sonora, México, at 27°22'04.64" latitude north and 109°55'28.26" longitude west, 37 masl, with warm climate (BW (h)) and extreme heat according to Koppen's classification modified by García (1988). Sowing dates were 15 and 22 November, 2012, using 8 g of seed for each 0.7-m row in a bed with two rows in a clay soil with pH 7.8. For agronomic management, INIFAP's technical recommendations were followed (Figueroa-López et al. 2011). Inoculum was prepared by isolating teliospores from infected grain, followed by centrifugation in a 0.5% sodium hypochlorite solution and plating on 2% water-agar Petri plates. After teliospore germination, fungal colonies were transferred and multiplied on potato-dextrose-agar. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage in five heads from each line. High relative humidity in the experimental area was provided by an automatic mist spray-irrigation system (Fig. 4) five times a day for 20 min each time. To avoid bird damage, an anti-bird net system was installed in the area used for evaluation of the wheat lines (Fig. 5). Harvest was done manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. Evaluated lines originated from the collaborative project between the Global Wheat Program of the International Maize and Wheat Improvement Center (CIMMYT) and the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP).



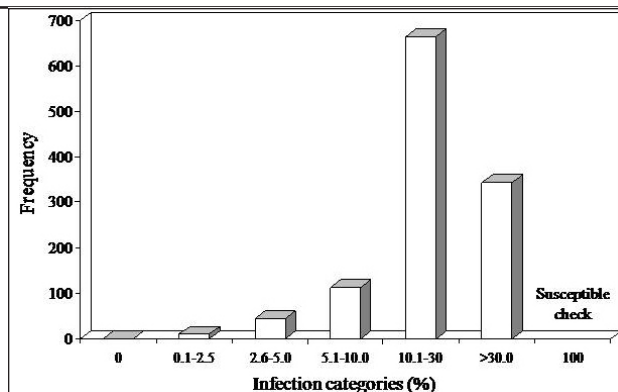
**Fig. 4.** Mist-irrigation system in the are used to evaluate advanced bread wheat lines for resistance to *Tilletia indica*.



**Fig. 5.** Anti-bird net system in the are used to evaluate advanced bread wheat lines for resistance to *Tilletia indica*.

**Results.** The range of the percentage of infection of the advanced lines in the first planting date was 0.0–92.1%, with an average of 30.4%, and 0.0–76.8% at the second with an average of 17.8%. The range of the average infection was 0.28–69.8% with an average of 24.1%. Overall, ten lines fell into the 0.1–2.5% infection category, 44 within 2.6–5.0%,

114 within 5.1–10.0%, 665 within 10.1–30.0%, and 343 with greater than 30.0% infection (Fig. 6, p. 27). The average of the three highest percentage of infection of the susceptible check KBSUS 1 was 100%. Five lines consistently showed a percentage of infection below 2.5% at both planting dates (Table 2, p. 27) and 14 were below 5.0% (Table 3, pp. 27-28). Lines with less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). The lines with the lowest average percentage of infection were ‘VILLAJUAREZF2009/5/BABAX/LR42//BABAX\*2/4/SNI/ TRAP#1/3/KAUZ\*2/TRAP//KAUZ’ with 0.28%, ‘PFAU/MILAN/3/BABAX/LR42//BABAX/4/ KA/ NAC//TRCH’ with 0.49%, ‘WHEAR/VIVITSI//WHEAR/3/ PANDORA’ with 1.04%, ‘WHEAR/ VIVITSI//WHEAR/3/ BECARD’ with 1.14%, ‘ATTILA/4/WEAVER/TSC// WEAVER/3/WEAVER /5/PAURAUQUE#1’ with 1.86%, and ‘FRET2\*2/KIRITATI//KIRITATI/2\*TRCH/3/WBLL1\*2/ BRAMBLING’ with 2.0%. The highest lines were ‘QUAIU/BECARD//BECARD’ with 63.9%, ‘KIRITATI// HUW234+LR34/PRINIA/3/BAJ #1’ with 64.4%, ‘ND643/



**Fig. 6.** Karnal bunt infection categories (%) in 1,176 advanced bread wheat lines artificially inoculated in the field at two dates during the 2012–13 crop season, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. The average of the three highest scores of infection of the susceptible check was 100%.

**Table 2.** Advanced bread wheat lines that showed less than 2.5% infection with *Tilletia indica* at two planting dates after artificial field inoculation, during the 2012–13 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Entry	Pedigree and selection history	Range of infection	Average
435	WHEAR/VIVITSI//WHEAR/3/PANDORA CMSS08B00073S-099M-099NJ-099NJ-8WGY-0B	0.0–2.1	1.0
451	VILLA JUAREZ F2009/5/BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ CMSS08B00178S-099M-099NJ-099NJ-2WGY-0B	0.0–0.6	0.3
543	WHEAR/VIVITSI//WHEAR/3/BECARD CMSS08B00518S-099M-099NJ-099NJ-22WGY-0B	0.0–2.3	1.1
588	FRET2*2/KIRITATI//KIRITATI/2*TRCH/3/WBLL1*2/BRAMBLING CMSS08B00684T-099TOPY-099M-099NJ-099NJ-9WGY-0B	1.7–2.3	2.0
961	PFAU/MILAN/3/BABAX/LR42//BABAX/4/KA/NAC//TRCH CMSA08M00419S-040ZTM-050Y-22ZTM-010Y-0B	0.0–1.0	0.5

**Table 3.** Advanced bread wheat lines that showed a percentage of infection with *Tilletia indica* below 5.0% at two planting dates after artificial field inoculation, during the 2012–13 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Entry	Pedigree and selection history	Range of infection	Average
21	FRET2/KUKUNA//FRET2/3/KIRITATI/2*TRCH CMSS08Y00117S-099Y-099M-099NJ-099NJ-14WGY-0B	4.4–5.0	4.7
45	KACHU/DANPHE CMSS08Y00151S-099Y-099M-099NJ-099NJ-21WGY-0B	3.1–4.2	3.7
109	PFAU/SERI.1B//AMAD/3/WAXWING/4/ND643/2*WBLL1 CMSS08Y00274S-099Y-099M-099NJ-2WGY-0B	3.8–4.9	4.3
115	PFAU/SERI.1B//AMAD/3/WAXWING/4/ND643/2*WBLL1 CMSS08Y00274S-099Y-099M-099NJ-099NJ-10WGY-0B	1.1–5.0	3.1
118	PFAU/SERI.1B//AMAD/3/WAXWING/4/FRNCLN CMSS08Y00278S-099Y-099M-099Y-3M-0WGY	4.5–4.6	4.6
363	MUNAL/3/HUW234+LR34/PRINIA//PFAU/WEAVER/4/MUNAL #1 CMSS08Y00888T-099TOPM-099Y-099M-099NJ-19WGY-0B	1.0–3.3	2.1
364	MUNAL/3/HUW234+LR34/PRINIA//PFAU/WEAVER/4/MUNAL #1 CMSS08Y00888T-099TOPM-099Y-099M-099NJ-20WGY-0B	2.0–3.4	2.7



**Table 3.** Advanced bread wheat lines that showed a percentage of infection with *Tilletia indica* below 5.0% at two planting dates after artificial field inoculation, during the 2012–13 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Entry	Pedigree and selection history	Range of infection	Average
399	SWSR22T.B./5/KAUZ//ALTAR 84/AOS/3/KAUZ/4/ SW94.15464/6/2*PRL/2*PASTOR CMSS08Y01067T-099M-099Y-099M-099Y-8M-0WGY	2.2–4.0	3.1
456	BECARD/MUNAL #1 CMSS08B00204S-099M-099Y-14M-0WGY	2.7–4.0	3.4
506	PASTOR/3/VORONA/CNO79//KAUZ/4/MILAN/OTUS// ATTILA/3*BCN/5/MUNAL #1 CMSS08B00441S-099M-099Y-11M-0WGY	1.4 – 2.9	2.1
596	FRET2/KUKUNA//FRET2/3/KIRITATI/2*TRCH/4/MUNAL #1 CMSS08B00688T-099TOPY-099M-099NJ-099NJ-27WGY-0B	1.8–3.9	2.8
692	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/KRONSTAD F2004/5/MU- NAL/6/MUNAL #1 CMSS08B00828T-099TOPY-099M-099Y-20M-0WGY	1.6–4.9	3.3
729	FRNCLN/DANPHE//FRANCOLIN #1 CMSS08B00863T-099TOPY-099M-099Y-7M-0WGY	1.4–4.8	3.1
771	WHEAR/KIRITATI/3/C80.1/3*BATAVIA//2*WBLL1*2/4/ KIRITATI/2*TRCH CMSS08B00907T-099TOPY-099M-099NJ-6WGY-0B	0.0–4.4	2.2
820	FALCIN/AE.TAUSCHII (312)/3/THB/CEP7780//SHA4/LIRA/4/ FRET2/5/MUU/6/ MILAN/KAUZ//DHARWAR DRY/3/BAV92 CMSA08Y00099T-099B-050Y-040M-0NJ-0NJ-8Y-0B	1.8–4.4	3.1
841	ATTILA/4/WEAVER/TSC//WEAVER/3/WEAVER/5/PAURAQUE #1 CMSA08Y00445S-050Y-050ZTM-050Y-30BMX-010Y-0B	0.0–3.7	1.9
870	AGT YOUNG/3/2*KA/NAC//TRCH CMSA08M00004T-040Y-050ZTM-050Y-9ZTM-010Y-0B	0.0–4.6	2.3
966	NING MAI 96035/FINSI//HEILO/3/ATTILA/PASTOR CMSA08M00445S-040ZTM-050Y-9ZTM-010Y-0B	3.5–4.0	3.8
989	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SOKOLL/WBLL1 PTSA08M00053S-050ZTM-050Y-105ZTM-010Y-0B	4.1–4.2	4.1
1143	KA/NAC//TRCH/3/2*VORB CMSA08Y00083T-099B-050Y-050ZTM-050Y-41BMX-010Y-0B	1.7–3.9	2.8
1151	BAVIS/VORB/5/CROC_1/AE.TAUSCHII (205)//BORL95/3/PRL/ SARA//TSI/ VEE#5/4/FRET2 CMSA08M00052T-050Y-040M-0NJ-10Y-0B	1.5–4.7	3.1

2\*WBLL1//VILLA JUAREZ F2009' with 65.6%, 'QUAIU#2\*2/TINKIO#1' with 66.4%, and 'TACUPETOF2001\*2/BRAMBLING//WHEAR/SOKOLL' with 69.9%. The advanced bread wheat lines with resistance shown to *T. indica* may be prospects for release in regions where Karnal bunt constitutes an economic constraint if attributes such as resistance to rusts, yield, and quality are met, or they may be part of a resistant pool in a wheat breeding program, once they are re-evaluated for two or three more crop seasons.

### Conclusions.

The range of the average percentage of infection of 1,176 advanced bread wheat lines evaluated for resistance to Karnal bunt during the autumn–winter 2012–13 crop season, was 0.28–69.8% with an average of 24.1%. Five lines consistently showed a percentage of infection below 2.5% and fourteen below 5.0% at both planting dates. Lines with the lowest average percentage of infection were 'VILLAJUAREZF2009/5/BABAX/ LR42//BABAX\*2/4/SNI/TRAP#1/3/KAUZ\*2/TRAP//KAUZ' with 0.28% and 'PFAU/MILAN/3/ BABAX/LR42//BABAX/4/KA/NAC//TRCH' with 0.49%. Lines with the highest average percentage of infection were 'QUAIU#2\*2/TINKIO#1' with 66.4% and 'TACUPETOF2001\*2/BRAMBLING//WHEAR/SOKOLL' with 69.9%. The average of the three highest levels of infection of the susceptible check was 100%.

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### ***Biological effectiveness of Opus, Folicur, Juwel, and Bemistop for control of Karnal bunt (Tilletia indica) of wheat, in the field.***

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**Abstract.** The commercial fungicides Opus, Folicur, Juwel, and Bemistop were evaluated in the field to determine their biological effectiveness to control Karnal bunt of wheat. A completely randomized design was used with four replications. Twenty heads of cultivar Tacupeto F2001 were inoculated during the boot stage with an allantoid sporidial suspension (10,000/mL). Commercial rates recommended for each product were followed. The first application was carried out ten days after inoculation (Zadoks 56–58; Feekes 10.4–10.5), and a second ten days later. Inoculated spikes were threshed by hand, and healthy and infected kernels were counted to determine the percentage infection. The biological effectiveness of the products evaluated were Opus, 98.2%; Juwel, 97.7%; Bemistop, 95.4%; and Folicur, 95.2%. The untreated inoculated check had a mean of 24.0% infection. No statistical differences were observed for the products evaluated for level of infection after arcsin transformation (Tukey,  $p = 0.05$ ), and the coefficient of variation was 10.2%. No phytotoxic effects of treatments applied to the wheat plant were observed.

**Introduction.** Karnal bunt of wheat, caused by the fungus *Tilletia indica* (syn. *Neovossia indica* Mitra (Mundkur), is the most important disease of wheat seed and grain in northwest Mexico (Fuentes-Dávila 1997). Losses are due primarily for the negative effect on flour quality and quarantine regulations, both national and international (SARH 1987; Brennan et al. 1900; SAGARPA 2002). Because no wheat cultivars are immune to Karnal bunt, chemical control is considered an important measure of an integrated management program of the disease. Due to the biological cycle of *T. indica*, the application of agrochemicals during heading–flowering–anthesis of the wheat plant provides greater control of the disease and allows a more profitable economical margin.

Research on chemical control of the disease by foliar applications has been carried out. Singh and Prasad (1980) reported a significant reduction in the level of infection in the field, with a single application during the boot stage with benomyl (Benlate), carbendazim (Bavistin), mancozeb (Dithane-M45), or triphenyltin hydrate (Duter). Singh and Singh (1985) reported that, of the fungicides Bavistin, Baycor, Baytan, Bayleton, Benlate, Blitox, Ceresan, Dithane M-45, Topsin, and Vitavax, only Baytan and Bayleton were effective at reducing disease severity. Smilanick et al. (1987) reported that in artificially inoculated experimental wheat plots, control of the disease was greater than 80% with two applications of propiconazole or etaconazole and with four applications of mancozeb or copper hydroxide. The best results were obtained when products were applied 72 h after inoculation with the fungus. Figueroa and Valdés (1991) reported the superiority of propiconazole for control of Karnal bunt with foliar applications when compared with the fungicides diniconazole, tebuconazole, flutriafol, fluzilazol, triadimenol, and procloraz. Salazar-Huerta et al. (1997) reported that during 1986–89, in both experimental plots and commercial fields, propiconazole (Tilt) was the product with the greatest biological effectiveness in controlling the disease, with two applications at the rate of 0.5 L/ha of commercial product. The first application was made when the crop was at 25% heading and the second one ten days later. Figueroa-López and Alvarez-Zamorano (2000) reported that epoxyconazole (Opus) showed similar levels of efficiency as that of propiconazole in field trials under artificial inoculation. Fuentes-Dávila et al. (2005) reported that tebuconazole (Folicur) and propiconazole (Tilt) had a biological effectiveness greater than 89% for control of Karnal bunt in artificially inoculated field trials. In 2007, they reported that the biological effectiveness of tebuconazole (Folicur), epoxyconazole (Opus), and

propiconazole (Tilt) was 99.8%, 99.6%, and 99.9%, respectively, and in 2016, the biological effectiveness of tebuconazole (Varon) was 97.5%, flutriafol (Pointer) 97.2%, Opus 96.9%, and piraclostrobina (Headline) 86.87%.

In southern Sonora, leaf rust (*Puccinia recondita* Eriksson) is an endemic and important disease of wheat that has caused epidemics (Dubin and Torres 1981; Figueroa-López et al. 2001) that can only be controlled by proper fungicide applications, once a new race or races are generated that affect the current cultivars. Headline and Pointer were evaluated for control of Karnal bunt in 2016 after the reports of Figueroa-López and Cantúa-Ayala (2006) and Figueroa-López et al. (2010) about their effectiveness in controlling rust. Varon also was evaluated in that trial because it was available on the market for rust control. More recently, other commercial products, such as Juwel from BASF and Bemistop from Arysta, are available on the market for control of leaf rust. Therefore, our objective was to evaluate the biological effectiveness of Opus SC (BASF, epoxiconazol 12% a.i. in weight), as the regional check; Folicur 25 EW (Bayer, tebuconazole); Juwel (BASF, epoxyconazol 11.50% + kresoxim-metil 11.50% CS); and Bemistop (Arysta Lifescience, propiconazol 25.50 EC); for controlling Karnal bunt in the field under artificial inoculation.

**Materials and methods.** The experiment was carried out during the 2017–18 crop season at the Norman E. Borlaug Experimental Station, located in block 910 of the Yaqui Valley at 27°22'04.64" latitude north and 109°55'28.26" longitude west, 37 masl, with a warm (BW (h)) and extremely warm and dry (BS (h)) climate, according to Koppen classification modified by Garcia (1988). Sowing date was 1 December, 2017 with a rate of 80 kg of seed/ha. Treatments were established in a completely randomized experimental design (Fig. 7) with four replications using the commercial bread wheat cultivar Tacupeto F2001. The experimental plot consisted of four beds with two 3-m rows and 0.80 m between beds (Fig. 8). Inoculations were made during the boot stage by injection applying 1 mL per spike with an allantoid sporidial suspension (10,000/

20 R4 Untreated check	19 R4 Juwel	18 R4 Opus	17 R4 Folicur	16 R4 Bemistop
11 R3 Opus	12 R2 Folicur	13 R3 Untreated check	14 R3 Bemistop	15 R3 Folicur
10 R3 Juwel	9 R2 Untreated check	8 R2 Juwel	7 R2 Opus	6 R2 Bemistop
1 R1 Folicur	2 R1 Bemistop	3 R1 Opus	4 R1 Juwel	5 R1 Untreated check

**Fig. 7.** Randomized complete distribution of treatments in the field for control of Karnal bunt (*Tilletia indica*) by foliar applications during the autumn–winter 2017–18 crop season in the Yaqui Valley, Sonora, Mexico.



**Fig. 8.** Experimental plots with cultivar Tacupeto F2001 used for evaluation of fungicides for control of Karnal bunt (*Tilletia indica*) during the autumn–winter 2017–18 crop season in the Yaqui Valley, Sonora, Mexico.



**Fig. 9.** A. Teliospore germination; a promycelium and a whorl of primary sporidia can be observed. B. Allantoid secondary sporidia. C. Use of a haemocytometer to determine number of secondary sporidia. D. Inoculation by injection into the booting flower spike.

mL) in 20 spikes, in the central rows of each plot (Fig. 9). Inoculum was prepared as described by Fuentes-Bueno and Fuentes-Dávila (2007). Commercial rates indicated for each product were followed: Opus 1 L/ha c.p., Folicur 0.50 L/ha c.p., Juwel 1 L/ha c.p., and Bemistop 0.5 L/ha c.p. (Table 4). For application of fungicides, a manual Solo

**Table 4.** Fungicides, formulations, concentrations, and rates used to control Karnal bunt by foliar applications during the 2017–18 crop season in the Yaqui Valley, Sonora, Mexico. Concentration is active ingredient in weight and Rate is liters of commercial product.

Treatment	Formulation and concentration	Rate (CP/ha)
Juwel	250 SC 23.0% a.i.	1.00
Bemistop	25.5 EC ≥ 25% a.i.	0.50
Folicur	250 EW ≥ 25% a.i.	0.50
Opus [untreated check]	SC 12% a.i.	1.00

backpack sprayer (15 L) with a single nozzle was used; the volume based on 250 L of water/ha. To avoid carry over of the products, plastic barriers were used between each plot during the applications (Fig. 10). The first application was carried out ten days after inoculation (Zadoks 56–58, Feekes 10.4–10.5) and the second ten days later. Inoculated spikes were threshed by hand, and the percentage of infection was obtained by counting the number of infected and healthy grains from 20 inoculated spikes from each plot treated with the fungicides, and from 20 inoculated spikes from the untreated check. The biological effectiveness was obtained using Abbot's formula, effectiveness of treatments = average percentage of infection of the check – average percentage of



**Fig. 10.** Application of fungicides in experimental plots for control of Karnal bunt (*Tilletia indica*), during the autumn–winter 2017–18 crop season in the Yaqui Valley, Sonora, Mexico.

infection of the treatment / average percentage of infection of the check x 100. The ANOVA was performed and mean comparison by Tukey's test ( $p = 0.05$ ) to determine statistical differences among treatments, previous arcsin transformation  $\sqrt{X + 0.5}$  (Steel and Torrie 1980). Phytotoxicity was evaluated ten days after each application of fungicide according to the EWRS (European Weed Research Society) scale (Table 5) (Champion 2000).

**Results.** Significant statistical differences were detected between the product treatments and the untreated check with respect to the percentage of infection. The coefficient of variation was 10.2%. Mean comparison by Tukey's test (Table 6) indicated that all treatments with fungicide application were effective on reducing the percentage of infection when compared with the untreated inoculated check, which showed the highest average percentage of infection (23.9%), with a range of 18.7–27.9. The real range of the mean percentage of infection obtained in spikes treated with the different products was 0.21–1.88% (Opus average 0.44%, Jewel 0.56%, Bemistop 1.11%, and Folicur 1.12%). The biological effectiveness of the products evaluated were Opus 98.2%, Jewel 97.7%, Bemistop 95.4%, and Folicur 95.2%.

**Conclusions.** The biological effectiveness of Opus, Jewel, Bemistop, and Folicur for control of Karnal bunt of wheat by foliar applications during heading–flowering–anthesis was 98.2%, 97.7%, 95.4%, and 95.2%, respectively, being statistically similar. According to the EWRS scale, no phytotoxicity was detected on wheat plants treated with the four fungicides.

**Table 5.** European Weed Research Society (EWRS) scale (1–9) to evaluate phytotoxicity in experimental plots inoculated with Karnal bunt and treated with Opus, Folicur, Jewel, and Bemistop in the Yaqui Valley, Sonora, Mexico, during the autumn–winter 2017–18 crop season.

Value	Effect on plant
1	no effect
2	very light symptoms
3	light symptoms
4	symptoms that are not reflected on yield
<b>LIMIT OF ACCEPTABILITY</b>	
5	medium damage
6	elevated damage
7	very elevated damage
8	severe damage
9	complete death
Transformation of the EWRS punctual logarithmic scale to percentage	
Punctual value	Phytotoxicity (%)
1	0.0–1.0
2	1.0–3.5
3	3.5–7.0
4	7.0–12.5
5	12.5–20.0
6	20.0–30.0
7	30.0–50.0
8	50.0–99.0
9	99.0–100

**Table 6.** Mean separation using Tukey's test ( $p = 0.05$ ) of the transformed percentage of Karnal bunt infected grain in spikes treated with Opus, Folicur, Jewel, and Bemistop during the autumn–winter 2017–18 crop season in the Yaqui Valley, Sonora, Mexico.

Treatment	Infected grain		Mean separation
	Real	Transformed	
Opus	0.44	4.73	A
Jewel	0.56	4.70	A
Bemistop	1.11	5.91	A
Folicur	1.12	5.13	A
Untreated check	23.9	25.6	B

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## ITEMS FROM THE RUSSIAN FEDERATION

**AGRICULTURAL RESEARCH INSTITUTE FOR THE SOUTH-EAST REGIONS  
(ARISER)****Department of Genetics, Laboratory of Genetics and Cytology, 7 Toulaiikov St., Saratov,  
410010, Russian Federation.*****Enlarging the bread wheat gene pool in 2017 by introgressing desirable genes from alien species  
at ARISER, Russian Federation.***

S.N. Sibikeev, A.E. Druzhin, L.T. Vlasovets, T.D. Golubeva, and T.V. Kalintseva.

We found that 107 samples from the collection of the Heilongjiang Academy of Agricultural Sciences, PR China, were resistant to the leaf pathogens under severe epidemics of leaf rust and leaf blotch; 10 samples has an IT = 0, 7 had an IT = 1, 17 had an IT = 2, and the remaining lines (73) showed an IT = 3–4. To leaf blotch, all (107) samples were resistant, with the percent lesion from 0 to 5%. By hybridization analysis in one sample, Kefen 12 was found to be resistant to leaf rust that is inherited by two dominant, complementary genes. In the *T. turgidum* subsp. *dicoccum* lines, resistance to leaf rust and leaf blots were confirmed in k10456, k12133, k13659, k19352, k19357, and k40030, all with an IT = 0–1. In hybrids between samples k10456 and k13659, the resistance to leaf rust is dominant. In a set of lines with different chromosomes of *Ae. columnaris* k1193, the ITs to leaf rust were chromosome 2U = 2–3; 3U = 0; 6U = 3; 1X = 3; 3X = 3; 5X = 2; 6X = 0; 6XS = 0; 5X–6X = 0; 6X–3X = 0; 3X–5X–6X = 0; and 7US–6XS = 0. Chromosomes 3U and 5X are normally (without deviations) transmitted in the offspring of hybrids.

***The reaction of introgression lines of spring bread wheat to leaf rust and leaf blotch in 2017.***

S.N. Sibikeev, A.E. Druzhin, T.L. Vlasovec, T.D. Golubeva, and T.V. Kalintseva.

Under severe epidemics of leaf rust and leaf blotch, the sets of the original NILs with a combination of alien translocations, a set of introgression lines with genetic material from various wheat relatives, and lines derived from crosses of CIMMYT synthetics with Saratov-bred cultivars were evaluated. The effect of double substitution 3B (3Age) and 3D (3Age) chromosomes from *Th. elongatum* in the cultivar Saratovskaya 29 for resistance to leaf blotch was detected. In the substitution lines, we observed 0% affected leaves and, in the recipient cultivar, 40%. The all introgression lines were resistant to leaf rust with an IT = 0–0;

For the NILs, a statistically insignificant decrease of grain productivity was detected for translocations T7DS–7DL–7Ae#1L + T1BL–1R#1S, T7DS–7DL–7Ae#1L + T6BS–6BL–6U#1L, T7DS–7DL–7Ae#1L + T3DS–3DL–3Ae#1L, T7DL–7Ae#1L + 4TBS–4BL–2R#1L, T7DL–7Ae#1L + T2AL–2AS–2MV#1, and T4AS–4AL–7S#2S. At the same time, an insignificant increase for grain yield was observed in NILs with the 6D (6Agi) substitution and significant for lines of Saratovskaya 29 with the substitutions 3B (3Age) and 3D (3Age) and a T7DL–?Age translocation. Among the introgression lines, the maximum grain productivity (5,382 kg/ha) was observed in line L449/16 (a combination of translocations T7DS–7DL–7Ae#1L + T1BL–1R#1S and substitution 6D (6Agi)); the standard cultivar Favorit was 4,922 kg/ha (substitution 6D 6Agi only). A significant increase in grain yield was obtained in line L609/16 (pedigree ‘Favorit/*T. turgidum* subsp. *persicum*), 4,808 kg/ha compared to 4,317 kg/ha in Favorit.

Long-term data analysis of the influence of the 6D (6Agi) substitution in sib pair NILs of L400R (6D (6Agi)) and L400S (6D 6D) showed that substitution 6Agi for 6D significantly increases the period between germination and flowering, plant height, number of productive stems/m<sup>2</sup>, spike length, and number of grain/spike, almost no effect on the weight of grain/spike, and significantly reduces the 1,000-kernel weight. A comparative analysis of lines L400R and L400S for protein content and gluten quality, flour strength, SDS, dough elasticity, and baking properties, showed that, on average, protein and gluten contents were significantly higher in line L400R than in those of the L400S sibs. Furthermore, we noted a positive influence of the presence of the 6Agi (6D) substitution for SDS sedimentation. For bread

making parameters, such as gluten strength, volume of bread, dough elasticity (P), and flour strength (W), the 6D (6Agi) substitution did not have a significant influence.

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### *The effect of aluminum ions, potassium, and their combined effect on the growth of wheat plants in vegetation experiments.*

Nina V. Poukhalskaya.

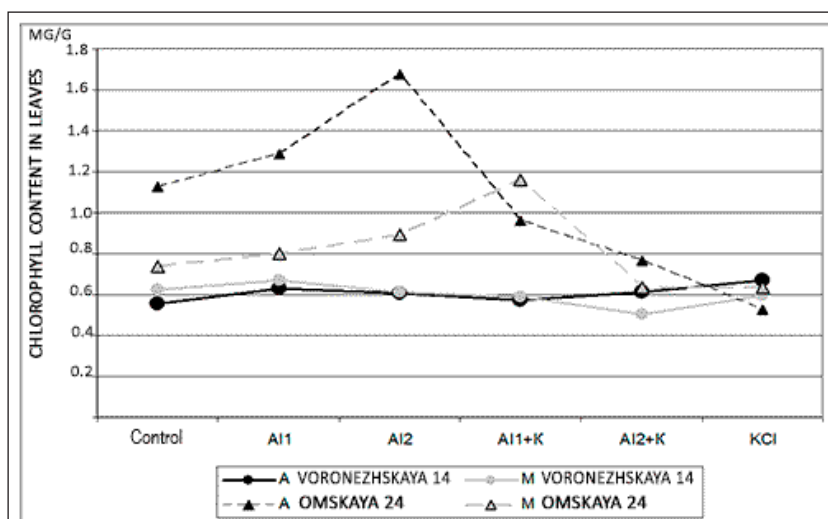
We used two concentrations of aluminum in vegetation experiments; 1 mg/100 g of soil (low) and 4.3 mg/100 g of soil (high). Our purpose was to determine how the photosynthetic apparatus reacts to aluminum toxicity. The reaction of plants to aluminum is ambiguous and can manifest itself by activating the growth of the vegetative part of wheat cultivars at low concentrations. Wheat cultivars were divided into two groups, those distinguished by high activity of the root system (biotype A) and those with decreased activity of the root system (biotype M). The division of the biotypes within a single cultivar is made on the basis of the acidifying activity of the root system, i.e., the acidification activity of root system (Poukhalskaya et al. 2006, 2008). We tested the spring wheat cultivars Voronezhskaya 14 and Omskaya 24.

**Results.** At the 3-leaf stage in biotype A, those with high activity of the root system, larger leaf areas were observed than in plants of biotype M. The leaf surfaces of plants of biotypes A and M of Voronezhskaya 14, compared with other cultivars, in the presence of aluminum in the soil, increased markedly (by an average of 46.8%) compared to those of the control; and 26.5% have a larger area than the plants of biotype M. When potassium is added to soil with aluminum, the leaf area in all cultivars decreased, especially in plants with a less active root system (biotype M).

This reaction to potassium salts deserves attention, because the presence of potassium ions in the soil could compensate for the negative effect of aluminum. However, this does not happen, and plants subjected to edaphic stress in the presence of aluminum ions in the soil solution show a decrease in growth processes with the addition of potassium ions. In response to aluminum ions, wheat plants initiate growth, but when potassium is added, this gain is not observed.

Similar to the development of the area of the assimilative surface, chlorophyll content also changes, increasing in plants in the presence of aluminum (Fig.1). Of the two cultivars represented differing in sensitivity, the content of chlorophyll increases in plants of the active group of Omskaya 24, the cultivar less sensitive to aluminum. No significant differences were found in plants of Voronezhskaya 14. Adding potassium to aluminum led to a decrease in the chlorophyll concentration to that of the level of the control. The data indicate that potassium nutrition can reduce the effect of aluminum in the soil.

The increase in the assimilative surface of wheat leaves in the presence of aluminum is an adaptive mechanism



**Fig.1.** Chlorophyll content in leaves of biotypes A (high activity) and M (low activity) of spring wheat cultivars Voronezhskaya 14 and Omskaya 24 in the presence of aluminum salts and potassium ions (mg/g dry weight).



by which plants try to compensate for the effect of stress in soils with aluminum ions. The answer to the question is whether or not such a strategy effects only yield. In the vegetative experiments, an increase in yield was obtained in variants with low doses of aluminum, which caused the activation of leaf growth.

The productivity of plants of biotype A of the spring wheat Voronezhskaya 14 in the presence of aluminum is significantly higher than that in biotype M by an average of 37%. Consequently, potassium ions can reduce the response of plants to stress. However, this leads to a decrease in productivity, since timely compensatory reactions do not develop that allow the plant to adapt to unfavorable conditions. The same effect of aluminum was observed in Omskaya 24. Here, the productivity surge falls on a higher dose of aluminum, but when potassium is added to aluminum, productivity is again reduced by 16% (biotype A) and by 31% (biotype M). Plants with a less active root system suffered more from the addition of potassium to the soil in the presence of aluminum than the plants of the biotype with a more active root system.

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## VAVILOV INSTITUTE OF GENERAL GENETICS – RUSSIAN ACADEMY OF SCIENCES

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### *Genotype analysis of a spring-type cultivars of common wheat carrying the Lr13 gene for the presence of the Ne2<sup>m</sup> gene.*

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Hybrid necrosis is caused by two complementary genes *Ne1* and *Ne2* (Kostyuchenko 1936; Hermesen 1960) located on chromosomes 5BL and 2BS, respectively (Tsunewaki 1960; Nishikavaki 1974). For each of these genes, a series of alleles are known: *Ne1<sup>w</sup>*, *Ne1<sup>m</sup>*, and *Ne1<sup>s</sup>* and *Ne2<sup>w</sup>*, *Ne2<sup>wm</sup>*, *Ne2<sup>m</sup>*, *Ne2<sup>ms</sup>*, and *Ne2<sup>s</sup>* (Hermesen 1963). A combination of these genes in the hybrid causes lethality or sublethality in the plants. McIntosh et al. (1995) showed that *Lr* genes, including *Lr13*, that are responsible for wheat leaf rust resistance, also are located on chromosome 2B. During crossing of the tester cultivar of the *Ne1<sup>s</sup>Ne1<sup>s</sup>ne2ne2* genotype lacking *Lr13* with the *Lr13*-carrier, the *Ne2<sup>m</sup>* gene usually was identified. Determination of the genetic distance between the *Lr13* and *Ne2<sup>m</sup>* genes showed that the recombination coefficient was 33.27±4.12% (Anand et al. 1991). As a result, we conclude that because the linkage is weak, the presence of the *Ne2<sup>m</sup>* gene cannot be used to identify *Lr13*.

However, Zhang et al. (2012) reported on the relationship of *Lr13* and hybrid necrosis gene *Ne2<sup>m</sup>* postulating that these genes are not only tightly linked, but that *Lr13* and the *Ne2<sup>m</sup>* allele are the same gene. Thus, wheat cultivars, noncarriers of hybrid necrosis genes, do not have the *Lr13* gene in their genotype either. To check this idea, we selected spring-type cultivars of common wheat carrying the *Lr13* gene (Table 1). These cultivars were crossed with the cultivars Marquillo (*Ne1<sup>s</sup>Ne1<sup>s</sup>ne2ne2* genotype) and Balaganka (*ne1ne1Ne2<sup>s</sup>Ne2<sup>s</sup>* genotype). The development of hybrid necrosis symptoms or their absence in the first and second hybrid progeny was recorded in the field at different growth stages.

Cultivar	Pedigree	Reference indicating the presence <i>Lr13</i>
Druzhdina	PV-18 / Saratovskaya-29	Singh et al. 1995
Erythrospermum-652	PV-18 / Saratovskaya-36	Vyushkov 1998
Erythrospermum-603	PV-18 / Dimitrovka-14	Vyushkov 1998
Lutescens-576	PV-18 / Dimitrovka-14	Vyushkov 1998
Krestyanka	Saratovskaya-46 / Merit	Singh et al. 1995

The presence of the *Ne2<sup>m</sup>* gene was shown only in the cultivar Lutescens-576 (genotype *ne1ne1Ne2<sup>m</sup>Ne2<sup>m</sup>*), whereas cultivars Druzhina, Erythrosperrum-652, Erythrosperrum-603, and Krestyanka are noncarriers of hybrid necrosis genes (genotype *ne1ne1ne2*), proving that the *Lr13* gene and the *Ne2<sup>m</sup>* allele are not the same gene.

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#### *Response of bacteria-treated wheat seedlings to osmotic stress.*

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Culturing plant cells and tissues *in vitro* is effective for modeling various biological processes under artificial, independent conditions. The effect of stressors, including drought, which is modeled with polyethylene glycol (PEG), largely depends on the biological characteristics of the plant species, the magnitude of the stress, and attendant factors, such as plant-associated microorganisms. Plant growth-promoting rhizobacteria (PGPR) are important in the life of the host plant. They supply the plant with additional mineral and organic nutrients, phytohormones, and available nitrogen. They also participate in the competitive bioregulation of microbial associations in soil and induce systemic resistance of the plant to abiotic and biotic factors of the external environment (Bashan et al. 2014; Maksimov et al. 2011; Tkachenko et al. 2015). The proposed mechanisms used by PGPR to protect plants from these stressors include the production of phytohormones, ACC-deaminase, and exopolysaccharides. Bacteria also affect proline levels in plants, which is a universal osmoprotector and antioxidant (Garcia et al. 2017).

We evaluated the effect of *Azospirillum brasilense* strain Sp245, a growth-promoting associative rhizobacterium, on the physiological and morphological parameters and the content of proline in wheat seedlings under conditions

of osmotic stress in culture *in vitro*. There were four experimental treatments: a control without application of bacteria and osmotic stress (control 1); bacteria without stress (control 2); a variant without bacteria with osmotic stress (control 3); and a variant with bacteria and stress (experiment).

In the first stage, explants (embryos isolated from mature wheat grains) were cultivated on hormone-free Murashige and Skoog (MS) liquid media (Murashige and Skoog 1962). On the 5th day, a bacterial suspension, prepared according to Döbereiner and Day (1976), was added to the tubes at a concentration of  $10^6$  cells/mL. After 3 days, the medium was replaced with another of similar composition but with 5% polyethylene glycol (PEG, Mm 6000). The stress lasted 5 days, after which the nutrient medium with PEG was again replaced by the standard MS medium. At 5 days after the stress was removed, the repair efficiency was evaluated. The following morphological-physiological variables were determined: length of the leaf, number of roots, average root length, wet weight of the roots, and raw weight of the shoot. Proline in plant parts (roots and leaves) was determined colorimetrically according to a standard procedure (Bates et al. 1973). The results were processed by ANOVA with calculation of the least significant difference (LSD) and with multiple comparisons by the Duncan test at a significance level of 95% ( $p \leq 0.05$ ).

We found that, under optimal growth conditions, inoculation with bacteria led to a 37% increase in leaf length in wheat seedlings. The wet weight of the leaves and roots of the seedlings under the influence of the bacteria increased approximately 1.7 times. The addition of PEG to the nutrient medium (5%) caused a significant inhibition of growth in the wheat seedlings, especially root growth, to the point of death. The proline content in the leaves and roots increased significantly under the influence of stress in both the control and the experiment (Table 1).

**Table 1.** Influence of *Azospirillum brasilense* Sp245 on physiological and morphological variables in wheat seedlings and the proline content in the leaves and roots of stressed plants.

Treatment		Leaf length (cm)	Root number (pcs)	Average root length (cm)	Leaf weight (mg)	Root weight (mg)	Proline content ( $\mu\text{mol} / \text{g}$ of wet weight)	
Designation	Presence of bacteria or PEG						leaf	root
Control 1	– bacteria – PEG	5.13a	2.90	1.43	327.00 a	83.00 a	1.000 a	102.000 a
Control 2	+ bacteria – PEG	7.03b	3.53	1.53	87.30 b	22.30 b	0.820 a	1.330 a
Control 3	– bacteria + PEG	3.93a	3.20	1.23	50.70 a	3.67 a	7.060 bc	4.090 bc
Experiment	+ bacteria + PEG	4.17a	3.37	1.63	35.70 a	3.33 a	8.700 c	5.700 c
$F_{\text{fact}}$	–	7.31 *	1.85	1.05	6.94 *	32.50 *	39.802 *	8.602 *
$LSD_{0.05}$	–	1.81	–	–	33.00	5.41	2.240	2.658

**Table 2.** Influence of *Azospirillum brasilense* Sp245 on physiological and morphological variables of wheat seedlings and the content of proline in the leaves and roots of plants during after-stress repair.

Treatment		Leaf length (cm)	Root number (pcs)	Average root length (cm)	Leaf weight (mg)	Root weight (mg)	Proline content ( $\mu\text{mol} / \text{g}$ of wet weight)	
Designation	Presence of bacteria or PEG						leaf	root
Control 1	– bacteria – PEG	3.13 a	4.33	1.20	46 b	3.10 a	6.740	5.460 a
Control 2	+ bacteria – PEG	6.13 b	5.27	1.40	106 d	14.90 b	3.470	3.870 a
Control 3	– bact. + PEG	1.77 a	3.23	1.17	24.7 a	4.00 a	9.410	16.200 c
Test	+ bacteria + PEG	2.57 a	4.00	0.90	57.7 c	6.00 a	9.650	13.900 bc
$F_{\text{fact}}$	–	9.21 *	4.71	2.0	280 *	16.90 *	0.210	31.507 *
$LSD_{0.05}$	–	2.17	–	–	7.12	4.56	–	3.756

During after-stress repair in the presence of the bacteria, the wet weight of the leaves of wheat seedlings increased 2.3 times, as compared to the control samples (control 3) (Table 2, p. 38). The level of proline continued to rise within 5 days after the removal of the stress (Table 2).

Thus, *Azospirillum brasilense* Sp245 bacteria promote the growth in wheat during culture *in vitro* as well as during repair under model conditions of osmotic stress. Increasing the adaptation potential of plants in purposefully created plant-microbial associations seems promising from the point of view of general approaches to ecologically friendly agriculture.

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## ITEMS FROM UKRAINE

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### *Breeding hexaploid triticale (x. Triticosecale Wittmack) with high bread-making quality.*

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**Summary.** Results (1980–2017) of breeding the hexaploid triticale for increase of adaptability, productivity, and grain quality are presented. Using intraspecific hybridization of the lines showing contrast for growth habit in interzonal tests of populations, lines, and cultivars, a winter and alternate triticale with high baking properties were created.

Breeding hexaploid triticale is aimed at increasing productivity, stability, and improving grain quality with retention of a complex of adaptive properties. Triticale cultivars created in Poland, Russia, Romania, Belarus, and other countries successfully compete with wheat, rye, and barley, and exceed their grain yield/ha by 20–30% (Grabovets 2010). In Ukraine, triticale cultivars specialized for a destination are introduced into agrarian production differing significantly in economic valuable signs (Schipak 2016; Schipak et al. 2017). Fodder triticales Amphidiploid 256, Garne,

Bouquet, and Shalanda, which spread to all agroecological zones of Ukraine, ensure high grain yields (7.5–10.5 t/ha) and a green crop (45–65 t/ha). Cultivars for food and universal appointment Amos, Nicanor, Raritet, Plastun volynskiy, and Yaroslava are characterized by good and excellent gluten quality and dough and bread grain productivity of 8.5–11.5 t/ha. These cultivar groups are semi-intensive types and are well adapted to a complex of adverse factors of wintering and vegetation. Nevertheless, they are prone to lodging in abnormally damp years, which reduces yield capacity, especially on rich soils. For these conditions, triticale cultivars with a plant height of 85–100 cm were created. Triticale with a high-yield capacity and shorter stem were created in Poland, Romania, Slovakia, and the Russian Federation. However, they lag behind local cultivars with medium stem height for grain productivity and quality in the drought conditions of the Steppe and Forest-steppe of Ukraine.

Our research was to create a gene pool of short-stem triticale with high productivity potential and improved grain quality, forming multiline triticale cultivars with a stem length of 85–105 cm, elastic-strong and, at the same time extensible, and balanced at a high-gluten level that is necessary for producing high-quality bread without the need for improvers.

**Materials and methods.** Hybrid populations were created by crossing the hexaploid triticale of various eco-geographical origin and growth habit. Selection for a complex of adaptive and economically valuable traits was carried out in contrasting conditions. Evaluating the populations and lines for resistance to drought, heat, and germination at grain ripening stage and grain quality was carried out in the droughty Steppe region of Ukraine (Seaside Experimental Breeding Station, Yalta, southern Donetsk Region). Hybrids and breeding material were evaluated for productivity, quality, and resistance to adverse factors of wintering and vegetation in the zones of western Forest (Volynskaya Experimental Station, Rokini) and eastern Forest-Steppe regions (Plant Production Institute named after V.Ya. Yuryev). In the  $F_3$ – $F_4$  generation, protein content, starch, carotenoids, sedimentation, grain hardness, and falling number were defined. After the  $F_4$  generation, a full technological analysis was made. Grain and flour quality and baking properties were determined as defined by Methodical recommendations (Leonov et al. 2011), without the application of improvers. Grain samples were ground in a MLU 202 milling apparatus to 67–70% flour. Recipe dough was 100 g of flour at 14% humidity, 1.3 g dry yeast, 4.5 g of sugar, 1.5 g of salt, and water at absorption farinograph. Glutenin electrophoresis was carried out in the Wibex laboratory (Poland).

**Results and discussion.** Hexaploid triticale is a unique crop with grain suitable for production of various foodstuffs, including high-quality bread. Among the European countries, Ukraine is one of the greatest consumers of bread. About 42% of protein in the Ukrainian diet come from wheat bread. This type of bread, however, is insufficient in lysine, one of the most important amino acids. Bread with increased lysine content can be produced from the cereal crop triticale. The future of this bread highly depends on the availability of suitable triticale cultivars with high productivity, adaptability, and increased grain protein and lysine content, in combination with increased bread-making quality. White and whole meal triticale bread is preferred by a large number of people who suffer from obesity, hypertension, and diabetes. This study examines the suitability of new triticale cultivars for use in the production of triticale bread.

From the correlation analysis of quality indexes of grain, dough, and bread in 7,300 samples of triticale with average and tall stem height for 1983–95, only some of the baking properties had an essential influence (Table 1, p. 41). Loaf volume was influenced positively by crumb porosity ( $r = 0.42$ ), grain vitreousness ( $r = 0.53$ ), and gluten content ( $r = 0.41$ ). The general baking value had a strong negative dependence on gluten content ( $r = -0.71$ ), DIG index ( $r = -0.77$ ), and gluten quality ( $r = -0.66$ ). A positive, average correlation is shown between general baking value and flour strength ( $r = 0.40$ ) and dough elasticity ( $r = 0.51$ ). Bread quality is determined to the greatest extent by crumb porosity ( $r = 0.90$ ). Flour strength, as an important index of flour and gluten quality, has a reliable, positive influence on porosity ( $r = 0.43$ ) and general baking value ( $r = 0.40$ ). The connections between flour strength and gluten quality ( $r = 0.51$ ), dough elasticity ( $r = 0.66$ ), and tensile properties ( $r = 0.67$ ) were stronger.

Winter triticale with a high gluten content is characterized by weak gluten quality, inelastic blurring dough ( $r = -0.42$ ), made bread with poor porosity ( $r = -0.46$ ), and had a low general baking rating ( $r = -0.71$ ). A broad search of triticale lines with large gluten yields, which occurred in the 1970s and 1980s, did not lead to the creation of triticales with high baking properties. The limits of the gene pool of the crop and the blocking corresponding wheat loci by the rye genome are not what theoretically prevented the possibility of synthesizing of triticale with unique qualities of a gluten. During breeding of baking triticales, the search should be expanded for hybrid combinations with the minimum negative influence of rye chromosomes. Selecting lines with complementary interactions between the wheat and rye genomes should be carried out among forms not only with low gluten content but with high rates of elasticity and tensile proper-

**Table 1.** Mean values for morphological and technological traits of hexaploid triticale and wheat during 2014–17 (\*= spring crop; \*\*= autumn crop).

Cultivar	Plant height (cm)	Yield capacity (t/ha)	Grain protein (%)	Gluten in flour (%)	GDI units	Falling number (sec)	Dough elasticity (mm)	Tensile strength of dough (mm)	Flour strength (ua)	Loaf volume (mL)	General bread making rating point
<b>WINTER TRITICALE</b>											
Amphidiploid 256 (standard)	136	5.61	12.30	16.7	82	206	39	37	57	473	6.6
Raritet (standard)	125	6.87	11.52	17.4	55	254	71	74	194	627	9.0
Shalanda	138	7.64	12.27	14.8	117	156	46	51	55	465	6.5
Bouquet	139	7.95	11.85	16.9	75	208	48	62	98	486	8.1
Nikanor	127	8.02	11.62	18.5	55	195	69	78	180	590	8.5
Amos	123	7.33	11.48	16.9	58	246	75	79	203	640	9.0
Timofey	92	9.94	11.67	17.0	54	152	84	81	210	698	8.7
Pudik	90	10.14	11.39	20.3	45	226	81	77	226	727	9.0
Yelan	94	10.36	11.87	19.0	50	199	72	77	229	800	9.0
<b>ALTERNATE TRITICALE</b>											
Yaroslava *	98	3.72	12.80	22.0	68	180	58	65	132	498	8.3
Yaroslava **	125	8.68	12.18	20.4	63	203	65	77	157	617	8.7
Aleksandra *	102	4.10	12.69	21.8	65	178	84	62	156	600	8.5
Aleksandra **	128	8.56	12.06	18.6	50	206	88	57	196	640	8.6
<b>SPRING TRITICALE</b>											
Aist x *	102	3.01	12.96	21.5	70	231	57	64	124	417	6.6
Aist x **	135	6.14	12.34	19.0	70	207	71	50	131	440	7.1
Hlibodar *	112	3.32	12.04	23.4	70	197	57	66	129	426	7.4
Darthliba *	116	3.51	12.02	17.0	63	183	56	55	109	490	7.6
<b>WINTER WHEAT</b>											
Podolyanka (standard)	102	6.25	12.44	27.0	63	263	72	69	207	657	8.8
HIP <sub>05</sub>		0.43									

ties of dough, thus achieving a balance in the gluten complex at a high level. For this purpose, from 1980 to 2017, 16,300 combinations, including 67.9% intraspecific crossings, were made. Based on the hybridization of ‘triticale 2n=42/2n=42’ with various growth habits, we created and transferred to state testing 26 cultivars from which two, Yunga and Stepan, were not registered.

Crossing the tall, winter cultivar Amphidiploid 3/5 with the average-height, spring triticale line L-5, created earlier by selection from the combination ‘GTA418/Amphidiploid 206’, was executed in 1980. The hybrids were tested during by alternating spring crops with autumn ones, leading to the creation of alternative triticale with high winterhardiness (Schipak 1998). The short-stem, productive line of alternative growth habit, D77/75, was selected from triticale D77 and was widely used in crosses. In the F<sub>1</sub> population (spring triticale Kharkivskiyi 41/D77/75), we

**Table 2.** Physical properties of dough and bread volume of triticale and wheat during 2014–17.

Cultivar	Country	Flour strength (au)	Water absorption (%)	Formation time (min)	Dough				General valorimetric value (uv)	Loaf volume (mL)
					Resilience (min)	Resistance (min)	Stability (min)	Softening (uf)		
Amphidiploid 256 (standard)	Ukraine	57	56.0	1.95	2.29	4.24	4.03	156	48	473
Raritet (standard)	Ukraine	194	55.1	2.65	6.46	9.17	9.10	87	74	627
Markiyan	Ukraine	180	57.0	2.45	4.23	6.44	7.73	99	71	610
Nikanor	Ukraine	180	57.6	2.98	3.50	5.98	7.15	105	69	590
Amos	Ukraine	203	54.1	2.50	6.50	9.00	9.15	82	78	640
Yaroslava	Ukraine	157	59.0	2.50	4.00	5.62	6.45	140	61	617
Timofey	Ukraine	210	53.4	2.85	10.75	13.60	15.15	81	84	698
Pudik	Ukraine	226	55.5	3.20	12.50	15.70	17.20	62	90	727
Yelan	Ukraine	229	54.8	2.90	10.50	13.40	13.85	75	86	800
Valentin 90	Russia	140	57.8	1.99	3.00	5.45	4.66	140	57	490
Hermes	Russia	59	48.0	1.80	0.50	2.30	3.00	140	34	420
Kapriz	Russia	93	58.3	2.33	2.75	5.08	5.00	169	55	465
Kroha	Russia	20	49.8	2.00	1.00	3.00	4.00	210	25	390
Lamberto	Poland	102	57.9	1.30	3.00	4.30	5.00	220	49	420
Pawo	Poland	65	55.6	2.10	2.03	4.27	3.47	180	48	390
Domital	Poland	39	49.8	2.20	2.00	4.20	4.80	160	34	430
Baltiko	Poland	39	54.0	1.80	1.50	3.30	5.40	170	32	360
Titan	Romania	26	49.2	1.90	1.30	3.20	3.20	190	39	390
Goron	Romania	52	50.0	1.50	0.50	2.00	3.70	185	30	420
Stil	Romania	39	53.0	2.00	1.20	3.20	4.00	200	39	400
Kandur	Slovakia	26	51.6	1.90	1.10	2.90	4.00	170	29	390
Amphidiploid 206	USSR	103	55.1	2.10	0.50	2.60	1.50	220	34	467
Podolyanka (soft wheat)	Ukraine	207	59.7	2.82	10.20	13.07	15.47	73	85	657

selected in 1988 the alternative line D8-192, which was easy threshed and had grain with a wheat morphology.

.....One of the most valuable hybrid combinations, 'F<sub>1</sub> (Amphidiploid 547/D8-192)/spring triticale Aist Kharkivskiy', was made in 1989. From this hybrid, repeated selections in the contrasting conditions of the Forest Steppe and sharply arid Steppe, valuable lines were obtained that have various gluten qualities, from weak to very strong (GDI 45–120 units), falling number (236–394 sec), dough elasticity (40–95 mm), and tensile strength (30–110 mm). The gluten complex was stabilized at a high level by creating a cultivar by association of respective complementary lines. The mixing effect was intensified due to the increased elasticity of dough of some lines and unique tensile ability of other lines (Patent #44901, 2009). The genetic basis of the cultivar Raritet was made by lines with contrasting dough quality indices, a tensile strength to 86 mm and elasticity of 79 mm, which promoted formation of a gluten complex balanced at a high level (P/L = 82/77), increased flour strength (to 222 a.u.), and high-quality bread without improvers (550–600 mL). The cultivar was transferred to the State Test in 2004 and registered in 2008.

The new cultivar Raritet is distinguished by an increased productivity in all zones, immunity to diseases, and steadily high baking properties (Schipak et al. 2013). The wide use of

the Raritet in intraspecific crosses revealed its extraordinary combining ability, including quality of gluten, dough, and bread. Raritet offered new opportunities to increase the baking properties of triticale, but was limited by very strong but insufficient gluten tensile strength. To improve cultivar for bread making, numerous crosses were made. The most valuable combinations recognized the participation of forms with weak but viscous, excessively extensible gluten, i.e., 'Amphidiploid 206/Raritet', 'Raritet/Valentin 90', and 'Raritet/HAD 7', from which lines with stronger elasticity and tensile strength gluten were selected. On this basis, the following new, multiline cultivars of baking and universal type were created: Amos (registered in 2014), Markiyon (2015), and Nicanor (2016). Creating these cultivars significantly increased the quality of triticale bread; the volume increased to 650 mL at a general baking value of 9.0 points.

Improving triticale competitiveness requires combining increased grain yield with short stem and high baking quality in one cultivar while maintaining complex resistance to unfavorable factors. Such forms were absent in the available assortment. Undersized cultivars from Poland, Romania, Slovakia, and the Russian Federation possess high potential productivity but have weak gluten and are used mainly for fodder and technical purposes. Using perennial tests of the 'Raritet/HAD 7' population in contrasting conditions, we selected consistently highly productive triticale with a plant height of 40–105 cm. Obtaining short-stem forms when crossing tall components is not a unique phenomenon, because the genealogy of Raritet includes forms of triticale and wheat with short stems. The complementation of the initial genotypes with the high rate of dough tensile strength of HAD 7 and the gluten complex elasticity in the Raritet increased probability of selecting, from a rather large sample size, short-stem lines with the excellent baking qualities that were better than that in the parental lines.

In the conditions of 2014–17, the short-stemmed lines of triticale (2,800 samples) from the cross 'Raritet/HAD 7' differed between good and excellent winterhardiness (8.2–9.0 points), had 530–640 ears/m<sup>2</sup>, and were 62–98 cm tall, which is equal to that of the short-stemmed, Polish cultivar Baltiko. In comparison with Raritet, plant height is reduced by 30–50% by shortening of all internodes, primarily the middle ( $I_4$ ) and lower ( $I_5$  and  $I_6$ ), which increased lodging resistance to 9 points. The duration of the vegetative period of the short-stemmed lines corresponds to that of the initial forms (275–278 days). The new triticale inherited somewhat high resistance to smut and foliar-stem diseases. These lines were selected in the acute arid steppe region and show high resistance to heat and form well-filled grain with 1,000-kernel weight of 44.3–62.5 g. In the drought conditions of 2014–17, grain productivity of the best short-stemmed cultivars Timofey, Pudik, and Yelan varied from 8.82 to 10.77 t/ha and averaged 9.94–10.36 t/ha, which exceeds that of the standard cultivars Raritet (by 3.07–3.49 t/ha), Baltiko (by 1.81–2.23 t/ha), and the wheat Podolyanka (by 3.69–4.11 t/ha).

An analysis of the interrelations of 30 morphobiological and technological traits in the short-stemmed cultivars and lines of triticale testifies that all studied traits influence grain quality but make significantly different contribution (Table 2, p. 42). The high bread volume (650–880 mL) relied on 15 traits, including dough stability ( $r = 0.58$ ), its resilience to mixing ( $r = 0.63$ ), and the overall calorimetric estimate ( $r = 0.71$ ). Loaf volume had a close, negative correlation with protein content ( $r = -0.53$ ), dough softening ( $r = -0.54$ ), GDI ( $r = -0.63$ ), and plant height ( $r = -0.72$ ).

Of the 18 general baking traits, the most effective are dough stability and resilience ( $r = 0.69$ ;  $0.70$ ), general calorimetric value ( $r = 0.76$ ), bread volume ( $r = 0.76$ ), crumb elasticity ( $r = 0.82$ ), and bread porosity ( $r = 0.87$ ). Falling number had no significant influence bread volume or the general bakery rating. The greatest number of reliable correlations were the general bakery rating (18), dough softening (20), and bread porosity (21). The probability of predicting with high reliability the bakery qualities of the short-stem triticale depended on a complex of morphological and technological traits was confirmed by the regression analysis was 93%. The interdependence of baking qualities formed the basis of creating genotypes with specific protein–gluten complex quality that were used further when forming multiline cultivars.

Grain properties of short-stem triticale are good to excellent. The test weight varied between 662–804 g/L, grain vitreosity between 17–52%, and grain hardness 76.4–123.0 N. Sedimentation indices (33–40 mL) in the new lines are higher when compared with the fodder triticale Amphidiploid 256 and Pawo (27–31 mL). We observed that the variability in the falling number (73–230 sec) had no essential impact on quality. Short-stem triticale is characterized by low grain protein content (9.8–11.9%), which is at the level of the Raritet parent. Quantity of a gluten in flour of short-stem amphidiploids varies between 10.0–22.0%. Raritet had a gluten output of 16.0–19.3% and wheat was 20.0–27.9%. Short-stem triticale exclusively form elastic and strong gluten: the GDI index varied from 30 to 55 u, with many lines surpassing both bread wheat (63 u) and Raritet (55 u), the best cultivar for this trait.

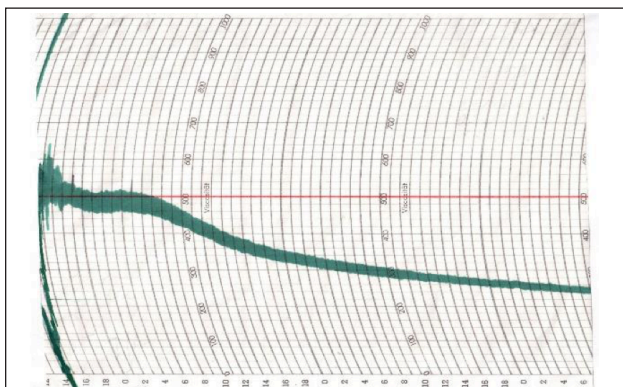
Triticale cultivars differ significantly in flour strength; 55–98 ua in fodder-type, winter triticale and 109–131 ua in spring triticale. Compared with spring amphidiploids, Yaroslava and Alesandra triticale, with an alternate growth



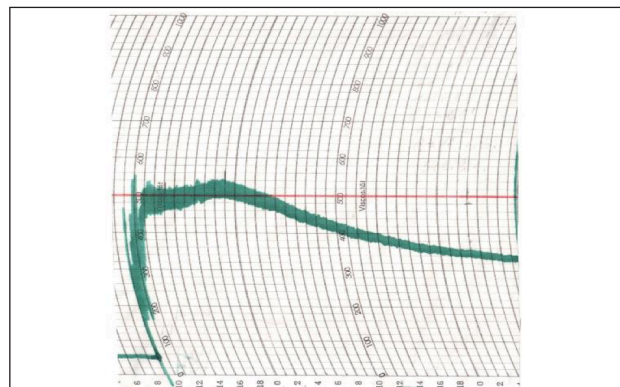
habit, form stronger flour especially when sown in autumn (157–196 ua). According to Shevchenko et al. (1976), the first grain triticale cultivar in the former USSR, Amphidiploid 206, flour strength fluctuated depending on the yearly climate conditions and forecrops (57–95 ua and averaged 72 ua); Mironovskaya 808 wheat was four-times greater at 288 ua. A steady, high value of flour strength was first in the cultivar Raritet. The 10-year average (2001–11) for Raritet was 193 ua, whereas the spring cultivar Aist was 121 ua, the spring wheat Kharkivska 26 was 200 ua, and the winter wheat Odesskaya 267 averaged 319 ua (Schipak et al. 2013). A similar ratio for flour strength in the various cultivars also was observed in 2014–17 (Tables 1 (p. 41) and 2 (p. 42)). The best short-stemmed, winter triticales have an advantage in flour strength compared with that of fodder and earlier cultivars bred for baking. In 2014–17, flour strength in the short-stemmed triticale was 190–353 ua, 57 ua in Amphidiploid 256, 194 ua in Raritet, and 157–262 ua in the winter wheat Podolyanka.

At the present stage of breeding, the important index of bakery qualities of triticale is a balance of dough properties at a high level. In triticale with weak gluten, dough elasticity is very low (39–52 mm). Fodder triticale are more variable for dough tensile strength (37–82 mm). Unlike the cultivars bred for feed, Raritet has a dough balanced at a high level of elasticity and tensile strength, averaging 71 and 74 mm, respectively, with a P/L equal to 1, for 2001–11. In 2014–17, Raritet formed a bread with a volume of 627 mL and a breadmaking rating of 9 points without the use of improvers. The line HAD 7 had a unbalanced dough with an elasticity of 50 and a tensile strength of 88 mm. The short-stemmed triticale lines from the combination ‘Raritet/HAD 7’ had dough elasticity of 72–96 and a tensile strength of 68–89 mm. The cultivars Timofey, Pudik, and Yelan, which were created with the involvement of the best short-stemmed lines, had elasticity–tensile strengths that were steadily high and averaged 84–81 mm, 81–77 mm, and 72–77 mm, respectively, for 2014–17. In the same years, the P/L in Raritet was 71–74 and 72–69 in the winter wheat Podolyanka.

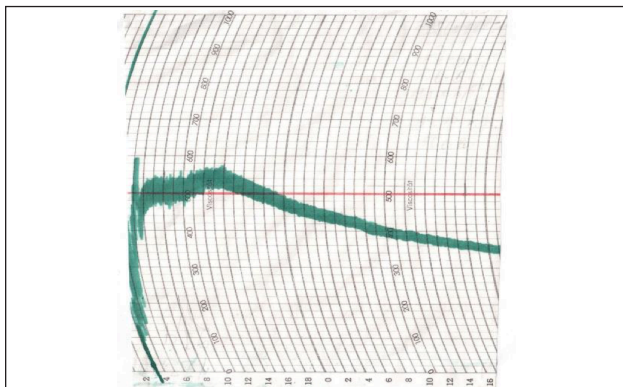
In fodder-type triticale (Amphidiploid 256, Pawo, Baltiko, and Titan), the physical properties of dough are low: formation times 1.30–2.10 min, resilience of 0.50–3.00 min, resistance of 2.00–4.24 min, stability of 3.00–5.40 min, and softening from 156 to 220 uf. The dough in such triticale forms quickly but its stability is five times less and the valorimetric value is twice less than those of strong wheat and baking-type triticales (Figs. 1–3). Thus, farinograms show that foddery-type triticale form a weak dough that is intensively diluted, it is less elastic, excessively plastic, very sticky,



**Fig. 1.** Farinogram of the triticale cultivar Amphidiploid 256 (2016).



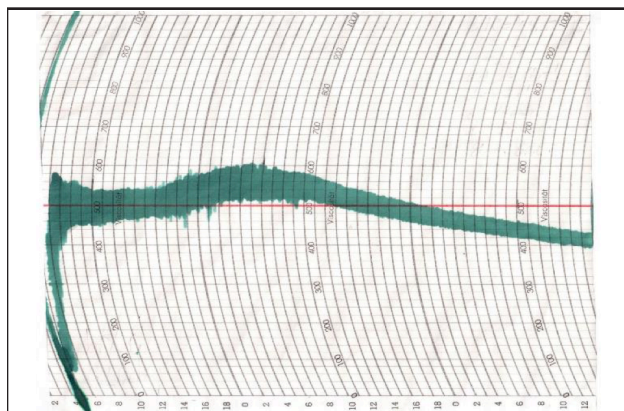
**Fig. 2.** Farinogram of the triticale cultivar Bouquet (2016).



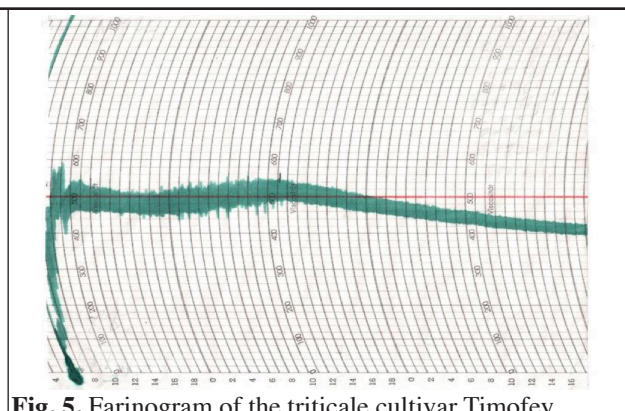
**Fig. 3.** Farinogram of the triticale cultivar Valentin 90 (2016).

and more resembles dough from rye, weak wheat flour, or sprouted, bug-damaged, or defective grain. Bread from the flour of similar triticale produced without improvers is of small volume (360–490 mL) with a condensed, crushed crumb. As a result, the general bread making rating does not exceed 5.5–7.5 points.

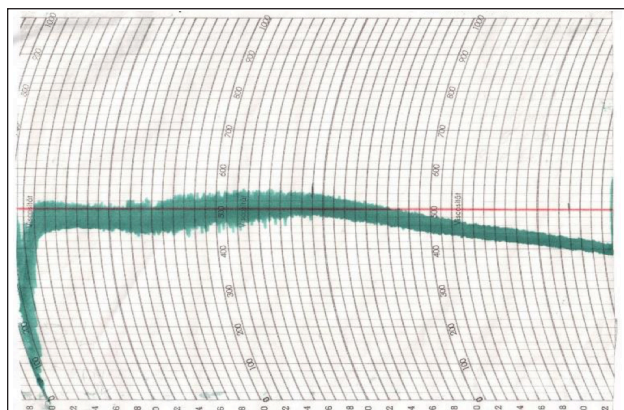
The best short-stem lines and cultivars of triticale have elastic dough, are steady against softening, tensile, and have a high gas-retaining ability, which is not inferior to the farinograms of valuable and strong wheats (Figs. 4–7, p. 45). So, in HAD 69, Timofey, Pudik, and Yelan, time of dough



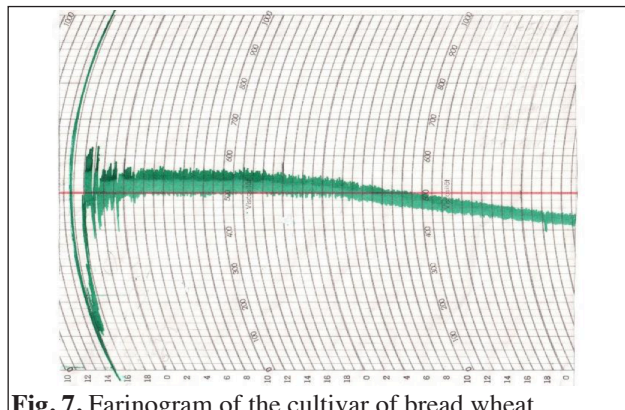
**Fig. 4.** Farinogram of the triticale cultivar Raritet (2016).



**Fig. 5.** Farinogram of the triticale cultivar Timofey (2016).



**Fig. 6.** Farinogram of the triticale cultivar Pudik (2016).



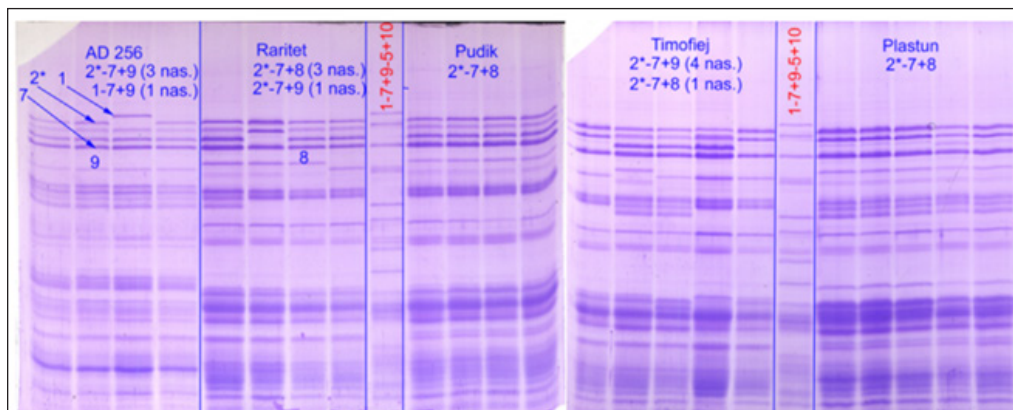
**Fig. 7.** Farinogram of the cultivar of bread wheat Podolyanka (2016).



**Fig. 8.** Bread from flour of triticale (1-3) and wheat (4) cultivars (1 = Amphidiploid 256, 2 = Raritet, 3 = Timofey, and 4 = Podolyanka).

formation is 2.8–3.5 min, resilience is 10.5–12.5 min, resistance is 13.4–15.7 min, stability is 10.5–17.2 min, dough liquefaction is 55–98 uf, and valorimetric value is 84–90 ev. Loaf volume without improvers is 610–880 mL with a general bread making rating of 8.6–9.0 points (Fig. 8). By color and appearance, bread from flour of baking-type triticales is similar to that from wheat but more nutritious, with better flavoring and aromatic qualities.

During the glutenin analysis of the short-stemmed cultivars Timofey and Pudik in comparison with the



**Fig. 9.** Glutenin electrophoresis of triticale cultivars Amphidiploid 256, Raritet, Pudik, Timofey, and Plastun.

standard fodder-type Amphidiploid 256, the parental forms Raritet and HAD 7 (Plastun), are revealed following subunit composition: Amphidiploid 256 has subunits 2\*-7+9 (75%) and 1-7+9 (25%); the maternal Raritet, with a high baking quality, has subunits 2\*-7+8 (75%) and 2\*-7+9 (25%); and

the paternal cultivar HAD 7, characterized by medium baking properties, has subunit 2\*–7+8 (Fig. 9). Timofey, created by combining two short-stemmed lines selected from the ‘Raritet/HAD 7’ hybrid, had two high-molecular subunits 2\*–7+9 (80%) and 2\*–7+8 (20%). The highest gluten quality is in cultivars Pudik and Yelan, having subunit 2\*–7+8. These morfo-biochemical indices, together with a complex molecular and genetic analysis of the expression of the genes defining grain quality, will produce new triticale cultivars capable of forming superfast, elastic gluten with a high-quality bread of volume over 700 mL without improvers. For further research of the nature of quality of strongly connected wheat–rye gluten complex with use of the new approaches, seeds of the best short-stemmed cultivars were sent to the U.S. (J. Dubcovsky, UC Davis), Australia (R. Trethowan, University of Sydney), Poland (H. Woś), Russian Federation (A.I. Grabovets, the Don ZNIISH), and Mexico (H.J. Braun, CIMMYT).

**Conclusions.** As a result of research spanning 1980–2017 for improvement the hexaploid triticale, we created medium-stemmed (Raritet, Amos, and Nicanor) and short-stemmed (Timofey, Pudik, and Yelan) cultivars with a yield capacity of 9.5–12.5 t/ha, complex immunity to disease, bread volume of 650–800 mL without improvers, and a general baking value of 9.0 points, which meet the requirements for valuable and strong wheats.

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## ITEMS FROM THE UNITED STATES OF AMERICA

**KANSAS****KANSAS STATE UNIVERSITY**

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<http://www.agronomy.k-state.edu/people/faculty/kirkham-mb/index.html>

***Mine site rehabilitation with grasses.***

M.B. Kirkham.

The past year has involved editing a book entitled 'Spoil to Soil: Mine Site Rehabilitation and Revegetation' (Bolan et al. 2018). Abandoned mine sites have left a legacy of contamination worldwide. The book presents fundamental and practical aspects of remediation and revegetation of mine sites at locations around the world, including Australia, Canada, Malaysia, New Zealand, and the United States. The Environmental Physics Group at Kansas State University contributed a chapter to the book (Alghamdi et al. 2018) dealing with the remediation of the abandoned lead and zinc mines in the Tri-State Mining District of southeast Kansas, southwest Missouri, and northeast Oklahoma. The District has a history of mining that goes back to the early 1800s. From 1850 to 1950, the District was the world's leading producer of lead and zinc. The mines provided the lead for artillery so that the United States could fight four major wars (Civil War, World War I, World War II, and the Korean War). The mines were closed in 1970. The waste materials around the mines are highly polluted, not only with lead and zinc, but also with cadmium, another heavy metal that co-occurs geologically with zinc. Lead and cadmium are toxic heavy metals. The wastes from these mines have polluted groundwater, rivers, lakes, and soil. Residents in Galena, Kansas, part of the District, have a higher incidence of kidney and heart diseases, skin cancer, and anemia compared to residents in control towns. These results suggest that toxic environmental agents, such as lead and cadmium, are associated with the causation of diseases among the residents.

Because biosolids (sewage sludge) had never been applied to the mine waste materials at Galena for remediation, an experiment was done to see their effect on plant growth and availability of heavy metals. In a greenhouse study, sudex (*Sorghum bicolor* (L.) Moench x *S. Sudanese* (P.) Staph) were grown in the mine waste materials with and without biosolids. Plants grew better with biosolids than without biosolids, and only the plants grown with biosolids produced heads. Plants grown without biosolids were stunted and showed severe heavy metal toxicity. Roots and shoots of plants grown with biosolids had lower concentration of lead and cadmium than roots and shoots of plants grown without biosolids. Organic carbon and phosphorus were increased in the mine waste materials after the addition of the biosolids. The increased growth of the plants grown with biosolids appeared to be due to the organic carbon and phosphorus that the biosolids added to the mine waste materials. They apparently immobilized the heavy metals and made them less available for uptake. The results suggested that biosolids, which are readily available from any town and continually produced, should be added to mine waste materials to revegetate the degraded land.

Although we used sudex, other plants in the grass family (Poaceae) have been used to remediate abandoned mine sites, including (pages in parentheses are those in Bolan et al. 2018) *Cynodon dactylon* (Bermuda grass, pp. 230 and 327), *Avena sativa* (oats, p. 299), barley (*Hordeum vulgare*, p. 299), *Elymus canadensis* (Canada wild rye, p. 299), *Bromus ciliatus* (fringed brome, p. 299), *Koeleria macrantha* (June grass, p. 299), *Festuca saximontana* (Rocky Mountain fescue, p. 299), *Agropyron trachycaulum* (slender wheat grass, p. 299), *Deschampsia caespitosa* (tufted hair grass, p. 299), *Festuca rubra* (creeping red fescue, pp. 301 and 341), *Agropyron cristatum* (crested wheat grass, p. 301), and *Agrostis capillaris* (browntop, p. 341). The book shows that grasses are widely used to rehabilitate and revegetate mine sites.

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**News.**

Dr. Oliver W. Freeman II has accepted a new job and is now Agriculture and Natural Resources Extension Field Specialist/Program Leader, Cooperative Extension Service, Central State University, 1400 Brush Row Road, Wilberforce, OH 45384.

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***Map-based cloning of the Hessian fly resistance gene H13 in wheat.***

Anupama Joshi.

*H13*, a dominant resistance gene transferred from *Aegilops tauschii* into wheat, confers a high level of antibiosis against a wide range of Hessian fly (HF, *Mayetiola destructor*) biotypes. Previously, *H13* was mapped to the distal arm of chromosome 6DS, where it is flanked by markers *Xcfd132* and *Xgdm36*. A mapping population of 1,368 F<sub>2</sub> individuals derived from the cross 'PI372129 (*h13h13*) / PI562619 (Molly, *H13H13*)' was genotyped, and *H13* was flanked by *Xcfd132* at 0.4cM and *Xgdm36* at 1.8cM. Screening of BAC-based physical maps of chromosome 6D of Chinese Spring wheat and *Ae. tauschii* coupled with high-resolution genetic and Radiation Hybrid mapping identified nine candidate genes co-segregating with *H13*. Candidate gene validation was done on an EMS-mutagenized TILLING population of 2,296 M<sub>3</sub> lines in Molly. Twenty seeds per line were screened for susceptibility to the *H13*-virulent HF GP biotype. Sequencing of candidate genes from 28 independent susceptible mutants identified three nonsense and 24 missense mutants for *CNL-1*, whereas only silent and intronic mutations were found in other candidate genes. 5' and 3' RACE was performed to identify gene structure and CDS of *CNL-1* from Molly (*H13H13*) and Newton (*h13h13*). Increased tran-

script levels were observed for the *H13* gene during incompatible interactions at larval feeding stages of GP biotype. The predicted coding sequence of *H13* gene is 3,192 bp, consisting of two exons with 618 bp 5'UTR and 2,260 bp 3'UTR. This sequence translates into a protein of 1,063 amino acids with an N-terminal coiled-coil, a central nucleotide-binding adapter shared by APAF-1, plant R and CED-4, and a C-terminal leucine-rich repeat domain. Conserved domain analysis revealed shared domains in Molly and Newton, except for differences in sequence, organization, and number of LRR repeats in Newton. Also, the presence of a transposable element towards the C terminal of *h13* was indicative of interallelic recombination, recent tandem duplications, and gene conversions in the *CNL* rich region near *H13* locus. Comparative analysis of candidate genes in the *H13* region indicated that gene duplications in *CNL* encoding genes during divergence of wheat and barley led to clustering and diversity. This diversity among *CNL* genes may have a role in defining differences in the recognition specificities of NB-LRR encoding genes. Allele mining for the *H13* gene in the core collection of *Ae. tauschii* and hexaploid wheat cultivars identified different functional haplotypes. Screening of these haplotypes using different HF biotypes would help in the identification of the new sources of resistance to control evolving biotypes of HF. Cloning of *H13* will provide perfect markers to breeders for HF resistance breeding programs and also provide an opportunity to study R-Avr interactions in the hitherto unexplored field of insect-host interactions.

### ***Genetic diversity of wheat wild relative, Aegilops tauschii, for wheat improvement.***

Narinder Singh.

Wheat is perhaps the most important component in human diet introduced since the conception of modern agriculture, which provides about 20% daily protein and calories to billions of people. With expected increase of population to  $9.5 \times 10^9$  by 2050, the risk to food security is imminent. Developing climate-resilient, high-yielding wheat cultivars could mitigate this problem in the wake of changing climate. However, eroding genetic diversity in elite germplasm decelerates wheat improvement. In contrast, untapped genetic diversity in wheat wild relatives, such as *Aegilops tauschii*, can be used to improve wheat for yield, quality, and tolerance to abiotic and biotic stresses. However, selecting and utilizing the wild genetic diversity is no easy task. Over 1,700 genebanks around the world hold more than  $7 \times 10^6$  accessions of these wild relatives, and selecting a few genetically diverse and unique accessions could be a daunting task. We developed and implemented a protocol to identify redundancy in genebanks using genomic tools, and identified over 50% duplicated accessions across three genebanks. After identifying the unique accessions, we selected a MiniCore consisting of only 40 accessions capturing more than 95% of the allelic diversity from 553 *Ae. tauschii* accessions. This MiniCore will facilitate the use of genetic diversity present in *Ae. tauschii* for tolerance to abiotic stresses and resistance to wheat rusts, and Hessian fly. Hessian fly is an important insect pest of wheat worldwide. Some of the strongest HF-resistance genes, such as *H26* and *H32*, were introgressed from *Ae. tauschii*, however, out of 34 known resistance genes, only six have been mapped on the D subgenome. In this study, we mapped three previously known genes, and a gene from *Ae. tauschii* accession KU2147. Genes were mapped on chromosomes 6B, 3D, and 6D. Further, identification and cloning of resistance genes will enhance our understanding about its function and mode of action. In conclusion, wild wheat relatives are genetically diverse species, and utilizing the intact genetic diversity in *Ae. tauschii* will be fruitful for wheat improvement in the wake of climate change to ensure future food security to expected  $2 \times 10^9$  newcomers by 2050.

### ***Efficient curation of genebanks using next-generation sequencing reveals substantial duplication of germplasm accessions.***

Narinder Singh.

Genebanks are valuable resources for crop improvement through the acquisition, ex-situ conservation and sharing of unique germplasm among plant breeders and geneticists. With over  $7 \times 10^6$  existing accessions and increasing storage demands and costs, genebanks need efficient characterization and curation to make them more accessible and usable and to reduce operating costs, so that the crop improvement community can most effectively leverage this vast resource of untapped novel genetic diversity. However, the sharing and inconsistent documentation of germplasm often results in unintentionally duplicated collections with poor characterization and many identical accessions that can be hard or impossible to identify without passport information and unmatched accession identifiers. We demonstrate the use of genotypic information from these accessions using a cost effective next generation sequencing platform to find and remove duplications. We identified and characterized over 50% duplicated accessions both within and across genebank collections of *Ae. tauschii*, an important wild relative of wheat and source of genetic diversity for wheat improvement. A pipeline identifies

and removes identical accessions within and among genebanks and curates globally unique accessions. We also show how this approach can also be applied to future collection efforts to avoid the accumulation of identical material. When coordinated across global genebanks, this approach will ultimately allow for cost effective and efficient management of germplasm and better stewarding of these valuable resources.

### **Genomic analysis confirms population structure and identifies inter-lineage hybrids in *Aegilops tauschii*.**

Narinder Singh.

*Aegilops tauschii*, the D-genome donor of bread wheat, is a storehouse of genetic diversity, and an important resource for future wheat improvement. A genomic and population analysis of 549 *Ae. tauschii* and 103 wheat accessions was performed by using 13,135 high-quality SNPs. Population structure, principal component, and cluster analysis confirmed the differentiation of *Ae. tauschii* into two lineages; lineage 1 (L1) and lineage 2 (L2), the latter being the wheat D-genome donor. Lineage L1 contributes only 2.7% of the total introgression from *Ae. tauschii* for a set of U.S. winter wheat lines, confirming the great amount of untapped genetic diversity in L1. Lineage L2 accessions, overall, had greater allelic diversity and wheat accessions had the least allelic diversity. Both lineages also showed intra-lineage differentiation with L1 being driven by longitudinal gradient and L2 differentiated by elevation. Little data is reported on natural hybridization between L1 and L2. We found nine putative inter-lineage hybrids in the population structure analysis, each containing numerous lineage-specific private alleles from both lineages. One natural hybrid was confirmed as a recombinant inbred between the two lineages. Seven putative hybrids from Georgia carry 713 SNPs with private alleles, which points to the possibility of a novel L1–L2 hybrid lineage. To facilitate the use of *Ae. tauschii* in wheat improvement, a MiniCore consisting of 29 L1 and 11 L2 accessions was developed based on genotypic, phenotypic, and geographical data. This MiniCore reduces the collection size by over 10-fold and captures 84% of the total allelic diversity in the whole collection.



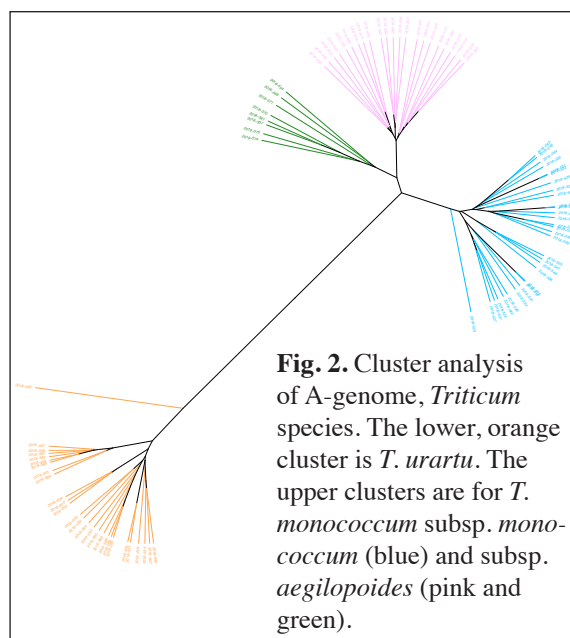
**Fig. 1.** Geographical distribution of the 90 A-genome species used in this study (*T. monococcum* subsp. *aegilopoides* (red), *T. monococcum* subsp. *monococcum* (green), and *T. urartu* (blue).

### **Studying the A genome of wheat using genotyping-by-sequencing.**

W. Jon Raupp, Narinder Singh, Shuangye Wu, Bikram S. Gill, and Jesse Poland.

Following on our analysis of *Ae. tauschii* and *Triticum turgidum* and *timopheevii* subspecies using genotyping-by-sequencing (GBS), we initiated a project on the A-genome species. In a small study, we selected 30 accessions each of the three A-genome species, *T. monococcum* subsp. *monococcum* and *aegilopoides*, and *T. urartu*, from diverse geographical areas (Fig. 1). Because of concern over heterogeneity in an accession, two samples were analyzed for each line, a single plant and a bulk of six plants. The analysis indicated no differences between the results for one versus six plants.

The GBS analysis indicated three separate groups for these species, one group comprised of the *T. monococcum* species and the other of *T. urartu* accessions (Fig. 2). The *T. monococcum* group could further be divided into two groups, one for subsp. *aegilopoides* and one for subsp. *monococcum*.



**Fig. 2.** Cluster analysis of A-genome, *Triticum* species. The lower, orange cluster is *T. urartu*. The upper clusters are for *T. monococcum* subsp. *monococcum* (blue) and subsp. *aegilopoides* (pink and green).

Furthermore, the grouping for subsp. *aegiloides* could further be divided into two groups based on whether they were collected in southern Turkey and Iraq or northern Turkey and Azerbaijan. Two *T. urartu* lines were misidentified and are actually *T. monococcum* subsp. *aegiloides*, which was verified by morphologically also. The remaining A-genome accessions (~800) will be analyzed by GBS this autumn 2018.

### ***Homoeologous recombination in the presence of the Ph1 gene in wheat.***

Dal-Hoe Koo, Wenxuan Liu, Bernd Friebe, and Bikram S. Gill.

A crossover (CO) and its cytological signature, the chiasma, are major features of eukaryotic meiosis. The formation of at least one CO/chiasma between homologous chromosome pairs is essential for accurate chromosome segregation at the first meiotic division and genetic recombination. Polyploid organisms with multiple sets of homoeologous chromosomes have evolved additional mechanisms for theregulation of CO/chiasma. In hexaploid wheat ( $2n = 6 \times = 42$ ), this is accomplished by pairing homoeologous (*Ph*) genes, with *Ph1* having the strongest effect on suppressing homoeologous recombination and homoeologous COs. In this study, we observed homoeologous COs between chromosome 5M<sup>5</sup> of *Aegilops geniculata* and 5D of wheat in plants where *Ph1* was fully active, indicating that chromosome 5M<sup>5</sup> harbors a homoeologous recombination promoter factor(s). Further cytogenetic analysis, with different 5M<sup>5</sup>/5D recombinants, showed that the homoeologous recombination promoting factor(s) maybe located in proximal regions of 5M<sup>5</sup>. In addition, we observed a higher frequency of homoeologous COs in the pericentromeric region between chromosome combination of rec5M<sup>5</sup>#2S:5M<sup>5</sup>#2L and 5D compared to 5M<sup>5</sup>#1/5D, which may be caused by a small terminal region of 5DL homology present in chromosome rec5M<sup>5</sup>#2. The genetic stocks reported here will be useful for analyzing the mechanism of *Ph1* action and the nature of homoeologous COs.

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### **KANSAS WHEAT**

**1990 Kimball Avenue, Manhattan, KS 66502, USA.**

Marsha Boswell.

### ***Kansas Hard Red Winter Wheat Tour 2018.***

**Day 1:** More than 90 people from 30 U.S. states and three countries traveled on six routes between Manhattan and Colby, KS, 1 May, stopping at wheat fields every 15–20 miles along the routes. Many tour participants had never stepped foot in a wheat field before and had only seen these Kansas plains from the window seat of passing airplane. These people are the millers, bakers, food processors, and traders who buy the wheat that Kansas farmers grow. If these fields make



it to harvest, the resulting crop will go into breads, but also a number of other food items, from snack cakes to donuts to seasonings, batters and coatings for fish, chicken and appetizers.

Dan Dogs buys wheat for Kerry Inc., a company that focuses on taste and nutrition to give consumers the foods and beverages they enjoy and feel good about consuming. This is his first time on the tour. Flour millers who grind that wheat into flour for his products and food companies who are his customers are also on the tour. Some of the Kansas wheat he saw today will eventually end up in his food products, such as the breading for chicken strips or similar foods.

Every tour participant makes yield calculations at every stop based on three different area samplings per field. These individual estimates are averaged with the rest of their car mates and eventually added to a formula that produces a final yield estimate for the areas along the routes. Although yields tend to be the spotlight of the Wheat Quality Tour, the real benefit is the ability to network among the 'grain chain.' This tour gives Kansas farmers the chance to interact with and influence their customers around the globe.

The 24 cars of wheat tour scouts made 317 stops at wheat fields across north-central, central, and northwest Kansas, and into southern counties in Nebraska. The calculated yield from all cars was 38.2 bushels/acre, but at the evening wrap-up meeting, tour scouts were quick to point out that this calculation likely is high, attributed to the fact that the wheat is about three weeks behind in development compared to a normal year. Not only that, but the wheat is short, which will make harvesting it difficult. The climate is dry, so without adequate moisture during the grain-fill period, achieving the tour calculated yields will be hard. Head size is determined right after dormancy. In the plants that were split open and examined, heads were small, which will negatively affect yields. Abandoned acres will likely be higher than normal, but how much depends on the next few weeks.

In addition, scouts from Nebraska and Colorado met the group in Colby, KS, to give reports from their states. The estimate for the Nebraska wheat crop is  $43.7 \times 10^6$  bushels, down from  $46.92 \times 10^6$  million bushels last year. The estimated yield average is 43 bushels/acre. In Colorado, the estimated yield was only 35 bushels/acre. Production in Colorado is estimated at  $70 \times 10^6$  bushels, down from  $86.9 \times 10^6$  bushels last year.

**Day 2:** On 2 May, 87 people on the Wheat Quality Council's 2018 winter wheat tour in 21 cars continued their way from Colby to Wichita, stopping in wheat fields along six different routes. One route included a trip to northern Oklahoma as well.

Although everyone thinks of Kansas wheat being used mainly for breads, tour participants from companies such as Tyson Foods use Kansas wheat in its breading for chicken nuggets and other products. These foods are sold directly to consumers through grocery stores and through restaurants such as McDonald's. Other participants included grain companies, flour mills, government agencies, wheat growers, and other food manufacturers.

The wheat tour scouts made 284 stops at wheat fields across western, central, and southern Kansas, and into northern counties in Oklahoma. Many cars experienced severe weather, hail, and limited visibility. A few even reported seeing funnel clouds. Although the weather was concerning, especially to those who had never been to Kansas before, the Kansas wheat fields will certainly benefit from the rainfall.

Scouts reported seeing some disease pressure, mostly in the early stages, including some reports of stripe rust, leaf rust, and barley yellow dwarf and wheat streak mosaic viruses. Short plants and wheat that is consistently 2–3 weeks behind schedule continued. The next few weeks will be critical for the crop. Dr. Romulo Lollato, Kansas State University wheat extension specialist, reported that if weather is similar to 2016, where rains began on 2 May, we could have an average crop. Despite the drought stress that year, grain fill conditions were very good.

The calculated yield from all cars was 35.2 bushels/acre, but at the evening wrap-up meeting, tour scouts again talked about the wheat being behind schedule and very small. Head size has already been determined, and heads will be small this year, affecting final yields. Abandoned acres were scattered along the Kansas routes, but scouts traveling in Oklahoma reported an even higher percentage of fields being grazed by cattle.

Mark Hodges from Oklahoma reported that the state's production is estimated at  $58.4 \times 10^6$  bushels, which is half of a normal crop. While  $4.1 \times 10^6$  acres were seeded last autumn, and only  $2.355 \times 10^6$  acres are estimated to make it to harvest because of drought conditions, poor root systems, few tillers, and small heads.

**Day 3:** The 2018 Wheat Quality Council's Hard Winter Wheat Tour across Kansas wrapped up on 3 May. During the three days of wheat scouting, four participants traveled six routes from Manhattan to Colby to Wichita and back to Manhattan.

The three-day average yield for the fields that were calculated was 37 bushels/acre. An estimated  $7.8 \times 10^6$  acres of wheat were planted in the autumn and most of Kansas has been in a severe drought since October. Tour participants saw wheat that was significantly behind schedule, with most areas three or more weeks behind normal development. Not only that, but the wheat is short, which will make harvesting difficult. Head size is determined right after the wheat comes out of dormancy, and most of the heads were small, which will negatively affect yields. Abandoned acres will likely be higher than normal, but how much depends on the next few weeks.

The official tour projection for total production of wheat to be harvested in Kansas is  $243.3 \times 10^6$  bushels. If realized, this would be about  $90 \times 10^6$  bushels less than last year's crop and the lowest production in Kansas since 1989. This number is calculated based on the average of estimated predictions from tour participants who gathered information from 644 fields across the state.

For more information about what participants saw statewide, search #wheattour18 on Twitter.

## MINNESOTA

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J.A. Kolmer and Y. Jin.

### *Wheat leaf rust in 2017.*

Wheat leaf rust (caused by *Puccinia triticina*) was at low to moderate levels throughout much of the hard red winter, soft red winter wheat, and hard red spring wheat growing regions of the U.S. in 2017. Moisture and temperature conditions throughout much of the southern Great Plains region allowed stripe rust (caused by *P. striiformis*) to spread and increase rapidly, which reduced the available leaf tissue for *P. triticina* to infect. The early and widespread stripe rust infections caused many wheat fields to be sprayed with fungicide, which also reduced the spread and increase of *P. triticina*. The reduced levels of leaf rust in the southern plains resulted in lower amounts of *P. triticina* being carried in the southerly winds to the northern hard red spring wheat region, which resulted in lower severity levels in this region.

Leaf rust caused an estimated 5% loss in wheat in Oklahoma. Estimated losses in other states were less than 1% or are not known.

A total of 65 races were found in the U.S. in 2017 (Tables 1 (p. 54-55) and 2 (p. 56)). Race MBTNB with virulence to *Lr1*, *Lr3a*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, and *Lr14a* was the most common race overall in the U.S. at 11.3% of isolates. This race also was predominant in the soft red winter wheat regions of the southeast and Ohio Valley states. In the soft red winter wheat area, races with virulence to *Lr11* were predominant. In Kansas and Nebraska, race MBDSB with virulence to *Lr1*, *Lr3a*, *Lr17*, *LrB*, *Lr10*, *Lr14a*, and *Lr39*, was the most common race. Race TFTSB, with virulence to *Lr2a*, *Lr24*, *Lr26*, and *Lr11* was the most common race in Texas and Oklahoma. In the southern-mid Great Plains region, races with virulence to *Lr39* were common. In the northern spring wheat area of Minnesota, North Dakota, and South Dakota, race TNBJJ, with virulence to *Lr2a*, *Lr9*, *Lr24*, and *Lr39* was the most common race. Race TBBGS with virulence to *Lr2a*, *Lr21* and *Lr39* also was common in this region.

**Table 1.** Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2017 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, *Lr39*, and *Lr42*.

Race	Virulence combination (ineffective Lr genes)	Southeast		North-east		Ohio Valley		OK-TX		KS-NE		MN-ND-SD		CA		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
		LBDSG	1,17,B,10,14a,28	0	0.0	0	0.0	0.0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	45.5
LCDSG	1,26,17,B,10,14a,28	1	0.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	31	3.6	4	0.9
MBDSB	1,3,17,B,10,14a	0	0.0	0	0.0	0	0.0	3	2.0	.6	0.0	0	0.0	0	0.0	0	0.0	03	0.6
MBDSD	1,3,17,B,10,14a,39	6	5.0	0	0.0	0	0.0	5	4.3	7	17.5	7	5.5	1	50.0	0	0.0	26	5.5
MBDSG	1,3,17,B,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	9.1	2	0.4
MBPSB	1,3,3ka,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	4	3.4	0	0.0	0	0.0	0	0.0	0	0.0	4	0.9
MBPSD	1,3,3ka,17,30,B,10,14a,39	2	1.7	0	0.0	0	0.0	4	3.4	0	0.0	2	1.6	0	0.0	0	0.0	8	1.7
MBTNB	1,3,3ka,11,17,30,B,14a	33	27.5	0	0.0	17	44.7	0	0.0	1	2.5	2	1.6	0	0.0	0	0.0	53	11.3
MCDSB	1,3,26,17,B,10,14a	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MCSD	1,3,26,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	50.0	0	0.0	1	0.2
MCDSG	1,3,26,17,B,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	2.4	0	0.0	6	27.3	9	1.9
MCPSB	1,3,26,3ka,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	2	1.7	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
MCPSD	1,3,26,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	2	1.6	0	0.0	0	0.0	3	0.6
MCTNB	1,3,26,3ka,11,17,30,B,14a	24	20.0	0	0.0	7	18.4	0	0.0	2	5.0	0	0.0	0	0.0	0	0.0	33	7.0
MDBBG	1,3,24,28	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MDPSD	1,3,24,3ka,17,30,B,10,14a,39	4	3.3	0	0.0	0	0.0	0	0.0	0	0.0	2	1.6	0	0.0	0	0.0	6	1.3
MFGJG	1,3,24,26,11,10,14a,28	4	3.3	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	5	1.1
MFGJJ	1,3,24,26,11,10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	2.5	0	0.0	0	0.0	0	0.0	1	0.2
MFGKG	1,3,24,26,11,10,14a,18,28	1	0.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MFJSB	1,3,24,26,11,17,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	1	0.2
MFPSB	1,3,24,26,3ka,17,30,B,10,14a	1	0.8	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	2	0.4
MFPSD	1,3,24,26,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	1	2.6	2	1.7	1	2.5	0	0.0	0	0.0	0	0.0	4	0.9
MFTSB	1,3,24,26,3ka,11,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	1.6	0	0.0	0	0.0	2	0.4
MGPSB	1,3,16,3ka,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	1	0.2
MLPSD	1,3,9,3ka,17,30,B,10,14a,39	3	2.5	0	0.0	0	0.0	1	0.9	3	7.5	2	1.6	0	0.0	0	0.0	9	1.9
MMSD	1,3,9,26,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MMNSD	1,3,9,26,3ka,17,B,10,14a,39	1	0.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MMPSD	1,3,9,26,3ka,17,30,B,10,14a,39	1	0.8	0	0.0	0	0.0	1	0.9	0	0.0	1	0.8	0	0.0	0	0.0	3	0.6
MNPSD	1,3,9,24,3ka,17,30,B,10,14a,39	5	4.2	0	0.0	0	0.0	9	7.7	6	15.0	10	7.9	0	0.0	0	0.0	30	6.4
MPDSD	1,3,9,24,26,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MPPSD	1,3,9,24,26,3ka,17,30,B,10,14a,39	3	2.5	0	0.0	1	2.6	16	13.7	5	12.5	12	9.4	0	0.0	0	0.0	37	7.9
PBDGG	1,2c,3,17,10,28	0	0.0	3	100.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	0.6
PBDGJ	1,2c,3,17,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	2.4	0	0.0	0	0.0	3	0.6
PBDJG	1,2c,3,17,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	4.5	1	0.2
TBBGJ	1,2a,2c,3,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	1	0.2
TBBGS	1,2a,2c,3,10,21,28,39	0	0.0	0	0.0	0	0.0	7	6.0	4	10.0	17	13.4	0	0.0	0	0.0	28	6.0
TBBKG	1,2a,2c,3,10,14a,18,28	0	0.0	0	0.0	2	5.3	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TBBQJ	1,2a,2c,3,B,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	1	0.2
TBGJG	1,2a,2c,3,11,10,14a,28	0	0.0	0	0.0	1	2.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	7	5.8	0	0.0	1	2.6	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	9	1.9
TCGJG	1,2a,2c,3,26,11,10,14a,28	0	0.0	0	0.0	1	2.6	0	0.0	0	0.0	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 2017 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, *Lr39*, and *Lr42*.

Race	Virulence combination (ineffective Lr genes)	Southeast		North-east		Ohio Valley		OK-TX		KS-NE		MN-ND-SD		CA		WA		Total			
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%		
TCGKG	1,2a,2c,3,26,11,10,14a,18,28	1	0.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TCJSB	1,2a,2c,3,26,11,17,B,10,14a	2	1.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TCJTB	1,2a,2c,3,26,11,17,B,10,14a,18	2	1.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TCRFG	1,2a,2c,3,26,3ka,11,30,14a,18,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	0	0.0	1	0.2
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	4	3.3	0	0.0	0	0.0	0	0.0	1	2.5	4	3.1	0	0.0	0	0.0	0	0.0	9	1.9
TCSQB	1,2a,2c,3,26,3ka,11,17,B,10	3	2.5	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	0.6
TCTNB	1,2a,2c,3,26,3ka,11,17,30,B,14a	5	4.2	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	5	1.1
TCTSB	1,2a,2c,3,26,3ka,11,17,30,B,10,14a	1	0.8	0	0.0	1	2.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TDBGD	1,2a,2c,3,24,10,39	0	0.0	0	0.0	0	0.0	0	0.0	1	2.5	0	0.0	0	0.0	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	2.6	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TDRKG	1,2a,2c,3,24,3ka,11,30,10,14a,18,28	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TDTSB	1,2a,2c,3,24,3ka,11,17,30,B,10,14a	0	0.0	0	0.0	1	2.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TFBJQ	1,2a,2c,3,24,26,10,14a,21,28	0	0.0	0	0.0	0	0.0	0	0.0	1	2.5	2	1.6	0	0.0	0	0.0	0	0.0	3	0.6
TFPSB	1,2a,2c,3,24,26,3ka,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	2.4	0	0.0	0	0.0	0	0.0	3	0.6
TFTNB	1,2a,2c,3,24,26,3ka,11,17,30,B,14a	0	0.0	0	0.0	1	2.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TFTSB	1,2a,2c,3,24,26,3ka,11,17,30,B,10,14a	1	0.8	0	0.0	3	7.9	43	36.8	0	0.0	4	3.1	0	0.0	0	0.0	0	0.0	51	10.9
TNBJJ	1,2a,2c,3,9,24,10,28,39	1	0.8	0	0.0	0	0.0	4	3.4	2	5.0	20	15.7	0	0.0	0	0.0	0	0.0	27	5.8
TNBJJ	1,2a,2c,3,9,24,10,14a,28,39	1	0.8	0	0.0	0	0.0	0	0.0	4	3.4	2	5.0	20	15.7	0	0.0	0	0.0	27	5.8
TNMJJ	1,2a,2c,3,9,24,3ka,30,10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	0	0.0	1	0.2
TNPSD	1,2a,2c,3,9,24,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,14a,28,39	4	3.3	0	0.0	0	0.0	1	0.9	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	5	1.1
TPBGJ	1,2a,2c,3,9,24,26,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	4	3.1	0	0.0	0	0.0	0	0.0	4	0.9
TPBJJ	1,2a,2c,3,9,24,26,10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	1.6	0	0.0	0	0.0	0	0.0	2	0.4
TPDQJ	1,2a,2c,3,9,24,26,17,B,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	2.4	0	0.0	0	0.0	0	0.0	3	0.6
Total		120		3		38		117		40		127		2		22		469			

**Table 2.** Number and frequency (%) of isolates of *Puccinia triticina* in the United States in 2017 virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance gene	Southeast		Northeast		Ohio Valley		OK-TX		KS-NE		MN-ND-SD		CA		WA		Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
<i>Lr1</i>	120	100.0	3	100.0	38	100.0	117	100.0	40	100.0	127	100.0	2	100.0	22	100.0	469	100.0
<i>Lr2a</i>	31	25.8	0	0.0	12	31.6	65	55.6	14	35.0	75	59.1	0	0.0	0	0.0	197	42.0
<i>Lr2c</i>	31	25.8	3	100.0	12	31.6	65	55.6	14	35.0	78	61.4	0	0.0	1	4.5	204	43.5
<i>Lr3</i>	119	99.2	3	100.0	38	100.0	117	100.0	40	100.0	127	100.0	2	100.0	9	40.9	455	97.0
<i>Lr9</i>	18	15.0	0	0.0	1	2.6	41	35.0	21	52.5	67	52.8	0	0.0	0	0.0	148	31.6
<i>Lr16</i>	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	0	0.0	1	0.2
<i>Lr24</i>	24	20.0	0	0.0	8	21.1	86	73.5	22	55.0	80	63.0	0	0.0	0	0.0	220	46.9
<i>Lr26</i>	55	45.8	0	0.0	15	39.5	68	58.1	11	27.5	46	36.2	1	50.0	9	40.9	205	43.7
<i>Lr3ka</i>	102	85.0	0	0.0	34	89.5	88	75.2	19	47.5	50	39.4	0	0.0	0	0.0	293	62.5
<i>Lr11</i>	92	76.7	0	0.0	33	86.8	46	39.3	5	12.5	15	11.8	0	0.0	0	0.0	191	40.7
<i>Lr17</i>	98	81.7	3	100.0	33	86.8	96	82.1	25	62.5	61	48.0	2	100.0	22	100.0	340	72.5
<i>Lr30</i>	98	81.7	0	0.0	34	89.5	88	75.2	19	47.5	50	39.4	0	0.0	0	0.0	289	61.6
<i>LrB</i>	98	81.7	0	0.0	33	86.8	96	82.1	25	62.5	59	46.5	2	100.0	21	95.5	334	71.2
<i>Lr10</i>	58	48.3	3	100.0	13	34.2	116	99.1	37	92.5	124	97.6	2	100.0	22	100.0	375	80.0
<i>Lr14a</i>	117	97.5	0	0.0	38	100.0	103	88.0	30	75.0	86	67.7	2	100.0	22	100.0	398	84.9
<i>Lr18</i>	15	12.5	0	0.0	3	7.9	2	1.7	1	2.5	5	3.9	0	0.0	0	0.0	26	5.5
<i>Lr21</i>	0	0.0	0	0.0	0	0.0	7	6.0	5	12.5	19	15.0	0	0.0	0	0.0	31	6.6
<i>Lr28</i>	23	19.2	3	100.0	5	13.2	21	17.9	14	35.0	75	59.1	0	0.0	22	100.0	163	34.8
<i>Lr39</i>	30	25.0	0	0.0	2	5.3	60	51.3	35	87.5	102	80.3	2	100.0	0	0.0	231	49.3
<i>Lr42</i>	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0

## SOUTH CAROLINA

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### *Novel wheat genotypes designed to meet the future needs for safe and surplus food.*

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Wheat supplies about 20% of the total food calories consumed worldwide and approximately half of the global demand for dietary proteins (Brenchley et al. 2012). Wheat is a national staple in many countries. In the United States, the per capita consumption of wheat exceeds that of any other single food staple. The demand for wheat and wheat products is strengthening worldwide. Besides being a major source of energy and nutrition, wheat grains are also a cause of many dietary disorders such as celiac disease, gluten sensitivity, and wheat allergy. Wheat grains also suffer from reduced bioavailability of dietary fibers (arabinoxylan and gluten) to the consumers. Additionally, wheat is susceptible to a large number of insects and fungal pests, which limits its productivity.

Unfortunately, all extant wheat genotypes under cultivation carry immunogenic epitopes and exhibit susceptibility to the root and crown rot pathogens (*Rhizoctonia solani* and *Fusarium* spp.) (Suligoj et al. 2013; Smiley et al. 2009). Therefore, to meet the global demand for safe and surplus food it is imperative to develop wheat genotypes with reduced immunogenicity, improved bioavailability of dietary fibers, and resistance to major fungal pathogens via genetic engineering. However, the conceived solution relies on genetic engineering it is noteworthy that the wheat genotypes

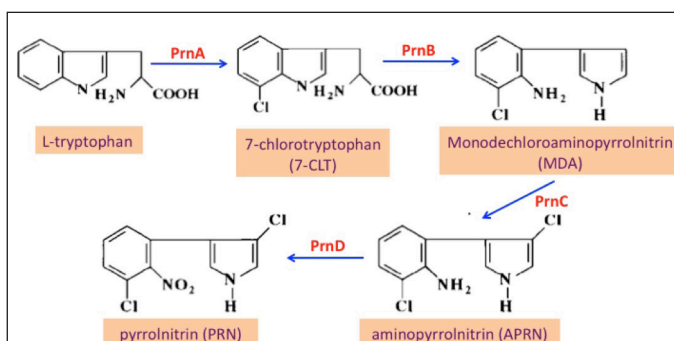
lacking immunogenic gluten proteins or expressing enzymes to increase nutrient bioavailability are designed to benefit the consumer unlike most of the contemporary transgenic crops, which were essentially developed to benefit producers. Therefore, wheat genotypes with these novel characteristics are expected to be readily acceptable to the general public and the regulatory authorities. Genetically engineered wheat has not yet received general acceptance hence we consider development of such genotypes analogous to an investment in the future. As quoted by Dr. Sanjaya Rajaram, the World Food Prize winner, "Feeding the world with wheat without using genetic modification will lead to food shortages". Therefore, we believe that under the pressing needs for safe and surplus food the so-called genetically modified (GM) wheat will eventually gain consumer acceptance. Since the development of a new wheat cultivar generally takes about a decade, it is worthwhile to develop the desired wheat genotypes today rather than waiting for the general acceptance for the GM wheat or encountering an urgent need.

**Wheat genotypes resistant to root and crown rot diseases.** About 86% of the U.S. wheat and 50% of the world's wheat is cultivated under water scarcity (<http://drought.mssl.ucl.ac.uk>). Management practices, such as direct seeding (no-tillage) or conservation tillage, are practiced to conserve moisture, limit wind erosion, maintain the soil profile, and conserve organic matter content to reduce emission of the greenhouse gasses into the atmosphere (Papendick and Parr 1997). In view of these benefits, direct seeding operations were adopted in 35.5% of the U.S. cropland (88 x 10<sup>6</sup> acres) planted to wheat, barley, corn, cotton, oats, rice, sorghum, and soybeans, which, according to the USDA Agricultural Resource Management Survey, represented 94% of the total planted acreage for the year 2009 (Horowitz et al. 2010).

Management practices that leave crop residues on the surface also create an ideal environment for the increase of necrotrophic soilborne pathogens, including *Rhizoctonia solani* and *Fusarium culmorum*, the causal agents of Rhizoctonia root rot and Fusarium crown rot, respectively. Yield losses due to such pathogens make them main limiting factors to the adoption of direct seeding (Weller et al. 1986; Cook 2000, Paulitz et al. 2002) in dryland cropping systems in the Pacific Northwest (PNW) and around the globe (Backhouse and Burgess 2002; Demirci 1998; MacNish and Neate 1996).

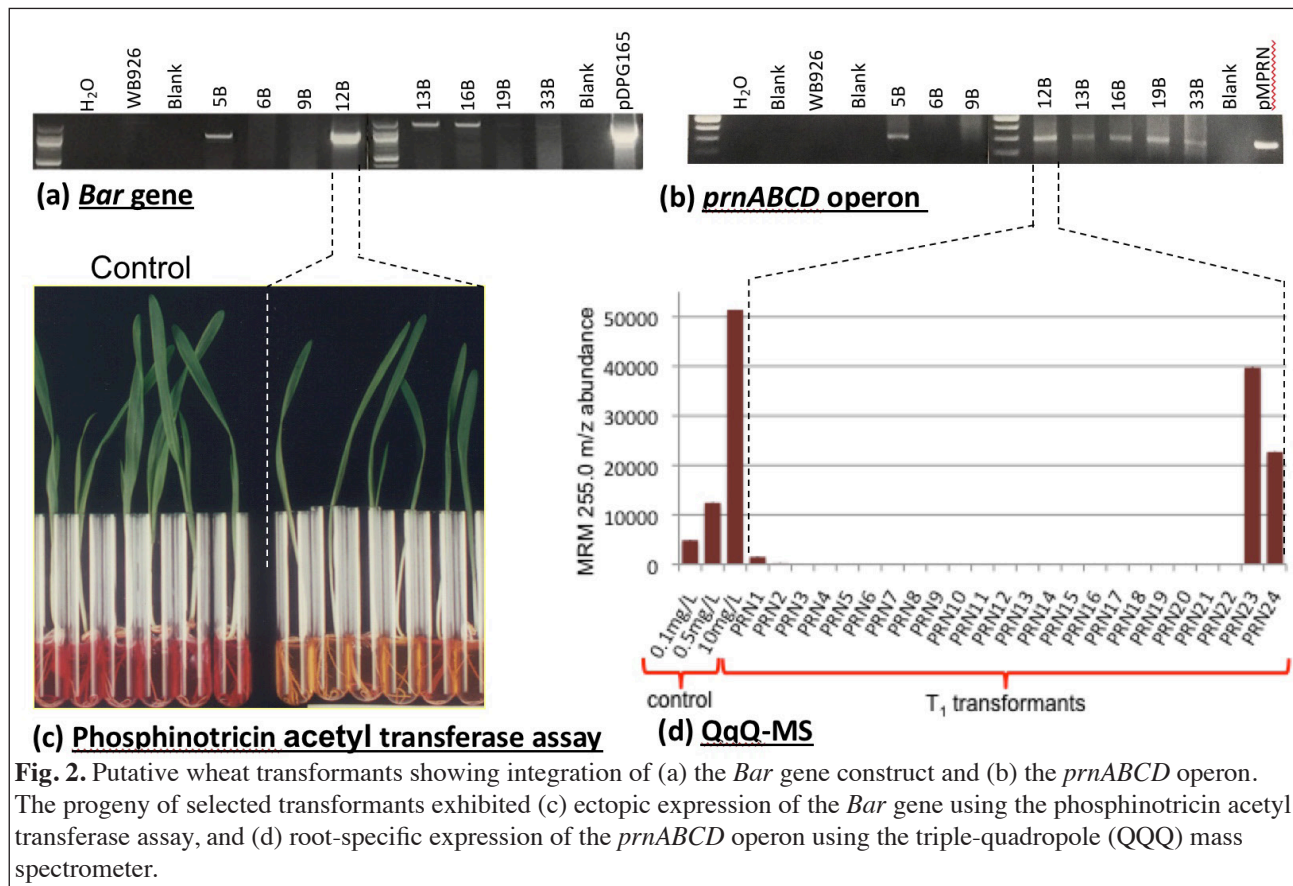
To deal with this problem, we adapted two different strategies.

- 1) Ectopic expression of the *Trichoderma* endochitinase gene in wheat. The chitinase enzyme catalyzes degradation of chitin molecules, a major component of the cell wall in true fungi including *Rhizoctonia* and *Fusarium*. Different strains of the mycoparasitic fungus *Trichoderma* have been effective as biological control agent against *R. solani*. Taking leads from these early studies, we decided to express the *Trichoderma harzianum* *ThEn42* gene in wheat plants. The soft white spring wheat cultivar Louise was transformed with a construct of *Th-En42* gene cloned in frame with the constitutive 35S promoter (Brew-Appiah et al. 2013). Louise plants were selected and assayed for endochitinase activity in roots, with a quantitative method using the fluorogenic substrate methylumbelliferyl-chitotrioside. Out of the four transformants, high root endochitinase activity was observed in two cases and, interestingly, these lines also showed resistance against both fungal pathogens in glasshouse.
- 2) Production of a natural fungicide pyrrolnitrin in wheat roots. Pyrrolnitrin is one of the natural agricultural fungicides produced by fluorescent *Pseudomonas* that exist naturally in suppressive soils. This antibiotic is synthesized from an amino acid tryptophan by the concerted action of four enzymes encoded by an operon that means these genes are components of a transcription unit and hence are co-regulated, which is necessary for maintaining stoichiometry of biosynthesis intermediates leading to the production of pyrrolnitrin (Fig. 1). In order to assure pyrrolnitrin production in wheat roots we engineered an expression vector by optimizing *prn* operon genes for expression in wheat. To assure root specific expression the operon was provided with the shared rice root specific *RCg2* promoter and to allow transfer of the products of *PRN* operon from cytosol to plastid, the site of tryptophan biosynthesis, each gene was supplemented with a transit peptide. In a nutshell this specific design has allowed high-level expression of the bacterial operon in bread



**Fig. 1.** Pyrrolnitrin biosynthetic pathway showing different steps involved in the production of pyrrolnitrin from L-tryptophan.

wheat. Although the pyrrolnitrin construct was co-transformed with the *Bar* gene construct in bread wheat, the transformants were first checked for integration of the *Bar* gene construct and its expression using the phosphinotricin acetyl transferase assay. Analysis of pyrrolnitrin content in the root extracts of selected T<sub>1</sub> transformants was later performed using the triple-quadropole (QQQ) mass spectrometer (Fig. 2). Synthetic pyrrolnitrin was used as control to make a standard curve to determine pyrrolnitrin concentration in these experiments.



**Fig. 2.** Putative wheat transformants showing integration of (a) the *Bar* gene construct and (b) the *prnABCD* operon. The progeny of selected transformants exhibited (c) ectopic expression of the *Bar* gene using the phosphinotricin acetyl transferase assay, and (d) root-specific expression of the *prnABCD* operon using the triple-quadropole (QQQ) mass spectrometer.

**Production of nutritionally enhanced ‘celiac-safe’ wheat genotypes.** Prolamins dubbed as gluten represent the major seed storage proteins in wheat grains and cherish the glory of being one of the most consumed dietary proteins in the world. In addition, gluten was also found responsible for a variety of dietary disorders in the susceptible individuals (Sapone et al. 2012). According to an estimate about 7.5% of the U.S. population is affected by the ‘gluten syndrome’. The only effective therapy known so far is lifelong adherence to abstinent diet, which is difficult to practice if not impossible. The known solution to this problem is strict adherence to the abstinent diet, which is difficult to follow. Moreover, this solution is associated with penalties, for instance i) strict adherence to a diet totally devoid of gluten-containing grains deteriorates gut health by its negative influence on the gut microbiota, and ii) long-term adherence to carbohydrate rich gluten-free diet results in multiple deficiencies and change in patient’s body mass index (BMI). No extant wheat genotype under cultivation or in wild is safe for celiac patients. Therefore, in order to develop celiac safe wheat cultivars, we undertook three different strategies: i) Epigenetic elimination of gliadins and low molecular weight glutenins by silencing of the wheat genes encoding a DNA glycosylase *DEMETER* and an iron-sulfur biogenesis enzyme *Dre2*, which are responsible for transcriptional de-repression of prolamin genes in the developing endosperm, ii) post-transcriptional elimination of immunogenic prolamins by RNA interference using a chimeric hairpin construct, and iii) post-translational detoxification of ‘gluten’ proteins by ectopic expression of glutenases in wheat endosperm.

Because gluten is a complex mixture of about 100 proteins encoded by a large number of genes, we devised a clever approach to deal with this problem by silencing a master regulator of prolamin accumulation in wheat grains. This strategy is based on the fact that there are two categories of promoters for endosperm specific gene expression: one that

are silenced by methylation in vegetative tissues and have to be demethylated before transcription in endosperm, and the other depends solely on the removal of repressors or induction of endosperm-specific transcription factors. In wheat, the promoters of LMWgs and gliadins belong to the first category and the promoters of HMWgs belong to the second category and are protected for methylation by the presence of CpG-islands. Similar to a high lysine barley mutant Risø 1508, the gliadins and LMW glutenins in wheat can be eliminated by epigenetic regulation without affecting the synthesis of HMW glutenins, which are indispensable for baking and are largely non-immunogenic.

As inducing mutations in the *DEMETER* gene leads to sterility, we adapted an RNA interference-based method for tissue specific silencing of the *DME* gene. For this purpose, a 938-bp hairpin with a 185-bp stem and a 568-bp loop was synthesized and cloned under the control of the wheat HMWg promoter. The construct was used for biolistic transformation of wheat scutellar calli and 118 putative transformants were obtained. Out of these 118 candidates, only seven plants exhibited 45–76% reductions in the amount of immunogenic prolamins (Wen et al. 2012). Interestingly, these transformants showed reductions in amount of different prolamins.

As hairpin construct could lead to off targeting of genes, we designed miRNA from the active site and the N-terminal region of the wheat *DEMETER* homoeologues. Three amiRNA sequences were selected and assembled on rice MIR528 template using overlapping primers, and cloned with the wheat HMWg promoter. The constructs were delivered to wheat via biolistic approach. The selection scheme yielded a total of 215 candidate transformants and 39 lines showing transgene integrations. Out of these 39 putative transformants, 12 lines showed 40–75% reduction in the amount of immunogenic prolamins (Rustgi et al. 2014). Protein profiling of these transformants exhibited elimination of specific prolamins and/or prolamins groups. Additionally, these lines showed many desirable characteristics such as compensatory increases in the amount of HMW glutenins, albumins, and globulins; increased grain lysine content; and gluten strength.

To increase the level of gluten elimination and *DEMETER* suppression in wheat, we undertook a site-directed insertional mutagenesis approach. To get the full benefit of this approach, the *DME*-specific TALE repressor is introduced in the wheat *Dre2* gene via a CRISPR Cas9 construct. The *Dre2* or Derepressed for Ribosomal protein S14 Expression, facilitates deposition of iron-sulfur (Fe-S) cluster to the *DME* apozyme, which is vital for its interaction with genomic DNA and its subsequent demethylation. In this approach, the double-stranded breaks introduced in the wheat *Dre2* homoeologues are repaired with the help of a donor construct carrying the *DME*-specific TALE repressor. This approach of simultaneous silencing of the *DME* and *Dre2* genes is expected to check *DME* activity at two time points, i.e., transcriptional and post-translational levels with the concomitant effect on the accumulation of immunogenic prolamins.

In order to achieve post-transcriptional silencing of prolamins genes, we designed a novel hairpin construct, which contain a chimeric stem derived from a number of small interfering RNAs each designed from a conserved region identified by individually aligning different kind of gliadins and LMWgs. A truncated version of wheat TAK14 intron was used as loop. The construct was cloned in the gamma subgenome of BSMV to be used in VIGS and also with HMWg promoter and Nos terminator for RNAi. The results showed significant reduction in the amounts of gliadins and LMWgs and in some instances showed complete elimination of specific prolamins.

To develop a dietary therapy for celiac patients we decided to express glutenases in wheat endosperm. Based on the parameters like target specificity, substrate length, optimum pH, and site of action a prolyl endopeptidase from *Flavobacterium meningosepticum* and a glutamine specific endoprotease from barley were selected for expression in wheat endosperm. Wheat transformants expressing these glutenases were obtained, and a few transformants exhibited significant reductions in amount of indigestible gluten peptides on the tricine PAGE gels and RP-HPLC. The wheat grains expressing 'glutenases' are expected to benefit all consumers due to improved bioavailability of storage proteins.

**Production of wheat genotypes with improved bioavailability of dietary fibers.** Arabinoxylans or pentosan are the predominant component of the wheat endosperm cell wall and constitutes 6–7% of the dry matter in grain. Unfortunately, mammals cannot digest these biological fibers, which significantly reduce their bioavailability to the consumer, and also cause discomfort on the consumption of these fibrous foods. Because of the great emphasis on the consumption of whole-grain products, we transformed wheat microspores by co-cultivating them with disarmed *Agrobacterium* strain AGL-1 to express codon-optimized version of 1,4- $\beta$ -xylanase from *Bacillus subtilis*. The obtained T<sub>2</sub> grains secreted  $\beta$ -xylanase into the medium containing oat-spelt xylan stained with Congo Red and de-polymerized xylans resulting in an unstained yellow hallow around the transformed grains (Brew-Appiah et al. 2013). These transformed wheat lines will be tested in the feeding trials with mice and are expected to exhibit high nutritional value.



**Meiotic manipulations in wheat to increase or decrease the recombination frequency.** Despite significant progress made in the field of molecular cytogenetics, the mechanism of diploid like chromosome-pairing behaviors in polyploids remain unresolved, and its key regulators unidentified. The genetic control of strict-homologous pairing evolved in polyploids to maintain fecundity and to assure success as a species. However, genes controlling strict-homologous pairing in polyploids are like a ‘blessing in a disguise’, as on one hand they provide stability to the plant genome and on the other hand prevent exchange of genetic material between homoeologous or related chromosomes. This genetic regulation prevents exchange of genetic material or transfer of traits between distantly related but sexually compatible species. Therefore, it is of paramount importance to decipher the genetic control of diploid-like chromosome pairing behavior in polyploids like wheat and manipulate it at will to expand their genetic bases to meet the future demand for food and feed.

In order to get insight into the genetic regulation of diploid like chromosome pairing behavior of polyploid wheat and the homologous recombination process, we undertook transient silencing of the essential meiotic genes in bread wheat using virus induced gene silencing approach. For this purpose, we used the disarmed Barley Streak Mosaic Virus as vector. VIGS of an essential meiotic gene *DMC1* (Disrupted meiotic cDNA 1) showed an average 30 univalents and six bivalents compared to the control where only bivalents were observed. This is in consistency with the known function of the *DMC1* gene in the repair of double stranded breaks at the meiotic prophase I (Bennypaul et al. 2012). Similarly, VIGS of wheat *Asy1* (Asynopsis 1) gene showed formation of multivalents, which is in consistency with what was observed for RNA interference lines of this gene in bread wheat (Boden et al. 2009). When VIGS was performed on the pairing homoeologous locus *Ph1* candidates, interestingly, one of the genes *dubbed RAFTIN like 1* showed quadrivalents or higher order pairing upon silencing, which is a characteristic of *ph1* mutants (Bhullar et al. 2014). These results indicate towards the possibility of enhancing and reducing the recombination frequency, which has far reaching implications in plant breeding.

Collectively, the major outcomes of this research is the development of wheat genotypes with near complete elimination/detoxification of immunogenic prolamins, efficiency to combat major root and crown rot pathogens or with efficiency of homoeologous recombination. Moreover, these wheat genotypes will serve the future need for safe and surplus food and feed.

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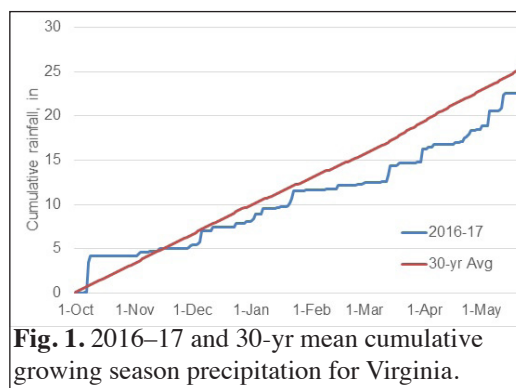
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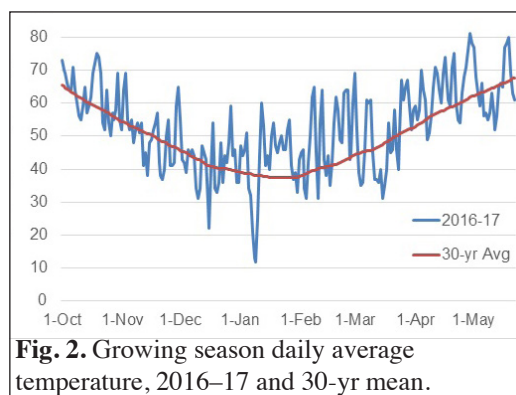
### *2017 Wheat Production in the Commonwealth of Virginia.*

**Growing conditions.** Statewide temperatures and rainfall in autumn 2016 were generally favorable for wheat seeding after fields dried from the soaking rains from Hurricane Matthew (Figs. 1 and 2). By mid-October, wheat planting reached 20% of intentions, compared with a five-year average of 25% by this date. Continued favorable weather allowed 41% of the wheat crops to be planted by 3 October. By mid-November, planting progress was near the 5-year average for all small grains reported with 60% of wheat acres reported as good or excellent. Dry conditions persisted through late November resulting in a decline in the number of wheat acres rated excellent, although this did allow successful late seeding in some areas. Rainfall in early December returned the total season precipitation to near normal, followed by mild and wet conditions through much of January. February was unseasonably warm with limited rainfall, resulting in soil moisture depletion. Wheat was rated good or excellent on 68% of acres. March brought mostly mild temperatures with a freeze mid-month. Seventy-five percent of the winter wheat crop was rated good or excellent for the week ending 26 March. Statewide rains were received in mid-March, but season total rainfall continued below normal. By the end of the third week of March, 33% of the wheat crop was reported as headed, up 14% from last year and 23% from the 5-year average. Dry soil conditions continued through mid-April with temperatures above average through the last half of the month. At the end of April, 75% of the winter wheat crop was still rated good or excellent. Wet weather in May resulted in a decline in wheat, with 65% rated good or excellent. By 20 May, approximately 94% of the wheat crop was headed, compared with 90% last year. By 19 June, about 51% of the wheat for grain was harvested, up significantly from 2016 and the 5-year average.

**Production.** According to the United States Department of Agriculture's National Agriculture Statistical Service, Virginia farmers planted 210,000 acres (85,050 hectares) of wheat in 2017 of which 145,000 acres (58,725 hectares)



**Fig. 1.** 2016–17 and 30-yr mean cumulative growing season precipitation for Virginia.



**Fig. 2.** Growing season daily average temperature, 2016–17 and 30-yr mean.

were harvested for grain. Wheat yields averaged around 66 bushels/acre (4,435 kilograms per hectare). In total  $9.6 \times 10^6$  bushels (261,504 metric tons) of wheat were produced in Virginia in 2017.

**Disease incidence and severity.** Many wheat diseases were prevalent and widespread throughout the Commonwealth in 2017. Stripe rust was widespread but not as severe as in 2016. Entries in Virginia's 2017 state wheat cultivar trials were rated for disease severity (0 = no infection to 9 = severe infection) at two to three diverse locations. The 139 entries in the 2017 trial had mean powdery mildew ratings that varied from 0 to 7 at three test sites, and mean ratings of 1.8 on the Eastern Shore (Accomack County), 1.8 in the northeastern region (Richmond County), and 2.2 in the southern Piedmont region (Nottoway County). *Barley/Cereal Yellow Dwarf Virus* infection was moderate, and entries had mean disease scores from 1 to 4 over three test sites; mean disease scores varied from 1.7 in the southern Piedmont, 2.3 in the northern Piedmont (Orange County), and 1.1 in the Tidewater (City of Suffolk) regions. Leaf rust was prevalent in several regions with ratings ranging from 0 to 9 at three sites. Mean leaf rust ratings varied from 3.3 on the Eastern Shore, 2.2 in the northeastern and 1.6 in the southwestern regions of the state. Race surveys, by Dr. James Kolmer at the USDA-ARS Cereal Disease Lab, conducted on 20 *P. triticina* collections from Blacksburg, Blackstone, Holland, Painter, and Warsaw, VA, identified 11 different races with races MBTNB and MCTNB being common at all five locations. Race MFGJG was identified at Holland, Painter, and Warsaw, VA. Race TCTNB was identified at Blacksburg and Painter, VA. Other races identified at Blacksburg included MMNSD, MNPSD, and MPPSD, and other races identified at Painter included TCJSB, TCRKG, and TNRJJ. Race TCSQB was identified at Blackstone, VA. Mean stripe rust ratings of entries in the state wheat trial ranged from 0 to 6 over two locations, and mean test ratings varied from 0.5 on the Eastern Shore to 0.4 in northeastern regions. Stripe rust samples from Blacksburg, Painter, and Warsaw, VA, were sent to Dr. Xianming Chen at USDA-ARS in Pullman, WA. Three races were identified, including PSTv-37 (virulence for *Yr6*, 7, 8, 9, 17, 27, 43, 44, *Tr1*, and *Exp2*) at all three locations; PSTv-47 (*Yr1*, 6, 7, 8, 9, 17, 27, 43, 44, *Tr1*, and *Exp2*) from Painter; and PSTv-305 (*Yr1*, 6, 7, 8, 9, 17, 27, 43, 44, *SP*, *Tr1*, *Exp2*) from Blacksburg. Stem rust was identified in one wheat plot at Painter, VA, and initial screening at the Cereal Disease Lab confirmed that it was a race common to the U.S. and not a strain of Ug99.

**State cultivar tests.** Wheat trials were planted no-till at the Tidewater test site at 48 seeds/ft<sup>2</sup>. Tests in the southwestern and northeastern regions, Eastern Shore, and southern and northern Piedmont regions were planted conventional-till at 44 seeds/ft<sup>2</sup>. Past seasons across Virginia have provided the opportunity to evaluate day length sensitivity, spring freeze damage, and resistance of lines to many diseases as noted above. In 2017, spring freeze damaged many of the entries that were either early heading and/or day length insensitive. Entries susceptible to one or more of the major diseases noted above also were damaged significantly. Mean grain yields over six test sites of the 139 entries in the 2016-17 trial varied from 45.4 bu/acre (3,051 kg/ha) in the southeastern Tidewater region to 90.3 bu/acre (6,068 kg/ha) in the northeastern Coastal Plains region. Forty-five entries produced mean grain yields that were significantly higher than the overall trial average of 69.7 bu/acre (4,684 kg/ha). The cultivar CROPLAN 8550 had the highest overall mean yield at 82.3 bu/acre (5,531 kg/ha). Ten other cultivars had similar mean grain yields varying from 78.9 to 82.2 bu/acre (5,302-5,524 kg/ha). Mean test weights of the 139 entries varied from 58.9 lb/bu (77.5 kg/hl) at the northeastern test site to 52.8 lb/bu (69.6 kg/hl) at the Eastern Shore site with an over locations mean test weight of 55.2 lb/bu (72.7 kg/hl).

### *Newly released cultivars.*

Three soft red winter (SRW) wheat cultivars, including VA11W-108PA (Dyna-Gro 9811), VA11W-279 (USG 3118), and VA12W-72 (16162692) were released by the Virginia Agricultural Experiment Station in May 2017.

### *Virginia Wheat Yield Contest results (<http://www.viriniagrains.com/yield/yieldcontests/>).*

Place	Grower	Farm	County	Yield bu/acre
1	Alan Welch	Welch Farms, Inc	Northumberland	122.3
2	Paul Davis	Davis Produce	New Kent	102.0
3	Boogie Davis	Davis Produce	New Kent	97.8

***Integrated disease management for soft red winter wheat in Virginia.***

Hillary Mehl and Navjot Kaur (PhD student).

Wheat disease management research in Virginia in 2017 included assessing the value of different fungicide application programs on varieties with different levels of Fusarium head blight (FHB) resistance, evaluating the profitability of different application timings of generic and premium fungicides for control of FHB and foliar disease in wheat, and screening wheat pathogens for sensitivity to different fungicide chemistries. Two major diseases in southeast Virginia are FHB and *Stagonospora nodorum* leaf blotch (SLB). Field experiments demonstrated the value of planting new, high-yielding wheat cultivars with moderate FHB resistance, which had higher yields and lower levels of deoxynivalenol contamination compared to susceptible cultivars regardless of fungicide program. When FHB pressure was low and SLB was the major disease, inexpensive triazole fungicides Folicur (tebuconazole) and Tilt (propiconazole) provided similar levels of disease control and yield response when compared to premium fungicides with mixed modes of action. Isolates of the fungi causing FHB and SLB were collected throughout Virginia in 2017, and currently the fungicide sensitivity and genetic diversity of these isolates are being evaluated. Research in the next few years will focus on evaluating the impact of management practices such as deployment of resistant wheat cultivars and fungicide applications on the phenotypic and genotypic diversity of fungal pathogens that are economically important on wheat in the region. This information will help to inform long-term approaches to sustainable, integrated management of wheat diseases in Virginia.

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Any opinions, findings, or recommendations expressed in this article are those of the authors and do not necessarily reflect those of our sponsors.

**WASHINGTON****USDA-ARS WESTERN WHEAT QUALITY LABORATORY****E-202 Food Quality Building, Washington State University, Pullman, WA 99164, USA.**[www.wsu.edu/~wwql/php/index.php](http://www.wsu.edu/~wwql/php/index.php)

Craig F. Morris, Douglas A. Engle, Mary L. Baldrige, Gail L. Jacobson, E. Patrick Fuerst, William J. Kelley, Shelle Lensen, Eric Wegner, Alecia Kiszonas, Shawna Vogl, Janet Luna, Stacey Sykes, Leonardo Pierantoni, Jessica Murray, Maria Itria Ibba, José Orenday-Ortiz, Derick Jiwani, and Eden Stout.

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. Our current activities and projects include grain hardness and puroindolines, waxy wheat, polyphenol oxidase (PPO), arabinoxylans, SDS sedimentation test, soft durum wheat, grain flavor, and Falling Number.

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## IV. CULTIVARS AND GERMPLASM

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***Recent PI Assignments in Triticum, X Triticosecale, Aegilops, and Secale.***

H.E. Bockelman, Agronomist and Curator.

Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN-Global): <https://npgsweb.ars-grin.gov/gringlobal/search.aspx?> 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* (JPR) 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.

**Table 1.** Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (JPR indicates that the cultivar was published in the *Journal of Plant Registrations*).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
682073 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Melba	United States	Washington
682074 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Ryan	United States	Washington
682075 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Achieve CL2	United States	Iowa
682076 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Banks	United States	Iowa
682077 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Benefit	United States	Iowa
682078 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Command	United States	Iowa
682079 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Dayton	United States	Iowa
682080 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Miskin	United States	Iowa
682081 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Raptor	United States	Iowa
682082 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Rugged	United States	Iowa
682083 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY 517 CL2	United States	Iowa
682084 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY 912	United States	Iowa
682089 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	U6714-B-056	United States	Michigan
682090 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	U6714-A-011	United States	Michigan
682091 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Thatcher-Lr53	United States	North Dakota
682092 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Lr56-157	United States	North Dakota
682093 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Lr59-151	United States	North Dakota
682094 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Lr62-129	United States	North Dakota
682147 PVP	<i>Triticum turgidum</i> subsp. <i>durum</i>	Alberto	United States	Arizona
682161	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	CDL002	United States	Minnesota
682660 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	ND VitPro	United States	North Dakota
682675	<i>Triticum turgidum</i> subsp. <i>durum</i>	PI624151-1-2	United States	Oklahoma
682676	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1121	United States	Nebraska
682677	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1132	United States	Nebraska
682678	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1094	United States	Nebraska
682679	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1073	United States	Nebraska
682680	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1055	United States	Nebraska
682681	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1117	United States	Nebraska
682682	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1115	United States	Nebraska
682683	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1056	United States	Nebraska
682684	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1018	United States	Nebraska
682685	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1049	United States	Nebraska



**Table 1.** Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (JPR indicates that the cultivar was published in the *Journal of Plant Registrations*).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
682686	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1108	United States	Nebraska
682687	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1010	United States	Nebraska
682688	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1095	United States	Nebraska
682689	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1058	United States	Nebraska
682690	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1011	United States	Nebraska
682691	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1126	United States	Nebraska
682692	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1024	United States	Nebraska
682693	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1075	United States	Nebraska
682694	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1074	United States	Nebraska
682695	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1109	United States	Nebraska
682696	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1041	United States	Nebraska
682697	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1044	United States	Nebraska
682698	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1112	United States	Nebraska
682699	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1026	United States	Nebraska
682700	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1009	United States	Nebraska
682701	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1124	United States	Nebraska
682702	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1033	United States	Nebraska
682703	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1052	United States	Nebraska
682704	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1086	United States	Nebraska
682705	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1045	United States	Nebraska
682706	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1076	United States	Nebraska
682707	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1107	United States	Nebraska
682708	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1091	United States	Nebraska
682709	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1019	United States	Nebraska
682710	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1039	United States	Nebraska
682711	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1130	United States	Nebraska
682712	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1065	United States	Nebraska
682713	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1125	United States	Nebraska
682714	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N15Y1071	United States	Nebraska
682715	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9012	United States	Nebraska
682716	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9117	United States	Nebraska
682717	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9140	United States	Nebraska
682718	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9275	United States	Nebraska
682719	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9268	United States	Nebraska
682720	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9046	United States	Nebraska
682721	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9276	United States	Nebraska
682722	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9204	United States	Nebraska
682723	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9074	United States	Nebraska
682724	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9153	United States	Nebraska
682740 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	AAC Brandon	Canada	Ontario
682809	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9085	United States	Nebraska
682810	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9056	United States	Nebraska
682811	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9070	United States	Nebraska
682812	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N16MD9209	United States	Nebraska
683485	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PRL/2*PASTOR	Mexico	
683486	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KUTZ	Mexico	
683487	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NADI	Mexico	
683488	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	CHIPAK	Mexico	
683489	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PBW65/2*PASTOR	Mexico	
683490	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MUTUS #1	Mexico	
683491	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	FRANCOLIN #1	Mexico	
683492	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	VENDA	Mexico	

**Table 1.** Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (JPR indicates that the cultivar was published in the *Journal of Plant Registrations*).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
683493	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	BONSU		Mexico
683494	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	BORLAUG100 F2014	Mexico	
683495	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MUCUY	Mexico	
683496	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KINGBIRD #1	Mexico	
683497	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	BAJ #1	Mexico	
683498	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KENYA SUNBIRD/ KACHU	Mexico	
683499	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KACHU #1	Mexico	
683500	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GID:3855011	Mexico	
683501	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GID:4577963	Mexico	
683502	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GID:3613474	Mexico	
683503	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GID:4314513	Mexico	
683504	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GID:4878569	Mexico	
683511 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Larry	United States	Kansas
683512 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Zenda	United States	Kansas
683518	<i>X Triticosecale</i> spp.	NT05421	United States	Nebraska
683519	<i>X Triticosecale</i> spp.	NT07403	United States	Nebraska
683520	<i>X Triticosecale</i> spp.	NT09423	United States	Nebraska
683521	<i>X Triticosecale</i> spp.	NT 11428	United States	Nebraska
683537 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Spur	United States	Montana
683538 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Iron	United States	Colorado
683539 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Luna	United States	Colorado
683540 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MS Camaro	United States	Colorado
683541 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Link	United States	Colorado
684572	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162107	United States	Nebraska
684573	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162109	United States	Nebraska
684574	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162111	United States	Nebraska
684575	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162112	United States	Nebraska
684576	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162113	United States	Nebraska
684577	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162115	United States	Nebraska
684578	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162116	United States	Nebraska
684579	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162120	United States	Nebraska
684580	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162121	United States	Nebraska
684581	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD162122	United States	Nebraska
684582	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PPO030	United States	Nebraska
684583	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PPO724	United States	Nebraska
684584	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PPO140	United States	Nebraska
684585	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PPO078	United States	Nebraska
684586	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PPO123	United States	Nebraska
684587	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	PPO538	United States	Nebraska
684588	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW14MD5111	United States	Nebraska
684589	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW14MD5543	United States	Nebraska
684590	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2469	United States	Nebraska
684591	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2470	United States	Nebraska
684592	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2471	United States	Nebraska
684593	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2475	United States	Nebraska
684594	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2481	United States	Nebraska
684595	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2482	United States	Nebraska
684596	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2483	United States	Nebraska
684597	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW06Y2487	United States	Nebraska
684598	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW15GH8079	United States	Nebraska
684599	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW15GH8083	United States	Nebraska

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PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
684600	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW15GH8087	United States	Nebraska
684601	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW15GH8151	United States	Nebraska
684602	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW15GH8168	United States	Nebraska
684603	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NN15GH8170R	United States	Nebraska
684604	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NN15GH8174R	United States	Nebraska
684605	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NN15GH8200R	United States	Nebraska
684606	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW15MD7089-50	United States	Nebraska
684607	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NEG2015-7235	United States	Nebraska
684608	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N14MD7134-113	United States	Nebraska
684609	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N14MD7156-50	United States	Nebraska
684610	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N14MD7163-143	United States	Nebraska
684611	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD1534103	United States	Nebraska
684612	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD1534233	United States	Nebraska
684613	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD1536142	United States	Nebraska
684614	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD1535162	United States	Nebraska
684615	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD153642	United States	Nebraska
684616	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N13MD2589W	United States	Nebraska
684617	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N11MD2166W	United States	Nebraska
684633 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	25R61	United States	Iowa
684634 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	25R74	United States	Iowa
684635 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	112370W	United States	Iowa
684636 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	112371W	United States	Iowa
684637 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	26R36	United States	Iowa
684638 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	112369W	United States	Iowa
684639 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WJ032015	United States	Iowa
684640 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162661	United States	Iowa
684641 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WJ022015	United States	Iowa
684642 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WJ082015	United States	Iowa
684643 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WJ012015	United States	Iowa
684644 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WJ052015	United States	Iowa
684645 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WJ072015	United States	Iowa
684646 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Aymeric	United States	Iowa
684647 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LA06146	United States	Iowa
684648 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MD GOL	United States	Maryland
684649 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Luisa	United States	Maryland
684659	<i>X Triticosecale</i> spp.	NT06427	United States	Nebraska
684660	<i>X Triticosecale</i> spp.	NT11406	United States	Nebraska
684661	<i>X Triticosecale</i> spp.	NT12414	United States	Nebraska
684662 PVP	<i>X Triticosecale</i> spp.	NT12434	United States	Nebraska
684669 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Oahe	United States	South Dakota
684671 PVP	<i>X Triticosecale</i> spp.	618491724	United States	Montana
684672 PVP	<i>X Triticosecale</i> spp.	641512175	United States	Montana
684673 PVP	<i>X Triticosecale</i> spp.	261216487	United States	Montana
684674 PVP	<i>X Triticosecale</i> spp.	841446398	United States	Montana
684977	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S1	United States	Washington
684978	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S2	United States	Washington
684979	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S3	United States	Washington
684980	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S5	United States	Washington
684981	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W7	United States	Washington
684982	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W9	United States	Washington
684983	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W10	United States	Washington
684984	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W11	United States	Washington

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PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
684985	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S13	United States	Washington
684986	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S14	United States	Washington
684987	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S15	United States	Washington
684988	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S17	United States	Washington
684989	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W19	United States	Washington
684990	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W20	United States	Washington
684991	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W21	United States	Washington
684992	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W22	United States	Washington
684993	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S25	United States	Washington
684994	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S26	United States	Washington
684995	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S27	United States	Washington
684996	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S28	United States	Washington
684997	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W31	United States	Washington
684998	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W32	United States	Washington
684999	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W33	United States	Washington
685000	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W35	United States	Washington
685001	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S38	United States	Washington
685002	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S39	United States	Washington
685003	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S40	United States	Washington
685004	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02S41	United States	Washington
685005	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W44	United States	Washington
685006	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W45	United States	Washington
685007	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W46	United States	Washington
685008	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	REA02W47	United States	Washington
685780 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	CW 7769	United States	Colorado
686368 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	TCG-Climax	United States	North Dakota
686369 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	AAC Penhold	Canada	Ontario
686371 PVP	<i>Triticum turgidum</i> subsp. <i>durum</i>	SNR-0068	United States	Arizona
686372 PVP	<i>Triticum turgidum</i> subsp. <i>durum</i>	SNR-0003	United States	Arizona
686410 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SY Gunsight	United States	Iowa
686411 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	UC-Patwin-RS	United States	California
686412 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	UC-Lassik-RS	United States	California
686413 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Resilience CL+	United States	Washington
686414 PVP	<i>Triticum turgidum</i> subsp. <i>durum</i>	UC-Desert King-RS	United States	California
686423 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9662	United States	Minnesota
686424 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9616CLP	United States	Minnesota
686425 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9590	United States	Minnesota
686426 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9719	United States	Minnesota
686427 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9479	United States	Minnesota
686428 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9578	United States	Minnesota
686429 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB4269	United States	Minnesota
686430 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB4575	United States	Minnesota
686431 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB1783	United States	Minnesota
686432 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB4311	United States	Minnesota
686436 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Lonerider	United States	Oklahoma
686437 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Smith's Gold	United States	Oklahoma
686438 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Spirit Rider	United States	Oklahoma
686478 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Dyna-Gro Caliber	United States	North Dakota
686842 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	26R45	United States	Iowa
686843 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	112378W	United States	Iowa
686844 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162665	United States	Iowa
686845 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162662	United States	Iowa

**Table 1.** Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (JPR indicates that the cultivar was published in the *Journal of Plant Registrations*).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
686846 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	XW16G	United States	Iowa
686847 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162678	United States	Iowa
686848 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162679	United States	Iowa
686849 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162668	United States	Iowa
686850 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162667	United States	Iowa
686851 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162666	United States	Iowa
686852 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	25W38	United States	Iowa
686854 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	16162692	United States	Virginia
686855 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	USG 3118	United States	Virginia
686856 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Dyna-Gro 9811	United States	Virginia
686859 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	TAM 204	United States	Texas
686860 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	TAM 114	United States	Texas
686878	<i>Aegilops tauschii</i>	AL8/78	Armenia	
686899 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Rebel	United States	Colorado
686900 PVP	<i>X Triticosecale</i> spp.	Forage FX 1001	United States	Montana
686941 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Pembroke 2016	United States	Kentucky
686965 PVP	<i>X Triticosecale</i> spp.	348612571	United States	Montana
686966 PVP	<i>X Triticosecale</i> spp.	530690862	United States	Montana
686967 PVP	<i>X Triticosecale</i> spp.	879684836	United States	Montana
686968 PVP	<i>X Triticosecale</i> spp.	690724516	United States	Montana
687030 PVP	<i>Secale cereale</i>	ND Dylan	United States	North Dakota
687038 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Lang-MN	United States	Minnesota
687144	<i>Triticum turgidum</i> subsp. <i>durum</i>	RHT-B1b-E529K	United States	California
687165	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GluB1-S60E	United States	California
687166	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GluB1-S62D	United States	California
687167	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GluB1-S101A	United States	California
687168	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GluB1-S239F	United States	California
687169	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GluB1-S261A	United States	California
687222 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Erisman	United States	Illinois
687331 PVP	<i>X Triticosecale</i> spp.	Hotshot		
687336 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Pakhtunkhwa 2015	Pakistan	
687795 PVP	<i>Triticum turgidum</i> subsp. <i>durum</i>	ND Grano	United States	North Dakota
687796 PVP	<i>Triticum turgidum</i> subsp. <i>durum</i>	ND Riveland	United States	North Dakota
687873 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	112373W	Germany	
687896 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Matterhorn	United States	Nebraska

**V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2018 SUPPLEMENT**

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The most recent version of the Catalogue, compiled for the 13<sup>th</sup> 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. Supplements 2013–14, 2015–16, 2017 also are available at those sites.

The 13<sup>th</sup> International Wheat Genetics Symposium in 2017 adopted the resolution that genetic loci in wheat should be designated in uppercase italics, e.g., *RHT1*, *SR35*, and that alleles be designated with first letter in uppercase for dominant alleles, e.g., *Rht1*, *Sr35*, and all lowercase letters for recessive alleles, e.g., *rht1*, *sr35*. The same procedure can be used in the case of nomenclature based on homoeologous sets, e.g., *RHT-D1* for the locus and *Rht-D1a*, *Rht-D1b* for alleles.

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## Morphological and Physiological Traits

### 1. Gross Morphology: Spike characteristics

#### 1.7. Multi-gynoecium

*Pis1*{10636}.            **i:**     Add: CM28TP {M10028}.

**ma:** Add: *KM69\_132294739* – 3.5 cM – *KM70\_136805221* – 3.0 cM – *Pis1* – 1.1 cM – *KM71\_140258883* {11228}.

**4. Aluminum Tolerance**

- Almt1.** *TaALMT1* {11242}. 4DL {11242}.  
**v:** CAR3911 {11242}.  
**ma:** *Xwmc457-4D* – 4.0 cM – *Almt1* – 2.0 cM – *Xwmc331-4D* {11242}.

**5. Anthocyanin Pigmentation****5.5. Purple grain/pericarp**

The location the second complementary gene is confusing: all three group-7 homoeologues may be involved in different materials.

**Pp1.**

- Pp-A1.** 7AS **v:** Saratovskaya 29 (not purple) {11312}.  
**Pp-B1.** 7BS Later renamed as *Pp3b*.  
**Pp-D1.** *TaPpm1a* {11313}. 7DS {11312}.  
**v:** Heixiaomai 76 *Pp3* {M1811}; Luozhen 1 *Pp3* {11313}.  
**c:** GenBank KM382421, a purple pericarp MYB 1, is strongly expressed in the pericarp {11313}. GenBank MG066451 {11313}.

**Pp3.**

- TaMyc1* {11312}, *TaPpb1a* {11313}. 2AS.  
**v:** Heixiaomai 76 *Pp3* {M1811}; Luozhen 1 *Pp3* {11313}.  
**c:** Encodes a protein with an anthocyanin bHLH regulatory factor {11313}. GenBank MG066455; has a 6x261 bp tandem repeat in the promoter {11313}. Specifically expressed in the seeds {11313}. The alternate allele has only a single 261-bp repeat {11313}.

Combinations of *Pp3* and one or other *Pp1* single purple allele gave light purple pericarp whereas combinations involving *Pp3* with multiple purple alleles gave a dark purple phenotype {11312}.

Add note at end of section: Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color {11285}. This may correspond to *TaPpm2* located on chromosome 4BL, one of three *Ppm* genes with no effect on purple pericarp {11313}.

**2. Chlorophyll Abnormalities****2.4 Yellow-green**

- yg** [{11238}]. Incompletely dominant. *y1718* {11238}. 2BS {11238}.  
**v:** Xinong 1718 mutant {11238}.  
**ma:** *Be498358* – 4.0 cM – *yg* – 1.7 cM – *Xwmc25-2B* {11238}.

The homozygous *yg**yg* genotype is extremely yellow, stunted and sterile and the mutant is easily maintained as a heterozygote {11238}.

**18. Dormancy (Seed)****18.3. Preharvest sprouting**

Add at end of section:

*QPhs.sicau-3B.1*, distally located on chromosome 3B in '*T. aestivum* subsp. *spelta* CSSR6 (res) / Lang (sus)'; nearest marker *wPt-6157*; transferred to durum cv. Bellaroi using SCAR markers {11246}.

**29. Glaucousness (Waxiness/Glossiness)****29.2 Epistatic inhibitors of glaucousness**

- W1.** **bin:** 2BS-0.84-1.00. **v:** P86 {11247}.  
**ma:** *Xgwm210-2B* – 0.77 cM – *XWGGC3197* – 0.81 cM – *W1* – 0.12 cM – *XWGGC2484* – 0.32 cM – *Xbarc35-2B* {11247}.  
**w1.** **v:** J87 {11247}.  
**Iw1.** **tv:** LDN<sub>DIC521-2B</sub> {11245}.  
**ma:** *Xgwm614-2B* – *Iw1/Xbarc35-2B/CD893659/CD927782/BQ788707/CD938589* – *Be498111* {11245}.

**Iw2.** Add synonym *IwT* {11207}.  
**v:** PBW114 /*Ae. tauschii* PAU14195 // 4\*WH542 backcross selections {11207}.  
**dv:** *Ae. tauschii* PAU14195 {11207}.  
**ma:** *Xcau96-2D* – 1.6 cM – *LrT (Lr39)* – 0.6 cM – *Xbarc124-2D* – 0.3 cM – *Xte6-2D* – 2.5 cM – *IwT* – 4.1 cM – *Xgdm35-2D* {11207}.

### 30.2. Flour, semolina, and pasta color

Add at the end of section:

Three QTL for peroxidase activity in the grain identified in a ‘Doumai (high POD activity) / Shi 4185 (low POD activity) ‘cross were named as *QPod.caas-3AL*, *QPod.caas-4BS*, and *QPod.caas-5AS* {11233}. Allelic variation was found at the *QPod.caas-3AL* locus {11233}.

**TaPod-A1a** {11233}. 3AL {11233}. **v:** Doumai {11233}.

**TaPod-A1b** {11233}. **v:** Shi 4185 {11233}.

There seemed to be no relationship to the *Per-* series identified by isozyme analyses and listed in the Protein section.

## 44. Height

### 44.2. Reduced Height: GA-sensitive

#### *Rht14.*

*GA2oxA9* expression was higher in Castelporziano than in its tall parent Capelli – see *Rht18* {11301}.

**Rht18.** **matv:** *Xbarc118-6A* – 1.4 cM – *Rht18/TdGA2Ox-A9/S470865SSR4/Xbarc37-6A* – 0.4 cM – *IWA4371* – 0.4 cM – *Xgwm82.1-6A* {11295}.

Independent ‘overgrowth’ mutants isolated from Icaris contained changes in the *GA2oxA9* coding region; this gene is predicted to encode GA 2-oxidase that metabolizes GA biosynthetic intermediates into inactive products thus reducing bioactive GA<sub>1</sub> {11301}.

**Rht24.** *Rht24b* {11293, 11294}. **v:** Solotar {11294}.  
**ma:** Excalibur\_rep\_c69275-346 {11294}.

*Rht24* is occurs at relatively high frequencies in European and Chinese wheat cultivars, and maps in the same region as *Rht14*, *Rht16*, and *Rht18* {11293}.

**Rht25** {11300}. *QHt.ucw-6AS* {11300}. 6AS {11300}.  
**bin:** 6AS1-0.35-1.00.  
**v:** UC1110 *Rht-D1b* {11300}.  
**ma:** *QHt.ucw-6AS* was located in a 0.2 cM interval flanked by *6A13699/6A13791/6A14397* and *6A14825* {11300}.

*Rht25* is proximal to *Rht14/Rht16/Rht18* {11300}.

### 44.3. Reduced height: temporary designations

**Rht\_NM9** {11273}. 2AS {11273}.  
**v:** Induced mutant NM9 {11273}.  
**ma:** *Xgwm122-2A* – 1.7 cM – *SNP34* – 1.9 cM – *Rht\_NM9* – 1.9 cM – *SNP41* – 14 .0 cM – *Xwmc261-2A* {11273}.

## 46. Hybrid Weakness

### 46.6. Hybrid weakness type II

**Add:** A gene named *NetJingW176* (after *Ae. tauschii* accession Jing Y176) was located in chromosome 2DS – *Xgwm-102-2D* – 4.5 cM – *Nec2* – 3.8 cM – *Xgwm515-2D* {11307}.



**48. Lack of Ligules**

Add to the introductory paragraph:

A dominant mutant allele for liguleless phenotype is reported in *Ae. tauschii* – this locus is located in chromosome 2DL but is independent of *LG2*.

**LG2.** **bin:** C-2DL3-0.49.  
**ma:** *Xbarc228-2D* – 12.7 cM – *Lg2/G3489\_1DL12del/G3489\_2DL11del* – 3.3 cM – *Xgdm6-2A* – 47.8 cM – *Xgwm301-2D* {11220}.

Following the *lg2* entry delete the sentence relating to diploid wheat.

**LG'** {11220}. Dominant mutation to liguleless phenotype. **bin:** C-2DL9-0.75.  
**Lg2'** {11220}. **dv:** Liguleless mutants of *Ae. tauschii* accession KU20-9 {11220}.  
**ma:** *Xgwm301-2DL*..... *Xbarc159-2D* – 9.3 cM – *LG'* {11220}.

**53. Male Sterility****53.1. Chromosomal**

**Ms1.** 4BS. **ma:** Located in a 0.05 cM region between *X27140346* and *X12360198* {11269}.  
**c:** Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is essential for pollen exine production {11269}. GenBank KX447407.  
**ms1d.** **c:** A G329A frameshift mutation in exon 1 {11269}.  
**ms1e.** **c:** A C1435T + 16-bp deletion in exon 2 {11269}.  
**ms1f.** **c:** A G155A frameshift mutation in exon 1 {11269}.  
**ms1g** {619}. See *ms5*.  
**ms1h** {11269}. **v:** Obtained in a TILLING population of QAL2000 {11269}.  
**c:** A G178A frameshift mutation in exon 1 {11269}.

**74. Stem solidness**

**Qsst.msub-3BL.** **bin:** 3BL11-0.81-1.00.  
**v:** Add: Fortuna {11230}; Genou {11230}; Judee {11230}; Rescue {11230}; S-615 {11230}; Vida {11230};

Add note before the present note: Haplotype analyses in a range of hexaploid and tetraploid accessions suggested the possibility of multiple alleles or loci in the QTL region {11230, 11239}. Conan with an intermediate level of stem solidness, represent, a different haplotype from other North American cultivars {11230}.

**Pathogenic Disease/Pest Reaction****89. Reaction to *Bipolaris sorokiniana***

**Sb2** {11255}. *Qsb.bhu-5B* {10709} 5BL {11255}.  
**bin:** 5BL1-0.55-0.75. **v:** YS116 {11255}.  
**ma:** Tightly linked to *Xgwm639-5B* and *Xgwm1043-5B* {11255}.  
**Sb3** {11256}. 3BS {11256}. **bin:** 3BS8-0.78 -1.00.  
**v:** Line 621-7-1 {11256}.  
**ma:** *Sb3/XWGGC3959* were mapped to a 2.2-cM interval between *Xbarc133/Xbarc147/Xcfp30-3B/XWGGC5911* and *XWGGC4320* {11255}; *XWGGC12798* – 0.08 cM – *SB3XWGGC9893/XWGGC10235* – 0.07 cM – *XWGGC6119* {11255}.

**90. Reaction to *Blumeria graminis* DC.****90.1. Designated genes for resistance**

**Pm2a.** **c:** NBS-LRR structure {11270}. GenBank CZT14023.1.  
**Pm4b.** **i:** 'VPM1 / 7\*Bainong 3217' {11287}.  
**ma:** *Xics13* – 1.3 cM – *Pm4b* – 1.7 cM – *Xics43* covering a 6.7 Mb physical region {11287}.

- Pm4e** {M11317}. 2AL {M11317}. **v:** D29 {M11317}.  
**ma:** *Xgdm93-2A* – 4.9 cM – *Pm4e/Xsts\_bcd1231* – 1.8 cM – *Xhbg327-2A* {113017}.
- Pm8.** **c:** Ortholog of *Pm3* with 81% homology with *Pm2a* at the nucleotide level {11276}.  
 GenBank AGY30894.1.
- Pm21.** **v:** Add: A derivative named HP33 was described as a ‘cryptic’ translocation {11275}.  
**c:** Add: NLR-V1, one of two NLR-V genes in HP33, was identified as the candidate for *Pm21* {11275}. GenBank MF716955. Silencing of *NLR-V1* compromised *Pm21* resistance in the T6AL-6VS lines described below and decreased the level of resistance in the T6DL6VS lines described below {11275}.
- Secondary recombinants 6AS<sub>10,6</sub> and 6AS<sub>16,6</sub> are reported in {11305}.
- Pm58.** **v:** U6714-A-011, PI 682090 {11320}; U6714-B-056, PI682089 {11320}.
- Pm59** {11214}. *Pm181356* {11214}. **bin:** 7AL15-0.00-1.00.  
**v:** PI 181356 {11214}.  
**ma:** *Xwmc525-7A* – 1.8 cM – *Xmag1759* – 0.5 cM – *Pm18156* – 5.7 cM – *Xmag1714* – 20.0 cM – *Xcfa2257-7A* {11214}.
- Pm60** {11250}. *PmR2* {M1800}. 7AL {11250}. **bin:** 7AL16-0.86-1.00.  
**dv:** PI 428196 {11250}; PI 428210 {11250}; PI 428215 {11250}; PI 428306 {11250}; PI 428309 {11250}; PI 428310 {11250}; PI 538737 {11250}; PI 538751 {11250}.  
**ma:** *Xwmc273.3-7A* – 3.9 cM – *scaf10-5.13* – 2.0 cM – *scaf14-17.9* – 0.3 cM – *Pm60/scaf13-6.30* – 0.7 cM – *scaf45-5.24* {11250}.  
**c:** NBS-LRR; the sequence in PI 428309 (GenBank MF996807) is 4,365 bp. The sequence of PI 428215 (GenBank MF996808) has a 240-bp insertion relative to PI 428309 whereas PI 428210 (GenBank MF996806) lacks the same sequence, which corresponds to two LRRs {11250}.
- pm60.** **dv:** G1812 {11250}.
- Pm61** {11290}. 4AL {11290}. **bin:** 4AL4-0.8-1.00.  
**v:** Xuxusanyuehuang {11290}.  
**ma:** *Xgwm160-4A* – 0.23 cM – *Pm61* – 0.23 cM – *Xicsx79* {11290}.

This gene was considered to be at a different locus to MIIW30, a dominant gene in *T. turgidum* subsp. *dicoccoides* accession IW30 and its hexaploid derivative Line 2L6 {11289}.

### 90.3. Temporarily designated genes for resistance to *Blumeria graminis*

- MIIW30** {11289}. MLIW30 [{11289}]. 4AL {11289}.  
**bin:** 4AL4-0.8-1.00  
**v:** Line 2L6 {11289}.  
**tv:** *T. turgidum* subsp. *dicoccoides* IW30 {11289}.  
**ma:** *Xbarc78-4A* – 1.00 cM – *XB1g2020.2* – 0.1 cM – *MIIw30* – 0.1 cM – *XB1g2000.2* – 2.6 cM – *Xgwm350-4A* {11289}.
- MIHLT** {18057}. 1DS {11257}. **v:** Hulutou {11257}.  
**ma:** *Xgwm-1D* – 1.7 cM – *Xwggc3026* – 1.5 cM – *MIHLT* – 2.1 cM – *Xwggc3148* – 4.0 cM – *Xcfd83-1D* {11257}.

**MIUM15** {11216}. Derived from *Aegilops neglecta*. 7AL {11216}.  
**bin:** 7AL15-0.99-1.00.  
**v:** NC09BGTUM15 {11216}.  
**al:** *Ae. neglecta* TTCC 223 {11216}.  
**ma:** *Xwmc525-7A/IWA8057* – 0.7 cM – *Xcfa2257-7A* – 0.4 cM – *MIUM15* – 0.8 cM –  
*Xcfa2240-7A* – 2.8 cM – *Xmag2185* – 3.4 cM – *IWA29295* – 4.0 cM – *IWA4434* {11216}.

**PmAF7DS** {11291}. 7DS {M10891}. **v:** Arina {11291}.  
**ma:** *Xpsr160-7D* – 1.3 cM – *Xgwm350a-7D* – 4.7 cM – *PmAF7DS* – 9.9 cM –  
*Xbarc184/Xgwm111-7D* {11291}.

Three of 61 Israeli *Bgt* isolates were avirulent: all three isolates were from tetraploid wheat accessions. It is possible that the gene may be present in many common wheat accessions.

**PmG3M** {M10102}. 6BL {11302}. **bin:** 6BL-0.7-1.00.  
**tv:** *T. turgidum* subsp. *dicoccoides* G-305-3M {11302}.  
**ma:** *Xgpw-6B* – 13.6 cM – *PmG3M* – 3.5 cM – *Xuhw213-6B* – 5.7 cM – *Xedm149-6B* {11302}.

**PmU** {11251}. 7AL {11251}. **dv:** UR206 {11251}.  
**ma:** *Xwmc273-7A* – 2.2 cM – *PmU* – 3.8 cM – *Xpsp3003-7A* {11251}.

*PmU* was transferred to, and was effective in, common wheat.

**PmX** [{11215}]. *pmX* {11215}. 2AL {11215}.  
**bin:** 2AL1-0.85-1.00.  
**v:** Xiaohongpi {11215}.  
**ma:** *Xhbg327-2A* – 0.6 cM – *PmX/Xsts-bcd1231* – 8.9 cM – *Xgpw4456-2A* {11215}.

## 95. Reaction to *Diuraphis noxia*

**Dn1.** **bin:** 7DS-0.36-0.73 {11225}.

**Dn1.** Add note: Tests of allelism indicated that *Dn1*, *Dn2*, *Dn5*, *Dn6*, and *Dnx* and four uncharacterized lines were identical or closely linked {11225}.

**Dn4.** Following the {863}. Add: ‘, 1DS {11225}’.  
 Add note: *Dn4* and an uncharacterized gene in PI 151918 were allelic or tightly linked {11225}.

**Dn6.** 7DS {0352, 18025}.  
**ma:** *Xgwm44-7D* – 11.6 cM – *Xgwm111-7D* – 3.0 cM – *Dn6* {11225}.

**Dn10** {11211}. 7DL {11211}. **bin:** 7DL-0.1-077.  
**v:** PI 682675 {11211}.  
**ma:** *Xcfd14-7D* – 2.3 cM – *Xgwm437-7D* – 9.0 cM – *Dn10* – 29.1 cM – *Xwmc488-7D* {11211};  
*Xcfd14-7D* – 3.6 cM – *Xgwm437-7D* – 11.3 cM – *Dn10* – 35 cM – *Xwmc488-7D* {11211};  
*Dn626580* – 2.0 cM – *Dn2401* – 8.4 cM – *Dn624151* {11211}.

**Dn2401.** **bin:** 7DS-0.37-0.61 {11211}.

**Dn100695** {11226}. 7DS M19026}. **v:** IG 100695 {11226}.  
**ma:** *Xgwm44-7D* – 13.0 cM – *Xcfd14-7D* – 15.7 cM – *Dn100695*.

**Dn626580** {11227}. 7DS {11227}. **v:** PI 626580 {11227}.  
**ma:** *Xgwm473-7D* – 3.2 cM – *Xbarc214-7D* – 1.8 cM – *Dn626580* {11227}.

**96. Reaction to *Eurygaster Integriceps***

Sunn pest

**Eil** {11201}. 4BS {11201}. **bin**: 4BS4-C-0.27.  
**v**: IG139431 {11201}; IG139883 {11201}.  
**ma**: *IWB73001 – Eil/BS00022785 – IWB9610* {11201}.

**97. Reaction to *Fusarium* spp.****97.1. Disease: Fusarium head scab, scab**

**Fhb1.** Modify or add:  
**v2**: Alsen *Fhb5* {11071, 11237}; Carberry *Fhb5* {11237}; ND744 *Fhb5* {11237}; ND3085 *Fhb5* {11237}; Sumai 5 *Fhb2 Fhb5* {10314, 11237}.  
**ma**: *Xgwm389-3B – 3.0 cM – Sr2/csr2 – 0.4 cM – Xgwm389-3B – 2.0 cM – Fhb1/UMN10/UMN<sub>v2</sub>* (coupling) {11210}. *Xgwm493-3B* and *Xgwm533-3B* were confirmed as useful markers {11237}.  
**c**: A pore-forming toxin-like gene product encodes a chimeric lectin with two agglutinin domains and an ETX/MTXZ toxin domain {11205}.

**Fhb5.** *Qfhs.ifa-5A* {10076}.  
**v2**: Modify or add: Alsen *Fhb1* {11237}; Carberry *Fhb1* {11237}; ND744 *Fhb1* {11237}; ND3085 *Fhb1* {11237}; Sumai 5 *Fhb1 Fhb2* {10314, 11237}.  
**ma**: *Xgwm150-5A*, *Xgwm304-5A*, and *Xgwm595-5A* confirmed as useful markers.

**97.2. Disease: Crown rot**

Three crosses involving EGA Wylie: *Qcrs.cpi-5Ds* ( $R^2 = 0.31$ ) and *Qcrs.cpi-2DL* ( $R^2 = 0.221$ ). Two additional QTL on chromosome 4BS were associated with plant height {11243}.

Nine NIL sets derived from three crosses of Australian wheat cultivars and *T. spelta* CSCR6: *Qcrs.cpi* was flanked by *Xcfp1822-3B* and *Xgwm181-3B* {11244}.

**98. Reaction to *Heterodera avenae* Woll., *H. filipjeva* (Madzhidov) Stelter, add: *H. latipons* Franklin**

At end of section:

For review {11309}.

**99 Reaction to *Magnaporthe grisea* (Herbert) Barr Add: *Syn. Pyricularia oryzae*****99.1** Current *Mg* list.**99.2 Reaction to *Magnaporthe oryzae*.*****Rmg8*.**

Add note: *Rmg8* also confers resistance to the wheat form of the pathogen. Its response is not sufficiently effective when present alone, but is enhanced in the presence of *RmgGR119* {11263}.

AVR-*Rmg8* was isolated and shown to be a small protein with a putative signal peptide. This protein was recognized by both *Rmg8* and *Rmg7* {11272}.

***RmgGR119*** {11263}. **v**: GR119 {11263}.

*RmgGR119* confers resistance to the wheat form of the pathogen and its response is enhanced in combination with *Rmg8* {11263}.

Add Note: Near-isogenic lines with the T2A–2NS translocation from *Ae. ventricosa* displayed reduced levels of spike blast, but there was little effect on seedling leaf blast response {11265}: **v**: Milan; VPM1.

**100. Reaction to *Mayetiola destructor* (Say)**

**H26.**                    **ma:** *Xrwgs-3D* – 3.2 cM – *H26/Xrwgs11-3D* – 1.0 cM – *Xrwgs12-3D* {M11318}.

**101. Reaction to *Meloidogyne* spp.**

**Rkn3.** Reference {11264} added to reference {10801} for this gene.

**103. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano); *Parastagonospora nodorum***

**Snn5** {11203}.                    4BL {11203}.                    **bin:** 4BL5-0.85-1.00.  
**tv2:** Lebsock *Tsn1 Snn3-B1* {11203}.  
**ma:** *Xbarc163/Xcfd22-4B* – 13.3 cM – *Snn5* – 2.8 cM – *Xwmc349-4B* {11203}.

**snn5.**                    **tv2:** PI 94749 {11203}.

**Snn6** {11206}.                    6AL {11206}.                    **v:** Opata 85 {11206}; RIL ITMI137 {11206}.

**snn6.**                    **v:** Synthetic W-7984 {11206}.  
**ma:** Flanked by XBE424987 and XBE403326 {11206}.

**Snn7** {11292}.                    Sensitive to SnTox7.                    2DL {11292}.  
**bin:** 2DL-9-0.75-1.00.  
**s:** CS(Timstein 2D) {11292}.  
**v:** Timstein {11292}.  
**ma:** *Xcdf267-2D* – 2.3 cM – *Xgdm6-2D* – 0.9 cM – *Snn7/Xcfd44-2D* – 1.8 cM – *Xgwm349-2D* – 11.3 cM – *Xgwm311-2D* {11292}.

**106. Reaction to *Puccinia graminis* Pers.**

**Sr2.**                    **ma:** *Xgwm389-3B* – 3.0 cM – *Sr2/csr2* – 0.4 cM – *Xgwm389-3B* – 2.0 cM – *Fhb1/UMN10/UMN<sub>v2</sub>* (coupling) {11210}.

**Sr5.**                    **ma:** Flanked by *Xbarc183-6D* and *wPt3879* {11232}.

**SR13.** Revised listing.

**Sr13** {674}.                    6AL {929}.                    **bin:** 6AL-8  
**ma:** *Xwmc59-6A* – 5.7 cM – *Sr13* {10607}; *CD926040* – *Sr13* – *BE471213* {10777}.  
**c:** *Sr13* was identified as a CC–NBS–LRR gene with three haplotypes in two specificities {11217}.

**Sr13a** {674, 11217}.

**i:** Khapstein /9\*LMPG {685, 11217}; Khapstein / 10\*Marquis Sr7b {686}.  
**v:** Machete {10607}.  
**v2:** Khapstein *Sr7a Sr14* {674}.  
**tv:** Kronos PI 576168 {11217}; Langdon {11217}; Maier {11217}; Renville {11217}; ST464-C1 {10473}.  
**tv2:** Khapli *Sr14* {674}.

**Sr13b** {11217}.                    **tv:** D99656 {11217}; Kofa PI 584336 {10777; 11217}; Medora PI496260 {10777, 11217}; Sceptre {10777}.

Haplotypes of other germplasm previously listed are unknown.

**v2:** French Peace *Sr7a Sr9a* {680}.  
**tv2:** Arrivato *Sr8b Sr9e* {10607}; ST464 *Sr9e* {10473}.

**Unspecified allele.** tv: PI534304 {11280}.

A resistance gene in 'Khapstein / 9\*LMPG' and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However, the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance locus mapped in {10778} could not be *SR13*.

**Sr21.** v: CSSr21 {M10115}.  
**madv:** *CJ961291* – 0.02 cM – *Sr21* – 0.04 cM – NLR pseudo-gene cluster {11315}; A diagnostic marker was developed from the cloned gene {11315}.  
 cc: *Sr21* is a CC–NBS–LRR gene of 4,872 bp; 44 diploid accessions with *Sr21* were classified as five haplotypes – i.e., Haplotype R1, MG582649, 28 accessions including DV92 (and CSSr21); Hap R2, GenBank MG601519, six accessions; Hap R3, MG601520, one accession; Hap R4, MG601521, six accessions; and Hap R5, MG601522, three accessions {11315}.

**Sr22.** cc: *Sr22* has CC–NBS–LRR structure: NCBI LN883743 {11213}.

**Sr25.** v: Misr 1 (Oasis/Skauz//4\*BCN/3/2\*Pastor) {11260}.

**Sr33.** cc: GenBank KF031291; 4,639 bp; protein CUM44200.1.

**Sr35.**

Add note: *Sr35* was postulated in 21 accessions of *T. monococcum* subsp. *monococcum* {11288}.

**Sr45.** cc: *Sr45* has CC–NBS–LRR structure: NCBI LN883757 {11213}.

**Sr46.** bin: 2DS5-0.47-1.00.

**dv:** *Ae. tauschii* var. *meyeri* AUS18913 {10538} = Clae 25 {11268}; *Ae. tauschii* TA1703 {11268}.

**ma:** *Xgwm210-2D* – 3.9 cM – *Sr46* – 5.6 cM – *Xcfd36-2D* – 0.3 cM – *Xwmc111-2D* {11268}.

Add note:

*Sr46* was more effective at higher temperatures in laboratory tests {11268}.

**Sr47.** Modify: 2B = T2BL–2SL–2BL·2BS.

tv: RWG35 {10872}; RWG36 {10872}; RWG37 {10872}.

Add note immediately following the **ma:** entry:

Further markers were used to identify the introgressions in RWG25, RWG26, and RWG27 {10872}. STS marker *Xrwgs38* was diagnostic for the *Sr47* segment in DAS35 and DAS36 {11319}.

**Sr50.** v: T1DL1RS–DR.A1 {11316}.

cc: *Sr50* is a CC–NBS–LRR gene homologous to barley *Mla* {11316}. GenBank KT725812, 3,508 bp.

**Sr60** {11208}. 5A<sup>m</sup>S {11208}. **dv2:** PI 306540 *Sr21* *SrTm4* *SrTm5* {11208}.

**ma:** *Pinb-5A<sup>m</sup>S.....GH724575/DK22976/CA5012332* – 0.25 cM – *Sr60/LRRK123.1* – 0.19 cM – *CJ942731/CJ884584* {11208}; *GH724575* – 1.56 cM – *Sr60/LRRK123.1* – 0.52 cM – *FD475316* {11208}.

**SrTm5** (11208). 7A<sup>m</sup>L {M11208}.

**dv:** *T. monococcum* subsp. *monococcum* PI 277131-2 {11208}.

**dv2:** *T. monococcum* subsp. *monococcum* PI 306540 *Sr21* *Sr60* *SrTm4* {11208}.

**ma:** *SrTm5/IWB25012/IWB44281/IWB405527/Sr22GMF/GMR* – 0.8 cM – *IWB6942* {11208}.

May be allelic with *Sr22* {112308}.

*Sr10526* {11249}. 6DS {11249}. v: C1tr 105026 {11249}.  
**ma:** *IWB36391/IWB34477* – 2.9 cM – *Sr15026* – 3.0 cM – *IWA4000* {11249}; *IWB36391* – 0.4 cM – *IWB262* – 2.6 cM – *Sr15026* – 1.3 cM – *IWB49086* {11249}.

*Sr150026* was detected with races QFCSC and TTTTF. When the same DH and RIL populations were tested with race TRTTF, there was evidence for complementary resistance genes on chromosomes 6DS and 6AS, one of which was *Sr10526*. When the populations were tested in the field in Kenya with Ug99 races *QSr.abr-6AS.1* ( $R^2 = 0.1-0.3$ ) was detected.

Add note at the end of the section: Consensus maps of many reported genes and QTL for stem rust resistance are provided in {11202}.

QTL:

‘Spark / Rialto’ DH population: *Sr5* and *Sr31* were derived from Rialto and *QDr.sun-3BS* (*Xgwm1034-3B* – *BS00010945* region and *QSR.sun-5A* (*Xgwm445-5A* – *Xgwm205-5A* region) were derived from Spark {11231}.

### 106.1. Designated genes for resistance to stripe rust

***Yr3a***. After ‘1B {185, 184}’ add:, revised to 5BL {11235}. 2B.

***Yr5***. **ma:** Add: Accurate prediction of *Yr5* was achieved with markers *IWA4096*, *IWA 6121* and *IWA7850* for which primer sequences are available in Cereals DB 11286}.

***Yr10***. **v:** Crest {11304}; 10 Chinese cultivars {11304}.  
**ma:** *Yr10/Xsdauw79* – 0.2 cM – *Xsdauw78* – 1.0 cM – *Yr10<sub>CG</sub>* – 2.1 cM – *Xsdauw75* – 0.5 cM – *Xpsp3000-1B* {11304}.  
**c:** AF149112 (*Yr10<sub>CG</sub>*) shown not to be the candidate gene {11304}.

***Yr15***. **v:** Add: Ochre {11240}.  
**ma:** Add: *Xbarc8-1B* – 0.26 cM – *R11/R5* – 0.51 cM – *Yr15* – 0.26 cM – *Xgwm413-1B/R8* {11240}.

***Yr17***. *YrHy1* {11308}, *YrMm58* {11308}.  
**v:** Huaiyang 1 {11308}; Kochu {11267}; Mengmai 58 {11308}; Milan {11267}; Mutus {11267}.

Add note at the end of section: Although *Yr17* was reported as a seedling-effective gene {62} some researchers report problems in obtaining repeatable seedling responses and prefer to treat this gene as conferring adult-plant resistance {11221}.

***Yr18***.

Add at end of section: *Yr18* conferred seedling resistance to leaf rust when transformed into durum wheat {M10114}.

***Yr24***. **v:** Neimai 836 {11259}.

***Yr29***. **v2:** Add: Druchamp {11235}.

***Yr34***. Add: Syn. *Yr48* {11266}.  
**v:** UC1110/PI610750 RIL#143 {11266}.  
**ma:** *Xgwm291-5A* – 0.5 cM – *B1* – 1.5 cM – *Yr34/Xgwm410.2-5A/Xcfa2149-5A/KASP\_109/KASP\_6988*/etc. {11266}; *Xgwm291-5A* – 2.3 cM – *B1* – 0.7 cM – *Yr34/Xgwm410.2-5A/Xcfa2149-5A/KASP\_109/KASP\_6988*/etc. {11266}.

*Yr34* is <1 cM from the awn inhibitor *B2* {11266}.

***Yr36***. **v:** Add: Shumai 1701 {11258}.  
**tv:** Add: *T. turgidum* subsp. *dicoccum* PI 415152 {M10058}.

Add note: Although originally described as conferring high-temperature, adult-plant resistance, this gene confers partial resistance in both juvenile and adult plants at temperatures less than 18°C {11277}.

**Yr46.** v: Add: Kundan {M0848}.

**Yr48.** Add: Syn. *Yr34* {11266}.  
v: UC1110/PI610750 RIL#143 {11266}.

**Yr79** {11222}. 7BS {11222}. **bin:** 7BL-0.40-0.45.  
v: PI 182103 {11222}; PI 679609, Avocet S / PI 679609 RIL#195 {11222}.  
**ma:** *IWA220* – 2.9 cM – *Yr79* – *Xwmc335-7B* – 0.9 cM – *Xbarc72-7B* – 1.7 cM – *Xgwm297-7B* – 1.6 cM – *Xgwm333* {11222}.

**Yr80** {11261}. Adult-plant resistance. *YrAW11* {11261}.  
3BL {11261}. **bin:** 3BL2-C-0.22.  
v: AUS27284 {11261}.  
**ma:** *Xgwm3763B* – 15.2 cM – *KASP\_5392/KASP\_65624* – 3.0 cM – *Yr80* – 4.9 cM – *KASP\_53113* {11261}.

**Yr81** {11262}. *YrAW5* {11262}. 6AS {11262}  
v: AUS27430/AvS RIL#16 {11262}.  
**v2:** AUS27430 *Yr18* {11262}.  
**ma:** *Xgwm459-6A* – 19.0 cM – *KASP\_3077* – 4.4 cM – *Yr81* – 2.8 cM – *KASP\_79351* {11262}

#### 107.2. Temporarily designated gene for resistance to stripe rust

**YrF** {11218}. 2B {11218}, 2BS {11219}.  
**v2:** Francolin#1 *Yr29* {11218, 11219}.  
**ma:** *Xgwm374-2B* – 2.0 cM – *YrF* – 1.8 cM – *Xwmc474-2B* {11219}.

**YrHu** {11229}. Derived from *Psathyrostachys huashanica*. 3AS {11229}.  
**bin:** 3AS4-0.45-1.00.  
v: H9020-17-25-6-4 {11229}.  
**ma:** *Xcfd79-3A* – 7.2 cM – *YrHu* – 0.7 cM – *BG604577* {11229}.

GISH failed to detect foreign chromatin {11229}.

**YrH62** {11303}. 1B {11303}.  
v: Line 03031-1-5 (ex CIMMYT) {11303}.  
**ma:** *Xgwm273-1B* – 3.7 cM – *Ax-109871410/Ax-109472792/Ax109352427* – 0.3 cM – *YrH62* – 0.8 cM – *Ax-109862469* – 2.1 cM – *Xbarc137-1B* {11303}.

**YrLk** {11252}. 7BL {11252}.  
v: Lankao 5 {11252}.  
**ma:** *Xbrac267-7B* – 4.4 cM – *YrLk* – 3.3 cM – *Xwmc396-7B* {11252}.

**YrLM168a** {11284}. Adult-plant resistance. 6BL {11284}  
v: LM16a {11284}; LM16b {11284}.  
**ma:** *Xwmc756-6B* – 4.6 cM – *YrLM168a* – 4.6 cM – *Xbarc146-6B* {11284}.

LM168a and LM168b are derivatives of Milan {11284}.

**YrMY37** {11282}. *yrMY37* {11282}. Recessive.  
7BL {11282} v: Mianmai 37 {11282}.  
**ma:** *Xwmc476-7B* – 1.57 cM – *Xgwm297-7B* – 0.79 cM – *YrMY37* – 0.38 cM – *Xbarc267-7B* {11282}.



YrMY41 {11271}.

1B {11271}.

v: Mianmai 41  
{11271}.

A cross with AvS+Yr26 failed to segregate. Although claimed to be a possible allele of Yr24/Yr26, the gene identified is likely to be the same.

### 107.3. Stripe rust QTL

‘Avocet (S) / Kundan (R)’: Yr46 plus *QYr.com-2AL* flanked by 3064488\_30:T>G ( $R^2 = 0.05-0.09$ ), *QYr.cim-3DS* flanked by 3021242 and 224356 ( $R^2 = 0.04$ ) and *QYr.cim-5AS* flanked by 3025355\_10:T>C and 1067590 ( $R^2 = 0.04-0.05$ ) {11248}.

‘Avocet S (S) / Napo 63 (R)’: *Qyrnap.nwafu-2BS* (11283).

2BS {11283}.

**bin:** 2BS-1-0.53. **ma:** Mapped to a 5.46 cM interval flanked by KASP markers 90K-AN34 and 90K-AN36; and by *Xbarc55-2B* and *Xgwm374-2B* {11283}.

‘Avocet R (S) / Chilero’: *Lr46/Yr29*, *QLr.cim-5DS/QYr.cim-5DS*, *QYr.cim.6BS* and *QYr.cim-7BL* from Chilero, and *QLR.cim-1DL/QYr.cim-1DL* from Avocet R {11306}.

‘Druchamp (R) / Michigan Amber (S)’: Eight QTL for high-temperature, adult-plant resistance: QTL in chromosomes 1BL (nearest marker *Xgwm131-1B*), 2BL (*IWA7583*) and 5BL (2, *IWA2558* and *IWA6383*) were stable across environments, whereas genes in chromosomes 1BL (*IWA8581*, probably *Yr29*), 1DS (*IWA22668*), 3AL (*IWA6834*), and 6BL (*IWA6420*) were not {11284}. In addition, three QTL for all-stage resistance were detected on chromosomes 5B (probably *Yr3*, *IWA6271*), 5DL (*IWA8331*), and 6BL (*IWA3297*).

‘Kariega / Avocet S’ DH population: Add to existing entry:

These locations were confirmed in a subsequent study; *QYr.sgi-2B.Ia* was located within the *wPt5556 – wPt6278* segment {11232}.

‘Mingxian (S) / P1057’ RIL population, and ‘Avocet S (S) / P10057’ and ‘Zhengmai 9023 (S) / P10057’  $F_2:F_3$  populations: Two strong QTL located in clustered QTL regions: *Qlrlov.nwafu-2BS* identified by *IAW5377*, *IWA2674*, *IWA5830*, and *Qyrlov.nwafu-3BS* identified by *IWB57990* and *IWB6491* {11279}.

‘Yaco S (R) / Mingxian 169 (R)’: Adult-plant resistance. *Qyryac.nwafu-2BS* located within a 1.3-cM region flanked by KASP markers *BS00022657\_51* and *IACX6411.BobWhite\_22503\_605* within the 10.4 cM *Xgwm148-2B – Xbarc55-2B* region {11241}.

Add at end of section: Markers associated with many stripe rust resistance genes are summarized in {11254}.

## 108. Reaction to *Puccinia triticina*

### 108.1. Genes for resistance

**Lr15.** **bin:** 2DS1-0.33-0.47.

**ma:** *Xgwm4562-2D – 3.1 cM – Lr15 – 9.3 cM – Xgwm102-2D* {11234}.

**Lr16.** **v2:** Francolin#1 Lr46 {11219}; Waxwing {11267}

**ma:** *Xwmc764-2B – 9.4 cM – Lr16 – 1.4 cM – Xwmc661-2B* {11219}.

**Lr21.** **ma:** Add: *Lr21*-mediated resistance requires expression of *RARI*, *SGT1*, and *HSP90* {11274}.

**Lr22a.** **i:** CH Campala Lr22a {11209}.

**v:** Line 98B34-T4B {10467}.

**ma:** *Xgwm455-2D – 0.39 cM – Lr22a – 1.1 cM – Xgwm296-2D* {11209}.

**c:** GenBank KY064064; NBS-LRR structure encoding an intracellular immune receptor homologous to the *Arabidopsis thaliana* RPM1 protein {11209}.

**Lr29.** **v:** Add: Kundan {11248}.

**Lr34.** Add at end of section

*Lr34* conferred seedling resistance to leaf rust when transformed into durum wheat {11314}.

**Lr36.** v: Add: CDC Bounty {11253}.

**Lr39.** Add: synonym *LrT* {11207}.

v: 'PBW114 / *Ae. tauschii* PAU14195 // 4\*WH542' backcross selections {11207}.

dv: *Ae. tauschii* PAU14195 {11207}.

ma: *Xcau96-2D* – 1.6 cM – *LrT (Lr39)* – 0.6 cM – *Xbarc124-2D* – 0.3 cM – *Xte6-2D* – *IwT* – 4.1 cM – *Xgdm35-2D* {11207}.

**Lr61** {11224}. *LrAW2* {11223}. 6BS {11223}.

tv: AUS 26579 {11224}; PI 244061 {11280}.

tv2: AUS 26582 *Lr79* {11224}.

ma: *sun682* – 0.7 cM – *Lr61/sun683/sun684* – 0.2 cM – *sunKASP\_60* {11223}; *sun682* – 0.6 cM – *Lr61/sun684* – 0.6 cM – *sunKASP\_59* {11223}.

**Lr67.** c: GenBank: coding sequence KR604817.2, 1,545 bp; protein sequence ALL26331.2, 514 amino acids.

**Lr74.** Add note:

'Tc\*3 / Caldwell' population: a gene for adult-plant resistance derived from Caldwell was identified with closest marker *Xcfb5006-3B*; the 'Tc\*2 / Caldwell 24-1' parent shared the same T allele at KASP marker IWB44132 as Spark and BT-Schomburgk Selection {11281}.

**Lr78** {11212}. *QLr.cdl.5D* {11212}. 5DS {11212}.

v: 'Tc\*3 / Toropi 4A212A' {11212}.

v2: Toropi (actual accession source not available) {11212}.

ma: *Lr70* – 5.6 cM – *Xbarc130-5D* – 1.8 cM – *Xwmc233-5D* .....*Xcfd189-5D* – 13.2 cM – *IWA2689* – 2.2 cM – *Lr78* – 8.0 cM – *Xcfa2104-5D* {11212}.

According to Somers et al. (2004) *Xbarc130* is in bin 5DS2-0.78-1.00 and *Xcfd189* in bin 5DS1-C-0.63.

**Lr79** {11224}. *LrAW3* {11224}. 3BL {11224}. bin: 3BL-0.63-0.90.

tv: 242/Bansi#149, C18.1 {11224}.

tv2: AUS26582 *Lr61* {11223, 11224}.

ma: *KASP\_31457* – 8.1 cM – *sun770* – 2.9 cM – *Lr79* – 1.8 cM – *sun786* {11224}.

*Lr79* conferred resistance to Australian common wheat Pt races, but not to durum-specific Ethiopian and Californian races {11224}.

**LrPI244061** {11280}. 2BS {11280}. tv: PI 244061 {11280}.

ma: *LrPI144061* – 11.5 cM – *KASP\_2BS\_IWB6117* {11280}.

Add note: This gene may be *Lr13* {11280}.

**LrPI287263** {11280}. 6BL {11280}. tv: PI 287263 {11280}.

ma: *LrPI287263* – 2.8 cM – *KASP\_6BL\_IWB44753* – 2.8 cM – *Xdupw217* {11280}.

**LrPI209274** {11218}. 6BS {11280}. tv: PI 209274 {11280}.

ma: *KASP\_6BS\_IWB39456* – 3.7 cM – *LrPI209274* – 1.0 cM – *KASP\_6BS\_IWB6117* – 8.1 cM – *Xdupw217-2B* {11280}.

This gene may be *Lr53* {11280}.

**108.3. QTL for reaction to *P. triticina***

‘Avocet / Kundan’ RIL population: *Lr29* (flanked by *10902272* and *02414*,  $R^2 = 0.5-0.65$ ), *QLR.cim-2BL* flanked by *1237388* and *1081780\_35C>T* from Avocet and *QLr.cim-2DS* flanked by *1237388* and *1081780\_35C>T* from Kundan {11248}.

‘Avocet R (S) / Chilero’: *Lr46/Yr29* and *QLr.cim-5DS/QYr.cim-5DS* from Chilero and *QLR.cim-1DL/QYr.cim-1DL* from Avocet R {11306}.

‘CI 13227 (R) / Lakin (MS)’ DH population: Adult-plant resistance conferred by *QLR.hwwg-2DS* ( $R^2 = 0.11-0.26$ ), *QLr.hwwg-7BL* ( $R^2 = 0.08-0.19$ , likely *Lr68*) and *QLr.hwwg-7AL* from CI 13227, and *QLr.hwwg-3BS* from Lakin {11311}.

‘Ning7840 / Clark’ RIL population: *QLr.hwwg-5AS* from Ning 7840; *QLr.hwwg-6AS* from Clark, flanked by *barc23-6A* and *IWA3321*; *QLr.hwwg3BS.I* from Clark, flanked by *IWA4654* and *IWA1702*, possibly *Lr74*; and *QLr.hwwg-7DS/Lr34* from Ning 7840 {11278}.

‘Thatcher\*3/Americano 44d’ RIL population: QTL for adult-plant resistance identified on chromosomes 3AS (*QLr.cdl-3A*), 3DS (*QLr.cdl-3DS*), and 6DS (*QLr.cdl-6D*); both the 3AS and 3DS QTL were required for expression of resistance {11296}.

Genotype lists: To Chinese cultivars: add reference {‘, 11310’}.

Add at end of section: See {18053} for historical review of leaf rust work in Canada.

**109. Reaction to *Pyrenophora tritici-repentis*****109.1. Insensitivity to tanspot toxin (necrosis)**

*Tsn1*. Insert at the end of the section, but before ‘A review.....’:

Tsn–ToxA interaction has a major role in SNB development in both common and durum wheat whereas it has a variable role in tanspot development in bread wheat and is not a significant factor for tanspot development in durum wheat {M18004}.

**116. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa***

**Bt9.** 6DL {11299}. v: PI 554099 {11299}.

**Bt10.** *QCbt.spa-6D* {M118098}. v: PI 554118 {11299}.

**Bt11.** 3B {11297}.

**ma:** May be associated with *Xbarc180*, *Xwmc623*, *Xwmc808*, and *Xgwm285* {11297}.

QTL:

‘Carberry / AC Cadillac’: AC Cadillac contributed QTL *QCbt.spa-6D* (*Bt10*) on chromosome 6D (markers *XwPt-1695*, *XwPt-672044*, and *XwPt-5114*). Carberry contributed *QCbt.spa-1B* (*XwPt743523*), *QCbt.spa-4B* (*XwPt 744434-Xwmc617*), *QCbt.spa-4D* (*XwPt-9747*), *QCbt.spa-5B* (*XtPt-3719*), and *QCbt.spa-7D* (*Xwmc273-7D*) {11298}.

At end of section: Additional QTL are listed in {18099}.

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**VI. ABBREVIATIONS AND SYNONYMS 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 mosaic 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* = *Septoria 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. *armeniicum* = *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 bessarabicum*

*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<sup>2</sup>** = square meters

**m<sup>3</sup>** = 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** = quantitative 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-HPLC** = 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 tagged 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 65 MANUSCRIPT GUIDELINES.**

The required format for Volume 65 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 44–64 of the *Newsletter* in coordinating 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](mailto:jraupp@k-state.edu).

**DISTRIBUTION:**

The only method of distribution of Volume 65 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* also will continue to be available (Vol. 37–64) through the Internet on Grain-Genes, the USDA–ARS Wheat Database at <http://wheat.pw.usda.gov/ggpages/awn/>.