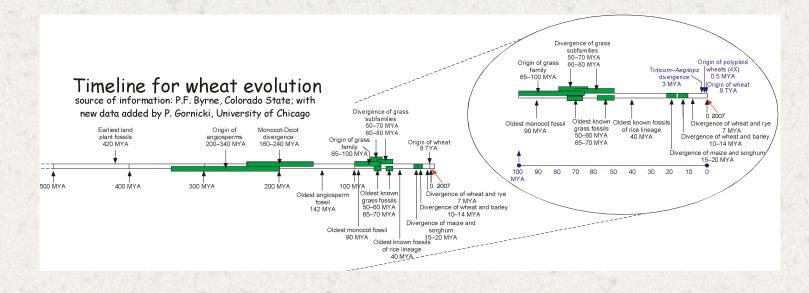
ANNVAL WHEAT NEWSLETTER

Volume 61



Contribution no. 16-066-B from the Kansas Agricultural Experiment Station, Kansas State University, Manhattan.

ANNUAL WHEAT NEWSLETTER

Volume 61

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

1 September, 2015.

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James S. Quick

Dr. James S. (Jim) Quick of Fort Collins, passed away early on the morning of 5 July, 2015, following a long illness, in the comfort of his home, surrounded by his loving family. He was born on 20 October, 1940, on a farm near Starkweather, North Dakota, to James Rodrick and Anna Selma (Sather) Quick, the oldest of seven children.

Jim's interest in plant breeding began with a 4-H crops projects and continued through his undergraduate experience with the wheat genetics project at North Dakota State University (NDSU) and the USDA. He received his B.S. degree from NDSU and his M.S. and Ph.D. degrees in plant breeding and genetics from Purdue University. Upon completion of his Ph.D., he served in India with the Rockefeller Foundation in sorghum research for three years and then returned to NDSU as an Associate Professor. He made significant contributions in



durum wheat breeding and cultivar development during his 12-year tenure at NDSU. In 1981, Jim joined Colorado State University (CSU) as a Professor and Leader of the Wheat Investigations project. In the next 23 years he made significant contributions in several areas: hard red winter wheat breeding and improved methodology, high-temperature tolerance, Russian wheat aphid resistance, and herbicide tolerance. He and his associates released more than 30 new wheat cultivars and several improved germplasm lines. One of Jim's most long-lasting contributions to the Colorado wheat industry was his idea to create the Colorado Wheat Research Foundation (CWRF) in collaboration with Colorado wheat industry leaders. The CWRF returns substantial research funding to the wheat breeding and wheat-related research programs annually based on seed sales of CSU-developed wheat cultivars that are marketed by the CWRF under the Plains Gold Brand.

Jim was especially proud to have served as major professor for 23 Ph.D. and M.S. candidates at NDSU and CSU. He also served the Crop Science Society of America as an Associate Editor of *Crop Science*. He also was the Editor of the *Annual Wheat Newsletter* from 1983 to 1994.

In 1996, Dr. Quick became Head of Soil and Crop Sciences at CSU and served in that role until his retirement in 2003. After retirement from CSU in 2003, Jim was employed as a consultant/ durum wheat breeder for the Dakota Growers Pasta Company and led the development of two new durum wheat cultivars.

Dr. Quick received numerous awards in recognition of his professional service. He was awarded Fellowships in the American Society of Agronomy and Crop Science Society of America; the



Agronomic Achievement Award, Crops, and the Agronomic Research Award from the ASA; and the Faculty Certificate of Merit Award from Gamma Sigma Delta. He was named a 'Legend' of the Department in 2009, our Centennial Year.

Jim was a scientist and teacher, world traveler, skier, family historian, and gardener extraordinaire. He also was a wonderful husband, loving father, and adoring grandfather. In 1993, he met his current wife, Jackie Panuska; they were married in Fort Collins on 13 June, 1994, and recently celebrated their 21st anniversary. He was preceded in death by his parents, James and Anna, and brothers, Richard and John.

He is survived by his wife, Jackie Panuska; three daughters, Alissa J. Quick of Bloomington, IN, Katie A. Quick May (Daniel Fairbank) of Fort Collins, and Jeanette S. Quick Sandlin (Mark) of Greensboro, NC; and their mother, Rosemary Davenport (Chris Reid) of Fort Collins; also step-children, Robin Horak of Boston, MA, and Jason Horak (Alice Kunce) of Little Rock, AR; grandchildren, Cassandra and Nathan May, and step-grandchildren, Kayli and Hunter Sandlin, Lyrian Ruesch, and Raymond Knight. He also is survived by siblings, Bobby Ann (Wayne) Paintner of Sundance, WY; Joan (Dennis) Bangen of Casper, WY; Mary Ellen (Jim) Spenningsby of Duluth, MN; and Marcia (Mike) Zimmerman of Garrison, ND; and sister-in-law, Joan Quick of Hickson, ND.

A Memorial to honor his life is planned for 22 August, 2015, from 2:00-4:00pm in the West Ballroom of the Lory Student Center at CSU.

Awards and Recognition

- Durum Industry Achievement Award, U.S. Durum Growers Association, 1976
- Member, US–USSR Spring Wheat Visit Team, 1976
- Sabbatical Leave, Plant Breeding Institute, Cambridge, United Kingdom, 1977-1978
- Fellow, American Society of Agronomy, 1985
- Fellow, Crop Science Society of America, 1986
- Shepardson Instruction Development Grant Award, CSU, 1985
- Distinguished Toastmaster Award, Toastmasters International
- Australian Wheat Research Council Grant Award, 1987
- Faculty Certificate of Merit, Gamma Sigma Delta Award, 1987
- Honor Society of Agriculture, CSU, 1989
- USDA NCISE□IARC Award for Study at CIMMYT, Mexico, 1995
- Agronomic Achievement Award, crops, American Society of Agronomy, 1996
- Agronomic Research Award, American Society of Agronomy, 2002

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 F₁ hybrid, synthetic, or multiline cultivar;
 - (e) Use as a recurrent parent in backcrossing;
 - (f) Mutation breeding;
 - (g) Selection of somaclonal variants; or
 - (h) Use as a recipient parent for asexual gene transfer, including gene transfer using molecular genetic techniques.
- 4. Plant materials of this nature entered in crop cultivar trials shall not be used for seed increase. Reasonable precautions to ensure retention or recovery of plant materials at harvest shall be taken.

ITEMS FROM BRAZIL

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

Wheat in Brazil – 2014 crop year.

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

In 2014, the Brazilian wheat production was a little bit higher than 5×10^6 tons (Conab 2015), which is enough to supply 50% of the domestic demand (Table 1). The southern region, comprised of the states of Rio Grande do Sul, Santa Catarina, and Paraná, accounts for 92.5% of the national production. Nonetheless, due to the characteristics of the cultivation system, average grain yield in this region is not the highest in the country.

The weather conditions in the south of Brazil were not favorable to wheat in 2014. High temperatures associated to high humidity during grain filling increased the incidence of Fusarium Table 1. Cultivated area, total production and grain yield ofwheat in Brazil in 2014 (* estimated value - March, 2015. Source:CONAB. 2015. Companhia Nacional de Abastecimento. Centralde Informações Agropecuárias/Grãos/Trigo. Available at: http://www.conab.gov.br/conabweb/index.php?PAG=131).

Region	Area (ha x 1,000)	Production (t x 1,000)	Grain yield (kg/ha)
North	—	—	—
Northeast	—	_	—
West-central	23.3	85.8	3,682.0
Southeast	130.5	354.6	2,717.0
South	2,576.6	5,463.5	2,120.0
Brazil [total]	2,730.4	5,903.9*	2,162.2*

head blight. Therefore, the grain quality was poor. Furthermore, the qualitative analysis of the grains indicated high concentration of micotoxin (DON).

Reference.

CONAB. 2015. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Available at: <u>http://www.conab.gov.br/conabweb/index.php?PAG=131</u>.

Performance of wheat cultivars in the state of Rio Grande do Sul, Brazil, 2013.

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

The Brazilian Commission of Wheat and Triticale Research (BCWTR) annually conducts the State Test of Wheat Cultivars in Rio Grande do Sul state (STWC–RS), aimed at supporting the indications of cultivars. This work has the objective of evaluating wheat cultivar grain yield performance of STWC–RS in 2013. The yield grain performance of 30 wheat cultivars (Ametista, BRS 327, BRS 328, BRS 331, BRS Guamirim, BRS Parrudo, Campeiro, CD 1440, CD 1550, Estrela Átria, Fundacep 52, Fundacep Bravo, Fundacep Horizonte, Fundacep Raízes, Jadeíte 11, JF 90, Marfim, Mirante, Quartzo, TBIO Alvorada, TBIO Iguaçu, TBIO Itaipu, TBIO Mestre, TBIO Pioneiro, TBIO Seleto, TBIO Sinuelo, TBIO Tibagi, TEC Frontale, TEC Vigore, and Topázio) was studied in 15 environments (Caxias do Sul, Coxilha, Cruz Alta – season 1, Cruz Alta – season 2, Cruz Alta – season 3, Não-Me-Toque, Passo Fundo – season 1, Passo Fundo – season 2, Sertão, Vacaria, Augusto Pestana, Eldorado do Sul, Independência, Santo Augusto, and São Borja), in Rio Grande do Sul in 2013. The experiments were carried out in a randomized block design with three or four repetitions. Each plot consisted of five 5-m rows with 0.2-m spacing between rows and a plant density of approximately 330 plants/m². Grain

yield data (kg/ha) were subjected an analysis of variance for individual (each) and group (all) environments. The grouped ANOVA was performed employing the mixed model (fixed cultivar effect and randomized environment effect). The grain yield performance of wheat cultivars was evaluated by analysis of adaptability and stability, employing the method of distance from the ideal cultivar, weighted by the coefficient of residual variation, proposed by Carneiro (1988). In this analysis, the ideal cultivar was considered as the cultivar with high grain yield, high stability, low sensitivity to adverse conditions of unfavorable environments, and able to respond positively to improvement of favorable environments. The general average of the STWC–RS in 2013 was 4,860 kg/ha. The experiment conducted in Santo Augusto had the highest average of wheat grain yield, 6,884 kg/ha. The maximum wheat grain yield was 8,223 kg/ha in Santo Augusto (cultivar Quartzo). The cultivars TBIO Sinuelo, Mirante, TBIO Mestre, and TEC Vigore had adaptability and stability in favorable environments with average of wheat grain yield higher than the general average). TBIO Sinuelo, TEC Vigore, and Estrela Átria had adaptability and stability in unfavorable environments (environments with average of wheat grain yield lower than the general average). In general, an average of all environments, TBIO Sinuelo (5,634 kg/ha), TEC Vigore (5,231 kg/ha), Mirante (5,317 kg/ha), and TBIO Mestre (5,208 kg/ha) came closest to the ideal cultivar.

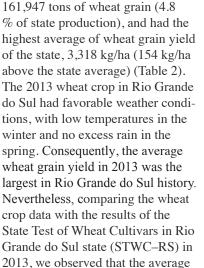
Reference.

Carnerio PCS. 1998. New methodologies for analyzing the stability and adaptability of behavior. Ph.D. thesis in genetics and breeding, Post-graduate Program in Genetics and Breeding, Federal University of Viçosa.168 pp.

Wheat crop in the state of Rio Grande do Sul, Brazil, in 2013.

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

The state of Rio Grande do Sul is one of the main wheat-producing states in Brazil. Our objective was to analyze the wheat crop in Rio Grande do Sul in 2013. In 2013, the state of Rio Grande do Sul harvested 1,059,032 ha of wheat (50.7 % of the total area harvested in Brazil), producing 3,351,150 tons of wheat (58.4 % of Brazilian production), with an average of grain yield of 3,164 kg/ha (415 kg/ ha above the Brazilian average of 2,749 kg/ha) (Table 2). Among the geographical mesoregions of Rio Grande do Sul (Fig. 1), the RS Northwest mesoregion harvested the largest wheat area, 834,788 ha (78.8 % of the cropped area in the state), and had the largest production, 2,675,218 tons of wheat grain (79.8 % of state production) (Table 2). However, the average grain yield obtained in this mesoregion was the third highest of the state, 3,205 kg/ha (41 kg/ha above the state average) (Table 2). The RS Northeast mesoregion harvested 48,803 ha of wheat (4.6 % of the cropped area in the state), produced 161.047 tons of wheat (4.6 % of the cropped area in the state), produced



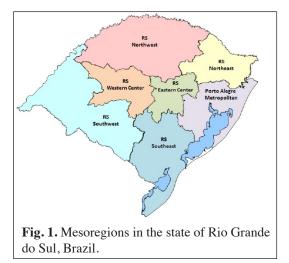


Table 2. Area harvested, production, and average of grain yield of wheat in each of the mesoregions (see Fig. 1) of the state of Rio Grande do Sul, Brazil, in 2013 (Source: IBGE 2015).

	Area harvested		Produc	Grain				
					yield			
Mesoregion	ha	%	tons	%	(kg/ha)			
RS Northwest	834,788	78.8	2,675,218	79.8	3,205			
RS Northeast	48,803	4.6	161,947	4.8	3,318			
RS Western Center	87,186	8.2	285,922	8.5	3,279			
RS Eastern Center	20,105	1.9	55,403	1.7	2,756			
Porto Alegre Metropolitan	2,500	0.2	7,111	0.2	2,844			
RS Southwest	51,150	4.8	129,159	3.9	2,525			
RS Southeast	14,500	1.4	36,390	1.1	2,510			
Rio Grande do Sul state	1,059,032	100.0	3,351,150	100.0	3,164			

of wheat grain yield of commercial crops was 1,696 kg/ha below the STWC-RS average (4,860 kg/ha).

Reference.

IBGE. 2015. Sistema IBGE de Recuperação Automática - SIDRA. Available at: <<u>http://www.sidra.ibge.gov.br/bda/tab-ela/listabl.asp?z=t&o=11&i=P&c=1612</u>>. Acessed 21 Mar 2015. Nota: Bank of aggregate data studies and research carried out by the IBGE.

ITEMS FROM THE CZECH REPUBLIC

CROP RESEARCH INSTITUTE Genebank, Drnovska 507, 16106 Praha 6 Ruzynze, Czech Republic.

An improvement of the genebank management system in the Czech republic.

Ludmila Papousková and Vojtech Holubec.

The existing documentation system for genetic resources in the Czech Republic, EVIGEZ, has not met the requirements of modern documentation systems (documentation of sets of characterization data, including molecular data, image analysis, and other aspects), so we currently are moving to a new documentation system, GRIN Global.

For proper data migration, first we needed to analyse the structure of two databases to avoid losing any recorded information. Although both systems contain parts for passport, characterization, and inventory data, they have different structures. The GRIN Global system allows, in most cases, more detailed information about genetic resources, for example, the recording of germination tests. In EVIGEZ, only the initial germination and subsequent records of germination test were recorded and stored outside the system in Excel tables. Now, it is possible to convert these records collectively to a database. System components also should report on the need for regeneration of material if germination reaches the critical value, contributing to more accurate control of the stored material.

The structure of the two systems of characterization and evaluation data did not differ significantly, however, a big advantage is the possibility of recording more sets of observation data relating to a single accession.

The greatest problem of data migration was, in our case, the transfer of taxonomic data. GRIN taxonomy does not fully correspond with the taxonomy in EVIGEZ. The GRIN system does not cover all taxa and synonyms and does not recognize lower taxonomic classification (to variety). However, EVIGEZ data can be transformed into GRIN Global without losing detailed taxonomy data using taxonomic synonyms.

Part of the GRIN Global system is a website of the database that will be used for all information and ordering genetic resources on-line via a shopping cart setup. Until now, it was possible to order genetic resources held in the Czech Republic only through e-mail.

This change of genebank management systems will help improve the quality of work in the genebank and, thus, improve the quality of service for users of genetic resources.

Germplasm conservation and seed longevity in the Czech genebank.

Vojtech Holubec and Ludmilla Papousková.

Seed longevity is a function of temperature and relative humidity. Decreasing moisture content by 1% results in a doubling of longevity. However, longevity depends on many factors, mainly the biologic quality of seed, pre- and post-harvest treatment, storage conditions, and gas composition. Seed genetic resources have been kept in the Genetic Resources

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Department at the Crop Research Institute, Ruzyne, since it was establisted in 1951. The initial 6.000 accessions were received from the organizations between 1880-1950. Samples in CRI Ruzyne genebank were stored in metallic boxes in the basement and regularly regenerated

Table 1. Viability of wheat in storage before establishment of the Czech Genebank.									
1985 winter wheat 1952–62 1963 1964 1968									
Viable accessions	834,788	2	25	131					
Storage years	19–27	18	17	13					
%	0	1.4	18.0	91.0					

in 5-year periods. Selected materials from the base collection were stored in commercial cold storage since 1985. Germination ability was regularly counted but not recorded in the EVIGEZ information system (Table 1). The new Genebank opened in 1989 and filled subsequently with materials from the commercial cold store and with newly regenerated material. Historiacal landmarks of the Czech Genebank include

- 1898–1950: early breeding and state variety testing institutes keep collections of landraces and cultivars mainly for their own use.
- 1951: Crop Research Institute founded, including the Department of Genetic Resources, 6,000 samples accepted from various sources before foundation of the CRI, including breeders, variety testing institutes, and other collections for storage.
- 1960s: seed stored in metallic boxes in the basement of a building and regenerated at intervals of 3–5 or 8 years.
- 1981–84: electronic documentation system EVIGEZ developed.
- 1985: climatized storage, selected items in commercial cold storage (2,200 accessions), ability to enter germination counts.
- 1889–90: Czech Genebank founded; 2,200 accessions moved from commercial cold storage and newly regenerated material added.

At present, there are data on seed longevity available for 23-28 years ending with the last germination tests in 2014 (Table 2). The standard germination ability of the 60 oldest wheat accessions did show an increase in germination by 2% from the initial 95.3%. Similarly, 44 winter barley

 Table 2. Viability of selected crops after 19–28 years of storage in the Czech Genebank
 (checked in 2014).

Сгор	#	Initial germination	Germination difference (%)	Years
Triticum L.	60	95.3	-2.0	23-28
<i>xTriticosecale</i> (winter type)	26	89.2	0.0	20
Hordeum L. (spring type)	44	89.8	11.9	20
Phaseolus L.	365	92.1	1.2	19
Pisum sativum L. convar. sativum	212	74.1	-14.6	19
Brassica napus L. var. napus	48	78.9	-0.1	20
Brassica napus L. f. bennis	16	79.5	0	20
Sinapis alba L.	6	72.6	0	20

accessions showed a 12% decrease in germination compared to the initial 89.8%, most likely because of lower initial quality. In legumes, 365 bean accessions showed a 1.2% decrease from the mean initial germination of 92.1%, and 212 pea accessions showed a 14.6% increase from the initial mean gennination of 74.1%. The oldest 60 accessions of Cruciferae species Brassica napus, B. rapa, and Sinapis alba had the same germination rate, as did triticale. The germination increase in pea possibly is due to dormancy, because this atribute was not originally counted in the germination rate.

ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK GATERSLEBEN Correnstraße 3, 06466 Stadt Seeland, OT Gerersleben, Germany.

A. Börner, M. Agacka-Mołdoch, F. Arana-Ceballos, A.M. Castro, P. Chamurlijski, Yu.V. Chesnokov, C. Clemenz, G. Gerard, E.K. Khlestkina, V. Koutev, T.V. Kukoeva, S. Landjeva, J. Ling, U. Lohwasser, G. Lori, I. Malbrán, M. Nagel, C.O. Qualset, D. Palejev, M.A. Rehman Arif, R. Rodeva, M.S. Röder, A. Sanabria, O.Y. Shoeva, M.R. Simon, Chr. Volkmar, K. Zaynali Nezhad, and Chr. D. Zanke.

Whole-genome, association mapping of plant height in winter bread wheat.

The genetic architecture of plant height was investigated in a set of 358 recent European winter wheat cultivars plus 14 spring wheat cultivars based on field data in eight environments. Genotyping of diagnostic markers revealed the *Rht-D1b* mutant allele in 58% of the investigated cultivars, whereas the *Rht-B1b* mutant was only present in 7%. *Rht-D1* was significantly associated with plant height by using a mixed linear model and employing a kinship matrix to correct for population stratification. Further genotyping data included 732 microsatellite markers, resulting in 770 loci, of which 635 markers were placed on the ITMI map plus a set of 7,769 mapped SNP markers genotyped with the 90k iSELECT chip. When Bonferroni correction was applied, a total of 153 significant marker-trait associations (MTAs) were observed for plant height and the SSR markers ($-\log_{10}(P-value) \ge 4.82$) and 280 ($-\log_{10}(P-value) \ge 5.89$) for the SNPs. Linear regression between the most effective markers and the BLUEs for plant height indicated additive effects for the MTAs of different chromosomal regions.

Analysis of syntenic regions in the rice genome revealed closely linked rice genes related to gibberellic acid (GA) metabolism and perception, i.e., GA20 and GA2 oxidases orthologous to wheat chromosomes 1A, 2A, 3A, 3B, 5B, 5D, and 7B; *ent*-kaurenoic acid oxidase orthologous to wheat chromosome 7A; *ent*-kaurene synthase on wheat chromosome 2B; GA-receptors, such as DELLA genes, orthologous to wheat chromosomes 4B, 4D, and 7A; and genes of the GID family orthologous to chromosomes 2B and 5B. The data indicated that, besides the widely used GA-insensitive dwarfing genes *Rht-B1* and *Rht-D1*, a wide spectrum of loci are available that could be used for modulating plant height in cultivar development.

Morpho-physiological and agronomic indices of plant water status in bread wheat.

We have assessed and mapped QTL for the manifestation of morpho-physiological and agronomic indices of plant water status and related quantitative traits, such as plant height, weight, and dry matter content, in spring wheat. Following the study of 10 agronomic traits, 13 QTL were mapped on linkage groups 1A, 1B, 2B, 2D, 4A, 5A, 5B, 5D, 6A, and 6D. Some of the identified QTL concurrently determined several traits. The physiological components of water status were shown to correlate with quantitative traits in wheat plants, such as plant height, weight, and dry matter content, and the correlation coefficients were calculated for all traits under study. Water retention capacity after 3 h correlated with water retention capacity after 24 h ($r_{xy} = 0.47$). Correlations also were found between water retention capacity after 3 h and plant height at booting stage ($r_{xy} = 0.29$) and between water retention capacity after 3 h and plant dry weight ($r_{xy} = 0.33$). Statistical calculations supported generally observed negative correlation (up to -1) between leaf water and dry matter contents, as well as between the root indices of variance in the mapping population of wheat lines. Obtained results will promote future efforts to fine-map the genes residing within the identified QTL, to eventually clone these genes in order to establish the physiological mechanisms for maintaining water homeostasis in higher plant cells and to accomplish the practical implementation of marker-assisted assessment of water status in wheat plants studied on the basis of morpho-physiological and economical indices.

Studies on salt tolerance in bread wheat.

A bi-parental mapping population (131 recombinant inbred lines) was investigated to study the change in the total root length after salt stress for 5 days. The population was developed by crossing a salt-resistant winter wheat cultivar with a salt-sensitive spring wheat. F_8 plants were used in this investigation. Seeds were germinated on germinating paper (21 x 30 cm) with seeds placed with the embryo down, to allow roots to grow downwards for observing differences in the total length of the roots. The germinating rolls were initially wetted and later placed in water up to a depth of 7 cm for 7 days. Afterwards, a half-strength, Hoagland's solution treatment was applied for the next 5 days. To identify differences in root and shoot length, 200 mM NaCl was added to the solution in comparison to the respective control. Rolls initially were soaked up to a depth of 21 cm for 15 minutes and then kept up to 7 cm from below for the remainder of the period. The coleoptile length of the whole collection in control ranged from 1.8 to 5.3 cm with mean of 3.5 ± 0.84 cm. Root length ranged from 37.1 to 108.3 cm with a mean of 68.08 ± 13.9 cm. Shoot length also showed great variation, where the mean shoot length was 17.0 ± 5.1 cm and ranged from 5 cm to 30 cm. The same population is planted in saline soils. The results obtained from the salt-infected field will be compared with this data to check whether or not the fast screening of wheat germplasm against salt stress is a useful method. The genetic map of this population is under construction. Consequently, the genetic and phenotypic data will be used to map loci for salt stress tolerance in this population.

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

Frost tolerance phenotype scores were collected from several locations in Germany and Russia during two seasons and were combined with the genotypic data in genome-wide association analyses. The genotyping was done employing an ILLUMINA infinium iSelect 90k wheat chip. The chip carries a total of 81,587 valid and functional SNPs. SNP associations were performed using liner mixed models that evaluated the effects of SNPs with minor allele frequencies >10% individually, adjusting for population structure and kinship. For the population structure analysis, the Q-matrix for three groups was chosen as the best option. Subsequent validation confirmed the results, and using an evolutionary tree calculated by the software PAUP, showed three genotype subgroups: North American, Russian, and North and Middle European. Genome-wide association analyses of the most significant SNP loci identified three and seven positive SNP associations on chromosomes 1B and 5A, respectively, using kinship. Haplotype analysis revealed that most of the significant SNP loci for these positions represent an advantage for the evaluated genotypes.

Induced resistance against fusarium head blight in bread wheat.

Fusarium head blight (FHB) or scab, mainly caused by *Fusarium graminearum* (Schwabe) and *F. culmorum* (WG Smith) Sacc, is one of the most important fungal diseases affecting wheat in cereal producing areas of the world. The economic losses caused by FHB include yield and quality reduction. The damages induced by the disease are further aggravated by the frequent presence of mycotoxins in affected grains. In the recent years, monoculture, reduced tillage, and maize/ wheat rotations have greatly increased the level of inoculum in the soil and, hence, the risk for epidemics of FHB in Argentina. Wheat resistance to FHB is inherited as a quantitative trait governed by polygenes and QTL have been detected on all wheat chromosomes. Because the genetic base of resistance is complex, we selected the most tolerant RILs from the ITMI population to see if their defences can be elicited by applying hormonal inducers or a bacterial suspension. Several of the resistance mechanisms are constitutively expressed or these are elicitated by a previous aspersion with hormonal or bacterial treatments. After the treatment, plant defences are 'primed' and respond faster in a more efficient mode when a pathogen attack occurs.

Several RILs, selected by their FHB tolerance, were treated with hormonal inductors of defences and a bacterial suspension (*Pseudomonas* spp.) before inoculation with one aggressive strain of *F. graminearum*. A complete factorial design was performed with untreated plants (controls) inoculated with Fusarium (I), pretreated with ethylene (E), treated with E and inoculated (E+I), treated with salicilic acid (SA), sprayed with SA and inoculated (SA+I), sprayed with a bacterial suspension (B), and inoculated after B treatment (B+I). Elicitation was performed 48 hours before anthesis (Zadoks growth stage 65). Afterwards, each spike was sprayed with 1 mL of the macroconidial suspension using a manual atomizer (constant volume). At harvest, the total number of grains/spike, the number of damaged kernels, the Fusarium index (FI = DK/GS), total weight/spike, and 1,000-kernel weight were calculated.

A part of the tolerant RILs were similar for grains/spike in the complete set of treatments. These lines also had a lower number of damaged kernels and Fusarium index, except when inoculated after SA induction, which showed a slightly higher damage. The TKW was not affected by inoculation in the treated and control plants. On the other hand, inoculated plants of a second group of RILs produced similar GS than control plants, except those sprayed with E, hormone that reduced significantly the grains/spike. The salicylic acid and B treatments induced better performance in this group of RILs, both in the inoculated or noninoculated plants.

Tolerant RILs would have two different types of inducible defense mechanisms. In the first group, the defenses seem to be mediated by ethylene and, in the second group, by the salicylic acid.

Genome-wide association mapping for resistance components to Zymoseptoria tritici in seedlings and its association with plant height and heading date in bread wheat.

Zymoseptoria tritici Desm. (Mycosphaerella graminicola (Fuckel) Schrot.) constitutes a major disease problem of wheat, host resistance being the most effective and economic tool to reduce yield losses. Resistance to the disease can be evaluated as percent necrosis and pycnidial coverage. Pycnidial coverage is often more accurate, because necrosis can be masked by senescence and other foliar diseases. An important fact in the search for resistance to this disease is its possible association with plant height and heading date. This work identifies i) marker-trait associations (MTAs) for resistance to Z. tritici expressed as necrosis and pycnidial coverage percentage through genome-wide association mapping DArTbased and ii) associations between resistance, plant height, and heading date. Three field experiments were conducted at the Experimental Station J. Hirschhorn, Faculty of Agricultural and Forestry Sciences, National University of La Plata, Argentina, during 2012 and 2013, in a split-plot design. Ninety-six winter wheat accessions from 21 countries were inoculated with two isolates from two locations from Argentina (Pla and Nueve de Julio) at the 3-leaf stage in both years. For two of the experiments, severity (expressed as necrosis percentage and pycnidial coverage percentage) in the first three leaves was scored, and heading date and plant height were evaluated for the three experiments.

A phenotype–genotype association analysis, employing the general linear model and the mixed linear model, was performed with the Tassel 2.1 software. Only MTAs significant with both models were considered. For necrosis percentage, three MTAs for Z. tritici resistance were detected on chromosomes 1A (two) and 6B with the isolate from Pla, whereas four significant MTAs on chromosomes 1B (two), 2A, and 2D were effective against the isolate from Nueve de Julio in the two experiments analyzed. Regarding pycnidial coverage percentage, six significant MTAs for Z. tritici resistance were detected on chromosomes 1A (two), 1B (two), 5B, and 7A with the Pla isolate, and five significant MTAs on chromosomes 1A (two), 1B (two), and 7D with the Nueve de Julio isolate, in the two experiments analyzed. On the other hand, five significant MTAs for heading date were detected on chromosomes 1B, 2B, 4B, 5D, and 6A, and four significant MTAs for plant height were identified on chromosomes 2B, 3A, 4A, and 7A, for the three experiments analyzed. Some of the MTAs for Z. tritici resistance were isolate specific whereas others were common to both isolates.

Additionally, a correlation analysis was performed in which both necrosis percent and pycnidial coverage percent were negatively associated with heading date (r = -0.18 and r = -0.23 for the Pla isolate and r = -0.41 and r = -0.36 for the Nueve de Julio isolate), whereas no significant association with plant height was found; except for percent necrosis for the Nueve de Julio isolate (r = -0.25).

Association mapping for resistance against insect pests in bread wheat.

A spring wheat panel consisting of 111 different genotypes from 27 countries and a winter wheat panel of 96 accessions from 21 countries were cultivated in the field on different places from 2011 to 2014. The population was used for a genome-wide association mapping analysis for resistance against different insect pests (aphids, Oscinella frit, orange and yellow wheat midges (Sitodiplosis mosellana (Géhin), Contarinia tritici (Kirby), and saddle gall midge (Haplodiplosis marginata)). The data was gathered using pheromone traps, white water traps, and evaluating wheats.

After sampling all traits, we calculated an association study to find characteristic MTAs for resistance. For resistance to Ocinella frit, we detected 41 MTAs in 2013, 44 MTAs on the different wheat chromosomes for the aphids, and nine MTAs for the saddle gall midge in 2012–13. The orange and yellow wheat midges were surveyed by white water traps. Highly significant, marker-trait associations were identified in 2013 on 18 out of 21 chromosomes. For orange

wheat midges adults and larvae, 43 and 25 MTAs, respectively, were detected. Alternatively, 22 and 19 MTAs for yellow wheat midge adult and larvae, respectively, were identified. The panels show wide differences between the individual insect pests.

Genetic diversity in old bread wheats from Bulgaria.

A collection of 60 historic wheat cultivars released in Bulgaria from the beginning of last century to the early 1970s as products of traditional farmers' selection and early breeding activities was assembled. This old germplasm had evolved from a broader gene pool and, therefore, is a valuable though yet underutilized resource for breeding purposes. Genetic diversity was studied in different sets of genotypes with regard to the phenotypic characteristics, growth habit, plant height, earliness, agronomic traits, disease resistance, nitrogen (N) use efficiency, and molecular variability. Among this germplasm, potential sources of good productive potential and lodging resistance were identified. One-third of the accessions demonstrated high to moderate resistance to yellow rust (*Puccinia striiformis*) in field conditions during the epiphytotic development of yellow rust throughout Europe in the spring of 2014. Depending on the environment, N use efficiency in 21 accessions at two N fertilizer levels (N₀ and N₁₂) and two environments differing by soil characteristics and crop predecessor showed variation with respect to the efficiency and N responsiveness. Under more extensive conditions with poorer soil characteristics and a maize predecessor, the majority of old genotypes were N efficient, whereas on haplic chernozem and a pea predecessor, the vast part of old gemplasm was N inefficient. The study of genetic variation and distinctiveness among 28 accessions as revealed by microsatellites showed high allelic richness (173 alleles at 25 loci on 14 chromosomes, 6.9 average number of alleles/locus), 0.68 average PIC, 49 unique alleles at 18 loci, and 30.9 % average cultivar heterogeneity.

Genetic diversity in Iranian bread wheat.

A study on 500 bread wheat accessions was conducted to determine genetic diversity based on morphological traits and ISSR makers. The accessions were provided kindly from the IPK–Gatersleben genebank and originated from Iran, Afghanistan, India, Turkey, Pakistan, Iraq, Nepal, Tajikistan, and some other countries. In order to evaluate genetic diversity based on morphological traits, pure lines, derived from the bread wheat accessions, were cultivated and evaluated in a field experiment based on an augmented design with three cultivars as control in 2013. Traits such as day-to-flowering, spike length, plant height, number of grains/spike, 1,000-kernel weight, grain length, grain width, flag leaf width, flag leaf length, peduncle length, and awn length were investigated. Results from these descriptive statistics showed that the maximum coefficient of variation of the phenotypic traits belonged to the awn length and the lowest for the days-to-flowering. A simple correlation analysis showed the highest correlation between the grain weight and grain width. A cluster analysis based on the morphological traits divided the genotypes into four groups.

Ten ISSR markers were used to study genetic diversity on the genome level among the genotypes. This part of study still is in progress and, after that, the results from each of the two parts can be compared. The above-mentioned genotypes are under investigation for salt stress based on hydroponic culture.

Seed longevity in bread wheat – artificial ageing vs. long-term storage.

Recombinant inbred lines (RILs) of the ITMI mapping population were analyzed after artificial ageing (treatment 1 was 100% RH, 43±0.5°C, 72h; and treatment 2 was 18% seed moisture content, 43±0.5°C, 72h) as well as after long-term storage (10°C/50% RH) for up to 14 years. The RILs were reproduced either at experimental fields at IPK in Gatersleben, Germany, or at the University of California Intermountain Research and Extension Center in Tulelake, USA. After ageing, two to four reps of 50 seeds were subjected to standard germination tests and data obtained were used for QTL analysis.

QTL detected after artificial ageing were found on chromosomes 1A, 1D, 2A, 2D, 3B, 3D, and 6B. In contrast, the loci detected after long-term storage were detected on chromosomes 4B, 5A, and 5B. Not only the different growing seasons, but also the different storage and ageing conditions, yielded different loci. The many different genomic regions contributing to the genetic determination of seed longevity underline the complexity and polygenic nature of this trait.

Contradictory mapping positions confirmed that growing and/or storage/ageing conditions exert a large influence on seed longevity.

The use of wheat-barley addition lines to verify a candidate gene for a regulator of anthocyanin biosynthesis in the leaf sheath.

Anthocyanins are implicated in plant resistance to a number of abiotic and biotic stress factors. Anthocyanin pigmentation of leaf sheath is determined by the *Pls-1* genes in wheat (chromosomes 7A, 7B, and 7D) and the *Ant1* gene in barley (chromosome 7HS). The whole set of wheat–barley addition lines (*T. aestivum* subsp. *aestivum* cv. Chinese Spring + *Hordeum vulgare* cv. Betzes) was used to localize the *HvMpc1* gene, a candidate gene for *Ant1*. The *HvMpc1* gene is a homolog of the maize gene *C1* encoding R2R3 MYB factor regulating anthocyanin biosynthesis. R2R3 MYB is a large family of transcription factors encoded by genes distributed on all chromosomes and, therefore, primary verification of the selected candidate genes should be the testing of their chromosome location. The sequence of *HvMpc1* was amplified using a specific primer pair in wheat–barley addition lines carrying chromosome 7H or its short arm, suggesting *HvMpc1* to be a proper candidate gene for *Ant1*. The *HvMpc1* sequence can be useful for further isolation of candidate genes for wheat *Pls-1*.

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ITEMS FROM HUNGARY

AGRICULTURAL INSTITUE Centre for Agricultural Research, Hungarian Academy of Sciences, Martonvásár, PO Box 19, H-2462, Hungary.

The Martonvásár Cereal Genebank.

M. Megyeri, G. Linc, P. Mikó, A. Farkas, I. Molnár, L. Láng, C. Kuti, and M. Molnár-Láng.

The main task of the Martonvásár Cereal Genebank is to collect, preserve, and maintain wheat species and genetic reserves from related species, and to make detailed investigation on the quality, agronomic value, and biotic and abiotic resistance of the accessions.

The Martonvásár Cereal Genebank is divided into three main parts: a breeder collection, the genetic stock collection, and a set of wheat wild relatives.

Breeder collection. The largest of the collections, the breeder collection consists of more than 11,500 accessions of breeding stocks, cultivars, and landraces. A majority of the accessions are *Triticum aestivum* (90%)

- genotypes, but other cultivated cereals (barley, triticale, and durum wheat) also are represented. The breeder collection is an important part of the cereal breeding program at Martonvásár.
- *Genetic stock collection.* Special attention is given to the high-value genetic stocks (1,000 accessions), such as an uploid material (nullisomic, monosomic, substitution, and addition series), special mutant stocks, and amphiploids. A majority of the genetic stocks were developed at Martonvásár during the last few decades, e.g., the Rannaya 12 monosomic series, and the other part was collected via international material exchanges. The genetic stock collection is used in basic genetic research and prebreeding activities. The maintenance of genetic stocks often requires cytogenetic control.
- *Wild wheat relatives.* This collection consists of about 1,700 accessions, including a majority of species of *Triticum*, *Aegilops*, *Secale*, *Hordeum*, and perennial species of *Agropyron* and *Elymus*. Many of these accessions possess excellent resistance for biotic and abiotic stresses. They are used mostly in prebreeding work. Several prebreeding programs were started at Martonvásár on the basis of genebank accessions to transfer useful traits of wild relatives in to hexaploid wheat. The *T. monococcum* collection, with more than 300 accessions, is outstanding among the European collections. The *Aegilops* collection has expanded in recent years by collecting 130 new accessions via European expeditions.

The entire genebank collection consists of around 14,000 accessions. The long-term, *ex situ* maintenance of the accessions take place in refrigerated storage (-28° C). The majority of the genebank accessions are stored for medium term at 4°C in a cold room. At the same time, perennial species also are maintained *in situ* in an isolated nursery.

Database management of the genebank uses the *Breeder* software, which was developed at Martonvásár for cereal breeding. Characterization of genebank accessions under field conditions is an important part of our activity. All phenotypic and agronomic data collected during the regeneration and conservation processes are recorded in the *Breeder* database, which also is used to manage seed production, storage, and exchange.

ITEMS FROM INDIA

BHABHA ATOMIC RESEARCH CENTRE Nuclear Agriculture & Biotechnology Division, Mumbai–400085, India.

Development of gamma ray induced mutant line in wheat variety PBW-343 having moderate resistance to wheat stem rust race Ug99.

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

Stem rust is a deleterious disease of wheat. In the recent past, the appearance of virulent races, such as Ug99, have broken many important stem rust resistance genes in wheat and barley. Under the aegis of an IAEA project (INT5150, 'Responding to the Trans-boundary Threat of Wheat Black Stem Rust (Ug99)'), the wheat cultivar PBW-343 was irradiated with gamma rays (250, 300, and 350 Gy). The M_1 was raised at Trombay in 2009–10. The M_2 population was sent to a hot-spot for Ug99 in Kenya in 2011 for screening for resistant mutants. Mutants were identified as moderately resistant (MR) or moderately susceptible (MS). These mutants were carried forward to the M_3 and M_4 generations in Kenya. Seed of one mutant line having an MR reaction were brought back to India, and this mutant line (TWM-97) is being multiplied at our station. Morphological characters were noted and molecular characterization of the mutant line is being carried out. Crosses were made with the parent cultivar for an alleleism study. We are thankful to Drs. P. J. L. Lagoda and T. Moleah (IAEA) for supporting this program and Prof. M. Kinyua (Eldoret, Kenya) for screening for Ug99 resistance.

ANNUAL WHEAT NEWSLETTER Development of an early maturing mutant line in wheat genotype MP-3054.

Vikas, G. Vishwakarma, A.S. Shitre, S. Bakshi, S.G. Bhagwat, G.A. Gadekar (Agriculture Research Station, Niphad, Maharashtra), and B.K. Das.

Due to changes in climate, particularly the rise in atmospheric temperature, wheat crop yields have been affected. Heat stress during the seedling, grain filling, and maturity stages are important, reducing the overall productivity. Wheat genotypes with longer duration to maturity suffer from terminal heat stress. Wheat genotype MP-3054 has moderate tolerance to heat stress, taking nearly 70 days to flower and 98 days to mature. Using gamma ray-induced mutation, we have developed early mutant lines (TWM-93 and TWM-94) that are 14-19 days earlier than the parent genotype. The mutant lines flower in 51–56 days and mature in 79–98 days. These mutants now are in the M_{e} generation and stable. These lines are being evaluated at Trombay, Niphad, and Akola. This work was carried out under an IAEA-RCA project RAS5056.

Induced mutation approach for improvement of yellow rust resistance in Indian wheat.

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

Rust is a very deleterious disease in wheat. Among the three rusts (black, brown, and yellow), yellow, or stripe, rust is more prevalent in the North-West Plain Zone and Northern Hill regions of India. In the recent past, due to the appearance of many virulent races of stripe rust, many newly released, high-yielding cultivars carrying important resistance genes to stripe rust have become susceptible. Therefore, we have initiated an induced-mutation approach for genetic improvement of yellow rust resistance in Indian wheat. We already have irradiated a few of the recently released wheat cultivars with gamma rays, and the M₁ was grown in Trombay. M₂ seeds were obtained and will be screened in a stripe rust infection hotspot and subsequent generations in laboratory and glass house conditions. This work is being carried out in collaboration with ICAR-IIWBR, Karnal; ICAR-IIWBR Regional Station, Flowerdale; and the G.B. Pant University of Agriculture & Technology, Pantnagar.

Induced mutation approach for genetic improvement of agronomic traits in the wheat cultivars HI-1500 and HI-1531.

G. Vishwakarma, V. Sai Prasad (IARI Regional Station, Indore, Madhya Pradesh), Vikas, and B.K. Das.

Wheat cultivars with maturity times of long duration are affected by terminal heat stress. The wheat cultivars HI-1500 and HI-1531 are popular as check cultivars and widely cultivated in the Central zone of India. Due to the long duration in maturity, the cultivars are affected by heat stress. In order to reduce the maturity period and height, an induced-mutation approach was followed. The two cultivars were irradiated with gamma rays, and the M, population was raised at Trombay. The M, population will be screened in the coming year. This work is being carried out in collaboration with the ICAR-IARI Regional Station, Indore.

A study of the inheritance and molecular characterization of an early maturing, mutant line TWM-89-2 in wheat cultivar C-306.

G. Vishwakarma, A. Saini (Molecular Biology Division, BARC, Mumbai), Vilkas, A. Shitre, and B.K. Das.

Using gamma rays, we earlier developed an early flowering and maturing mutant line in the wheat cultivar C-306 (under an IAEA-RCA project RAS5045). This line (TWM-89-2) has been deposited at the National Bureau for Plant Genetic Resources, New Delhi, with national id number IC0611305. Molecular markers (AP-PCR, STMS, and AFLP) are being used to characterize the mutant line and study polymorphism between the parent and the mutant line. In order to study the inheritance of the early maturing trait and develop molecular markers, crosses were made between the mutant and the parental cultivar. The F1 seeds were grown, and F2 seeds obtained. An F2 mapping population will be used for studying genetics and developing linked marker(s).

ANNUAL WHEAT NEWSLETTER VOL. 6 Inducing mutations in Indian wheat using physical mutagens, electron, proton, and ion beams.

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

In India, gamma rays are used most commonly for inducing mutations for crop improvement. However, by using other physical mutagens, such as electron, proton, or ion beams, many mutants were obtained in other countries. In order to explore the use of these mutagens, we have standardized the dose and other technical parameters in collaboration with the Raja Ramanna Centre for Advanced Technology, Indore (Dr. V.C. Petwal) and the BARC Pelletron Facility at TIFR, Mumbai (Drs. J.P. Nair and A.K. Gupta). Electron beam irradiation of three wheat cultivars was done and the GR50 determined. Technical standardization for irradiation of wheat seeds with proton and ion beams is in progress.

Validation of SCAR markers for leaf rust resistance gene Lr32 in Indian wheat genotypes.

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

The leaf rust resistance gene Lr32 has not yet been fully exploited in Indian wheat breeding programs. In order to use this gene in breeding and for pyramiding with other Lr genes, molecular markers linked to this gene will be very useful and efficient. A SCAR marker for this gene was reported by in 2010. Our aim was to validate this marker in Indian wheat genotypes and a segregating population. PCR amplification was done in five genotypes with Lr32 and 10 genotypes without Lr32. A 350-bp band was amplified in genotypes with Lr32, which was absent in noncarriers. For further confirmation, we are analyzing a segregating population from the cross 'Agra Local / TC+Lr32'.

Validation of SCAR marker for Glu-D1d (coding for HMW-glutenin subunits 5+10) in Indian wheat genotypes.

G. Vishwakrma, Vikas, and B.K. Das.

The HMW-glutenin subunits 5+10 (coded by Glu-D1d) are known to influence dough strength and bread-making quality. In our wheat breeding program, these subunits are selected using SDS-PAGE. However, a marker-assisted breeding program will ease the process. A SCAR marker (478 bp) is linked to this gene. We validated this marker in Indian wheat genotypes. The carriers amplified a 478-bp band that was not amplified in noncarriers. This marker is more robust than the 450-bp marker reported by D'Ovidio and Anderson (1994). For further confirmation, we are using a segregating population from the cross 'Kalyansona (Glu-Dla; coding for subunits 2+12) / PBW-343 (Glu-Dld; coding for subunits 5+10)'.

Improvement of wheat cultivar HD-2189 by incorporating rust resistance genes Sr24/Lr24 and HMW-glutenin subunits 5+10 (Glu-D1d) by marker-assisted backcross breeding.

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

The wheat cultivar HD-2189 is popular in the Peninsular zone of India. For improvement of rust resistance and dough strength, two genes, Sr24/Lr24 and Glu-D1d (coding for HMW-glutenin subunits 5+10), were incorporated from the genetic stock KS-3 (developed at our centre). Marker-assisted backcross breeding was carried out. The lines are now in the $BC_{c}F_{a}$ generation and are being evaluated for yield and other characteristics. We are proposing for a yield trial under special marker-assisted backcross breeding lines.

ANNUAL WHEAT NEWSLETTER VOL. Developing low-cost, high-throughput screening of SCAR and STMS markers in wheat using SYBR green-based, low-resolution melt profiling.

G. Vishwakarma, S.G. Bhagwat, and B.K. Das; and A. Saini, R. Sanyal, and N. Jawali (Molecular Biology Division, Bhabha Atomic Research Centre, Mumbai-400085, India).

PCR-based, single-locus, DNA markers, such as SCAR and STMS markers, commonly are used in crop breeding experiments for diverse applications. These markers are generally scored using agarose or polyacrylamide gel electrophoresis. However, these techniques are laborious, time consuming, and not cost-effective for analyzing large populations. Lowresolution melt profiling, based on low cost dyes (such as SYBR green), could be effectively utilized for detecting singlelocus, PCR markers (SCAR or STMS) in a gel-free manner. The feasibility of the approach was demonstrated using SYBR green-based, melt profiling in a few STMS and SCAR markers in ten bread wheat genotypes. Clean melt curve profiles were obtained for all markers with no background noise from unused template DNA or primer dimers. Individual STMS and SCAR markers could be detected easily in different genotypes. In addition, polymorphic STMS markers also could be identified in melt curve profiles. This approach is $\sim 20\%$ cheaper than the conventional, gel-based methods. Furthermore, the possibility of multiplexing and reducing the volume of reaction mix provides further scope for reducing the cost of screening. Screening STMS and SCAR markers by this high-throughput method will be useful in estimating linkage and gene mapping, genetic diversity and phylogenetic analyses, and marker-assisted selection. Although the current study was based on analysis of wheat samples, the method may be applicable to other crop plants.

Understanding the molecular mechanism of stem rust resistance genes in wheat.

G. Vishwakarma, A. Saini, N. Jawali (Molecular Biology Division, BARC, Mumbai), and B.K. Das.

Wheat production is affected by many biotic stress, of which stem rust, caused by *Puccinia graminis* f. sp. tritici (Pgt), is a potential threat worldwide and can cause 100% damage to yield. Understanding the molecular mechanism involved in resistance to stem rust is of utmost importance for achieving durable resistance against this disease. Two wheat genotypes, C-306 and Unnath C-306, hereafter UC-306 and C-306+Sr24, respectively, were injected with the Pgt pathotype 7G-11. A microarray analysis of the wheat transcriptome was done at three time points, 0, 10, and 72 hours post inoculation (hpi). Microarray results showed that before inoculation (0 hpi), a minimal number of genes were differentially regulated. However, at 10 hpi, approximately 300 genes were up-regulated in UC-306, indicating a major defense response against the pathogen. At 72 hpi, the transcriptome was comparable to that before inoculation. Differentially regulated transcripts were annotated using the DFCI gene indices database. Transcripts related to pathogenesis related proteins, phytoalexins, transcription factors, biotic stress, cell membrane transporters, kinases, and xylan synthase were found to be up regulated in the resistant cultivar and, hence, are key players in resistance to stem rust pathogen. Validation of transcription levels of a few important transcripts is being carried out using quantitative RT-PCR. This work is being carried out in collaboration with ICAR-IIWBR RS, Flowerdale, and the IARI Regional Station, Wellington.

Genetic variability of phytic acid and inorganic phosphorus in diverse wheat germplasm.

Suman Bakshi, Vikas Kumar, Abhijeet Shitre, and B.K. Das.

Phytic acid (myo-inositol hexakisphosphate), the major storage form of phosphorus in seeds, is believed to have a negative impact on nutritional quality. The phytic acid concentration reported in wheat germ and bran are 1.1–3.9% and 2.0-5.3%, respectively. More than half of the world population is affected by micronutrient malnutrition, and one-third of the world's population suffers from anemia and zinc deficiency, particularly in developing countries. Iron and zinc deficiencies are major health problems worldwide. Phytic acid chelates micronutrients and prevents their bioavailability in monogastric animals, including humans, because they lack the enzyme phytase in their digestive tract. Several methods have been developed to reduce the phytic acid content in food to improve its nutritional value, including the genetic improvement of food grain and several pretreatment methods. Because breeding for low phytic acid has been proposed for several cereals and legumes, it is important to evaluate genetic variation for phytic acid content among the available germplasm. Colorimetric estimation was done for both phytic acid and inorganic phosphate in 270 diverse wheat genotypes. Significant genotypic variation was found among the tested genotypes. The range for phytic acid content is 4.48 to 14.8 mg/g with a mean of 10.56 mg/g. The range for inorganic phosphate content is 0.30 to 1.8 mg/g. Wheat germplasm is not extensively evaluated for genetic variation for phytic acid. Screening of large diverse germplasm available indicated that phytic acid is a highly heritable trait ($h^2 = 0.76$) and selection for low phytic acid is possible.

Analysis of advance wheat genotypes of peninsular zone of India for phytic acid, inorganic phosphate, iron and zinc content.

A.S. Shitre, G.A. Gadekar (Agriculture Research Station, Niphad), V. Ramachandran, Vikas, and B.K. Das.

Malnutrition (particularly iron and zinc) is a common problem worldwide, more severe in developing countries. Biofortification and some other measures are available, but they are difficult to implement and use in day-to-day activities. One suggested method is genetic improvement of cereals with increased iron and zinc content and reduced phytic acid content, which binds with these minerals and makes them unavailable for digestion in nonruminants. One hundred advanced breeding lines of wheat, developed for the Peninsular zone of India, were analyzed for iron, zinc, phytic acid, and inorganic phosphate content and significant variability was observed. Iron content was 0.042–0.098 mg/g and and zinc content was 0.017–0.029 mg/g. Phytic acid content ranged from 4.97 mg/g to 15.02 mg/g (mean of 9.58 mg/g). Inorganic phosphate content was ranged from 0.128 to 0.234 mg/g of seed. The parameters exhibiting higher estimates of GCV, coupled with high heritability, indicate that considerable improvement in these parameters can be achieved through incorporating desired genotypes in a crossing program followed by pedigree selection.

News from our wheat research group.

Mr. G. Vishwakarma received the 'Best Poster' award for the presentation 'Low resolution SYBR green dye based melt profiling for analysis of STMS and SCAR markers in plants' during the National Symposium on Crop Improvement for Inclusive Sustainable Development held at Ludhiana, India, 7–9 November, 2014.

Publications.

- Vishwakarma G, Sanyal RP, Saini A, Jawali N, Bhagwat SG, and Das BK. 2014. Low resolution SYBR green dye based melt profiling for analysis of STMS and SCAR markers in plants. *In:* Proc Natl Symp Crop Improvement for Inclusive Sustainable Development, Ludhiana, India, 7–9 Nov. Abstracts and Short Communications. Pp. 713-714.
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GENETIC RESOURCE CENTRE Latvian State Forest Research Institute 'Silava', Rigas 111, Salaspils LV-2169, Latvia.

Long-term storage of plant genetic resources in the Latvian genebank.

A. Gailite, A. Gaile, and D. Rungis.

The Latvian genebank of cultivated plants preserves seed of 72 agriculturally important species and their hybrids. Most accessions are of Latvian origin, and information about stored accessions is available in the SESTO and EURISCO databases. The genebank stores material of Latvian origin collected and bred in Latvia, as well as Latvian accessions repatriated from other gene banks. Most regeneration activities have been concentrated on the repatriated accessions.

The first accessions were put in long-term storage conditions in freezers at $-18\pm2^{\circ}$ C in 1999. Germination tests of accessions representing 20 species (cereals, forage grasses, peas, and flax) were made after ten years of storage and only small changes were observed. Germination tests were repeated on the same accessions after 15 years of storage. A slight decrease in germination was observed in cereals, peas, and most of the grass species accessions (2–10%) depending on species and variety. A significant decline in germination was found only for three grass accessions (more than 15%). Close monitoring of grass accessions is required and, in case of a further decline in germination, regeneration will be necessary.

ITEMS FROM LITHUANIA

PLANT GENE BANK Stoties str. 2, Akademija, Kedainiai distr., Dotnuva, Lithuania.

Long-term seed conservation of plant genetic resources in Lithuania.

A. Baliuckiene, A. Blazyte, R. Baltrenas, A. Biviliene, S. Dapkuniene, B. Gelvonauskis, B. Markeviciene, and L. Sveistyte.

The collection and studies of the genetic diversity of agricultural crops in Lithuania were initiated by Professor D. Rudzinskas in 1922 after the Plant Breeding Station was established in Dotnuva.

In 1994, the Baltic-Nordic project for plant genetic resources was initiated by the Nordic Genetic Resource Center (formerly the Nordic Gene Bank). The main objective of the project was to develop a national plant genetic resources conservation network in Lithuania. In 1997, long-term seed storage was established at the National Plant Genetic Resources Coordinating Centre. The Nordic Gene Bank provided all necessary facilities.

The law on National Plant Genetic Resources was enacted in 2001 by the Parliament of Lithuania and the Plant Gene Bank was established in 2004. Currently, eight institutions in Lithuania are involved in the activity of collecting, investigating, and conserving plant genetic resources. The main activity of the Plant Gene Bank is long-term preservation of plant genetics resources. Seeds of old landraces and cultivars of agricultural crops, advanced cultivars, and valuable breeding material, and distinguished populations of wild relatives of cultivated plants and forest trees, ornamental, and medicinal plants are stored in the airtight aluminium foil bags at -18° C in the long-term seed storage.

To date, 3,014 accessions of 179 plant species are stored for the long-term conservation. Agricultural crops represent the largest number of accessions (2,176). Long-term seed storage is supplemented annually with new accessions.

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.

Reaction to Karnal bunt under artificial inoculation of advanced bread wheat lines selected for cultivation in the humid high lands of Jalisco, Mexico.

Guillermo Fuentes-Dávila, Javier Ireta-Moreno (NIFAP, Campo Experimental Centro–Altos de Jalisco, km 8 Carr. Tepatitlán-Lagos de Moreno, Tepatitlán, Jalisco 47600, México), Pedro Félix-Valencia, Pedro Figueroa-López, Miguel Alfonso Camacho-Casas, José Luis Félix-Fuentes, Gabriela Chávez-Villalba, and Joel Soto-Nolazco (Junta Local de Sanidad Vegetal del Valle del Yaqui, Rodolfo Elías Calles 711, Cd. Obregón, Sonora, México 85150).

Abstract. Twenty-four advanced bread wheat lines selected for cultivation in the humid, high lands of the state of Jalisco, Mexico, were evaluated for resistance to Karnal bunt by artificial inoculation during the 2013–14 crop season at two dates, in the Yaqui Valley, Mexico. The infection range for the first date was 0–73.16%, and 0–32.54% for the second date. Line SOKOLL*2/TROST (CMSA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-03Y-0B) did not show any infected grain on either date, three lines were within the 0.1–2.50 infection category (ROLF07/TUKURU/5/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ with 0.19%; GOUBARA-1/2*SOKOLL with 0.67%; and FRET2/KUKUNA//FRET2/3/TUKURU/4/FRET2/TUKURU//FRET2 with 1.46%), three in the 5.1–10.0% infection category, 13 at 10.1–30.0%, and four >30.0%. The mean of the three highest percentages of infection of the susceptible check was 99.02%.

Introduction. Wheat cultivation under rainfed conditions in Mexico has fluctuated from 62,110 to 239,000 ha between 1976 to 1997, with an average grain yield ranging from 1.3 to 2.1 t/ha (Villaseñor-Mir and Espitia-Rangel 2000). In 2013, the area grown with wheat in Mexico under these conditions was 122,321.10 ha, and 6,299 in the state of Jalisco with an average grain yield of 1.06 t/ha (Ireta et al. 2008; SIAP 2015), although, in the 1980s and early 1990s, wheat occupied about 12,000 ha each year with an average grain yield of 3 t/ha in the same state (Chávez and Ireta 1993). Despite the small area dedicated to rainfed wheat cultivation in Mexico, the perspectives are quite wide: more than 1 x 10⁶ ha can be used for wheat in 16 states; investment is lower than in irrigated land, the land is cheaper, and the water has no cost; technology can offer improvement in wheat production with a potential grain yield average of 3 t/ha; and costs due to transportation and storage, so that wheat produced during the summer in the central high plateau, may be more accessible than the imported one (Villaseñor-Mir and Espitia-Rangel, 2000). The potential area for wheat production under rainfed conditions in the state of Jalisco is 57,000 ha, and the more prevalent diseases are leaf (*Puccinia triticina*) and stripe (*Puccinia striiformis*) rusts, Septoria leaf (*Septoria tritici*) and glume (*Septoria nodorum*) blotches, Fusarium head blight (*Fusarium graminearum*), and spot blotch (*Bipolaris sorokiniana*) (Chávez and Ireta 1993). Although Karnal bunt is not

present in the state of Jalisco (SAGARPA 2002), it is important to screen wheat experimental germplasm for reaction to this and other diseases so that selected material has the attributes not only for rainfed conditions, but tolerance/resistance to diverse biotic factors. Karnal bunt of wheat caused by *Tilletia indica* (syn. *Neovossia indica*) has been reported from India (Mitra 1931), Mexico (Duran 1972), Pakistan (Munjal 1975), Nepal (Singh et al. 1989), Brasil (Da Luz et al. 1993), the United States of America (APHIS 1996), Iran (Torarbi et al. 1996), and the Republic of South Africa (Crous *et al.* 2001). *Triticum aestivum* is the most susceptible plant species to Karnal bunt (Fig. 1), which under artificial inoculation, may show more than 50% infected grain (Fuentes-Dávila et al. 1992; 1993). Although *T. indica* may affect durum wheat (*T. turgidum*) and triticale (X *Triticosecale*; Agarwal et



Fig. 1. Karnal bunt on the grain of bread wheat.

to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1988). Chemical control is accomplished by applying fungicides during flowering (Fuentes-Dávila et al. 2005); however, this measure is not feasible when quarantines do not allow tolerance levels for seed production. Resistant wheat cultivars are the best means to control this disease. Our objective was to evaluate 24 advanced bread wheat lines for resistance to Karnal bunt, which were selected from the Global Wheat Program of CIMMYT for their acceptable performance under rainfed conditions. These

Entry	ring the crop season 2013-2014, in the Yaqui Valley, Sonora, Mexico. Pedigree and selection history
· ·	FRET2/KUKUNA//FRET2/3/TUKURU/4/FRET2/TUKURU//FRET2
l	CGSS05B00149T-099TOPY-099M-099NJ-099NJ-2WGY-0B
	SW89-5124*2/FASAN/3/ALTAR 84/AE.SQ//2*OPATA
2	CMSA04M00335S-040ZTP0Y-040ZTM-040SY-16ZTM-04Y-0B
3	VEE/PJN//2*TUI/3/WH576
)	CMSS95Y00795S-0100Y-81DH-0B-10Y-0B-01Y
1	ACHTAR*3//KANZ/KS85-8-5/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92
т	CMSA05M00661T-050Y-040ZTM-040ZTY-26ZTM-02Y-0B
5	PRL/2*PASTOR*2//YANAC
	CGSS05B00211T-099TOPY-099M-099NJ-099NJ-4WGY-0B
5	SOKOLL*2/TROST
	CMSA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-03Y-0B
7	SOKOLL*2/TROST CMSA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-03Y-0B
8	WBLL1*2/VIVITSI/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*JANZ CMSS05B00713S-099Y-099M-099Y-099ZTM-4WGY-0B
	HUW234+LR34/PRINIA*2//WHEAR
9	CGSS05B00243T-099TOPY-099M-099NJ-1WGY-0B
	D67.2/PARANA 66.270//AE.SQUARROSA (320)/3/CUNNINGHAM/4/WBLL1*2/TUKURU
10	CMSA04M00492S-040ZTP0Y-040ZTM-040SY-22ZTM-02Y-0B
1.1	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX
11	CMSA05Y00325S-040ZTP0Y-040ZTM-040SY-38ZTM-04Y-0B
12	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX
12	CMSA05Y00325S-040ZTP0Y-040ZTM-040SY-21ZTM-03Y-0B
13	HUW234+LR34/PRINIA*2//WHEAR
5	CGSS05B00243T-099TOPY-099M-099NJ-099NJ-1WGY-0B
14	ROLF07/TUKURU/5/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ
	CGSS05B00115T-099TOPY-099M-099Y-099ZTM-2WGY-0B
15	ATTILA/BAV92//PASTOR/3/ATTILA*2/PBW65
	CMSA04M00070S-040ZTB-040ZTY-040ZTM-040SY-13ZTM-04Y-0B
16	ESDA/KKTS CMSA04M00178S-040LNB-040ZTY-040ZTM-040SY-5ZTM-03Y-0B
	GOUBARA-1/2*SOKOLL
17	GOUBARA-1/2*SOKOLL CMSA04M01020T-050Y-040ZTP0M-040ZTY-040ZTM-040SY-8ZTM-01Y-0B
	ATTILA*2/PBW65//TNMU
18	CGSS05Y00442S-0B-099Y-099M-099NJ-8RGY-0B
	GOUBARA-1/2*SOKOLL
19	CMSA04M01020T-050Y-040ZTP0M-040ZTY-040ZTM-040SY-8ZTM-01Y-0B
•	HUW234+LR34/PRINIA*2//YANAC
20	CGSS05B00242T-099TOPY-099M-099NJ-099NJ-28WGY-0B
1	HUW234+LR34/PRINIA*2//YANAC
21	CGSS05B00242T-099TOPY-099M-099NJ-099NJ-13WGY-0B
22	BABAX/LR43//BABAX/5/MOR/VEE#5//2*DUCULA/3/MILAN/4/BAU/MILAN/6/ SKAUZ/BAV92
22	CMSS05Y00558T-099TOPM-099Y-099M-099Y-099ZTM-5RGY-0B
23	PGO/SERI//BAU/3/DUCULA/4/FRET2/KUKUNA//FRET2
	CMSS05Y00357S-0B-099Y-099M-099Y-099ZTM-12WGY-0B
24	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX
	CMSA05Y00325S-040ZTP0Y-040ZTM-040SY-40ZTM-04Y-0B

Materials and methods. Twenty-four advanced bread wheat lines (Table 1, p. 21) were evaluated for resistance to Karnal bunt during the 2013–14 fall-winter crop season in block 910 in a clay soil with pH 7.8, in the Yaqui Valley, Sonora, Mexico. Sowing dates were 21 November and 3 December, 2013, using a 1-m bed with two rows. Inoculum was prepared by isolating teliospores from infected kernels, 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 by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage (Fig. 2) in ten heads/line. High relative humidity in the experimental area was provided by a mist-automized, irrigation system five times per day, 20 min each time (Fig. 3). Harvest was manual, and visual counting of healthy and infected grains determined the percent infection. Evaluated lines

originated from the collaborative project between the International Maize and Wheat Improvement Center (CIMMYT) and the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP).

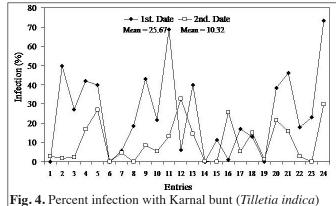
Results and discussion. The range of infection for the first planting date was 0-73.16% with a mean of 25.67 (Fig. 4). Four lines did not show any infected grain, one was in the 0.1-2.5% infection category, one at 2.6-5.0%, one at 5.1-10.0, eight at 10.1-30.0, and nine > 30%. The range of infection for the second planting date was 0 to 32.54%, with a mean of 10.32. Four lines did not show infected grains, five were in the 0.1-2.5%infection category, two at 2.6–5.0%, three at 5.1–10.0, nine at 10.1–30.0, and one > 30%. The average infection range for the two dates was 0-51.50% with a mean of 17.74% (Fig. 5, p. 23). The highest average percent infection was in line FRET2*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ/5/ ONIX (CMSA05Y00325S-040Z TP0Y-040ZTM-040SY-40ZTM-04Y-0B) with 51.50%, followed by FRET2*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ/5/ONIX (CMSA05Y 00325S-040ZTP0Y-040ZTM-040SY-38ZTM-04Y-0B) with 40.85%, PRL/2*PASTOR *2//YANAC with 33.41%, and HUW234+LR34/PRINIA*2//YANAC with 31.02%. In the resistant category, which is less than 5% infection (Fuentes-Dávila and Rajaram 1994), one line did not show any infected grain at both dates (SOKOLL*2/ TROST, CMSA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-03Y-0B). Three lines were within the



Fig. 2. Artificial inoculation of bread wheat with a sporidial suspension of Tilletia indica by boot injection in the field.



Fig. 3. A mist irrigation system in an experimental field.



of 24 advanced bread wheat lines artificially inoculated in the field during the 2013–14 crop season at two dates. Plots were in the Yaqui Valley, Sonora, Mexico.

0.1-2.50% infection category (ROLF07/TUKURU/5/ WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ with 0.19%, GOUBARA-1/2*SOKOLL with 0.67%, and FRET2/KUKUNA//FRET2/3/TUKURU/4/FRET2/ TUKURU// FRET2 with 1.46%) (Fig. 6, p. 23). Four lines were in the 5.1–10.0% infection category, 13 at the 10.1–30.0%, and four were >30%. The mean of the three highest percentages of infection of the susceptible check was 99.02%. Artificial inoculation in the field may be affected by various factors such as inoculum survival and viability, proper injection by the operator, proper amount of the suspension, distribution of sporidia in the suspension, weather conditions prevailing during and after the inoculation (primarily temperature, relative humidity, solar radiation), and the specific phenological

stage of the plant, therefore, variation in the percentage of infection within a single line is common. We recommend several sowing dates and in several crop seasons in order to avoid escapes. Lines in the resistant category that showed consistency in the level of infection at both dates were SOKOLL*2/TROST (CMSA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-03Y-0B) with 0 difference (Fig. 4, entry 6, p. 22), ROLF07/TUKURU/5/WBLL1*2/4/ YACO/PBW65/3/KAUZ*2/TRAP//KAUZ with a 0.38 difference (14), SOKOLL*2/TROST (CM-SA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-03Y-0B) with a 1.01 difference (7), GOU-BARA-1/2*SOKOLL with a 1.33 difference (19), and FRET2/KUKUNA//FRET2/3/TUKURU/4/FRET2/ TUKURU//FRET2 with a 2.93% difference (1). Several weather parameters that prevailed in southern Sonora during 1 January to 10 March, 2014, included a maximum average temperature in January, February, and March (1-10) of 27.1, 28.6, and 26.0°C, respectively; a minimum average temperature of 5.9, 6.5, and 10.2°C, respectively; and an average relative humidity of 70.4, 75.3, and 78.9, respectively (PIEAES 2015). Two days had rainfall in March with a total of 3.7 mm, which, based on the history of the incidence of Karnal bunt in the region, influenced the presence of the disease (out of 1,304 spike samples in seven localities, 21 were positive for infected grain, and out of 34,812 grain samples analyzed in eight counties, 621 were positive), although the number of infected grains/ kg was quite low (Ing. Joel Soto-Nolazco, personal communication, Yaqui Valley, Plant Health Council).

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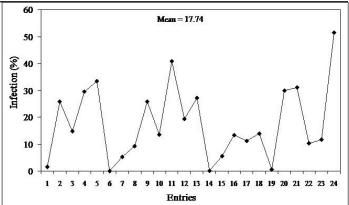
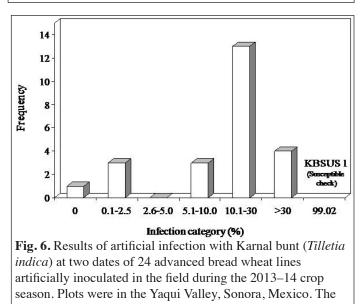


Fig. 5. Average percent infection with Karnal bunt (*Tilletia indica*) of 24 advanced bread wheat lines artificially inoculated in the field during the 2013–14 crop season at two dates. Plots were in the Yaqui Valley, Sonora, Mexico.



level of KBSUS1 infection is the mean of the three highest infection scores.

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Performance of bread wheat cultivars Ónavas F2009 and Villa Juárez F2009 in semi-commercial plots in southern Sonora during 2013–14.

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Abstract. We evaluated the performance of bread wheat cultivars Ónavas F2009 and Villa Juárez F2009 released by INIFAP for commercial cultivation, in semi-commercial fields during the 2013–14 crop season under the agronomic management of cooperating farmers. The trials were located in the Yaqui Valley: 1) Bacum County, block 113 (27°30' 23.87"–100°08'28.26", 20 masl), sowing date 2 December, 2013, cultivars sown in 12 x 0.8-m beds, 485-m long; and 2) Bacum County, block 809 (27°23'19.40"–110°06'42.21", 15 masl), sowing date 29 November, 2013, cultivars sown in 12 x 0.8-m beds, 477-m long. Six 10 x 0.8-m beds were used to evaluate stem fresh weight, leaf fresh weight, root fresh weight, spike fresh weight, and the number of spikes/m²; other variables evaluated were spike dry weight, 1,000-kernel weight, spike and grain length, and number of grains/spike. Grain yield was determined in the area sown using a Parker grain weigh cart model 1555. Variables in which Ónavas F2009 was superior to Villa Juárez F2009 were number of spikes, stem fresh weight in block 809, leaf fresh weight, and root fresh weight. Variables in which differences between blocks were detected included spike dry weight. In relation to grain yield, Ónavas F2009 performed better than Villa Juárez F2009 in both locations, with a difference of 533 and 608 kg/ha in blocks 809 and 113, respectively. Ónavas F2009 showed a maximum grain yield of 7.5 t/ha in block 113.

Introduction. National wheat production in Mexico in year 2010 was 3.9 x 10⁶ tons, which was not sufficient to supply the needs in the country. Since 2010, 3.3 x 10⁶ tons were imported (OEIDRUS 2011). Before the 1990s, bread wheat was the dominant class in northwest Mexico. In the state of Sonora, bread wheat occupied more than 50% of the area dedicated to wheat from the agricultural season 1983-84 to 1993-94. However, many wheat producers decided to start growing durum wheat, because the Mexican government implemented domestic quarantine No. 16 (SARH 1987), which limited the cultivation of bread wheat in fields where Karnal bunt had been detected at levels greater than 2% infected grains. Other important factors were that durum wheat showed greater grain yield than bread wheat and, that during that period of time, durum wheat did not have problems with leaf rust. In addition, there were opportunities for export of durum wheat. Despite the economic and operational problems caused by Karnal bunt at the beginning of the 1980s, during the 1990-91 agricultural season bread wheat was still grown in 220,409 ha, which represented 89% of the total area dedicated to wheat in the state. However, durum wheat was consolidated as the dominant class grown in Sonora from the 1994-95 agricultural season. The area grown with wheat during the 2010-11 crop season in the state of Sonora was 292,247 ha; 87% (254,531) corresponded to southern Sonora. Durum wheat cultivars CIRNO C2008 and Átil C2000 occupied 40% of the total area. The Mexican federal government has implemented a financial support program for commercialization to enhance the production of bread wheat, which is in demand by the national industry, and along with agriculture by contract, it is intended to increase the area with bread wheat in order to balance the relation with durum wheat. Our objective was to evaluate the performance of two bread wheat cultivars in semi-commercial fields, which were released by INIFAP for commercial cultivation in 2009.

Materials and methods. This work was carried out during the 2013–14 crop season with the bread wheat cultivars Ónavas F2009 (Fig. 7) (Figueroa-López et al. 2013a, b) and Villa Juárez F2009 (Fig. 8) (Valenzuela-Herrera et al. 2012a, b), under the agronomic management of cooperating farmers. The trials were located in the Yaqui Valley: 1) Bacum County block 113 (27° 30' 23.87"–100° 08' 28.26" at 20 masl; sowing date 2 December, 2013) and 2) Bacum County block 809 (27° 23' 19.40"–110° 06' 42.21" at 15 masl; sowing date 29 November, 2013).



Fig. 7. Bread wheat cultivar Ónavas F2009 has an average height of 97 cm. Plants present an intermediate growth habit and a very high frequency of recurved flag leaves. Grain shape is semi-elongated, and coloration after treatment with phenol is light.

Fig. 8. Bread wheat cultivar Villa Juárez F2009 has an average height of 91 cm. Plants are semiprostate and have a very high frequency of recurved flag leaves. Grain shape is semi-elongated, and coloration after treatment with phenol is nil or very light.

Agronomic management. Block 113, after irrigation of the land before sowing and once the land was ready for sowing, Faena was applied at 3 L of commercial product (c.p.)/ha, as well as 400 kg of urea, 12–40 kg of sulphur, 100 kg of zinc, and 1.5 liters of 2,4D amina for weed control. Cultivars were sown in 12 x 0.8-m beds 485-m long. The seeding rate was 130 kg/ha. Complementary irrigations were provided 35 days after sowing; the second 20 days later with an application of ammonia (NH₃, 70 kg/ha), the third 20 days later with an application of NH₃ (70 kg/ha), and the fourth 15 days later.

In Block 809, cultivars were sown in 12 x 0.8 m beds, 477-m long. Urea was applied at 200 kg/ha as well as mono-ammonium phosphate at 100 kg/ha before the land was sown and irrigated. The seeding rate was 150 kg/ha. Complementary irrigations were provided 49 days after sowing with the application of ammonia (60 kg/ha), the second 33 days later with an application of ammonia (50 kg/ha), and a third 23 days later. For aphid control, Velfidor was applied at 150 ml/ha c.p. on 15 January, 2014. For broadleaf weed control, Agramina 6 c.p. was applied at 500 ml/ha on 22 December, 2013, Situi XL at 20 g/ha on 10 February, 2014, and Agramina 6 at 1.5 l/ha on 10 March, 2014. For narrow-leaf weed control, Topik Gold was applied at 350 ml/ha on 27 December, 2013, and at 500 ml/ha on 18 February, 2014. A John Deere 8820 combine was used to harvest block 809 and a 5660 in block 113 (Fig. 9, p. 26). Grain yield (kg/ha) was determined using a Parker grain weigh cart, model 1555 (Fig. 10, p. 26). Six 10 x 0.8-m beds were used to evaluate the following variables: number of spikes, spike fresh weight, stem fresh weight, leaf fresh weight, and root fresh weight



Fig. 9. Combines used for harvesting wheat cultivars Ónavas F2009 and Villa Juárez F2009 in semicommercial blocks 809 and 113 in the Yaqui Valley, Sonora, Mexico, during the 2013-14 crop season.



Fig. 10. Grain yield determination of wheat cultivars Ónavas F2009 and Villa Juárez F2009 using a Parker grain yield cart model 1555 in semicommercial blocks 809 and 113 in the Yaqui Valley, Sonora, Mexico, during the 2013–14 crop season.

(three replications each), all per m²; spike dry weight (five replications); 1,000-kernel weight (three replications); number of grains/ spike (five replications); and grain and spike length (five replications each).

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Results and discussion. Based on the results

obtained, cultivars Ónavas F2009 and Villa Juárez F2009 were similar for spike dry weight (the average was a little higher in Ónavas in both blocks, Fig. 11), 1,000-kernel weight (Fig. 12), number of grains/spike (the average was a little higher in Ónavas in both blocks, Fig. 13), grain length (Fig. 14), spike length (Fig. 15, p. 27), and spike fresh weight

(the average was a little higher in Villa Juárez in both blocks, Fig. 16, p. 27). Variables in which Ónavas F2009 showed a greater average than Villa Juárez F2009 were number of spikes/m², with a difference of 58 and 24 in blocks 809 and 113,

season.

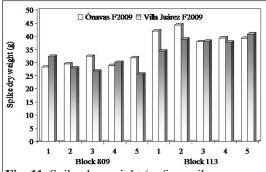


Fig. 11. Spike dry weight (g; five spikes (replicatons)) of wheat cultivars Ónavas F2009 and Villa Juárez F2009 in semicommercial plots in the Yaqui Valley, Sonora, Mexico, during the 2013–14 crop season.

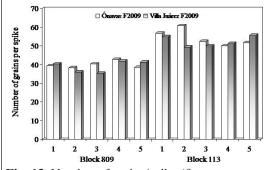


Fig. 13. Number of grains/spike (five replications) of wheat cultivars Ónavas F2009 and Villa Juárez F2009 in semicommercial plots in the Yaqui Valley, Sonora, Mexico, during the 2013-14 crop season.

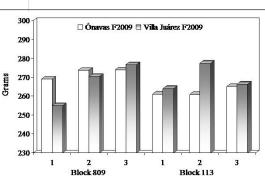
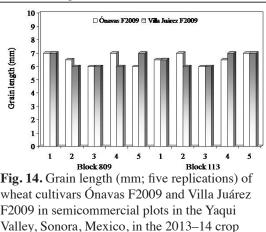
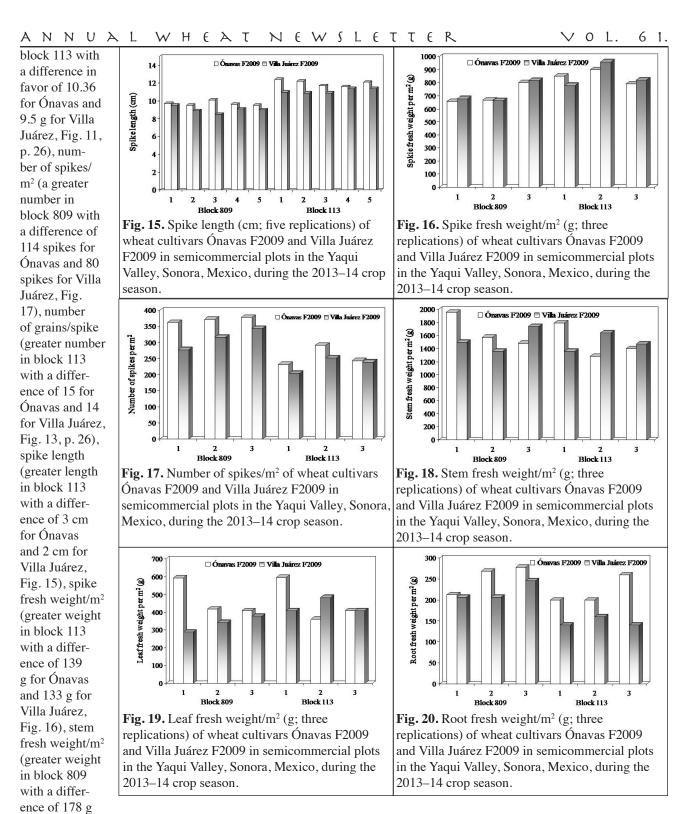


Fig. 12. 1,000-kernel weight (g; three replications) of wheat cultivars Onavas F2009 and Villa Juárez F2009 in semicommercial plots in the Yaqui Valley, Sonora, Mexico, during the 2013-14 crop season.



respectively (Fig. 17, p. 27); stem fresh weight in block 809 with a difference of 136 g (Fig. 18, p. 27); leaf fresh weight with a difference of 138 and 21 g in blocks 809 and 113, respectively (Fig. 19, p. 27); and root fresh weight with a difference of 33 and 74 g in blocks 809 and 113, respectively (Fig. 20, p. 27).

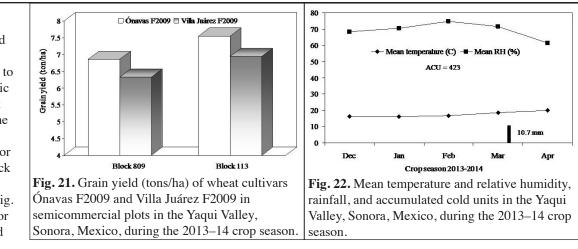
Variables in which differences between blocks were detected were spike dry weight (a greater weight in



for Ónavas and 42 g for Villa Juárez, Fig. 18), and root fresh weight/m² (greater weight in block 809 with a difference of 33 g for Ónavas and 74 g for Villa Juárez, Fig. 20).

For grain yield, Ónavas F2009 performed better than Villa Juárez F2009 in both locations, with a difference of 533 kg/ha and 608 kg/ha in block 809 and 113, respectively (Fig. 21, p. 28). This result agrees with that of Figueroa-López et al. (2013b) who indicate that Ónavas F2009 shows competitive grain yield (a maximum of 7.5 t/ha in block 113) with the durum wheat cultivars grown in southern Sonora. On the other hand, Villa Juárez F2009, previous to its release for commercial cultivation, showed a yield of 8.1 t/ha in semi-commercial plots (Valenzuela et al. 2012b),

which was not expressed in this work, possibly due to the agronomic management applied by the cooperating farmers and/or due to the lack of sufficient cold units (Fig. 22), which for optimal yield expression



should be at least 600 in this region (Fig. 22) (Félix-Valencia et al. 2009).

The validation plots represent an important tool for evaluating wheat candidate lines for commercial release by INIFAP, whose objectives are to 1) generate information about their performance and expression potential under the management of cooperating farmers, and to provide such information to the wheat farmers of the region and 2) enhance the cultivation of bread wheat in the region, since several years ago, more than 80% of the area cultivated with wheat has been under durum wheat (SIAP 2013). Efforts by the national wheat industry and the federal government have been implemented in order to increase bread wheat cultivation so as to diminish the import of this type of wheat.

Conclusions. Cultivar Ónavas F2009 was superior to Villa Juárez F2009 in number of spikes, stem fresh weight in block 809, leaf fresh weight, and root fresh weight. Ónavas F2009 performed better than Villa Juárez F2009 for grain yield in both locations, with a difference of 533 kg/ha and 608 kg/ha in blocks 809 and 113, respectively. Ónavas F2009 showed a maximum grain yield of 7.5 t/ha in block 113, therefore, it represents a good bread wheat option for wheat producers in southern Sonora.

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Reaction of bread wheat cultivars to artificial inoculation with Karnal bunt after fertilization with nitrogen and sulphur.

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Abstract. The reaction of cultivars Tacupeto F2001, Kronstad F2004, Navojoa M2007, and Roelfs F2007, to inoculation with Karnal bunt was evaluated at the Norman E. Borlaug Experimental Station during the 2012–13 crop season. Cultivars were subjected to two nitrogen treatments (200 and 300 kg/ha) and four sulphur treatments (0, 30, 60, and 90 kg/ha), with three replications. The trial was sown on 30 November and 15 December, 2012. For the 2013–14 crop season, cultivars Kronstad F2004 and Roelfs F2007 were used to study the effect of sulphur in two dates (28 November and 11 December, 2013), keeping the nitrogen rate at 300 kg/ha. Depending on the rate and opportunity of application of sulphur treatments as ammonium sulphate (21N-00P-00K-24S), the application of 121.5 kg N/ha in each of the two first complementary irrigations were complemented with urea. Therefore, within each sowing date and cultivar, sulphur treatments of 0-0, 15-0, 30-0, 45-0, 0-15, 0-30, 0-45, 15-15, 15-30, 15-45, 30-15, 30-30, 30-45, 45-15, 45-30, and 45-45, which allowed total sulphur applications from 0 to 90 kg S/ha, were studied. Inoculations were made by injecting 1 mL of an allantoid sporidial suspensión (10,000/mL) during the boot stage, in 10 heads/row in each treatment. The range of infection for cultivar Roelfs F2007 were 23.06–50.27% with a mean of 39.65%, and 8.07–37.80%, with a mean of 24.66%, for the 1^{st} and 2^{nd} sowing dates during the 2012–13 crop season, respectively; 8.94–36.89% and a mean of 18.62%, and 1.29-13.83% with a mean of 6.13% for Navojoa M2007; 30.02-64.66% and a mean of 51.33%, and 23.40-53.35% with a mean of 35.92% for Tacupeto F2001; and 17.83–37.90% with a mean of 29.72%, and 4.04–33.81% with a mean of 20.82%, for Kronstad F2004. The range of infection for cultivar Roelfs F2007 was 8.69 to 27.59, with a mean of 17.05%, and 4.60 to 25.77, with a mean of 16.77%, for the 1st and 2nd sowing dates during the 2012–13 crop season, respectively; and 2.98 to 16.42, with a mean of 8.07%, and 8.92 to 21.59, with a mean of 14.15%, for Kronstad F2004.

Introduction. Sulphur is an important element in sulphidryl and disulphur (S–S) bond formation, important for protein structure stabilization and partly responsible of the viscoelastic properties of wheat gluten (Naeem and MacRitchie 2003). A sulphur deficiency, in the presence of adequate nitrogen fertilization, modifies the dough properties (increasing maximum resistance and lowering extensibility) as the gluten sulphur-protein-rich proportions are reduced (particularly the low-molecular-weight glutenin subunits and the α , β , and γ -gliadins), although there is a higher proportion of polypeptides low in sulphur, such as ω -gliadins and high-molecular-weight glutenins (Randall and Wrigley 1986). Sulphur deficiency is dependent on soil type, locality, and climate. Soil pH also may affect the availability of sulphur (Freney and Williams 1983) and is volatized by debris burning. A 1.2 mg/g sulphur content and an N:S ratio of 16:1 or 17:1 in the wheat grain appears to be critical for optimal quality (Zhao et al. 1999). Usually, the maximum response to sulphur application in wheat is obtained between 10–20 kg/ha (McGrath et al. 1996). Tea et al. (2007) reported the synergy between nitrogen fertilizers and sulphur upon their intake increase in the grain and the influence of fertilization with sulphur in the quantities and proportions of the different types of gluten proteins (Wieser et al. 2004).

Karnal bunt occurs in bread wheat, durum wheat, and triticale. Generally, infected grains are partially affected, and completely infected kernels are uncommon (Mitra 1935). Control of this pathogen is difficult because teliospores are resistant to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1988). Chemical control is accomplished by applying fungicides during flowering (Salazar-Huerta et al. 1997). Resistant wheat cultivars are the best means for control. Our objective was to evaluate the reaction to Karnal bunt under artificial inoculation of the commercial bread wheat cultivars Tacupeto F2001, Kronstad F2004, Navojoa M2007, and Roelfs F2007, subjected to two nitrogen (200 and 300 kg/ha) and four of sulphur (0, 30, 60, and 90 kg/ha) treatments. Results of the general percent infection at two sowing dates and the highest percentage infection obtained with the different nitrogen–sulphur combinations follow.

Materials and methods. Bread wheat cultivars Tacupeto F2001, Kronstad F2004, Navojoa M2007, and Roelfs F2007 were subjected to two nitrogen (200 and 300 kg/ha) and four of sulphur (0, 30, 60, and 90 kg/ha) treatments, in a trial with three replications. Sowing was on 30 November and 15 December, 2012, with one irrigation to promote crop establishment and four complementary irrigations, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, in a clay soil with pH 7.8. Within each date, treatment combinations corresponding to nitrogen, sulphur, and cultivars were established in the field under a randomized, split-plot, experimental design. Cultivars were the main plot, and the nitrogen x sulphur treatment combinations were distributed randomly within each main plot. Four 5-m beds with two rows each were sown for each treatment. Inoculations were by injecting 1 mL of a secondary sporidial suspen-

sion (10,000/mL) in 10 spikes per bed, in two beds of each treatment in each sowing date (spikes of one replicate of the nitrogen x sulphur treatments in each cultivar), using a hypodermic syringe during boot stage. Inoculum preparation followed the methodology of Fuentes-Dávila et al. (2012). Spikes from the first sowing date were inoculated on 22 February, 2013, and the second on 1 March. Harvest and head threshing were done manually, and the counting of healthy and infected grains was done visually to determine the percent infection. For the 2013–14 crop season, cultivars Kronstad F2004 and Roelfs F2007 were used to study the effect of sulphur in two sowing dates (28 November and 11 December, 2013), while keeping the nitrogen rate at 300 kg/ha, because no differences were observed in yield and quality between that rate and 200 kg/ha in the previous crop season. According to Zhao et al. (1999), excess of nitrogen causes an imbalance in the relationship N:S in favor of N, which is reflected in a reduction in bread loaf volume. Nitrogen was divided into three applications: pre-sowing (57 kg N/ha using 100 kg of urea, 46N-00P-00K, and 100 kg of mono-ammonium phosphate (11-52-00)) and right before the first and second complementary irrigations. Depending on the rate and opportunity of application of sulphur treatments as ammonium sulphate (21N-00P-00K-24S), the application of 121.5 kg N/ ha in each of the two first complementary irrigations were complemented with urea. Therefore, within each sowing date and cultivar, sulphur treatments were 0-0, 0-15, 0-30, 0-45, 15-0, 15-15, 15-30, 15-45, 30-0, 30-15, 30-30, 30-45, 45–0, 45–15, 45–30, and 45–45, which allowed total sulphur applications from 0 to 90 kg S/ha to be studied. Inoculum preparation followed methodology previously described, and inoculations were made on 12 and 20 February, 2014.

Results. At the first sowing date of the 2012–13 crop season, the percent infection for cultivar Roelfs F2007 was 23.06–50.27%, with a mean of 39.65%; for Navojoa M207, 8.94–36.89%, with a mean of 18.62%; for Tacupeto F2001, 30.02–64.66%, with a mean of 51.33%; and for Kronstad F2004, 17.83–37.90%, with a mean of 29.72% (Table 2). The overall range for the four cultivars was 8.94–64.66 with a mean of 34.83%. The susceptible check showed 89.61% infection at the first date. The percent infection at the second sowing date for cultivar Roelfs F2007 was 8.07-37.80%, with a mean of 24.66%; for Navojoa M2007, 1.29–13.83%, with a mean of 6.13%; for Tacupeto F2001, 23.40–53.35%, with a mean of 35.92%; and for Kronstad F2004, 4.04–33.81%, with a mean of 20.82% (Table 2). The overall range for the four cultivars was 1.29–53.35% with a mean of 21.88%. The susceptible check showed 97.90% infection at the second date. The highest percent infection for cultivar Roelfs F2007 at the first sowing date, under different N-S combinations were 44.69%, 44.22%, and 43.41% for combinations 200–30, 200–90, and 300–30, respectively; for Navojoa M2007, 25.13%, 21.65%, and 20.17% for combinations 300–0, 300–60, and 200–30; for Tacupeto F2001, 60.89%, 60.81%, and 57.53% for combinations 300-0, 300-60 and 200-0; and for Kronstad F2004, 34.45%, 33.80%, and 32.19% for combinations 300-0, 200-30, and 300-30 (Table 3). The highest percent infection for cultivar Roelfs F2007 in the second sowing date were 36.80%, 29.98%, and 26.19% for combinations 300–0, 300–90, and 300–30, respectively; for Navojoa M2007, 11.53%, 7.28%, and 6.33% for combinations 300–60, 300–0, and 200–0; for Tacupeto F2001, 48.16%, 42.16%, and 37.05% for combinations 300-0, 200-60, and 200-0; and for Kronstad F2004 29.58%, 28.82%, and 27.49% for combinations 300-30, 300-60, and 200-60 (Table 3, p. 31).

2012–13 crop season.								
Tacupeto F2001, and Kronstad F2004, at the first and second sowing dates, in the Yaqui Valley, Sonora, during the								
Table 2. Percent infection with Karnal bunt of bread wheat commercial cultivars Roelfs F2007, Navojoa M2007,								

	30 Novem	nber, 2012			15 Decem	1ber, 2012	
Roelfs	Navojoa	Tacupeto	Kronstad	Roelfs	Navojoa	Tacupeto	Kronstad
47.48	22.91	56.60	34.03	27.64	5.43	37.61	8.41
41.91	8.94	38.98	27.00	32.32	6.49	36.49	24.34
39.76	16.15	40.81	30.86	16.40	2.38	23.40	4.04
45.79	14.90	36.98	30.61	21.62	5.37	37.75	17.96
23.06	11.37	57.12	29.71	21.19	7.38	39.14	27.69
47.57	23.47	64.66	37.90	22.65	7.18	45.19	8.98
37.40	18.72	62.15	31.29	19.74	9.22	25.99	33.24
40.30	15.96	59.47	30.19	8.07	13.83	38.36	24.41
36.56	23.38	54.20	35.14	22.35	5.65	35.85	29.61
50.27	19.92	60.85	29.24	30.02	7.01	26.91	29.56
40.97	21.33	30.02	31.66	35.80	7.75	25.45	23.32
47.47	19.01	51.63	37.23	37.80	1.29	37.95	9.58
23.44	20.04	52.51	22.86	14.72	7.89	25.10	10.47
39.74	11.59	58.26	29.36	31.98	2.42	43.19	26.62
34.59	36.89	60.14	17.83	26.17	5.31	53.35	21.17
38.16	13.37	36.85	20.64	26.02	3.47	42.98	33.81

ΑΝΝυΑΙ ΨΗΕΑΤ ΝΕΨΙΙΕΤΤΕΚ

Table 3. Percent infection with Karnal bunt of commercial bread wheat cultivars Roelfs F2007, Navojoa M2007, Tacupeto F2001, and Kronstad F2004, subjected to several combinations of nitrogen x sulphur (N–S) fertilization during the first and second sowing dates in the Yaqui Valley, Sonora, during the 2012–13 crop season.

	30	November, 2	012		15 Decen	nber, 2012				
N–S	Roelfs	Navojoa	Tacupeto	Kronstad	Roelfs	Navojoa	Tacupeto	Kronstad		
200–0	35.32	15.93	57.53	30.74	13.91	6.33	37.05	18.33		
200-30	44.69	20.17	40.82	33.80	21.92	4.52	31.70	16.37		
200-60	36.37	17.42	38.89	19.24	26.10	3.88	42.16	27.49		
200–90	44.22	15.53	55.38	26.11	23.35	5.16	30.57	16.45		
300–0	42.78	25.13	60.89	34.45	36.8	7.28	48.16	11.00		
300-30	43.41	17.34	47.79	32.19	26.19	5.96	32.18	29.58		
300-60	38.85	21.65	60.81	30.73	19.01	11.53	31.38	28.82		
300–90	31.59	15.81	48.50	30.51	29.98	4.39	34.14	18.54		

The percent infection in the first sowing date during the 2013–14 crop season for cultivar Roelfs F2007 was 8.69-27.59%, with a mean of 17.05%, and for Kronstad F2004, 2.98-16.42%, with a mean of 8.07%. The overall range for the two cultivars was 2.98-27.59% with a mean of 12.56% (Table 4). The susceptible check showed 88.98% infection at the first date. The percent infection at the second sowing date for cultivar Roelfs F2007 was 4.60-25.77%, with a mean of 16.77%, and for Kronstad F2004, 8.92-21.59% with a mean of 14.15% (Table 4). The overall range for the two cultivars was 4.60-25.77% with a mean of 15.46%. The susceptible check showed 89.95% infection at the second date. A marked difference in percent infection for Kronstad F2004 between dates was observed, which was higher at the second date with the exception of treatments 30-45 (13.21-12.35%) and 45–45 (16.42–9.50%); the difference between the second and first planting dates ranged from 0.64% to 15.45%. For Roelfs

Table 4. Percent infection with Karnal bunt of two commercial, bread wheat cultivars Kronstad F2004 and Roelfs F2007, subjected to several combinations of nitrogen x sulphur (N–S) fertilization at two sowing dates, in the Yaqui Valley, Sonora, during the 2013–14 crop season.

	30 Nover	nber, 2012	15 Decem	1012 nber, 2012
(N-S)	Kronstad	Roelfs	Kronstad	Roelfs
0–0	11.82	22.17	12.46	14.35
15–0	9.32	8.69	20.69	12.94
30–0	7.53	24.68	12.92	23.15
45–0	4.33	20.16	16.63	14.70
0–15	4.30	18.51	13.38	16.69
0–30	5.33	14.98	14.76	17.84
0–45	6.14	15.54	21.59	18.04
15–15	8.26	17.03	19.96	18.35
15-30	2.98	16.18	12.06	18.16
15–45	8.39	12.38	12.80	25.77
30–15	8.04	18.15	8.92	9.05
30–30	9.54	11.84	17.69	4.60
30–45	13.21	27.59	12.35	17.27
45–15	6.37	17.07	8.97	16.57
45-30	7.07	14.26	11.68	15.96
45–45	16.42	13.50	9.50	24.87

F2007, the percent infection was higher in eight treatments at the second date, ranging from 1.31% to 13.39%, whereas the other eight were higher at the first date, ranging from 0.51% to 10.32%.

Conclussions. Although there were clear interactions between levels for all factors for the reaction of bread wheat cultivars to artificial inoculation with Karnal bunt, the effects of sowing and inoculation dates and cultivar were apparent in both years. Higher levels of infection were observed at the earlier sowing and inoculation dates during the 2012–13 crop season, whereas the opposite occurred in 2013–14. The highest infection during the first season was recorded in Tacupeto F2001 (sowing 30/11/12, inoculation 22/02/13) and the lowest in Navojoa M2007 (sowing 15/12/12, inoculation 01/03/13). As the nitrogen rate increased, the greater the percent infection with no apparent effect by the sulphur rate, for all cultivars averaged across sulphur rates when the trial was sown on 15/12/12 and inoculated on 01/03/13. In the 2013–14 crop season, of the two cultivars evaluated, Roelfs F2007 had a higher percent infection than Kronstad F2004; and as in the first season, without an apparent effect by the sulphur rate.

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Effect of temperature, relative humidity, and rainfall on wheat grain yield in southern Sonora during the 2014–15 crop season.

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Abstract. The effect of temperature on wheat production for the 2014–15 crop season was evaluated using data obtained from 23 weather stations in southern Sonora. Temperature accumulated within the range >0 to <10°C at a >30°C threshold were measured and compared with data from three previous seasons. The effect of relative humidity, rainfall, and average temperature also were evaluated. The accumulation of cold hours, within the range >0 to <10°C, caused weak seedlings, and the tillers gave rise to spikes with various degrees of sterility, which, in turn, produced few or small grains. During the 2014–15 crop season, thermal hours in the temperature threshold >30°C increased to 2,610, which occurred frequently from 11 March on, coinciding with flowering and the initial and half-way development of the grain. Sterility increased during the reproductive stage, resulting in a few grains/spike, an increase in the number of wrinkled grains, and grains with low specific weight. The heat waves caused flower abortion and/or kernel development and a reduction of 176 kg; 112 kg for each 1% increase in relative humidity, starting at 67.1%, an average wheat production reduction of 176 kg; 112 kg for each 1 mm of rainfall accumulated from flowering onward; and 572 kg for each 1°C temperature increase, starting at 15.9°C, were observed. The temperature trend during this crop season had a greater negative effect than that of rainfall and relative humidity. The interaction between temperature and RH indicates that, as the average temperature increased at 2.1°C and 3.2% RH, the average wheat grain production was reduced by 1.945 ton.

Introduction. In the region of southern Sonora, the main economic activity is agriculture. Wheat is the most important crop, which is frequently affected by the presence of adverse climatic phenomena, such as the abscence or uneven distribution of the cold during the winter, early and/or late frosts, excess or lack of rainfall, and the presence of diseases and pests. Wheat production during the 2014–15 crop season had a an average reduction of 1.9 ton/ha, affecting more than 240,000 ha. Abiotic and biotic factors associated with this negative impact on wheat production were increases in temperature, relative humidity, and rainfall, which also were associated with the occurrence of several diseases. This study determined the factors highly associated with the reduction of wheat production during the 2014–15 crop season in southern Sonora.

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Materials and methods. To evaluate the effect of temperature on wheat production for the 2014–15 crop season, data obtained from 23 out of 29 weather stations in southern Sonora (Fig. 23) (PIEAES 2015), covering the Yaqui and Mayo Valleys, was used for the analysis. This data consisted of measuring the effect of the temperature accumulated within the range of >0 to $\leq 10^{\circ}$ C (conceptualized as accumulated cold hours) at a $\geq 30^{\circ}$ C threshold, compared with data from the 2011–12, 2012–13, and 2013–14 wheat seasons. The effects of relative humidity, rainfall, and average temperature also were evaluated. Damage to the spike was analyzed in several farmers' fields, by measuring the percent sterility, number of wrinkled grains, and number of grains with spots.

Results and discussion. The accumulation of cold hours, within the range $>0-\le10^{\circ}$ C (Fig. 24), was reduced from the early growth stages of the wheat plant (Fig. 25). Seedlings were weak and the tillers gave rise to spikes with various degrees of sterility, producing few or small grains. Because of their size, these grains were not retained by the combine during harvest (Fig. 26) (Félix et al. 2009). Weak stems are more susceptible to lodging and weak tillers exert an effect of competition as a weed with respect to the main stem. The lack of cold ($\Sigma > 0$ to $\le10^{\circ}$ C)

also causes a reduction of the foliar area index, equal to the foliar mass reduction. which is not compensated for during the rest of the season and is closely related with a drop in production (Félix et al. 2009). During the

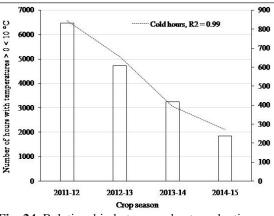


Fig. 24. Relationship between wheat production with thermal hour accumulation within $>0-\le10^{\circ}$ C conceptualized as accumulated cold hours (registered data from weather station in the Yaqui and Mayo Valleys, Sonora, Mexico.

2014–15 crop season, thermal hours in the temperature threshold \geq 30°C increased to 2,610 (Fig. 27, p. 34). This level of temperature occurred frequently from 11 March onward, coinciding with flowering and with the initial and half-way development of the grain (Table 5, p. 34). The increase in sterility during the reproductive stage, resulting in a reduction in number of grains/spike and an increase in the number of wrinkled grains and grains with low specific weight (Figs. 28 and 29, p. 34), were noticable. The heat



Fig. 23. Weather stations located in the Yaqui and Mayo Valleys, in southern Sonora, Mexico.

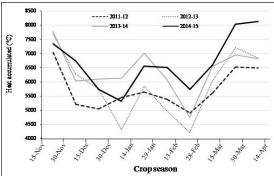
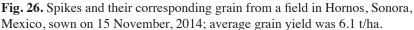


Fig. 25. Dynamics of heat acumulation during the 2011–12 to 2014–15 crop seasons in the Yaqui and Mayo Valleys, Sonora, Mexico.





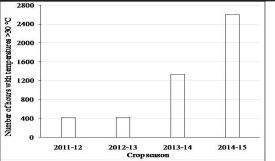
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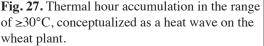
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Table 5. Temperatures greater than 30°C, time of exposure, and frequency, during March and April, 2015, in the Yaqui and Mayo Valleys, Sonora, Mexico (rows with the same color, indicate heat waves as temperatures above 30°C occurred during consecutive days).

Day/	Temperature	Number
month	(°C)	of hours
11/03	30.1	1
14/03	30.0-31.1	3
15/03	30.0	1
22/03	30.1	1
23/03	30.7–31.8	4
24/03	30.2-30.4	3
27/03	30.0-32.5	5
28/03	30.0-32.0	6
29/03	30.1-30.4	3
01/04	31.1–32.8	4
02/04	30.1–30.8	5
05/04	30.1-30.8	4
06/04	30.9-32.2	6
07/04	30.0-33.1	6
08/04	30.4–31.8	5
09/04	31.1–32.6	4
10/04	30.1-30.6	5
13/04	30.3–30.8	4
14/04	30.5-31.9	6
15/04	30.1-32.9	7

For each 1% increase in relative humidity, starting at 67.1%, wheat production was reduced by an average of 176 kg. For each 1 mm of rainfall accumulated (Fig. 30, p. 30) from flowering onward, average production was reduced by 112 kg, in response to damage by fungal diseases such as Karnal bunt (Tilletia indica) and black point (Alternaria spp.) (Fig. 31, p. 30), and spot blotch (Bipolaris sorokiniana). For each 1°C temperature increase, starting at 15.9°C, average wheat production was reduced 572 kg. The temperature trend present during this crop season had a greater negative effect than the effect of rainfall and relative humidity, although the interaction of temperature and RH indicates that as the average temperature increased during the crop season in 2.1°C and 3.2% RH. The average grain production was





wave (Table 5) had a negative impact on pollination causing flower abortion (Figs. 28 and 29) on those recently pollinated, which affected kernel development and the developing kernels from a quarter kernel to milky stage, coinciding with stages Z6.5-Z7.05 (described by Zadoks et al. 1974). This level of temperature stress was



manifested in a reduction of final grain weight.

Fig. 28. A commercial field with wheat cultivar CIRNO C2008 in block 1730, planting date 25 November, 2014, with a 160 kg/ha seeding rate, three complimentary irrigations, and flowering 83–86 days after sowing (~11–15 February, 2015). Fungicides were applied to control rusts and Karnal bunt. The average yield for 300 ha was 5.3 t/ha, fewer grains/m², and spikes with small grain. Black point at harvest was 6%; yellow berry was $\leq 1\%$.



Fig. 29. Spikes of wheat cultivar CIRNO C2008 and their corresponding grain and grain weight from an area on the north side of a low canal. Planting date was 18 November, 2014, with a 180 kg/ha seeding rate, three complimentary irrigations, and flowering 85–90 days after sowing (~11–15 February, 2015). No fungicides were applied. Grain yield was 5.9 t/ha, 1.5 t/ha less than in the 2013–14 growing season, fewer grains/m², and sterile spikes and spikes with small and wrinkled grain. Black point at harvest was 5%; yellow berry was 5%.

reduced to 1.945 ton in 240,000 ha, which is equivalent to a volume of 466,800 ton, significantly affecting the regional economy in southern Sonora.

Damage to the plant and floral organs occurs when extreme climatic conditions prevail. Temperature damage is typified by its levels, because plants will not tolerate it at a given specific phenological stage. Damage might occur depending on the level of expression of these three principles: temperature level, time of exposure, and frequency. According to Table 5, the data complies with the temperature level, time of exposure (hours), and the frequency in days, in order to consider this climatic parameter as a heat wave, the main abiotic factor that caused the low wheat grain yield during the 2014–15 crop season.

Conclusion. In what is considered a normal wheat season, the average temperature is 16.2°C with 64% relative humidity. During the 2014–15 season, the average temperature was 18.8°C with 77.4% relative humidity, which caused heat waves (temperature fluctuations between 30 and 33°C) during tillering, flowering, and part of grain filling. Several periods had more than 80% relative humidity during the season and atypical precipitation patterns occurred in January, February, March, and at the beginning of April. These climatic conditions caused general damage to the wheat plant, which was expressed in a significant reduction in grain production, as well as negative effects on quality for export.

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Fig. 30. Rainfall during January to April, 2015, in southern Sonora, Mexico.



Fig. 31. Symptoms of Karnal bunt (left) and black point (right) in wheat.

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Evaluation of synthetic wheat lines under normal irrigated conditions.

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Wheat is the most widely grown cereal in Pakistan. Abiotic and biotic stresses, especially rust diseases, are the main reasons for a low average national yield. Therefore, a dire need exists to develop genotypes with improved resistance to these diseases along with high yield potential. Synthetic hexaploid wheat (man-made wheat) is a novel source of wheat germplasm that may be used as a resource to break the yield barrier in the wheat crop. These synthetics (2n = 6x = 42;AABBDD) are a globally recognized, potent genetic stock and are used by several wheat-breeding programs (Mujeeb-Kazi et al. 2008, Trethowan and Mujeeb-Kazi 2008; Ogbonnaya et al. 2013).

The Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan, is working on wheat improvement and has developed high-yielding recombinants; some promising ones contributing in multilocation microtrials. In addition, a large number of recombinants and synthetics were evaluated in different trials/generations. In the current studies, synthetic lines were evaluated in two different field experiments. The first experiment consisted of a set of 13 wheat-breeding introductions, advanced synthetic-derived lines, and two check cultivars (Punjab-2011 and Galaxy-2013) sown in six 6-m rows with a row-to-row distance of 30 cm and plot size of 10.8 m². In the second experiment, 35 synthetic-derived lines were tested in the field along with the two check cultivars sown in a 4.95 m² plot. The material was sown in November 2013. Data were recorded on days-to-heading, plant height (cm), tiller number, spike length (cm), number of grains/spike, 1,000-kernel weight (g), grain yield (kg/ha), harvest index (%), and reaction to leaf rust, yellow rust, and stem rust.

Experiment I. The data of 13 synthetics, along with two checks, are presented (Table 1, p. 37). All synthetic lines were early heading compared to the checks, except four lines that were similar. Maximum plant height and tiller number were noticed in Nepal-AL/249, whereas Ehydral/13 and Kazi-09 were better for spike length and number of grains/spike, respectively. The 1,000-kernel weight ranged from 31.0 g to 51.8 g among the synthetic lines. Six lines (Kazi-09, EM, IBT-S/1069, Ehydral/13, ITMI/71, and Nepal-AL/186) all had a 1,000-kernel weight above 40.0 g and acceptable grain yield, and were selected for further evaluation in replicated yield trails next year.

Experiment II. A wealth of variability was observed in the synthetic-derived lines, represented by the range of various morpho-agronomic traits (Table 2, p. 37-38). Entry 140 had the earliest number of days-to-heading. Taller (plant height \geq 110 cm) entries with good seed size and higher grain yield, such as entries 30, 42, 44, 47, 52, 64, 123, 129, 147, and

Table 1. Morpho-agronomic traits of the advanced, synthetic-derived wheat lines (DH, days-to-heading; PH, plant height; TIL, tiller number; SL, spike length; NGPS, number of grains/spike; TKW, 1,000-kernel weight; and GY, grain yield).

<i>J</i> ¹⁰¹⁰):		1		1		1	
Entry	DH	PH (cm)	TIL	SL (cm)	NGPS	TKW (g)	GY (kg/ha)
Kazi-09 (5-101)	103	101.4	235	12.3	67	41.4	4,155
EM	101	91.8	216	11.9	74	47.6	3,484
IBT-S/1069 (5-133)	102	100.2	210	13.3	60	43.0	3,399
Nepal-AL/249	108	113.8	265	11.2	48	39.0	3,502
9X1/36	107	100.6	213	10.8	55	38.2	3,324
T/FCT/18	127	99.4	211	10.8	59	38.4	2,754
Ehydral/13 (5-151)	124	101.0	232	13.7	64	47.6	3,336
Nepal-AL/247	108	111.6	224	11.8	60	37.6	3,334
Nepal-AL/268	128	99.0	212	12.2	60	43.8	2,451
ITMI/71	126	104.6	240	12.3	46	51.8	3,265
Nepal-AL/186	105	102.6	235	12.6	48	44.6	3,694
9X1/26	107	99.0	238	10.6	48	39.8	2,841
T/FCT/73	109	100.4	215	11.4	63	31.0	2,737
Galaxy-2013 (check)	127	103.0	208	13.6	51	49.0	3,650
Punjab-2011 (check)	127	97.8	197	12.4	68	44.2	3,422

Table 2. Morpho-agronomic traits and disease performance of bread wheat x synthetic-derived wheat lines. Mean, range, and standard deviation of the synthetic derivatives also are presented at the bottom of the table (DH, days-to-heading; PH, plant height; TIL, tiller number; SL, spike length; NGPS, number of grains/spike; TKW, 1,000-kernel weight; GY, grain yield; HI, harvest index; Lr, reaction to leaf rust; Yr, reaction to yellow rust; and Sr, reaction to stem rust).

1031).	DH	PH		SL		TKW	GY	HI			
Entry	(50%)	(cm)	TIL	(cm)	NGPS	(g)	(kg/ha)	(%)	Lr	Yr	Sr
25	99	115	164	10.4	53.4	43.6	2,283	20	0	0	0
28	103	99	276	10.7	67.4	36.8	4,212	38	0	0	0
30	98	114	239	12.1	56.6	46.4	3,464	32	0	0	0
37	104	122	230	12.4	58.2	38.8	1,788	21	0	0	0
39	108	110	300	11.1	57.6	42.0	3,626	28	0	0	0
42	105	117	387	8.6	56.2	39.6	4,464	28	0	0	0
43	105	112	286	9.3	53.4	40.4	3,283	31	0	0	0
44	105	111	203	9.4	63.8	39.2	3,434	33	0	0	0
45	102	109	201	11.4	49.6	52.0	3,091	34	20R	0	0
47	102	113	316	12.7	50.2	49.0	3,858	32	10R	0	0
49	106	110	141	9.7	60.4	38.2	3,111	33	0	0	0
52	101	114	195	12.2	49.2	50.8	3,747	36	10R	0	0
64	99	115	259	12.0	54.2	46.0	3,313	31	0	0	0
73	102	83	273	11.2	64.8	36.2	3,343	36	0	0	0
74	107	100	223	11.5	54.0	41.8	3,081	33	0	0	0
76	103	98	265	11.6	55.8	41.8	3,343	36	0	0	0
83	98	104	188	10.9	44.8	47.8	2,374	32	0	0	0
84	99	113	245	11.8	47.4	45.6	3,010	31	0	0	0
90	100	112	201	10.2	61.4	41.4	2,949	26	0	0	0
109	98	107	241	11.5	59.2	38.4	3,515	35	0	0	0
116	102	110	100	11.4	56.8	32.8	1,737	26	0	0	0
117	102	107	166	11.3	67.6	35.2	1,990	29	0	0	0
120	104	108	365	12.1	78.4	33.0	2,475	29	0	0	0
121	105	106	217	13.1	57.8	34.8	3,121	33	0	0	0
123	106	112	235	13.3	61.0	42.6	4,424	32	0	0	0
125	102	106	240	11.1	62.6	39.4	3,919	32	0	0	0
126	101	109	225	11.7	63.2	39.4	3,313	38	0	0	0

Table 2. Morpho-agronomic traits and disease performance of bread wheat x synthetic-derived wheat lines. Mean, range, and standard deviation of the synthetic derivatives also are presented at the bottom of the table (DH, days-to-heading; PH, plant height; TIL, tiller number; SL, spike length; NGPS, number of grains/spike; TKW, 1,000-kernel weight; GY, grain yield; HI, harvest index; Lr, reaction to leaf rust; Yr, reaction to yellow rust; and Sr, reaction to stem rust).

Tust).	DH	PH	Ĭ	SL		TKW	GY	HI			
Entry	(50%)	(cm)	TIL	(cm)	NGPS	(g)	(kg/ha)	(%)	Lr	Yr	Sr
129	102	110	243	11.2	64.4	40.2	3,818	32	0	0	0
130	104	107	280	13.0	57.6	41.4	3,010	32	0	0	0
136	100	105	237	11.4	58.8	38.4	3,212	36	0	0	0
140	95	107	275	11.8	60.0	43.6	3,141	26	0	0	0
142	104	105	215	13.6	67.6	39.0	2,818	34	0	0	0
147	105	113	224	12.0	64.8	36.0	3,757	34	0	0	0
150	100	116	237	14.2	49.2	45.4	2,727	26	0	0	0
158	101	113	246	13.5	61.4	46.0	3,909	33	0	0	0
Punjab-2011	103	104	225	13.6	70.4	37.4	3,000	33	0	0	0
Galaxy-2013	102	108	226	13.3	56.3	46.5	3,882	38	0	0	0
Mean (synthetics)	102	109	238	11.6	58.5	41.2	3,264	32	0	0	0
Range (synthetics)	95–108	83-	100-	8.6-	44.8-	32.8-	1,737–	20-38	0	0	0
Kange (synthetics)	95-108	122	387	14.2	78.4	52.0	4,464	20-38	0		0
Standard deviation (synthetics)	±2.9	±6.8	±56.0	±1.2	±6.9	±4.8	±702	±4.4	0	0	0

158, are worth testing under drought conditions. Maximum tiller numbers were recorded in entries 42 (387) and 47 (316) when compared to checks Punjab-2011 (225) and Galaxy-2013 (226). Entry 42 also was the highest yielder, whereas the yeild of entry 47 was equal to that of the better check Galaxy-2013. Almost all the synthetic derivatives had comparatively shorter and more compact spikes than those observed in the checks. The selected synthetics were either equal to or higher in number of grains/spike or bold seed size, which contributed to thier higher grain yield. Entry 158 produced a higher number of grains/spike, a similar seed size, and was higher in yield compared to the Galaxy-2013 check. The maximum seed weight was observed in entry 52, which was coupled with a higher grain yield than both check cultivars. The highest grain yield was produced by entry 42 (4,464 kg/ha), followed by entries 123 (4,424 kg/ha) and 28 (4,212 kg/ha). Among the synthetic derivatives, entry 28 also had the maximum harvest index (38%), which is similar to the commercial check Galaxy-2013. No severe rust attack was observed in the synthetic derivatives and checks. Fifteen superior synthetics, entries 28, 30, 42, 44, 45, 47, 52, 64, 73, 76, 123, 125, 129, 147, and 158, with acceptable seed size/color and a yield higher than that of Punjab-2011, were finally selected. These selected synthetics are planted in replicated yield trials at NIAB, Faisalabad, for evaluation during the 2014–15 crop cycle.

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Field evaluation of synthetic and durum wheat lines in replicated yield trial.

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To broaden the genetic base of bread wheat, D-genome synthetic (2n=6x=42;AABBDD) derivatives and durum wheat advanced breeding lines were included in the wheat improvement program of the Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, during 2013–14. In this study, 65 wheat genotypes, including synthetic-derived wheat

lines, durum, and five check cultivars (Punjab-2011, Millat-2011, Galaxy-2013, Fakhr-e-Sarhad, and Lasani-2008), were evaluated in a preliminary yield trial under irrigated conditions. The trial was laid out in an alpha-lattice design with two replications keeping a row distance of 30 cm and plot size of 4.95 m². The material was planted on 18 November, 2013, at NIAB, Faisalabad. Irrigation was applied as and when required by the crop. Data were recorded on days-to-heading, plant height (cm), 1,000-kernel weight (g), grain yield (kg/ha), leaf rust, yellow rust, and stem rust. Five random plants/ replication were used for the measurements of PH, whereas all other traits were recorded on plot basis.

Enormous genetic variability for days-to-heading (98–113), plant height (82.7–119.7), 1,000-kernel weight (30.9–51.8), and grain yield (2,293–4,062) were observed among the tested material (Table 3, pp. 39-40). Seven genotypes showed were greater than 108 days-to-heading compared to 104 days for the bread wheat check Galaxy-2013. Three genotypes were taller than 110 cm, which also are worth evaluating under drought. Forty-five of the test genotypes produced 1,000-kernel weights in the range of 40–51.8 g, compared to 36.7 g for the check Lasani-2008. Genotype 69 (Fakhr-e-Sarhad), a T1BL·1RS cultivar of the Khyber Pakhtunkhwa Province, produced the highest grain yield (4,062 kg/ha) followed by genotypes 59 (durum, 3,754 kg/ha) and 68 (Galaxy-2013, 3,744 kg/ha). Forty-four test genotypes produced higher yields than those of three local checks (Punjab-2011, Millat-2011, and Lasani-2008). All genotypes were found to be nearly free from disease. Of the 65 test genotypes, 25 were selected based on their bold seed size and/ or higher grain yield. Among these, 17 were synthetic derivatives (1, 5, 7, 29, 31, 32, 35, 37, 43, 45, 46, 48, 49, 50, 52, 53, and 55) and eight were durum wheats (3, 56, 57, 59, 60, 61, 62, and 63). Among the durum genotypes, entry 3 was prominent because it had the highest 1,000-kernel weight (51.8 g), although it had a medium yield. Entry 3 could be crossed with high yielding genotypes, such as Fakhr-e-Sarhad, Galaxy-2013, and selected synthetic derivatives, to recover recombinants with improved seed size and grain yield.

Table 3. Agronomic traits and disease reaction of synthetic derivatives, durum wheat genotypes, and checks (DH, days-to-heading; PH, plant height; TKW, 1,000-kernel weight; GY, grain yield; Lr, reaction to leaf rust; Yr, reaction to yellow rust; and Sr, reaction to stem rust; TR, trace).

		PH	TKW	GY			
Entry	DH	(cm)	(g)	(kg/ha)	Lr	Yr	Sr
1. Bioremediation Plot. 7th EBWYT	99	95.9	48.8	3,596	10MR-MS	0	0
2. Bioremediation Plot. 7th EBWYT	105	103.1	40.0	2,627	TR	0	0
3. ITLY D-	113	82.7	51.8	2,643	TR	0	0
4. N-Lines	104	95.6	37.6	2,912	0	0	0
5. ICARDA	105	95.8	37.9	3,551	0	0	0
6. ICARDA	105	104.9	39.9	2,695	0	0	0
7. ICARDA	103	93.1	40.4	3,374	0	0	0
8. ICARDA	101	93.1	37.9	3,207	0	0	0
9. ICARDA	103	90.1	43.4	2,387	0	0	0
10. ICARDA	103	94.7	34.2	2,874	TR	0	0
11. KAGHAN selection	109	96.0	34.3	2,427	0	0	0
12. KAGHAN selection	107	103.7	36.6	2,609	0	0	0
13. KAGHAN selection	104	119.7	38.7	2,713	0	0	0
14. KAGHAN selection	107	109.9	37.7	2,530	0	0	0
15. KAGHAN selection	105	105.5	38.9	2,677	0	0	0
16. KAGHAN selection	105	104.5	38.0	2,916	0	0	0
17. KAGHAN selection	103	103.1	37.2	2,944	0	0	0
18. KAGHAN selection	106	97.8	33.2	2,338	0	0	0
19. KAGHAN selection	106	104.8	33.8	2,797	0	0	0
20. KAGHAN selection	106	105.3	33.1	3,367	0	0	0
21. KAGHAN selection	107	95.8	33.0	2,586	0	0	0
22. KAGHAN selection	107	99.3	33.2	2,952	0	0	0
23. KAGHAN selection	106	105.8	34.0	3,037	0	0	0
24. KAGHAN selection	102	97.7	37.5	3,055	0	0	0
25. KAGHAN selection	107	101.5	32.9	2,798	0	0	0
26. KAGHAN selection	105	96.8	33.7	2,394	0	0	0
27. KAGHAN selection	106	101.9	33.0	3,396	0	0	0

Table 3. Agronomic traits and disease reaction of synthetic derivatives, durum wheat genotypes, and checks (DH, days-to-heading; PH, plant height; TKW, 1,000-kernel weight; GY, grain yield; Lr, reaction to leaf rust; Yr, reaction to yellow rust; and Sr, reaction to stem rust; TR, trace).

		PH	TKW	GY			
Entry	DH	(cm)	(g)	(kg/ha)	Lr	Yr	Sr
28. KAGHAN selection	110	104.1	39.0	2,787	0	0	0
29. KAGHAN selection	106	112.6	39.0	3,739	0	0	0
30. KAGHAN selection	98	98.4	39.0	2,493	0	0	0
31. KAGHAN selection	100	99.4	43.7	3,243	0	0	0
32. KAGHAN selection	99	94.9	42.1	3,345	0	0	0
33. KAGHAN selection	101	102.6	38.2	3,177	0	0	0
34. KAGHAN selection	99	95.0	35.0	2,593	0	0	0
35. KAGHAN selection	99	104.2	39.3	3,226	0	0	0
36. KAGHAN selection	103	98.7	39.4	2,737	0	0	0
37. KAGHAN selection	103	100.3	39.5	3,372	0	0	0
38. KAGHAN selection	103	99.8	36.4	2,922	TR	0	0
39. T/FCT	106	94.0	38.5	3,491	0	0	0
40.12X2	103	97.0	37.2	3,170	0	0	0
41. Mayoor/FCT	105	100.5	34.3	2,562	TR	0	0
42. Mayoor/FCT	104	95.4	34.4	2,580	0	0	0
43. Th. curvifolium derivative	103	112.7	37.9	3,671	0	0	0
44. M/OPATA	107	91.0	30.9	2,850	0	0	0
45. SAWSN selection (2012–13)	101	107.6	44.3	3,090	0	0	0
46. SAWSN selection (2012–13)	103	104.7	39.9	3,724	0	0	0
47. SAWSN selection (2012–13)	104	103.7	41.7	2,675	0	0	0
48. SAWSN selection (2012–13)	103	107.8	44.3	3,526	0	0	0
49. SAWSN selection (2012–13)	103	104.6	42.4	3,644	TR	0	0
50. SAWSN selection (2012–13)	106	106.6	40.9	3,050	TR	0	0
51. SR selection	107	101.0	41.3	2,753	TR	0	0
52. SR selection	100	107.1	39.1	3,127	TR	0	0
53. SR selection	101	106.6	44.0	2,935	0	0	0
54. SR selection	106	92.1	43.4	2,370	0	0	0
55. SR selection	105	106.0	41.5	3,584	0	0	0
56. Durum selection (2012–13)	108	89.0	35.9	3,418	0	0	0
57. Durum selection (2012–13)	109	91.7	41.8	3,074	0	0	0
58. Durum selection (2012–13)	109	88.0	38.2	2,293	0	0	0
59. Durum selection (2012–13)	106	91.6	35.6	3,754	0	0	0
60. Durum selection (2012–13)	112	95.8	42.0	3,434	0	0	0
61. Durum selection (2012–13)	106	87.9	41.1	2,533	0	0	0
62. Durum selection (2012–13)	106	93.9	41.7	3,586	0	0	0
63. Durum selection (2012–13)	105	91.1	34.7	3,,084	0	0	0
64. Durum selection (2012–13)	107	91.0	41.3	2413	0	0	0
65. Durum selection (2012–13)	109	98.2	42.0	2,636	0	0	0
66. Punjab-2011	102	96.0	41.3	2,568	0	0	0
67. Millat-2011	99	101.8	42.0	2,746	0	0	0
68. Galaxy-2013	104	107.9	43.8	3,744	5R	0	0
69. Fakhr-e-Sarhad	104	104.0	42.7	4,062	0	0	0
70. Lasani-2008	102	92.9	36.7	2,749	0	0	0
Mean	104	100.0	39.0	2,999	_	_	_
Range	98– 113	82.7– 119.7	30.9– 51.8	2,293– 4,062	_	_	_
Standard deviation	±3.1	±6.8	±4.1	±435.5			
Standard deviation	L - 2.1	L -0.0	L - 1.1		1		

The selected synthetic and durum genotypes have been planted in separate replicated yield trials at NIAB for evaluation during the 2014–15 cropping season. In the durum trial, Durum-97 was added as a local check. Crosses will be attempted between these synthetics, the commercial checks, and other promising entries during 2014–15. We also are exploring the direct potential of the best durum wheat entries as a cultivar and embarking on a pentaploid-based, durum improvement program to improve durums and bread wheat germplasm using synthetic derivatives.

Genetic variation in exotic durum wheat accessions.

Babar Manzoor Atta, Sajid Shokat, and Kamran Saleem.

Durum is the only commercially cultivated tetraploid wheat species. Durum is a hard wheat, high in protein and strength, and used to prepare various products, such as breads, cakes, biscuits, pastas, noodles, and other bakery products. The Wheat Research Institute (WRI), at AARI, Faisalabad, released the durum wheat cultivars (2n=4x=28; AABB) Wadhanak-85 and Durum-96 during 1985 and 1996, respectively, for cultivation in the province of Punjab. The demand for durum wheat is increasing in Pakistan and augments our breeding efforts to improve yield potential and disease resistance. This will definitely lead to the development of cultivars to feed our local industry and for export to earn foreign exchange.

A set of 13 durum wheat accessions, mostly approved cultivars from Turkey, were planted at the NIAB, Faisalabad, in two 2.8-m rows to test their adaptability and productivity. Data were recorded on days-to-heading, plant height, spike length, number of grains/spike, 1,000-kernel weight, grain yield, and resistance to leaf rust, yellow rust, and stem rust. Five random plants were used for recording the data and means.

One accession, Karsakilcik, did not adapt to Faisalabad conditions; no heading and high susceptibility to rusts, rejected this cultivar in the field. Data for the other 12 accessions is presented (Table 4). Sufficient genetic variability was recorded for all the traits. Ceylan-95 (118) and Divarbakir-81 (117) were comparatively late in heading. Ceylan-95 also was the tallest (104 cm) and had the longest spike (10.2 cm) but had the minimum number of grains/spike (50.4), due to a lower spike density and resulting in a lower yield. Harran was the shortest accession (87.6 cm) with the highest number of grains/spike (75.6) but much lower seed weight (40 g) and the lowest grain yield (240 g). The most desirable accessions had a medium height, compact spike, and good seed weight. Firat-93 was the most promising cultivar, with a bold seed size (51.2) and highest yield (725 g). These accessions were found to be free from all the three rust diseases. Eight entries, with a yield ranging from 620 g to 725 g, were better adapted to the local conditions.

Table 4. Morpho-agronomic traits and disease performance of exotic durum wheat accessions (DH, days-to-heading; PH, plant height; SL, spike length; NGPS, number of grains/spike; TKW, 1,000-kernel weight; GY, grain yield; Lr, reaction to leaf rust; Yr, reaction to yellow rust; and Sr, reaction to stem rust; TR, trace disease).

		PH	SL		TKW	GY	,		
Entry	DH	(cm)	(cm)	NGPS	(g)	(g)	Lr	Yr	Sr
Altintoprak-98	102	90.2	7.7	60.8	47.2	490	0	0	0
Artuklu	101	102.6	9.1	66.8	50.4	660	0	0	0
Aydin-93	114	102.4	7.6	55.6	37.8	680	TR	0	0
Ceylan-95	118	104.0	10.2	50.4	44.6	565	0	0	0
Divarbakir-81	117	101.8	9.6	54.2	44.8	630	0	0	0
Eyyubi	102	96.4	7.7	66.4	45.2	715	0	0	0
Firat-93	103	91.0	7.9	54.8	51.8	725	0	0	0
Guneyyildizi	107	96.2	8.5	63.6	41.4	725	0	0	0
Harran	103	87.6	9.0	75.6	40.6	240	0	0	0
Saricanak-98	105	93.2	8.3	66.0	45.8	620	TR	0	0
Sahinbey	102	96.2	8.8	56.8	62.2	685	0	0	0
Zuhre	105	91.8	8.3	61.4	43.2	440	0	0	0

Babar Manzoor Atta, Sajid Shokat, and Kamran Saleem.

Wheat is the main cereal crop of Pakistan. Among the various environmental stresses affecting wheat production, drought is the major limiting factor. The current cultivars do not produce a maximum yield due to the large spatial variation in rainfall under arid and semi-arid conditions. Therefore, developing genotypes that are either tolerant to terminal drought or that mature early to escape this stress is a dire need.

We evaluated wheat genotypes for drought tolerance in two field trials and in an experiment under plastic tunnel conditions. The Wheat Station Yield Trial (WSYT (A-I)) was comprised of eight genotypes and a check (Punjab-2011). Similarly seven local and two exotic (Turkey) genotypes were tested in WSYT (A-II) along with two checks (Galaxy-2013 and Punjab-2011). The trials were conducted in a randomized complete block design with three replications keeping row to row distance of 30 cm and plot size of 4.95 m². The material was planted on 11 November, 2013. No supplementary irrigation was applied during the entire cropping season.

Thirteen local genotypes, one exotic line (Sitta), and four checks, including Marvi-2000 as a drought-susceptible check, were evaluated under water-limited conditions in a plastic tunnel. The material was planted in single rows per genotype with two replications. The material was saved from rain, although a single, life-saving irrigation was applied at grain development stage insure a seed harvest.

Table 5. Morpho-agronomic traits and disease performance of wheat genotypes in Wheat Station Yield Trial A-I (a) and A-II (b). Overall mean and p values also are presented (DH, days-to-heading; PH, plant height; TIL, tiller number; SL, spike length; NGPS, number of grains/spike; TKW, 1,000-kernel weight; and GY, grain yield).

SL, spike length	DH	PH	Grunners	SL	, 1,00	TKW	BI	GY			
Entry	(50%)	(cm)	TIL	(cm)	NGPS	(g)	(g)	(kg/ha)	Lr	Yr	Sr
Wheat Station	Yield Tri	al A-I									
NW-1-20	103	77.8	151.0	10.4	48.9	42.1	530.0	2,646	TR	TR	0
NW-3-2	91	83.6	141.0	14.0	53.1	48.8	536.7	2,244	0	10MS-S	0
NW-7-13	92	72.1	127.7	9.5	51.8	43.1	463.3	2,248	50MS-S	70S	0
NW-7-20	92	75.0	148.7	9.8	50.1	43.4	476.7	2,212	30S	80S	0
NW-7-19	93	76.8	131.3	9.8	52.1	43.6	523.3	2,538	30MR	60S	0
NW-7-24	92	78.1	140.7	10.2	54.9	44.1	550.0	2,318	0	60S	0
NW-10-19	100	85.7	134.0	10.7	57.7	44.1	546.7	2,386	0	20MS	0
NW-31-2	92	80.1	136.7	11.8	56.9	45.9	613.3	3,058	0	20R	0
Punjab-2011	94	79.1	139.7	11.5	49.9	43.6	526.7	2,355	10MR- MS	0	0
Mean	94	78.7	139.0	10.8	52.8	44.3	530.0	2,445	-	_	-
P value	<.001	<.001	0.94	<.001	0.214	0.002	0.722	0.035	-	-	-
Wheat Station	Yield Tri	al A-II									
NW-15-5-37	99	84.9	180.0	11.3	51.7	42.6	673.0	3,165	0	80S	0
NW-1-47-4	101	84.8	163.3	12.6	62.5	40.3	747.0	3,118	0	0	0
NW-7-1-9	105	87.7	185.0	12.2	55.7	41.5	677.0	3,229	60S	70S	0
NW-10-4-20	99	89.0	149.3	11.6	54.5	42.3	643.0	2,508	0	30MS	0
NW-7-28-13	101	79.6	149.3	10.3	54.0	36.3	520.0	2,545	40MS-S	30MS-S	0
NW-10-46-25	105	80.5	156.3	11.6	51.9	41.7	543.0	3,101	0	0	0
NW-1-27-3	99	84.3	130.0	12.7	57.2	48.1	583.0	2,885	TR	20R	0
PUNJAB-2011	95	84.3	174.3	11.5	56.2	43.9	707.0	3,151	TR	0	0
Galaxy-13	103	87.5	142.0	12.3	54.6	50.1	543.0	2,889	40MS-S	0	0
Karacadag-98	103	84.5	199.3	12.8	72.6	37.9	887.0	1,990	40MS-S	40MS-S	0
Nurekent-2008	109	87.0	148.7	13.2	65.9	37.6	700.0	1,656	50S	50S	0
Mean	102	84.9	162.0	12.0	57.9	42.0	657.0	2,749	—	_	_
P value	<.001	0.001	0.029	<.001	<.001	<.001	<.001	0.001	_	_	_

Data were recorded on days-to-heading, plant height (cm), tiller number, spike length (cm), number of grains/ spike, 1,000-kernel weight (g), biomass (g), grain yield (kg/ha or g), and resistance to leaf rust (Lr), yellow rust (Yr), and stem rust (Sr). Five random plants per replication were used for the measurements.

Morpho-agronomic data and disease response of the wheat genotypes tested in WSYT A-I and A-II are given (Table 5, p. 42). In trial A-I, significant differences between the genotypes were observed for days-to-heading, plant height, spike length, 1,000-kernel weight, and grain yield, whereas tiller number, grains/spike, and biomass were not significant, as showed by the p-values. Genotype NW-1-20 had a significantly higher days-to-heading (9 days) and grain yield (12.4 higher) than the check; NW-3-2 was comparatively taller, had the longest spike length, and the highest 1,000-kernel weight and grain yield, equal to that of the check cultivar. NW-10-19 was late (6 days), taller, and with a comparatively higher yield than that of the check. The plant height and spike length of genotype NW-31-2 was not significantly different than those of the check, but had a highter 1,000-kernel weight and the highest grain yield (29.9 higher than that of the check). These four genotypes were also disease resistant and were selected for further evaluation during 2014–15 crop season. The remaining four genotypes were found to be susceptible to either to leaf rust or stem rust or both.

In trial A-II, the genotypes showed significant differences for all traits. Among the seven local and two exotic genotypes, all were susceptible to the rusts with the exception of NW-1-47-4, NW-10-46-25, and NW-1-27-3. Genotype NW-10-46-25 did not qualify for visual selection. The remaining two genotypes (NW-1-47-4 and NW-1-27-3) were 2–4 days earlier in heading, equal to the check for spike length, had higher number of grains/spike and biomass. Their yiels was either equal to or higher than that of the Galaxy-2013 check. These genotypes were selected for further testing during next year.

In the tunnel experiment, all test genotypes were at equal to or earlier than Galaxy-2013 in days-to-heading; Sehar-06 was the earliest (Table 6). NW-3-3341-7 and Marvi-2000 were the tallest. NW-10-1111-3, NW-10-46-25, and Ingulab-91 had the highest biomass and grain yield at maturity. This trail confirmed the findings of the field trials and the same genotypes also were selected in this experiment, with the addition of new genotypes tested in this experiment. In total, eight genotypes that showed higher yield than the susceptible and latest checks Marvi-2000 and Galaxy-2013, respectively, were selected for subsequent evaluation, with the exception of three disease-susceptible genotypes.

 Table 6. Agronomic traits of wheat genotypes in drought experiment under plastic tunnel conditions.

tunnel conditions.				
	Days-to-heading	Plant height	Biomass	Grain yield
Entry	(50%)	(cm)	(g)	(g)
NW-1-9-47	81	44.2	65	20.0
NW-1-27-3	78	49.8	105	33.7
NW-1-47-4	80	53.0	135	44.5
NW-1-8183-8	78	56.3	105	34.5
NW-3-3341-7	80	62.3	120	33.4
NW-5-1212-1	78	52.1	75	16.6
NW-7-9-30-1	80	57.2	120	37.6
NW-7-28-13	77	52.2	90	26.4
NW-10-4-20	78	55.9	105	31.1
NW-10-46-25	79	56.1	170	62.0
NW-10-1111-3	77	51.3	170	63.2
Sehar-2006	73	52.1	95	32.5
Inqulab-91	76	59.3	155	51.1
Sitta	74	55.4	145	42.7
Marvi-2000	73	60.2	100	29.7
NW-3-2	75	54.2	115	30.8
NW-31-2	75	53.9	100	30.3
Galaxy-2013 (check)	80	51.4	60	23.8
Mean	77	54.3	112.8	35.8

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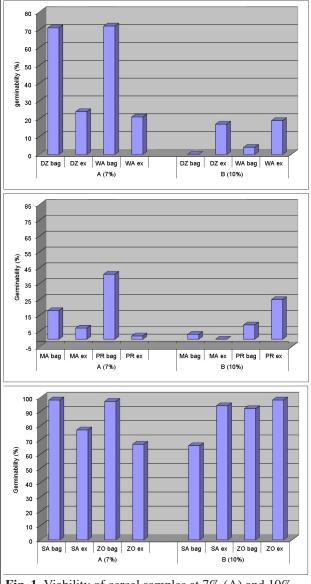
Maciej Niedzielski and Jerzy Puchalski (Botanical Garden) and Beata Cieślak and Mieczyslaw W. Obiedziński (Warsaw University).

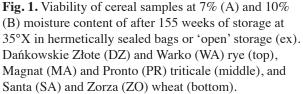
Seed longevity of cereal seed samples during hermetic vs. 'open' storage at 35°C and the effect of headspace gasses in hermetically stored samples.

Seed banks are the main *ex situ* method for the conservation of plant genetic diversity. According to the IPGRI recommendations for orthodox seed, dried samples are stored in hermetic containers at approximately -25° C. However, aging processes are not stopped completely. An important role in the aging of dry seed is played by the oxidative reactions of lipids due to free radical activity or auto-oxidative processes. Low-molecular volatiles, the end-products of these reaction, could be accumulated In hermetic storage containers. Due to their chemical activity, they may react with proteins and/or nucleic acids, negatively affecting seed viability. This experiment analyzed the changes in germinability of cereal samples stored in mild, artificial ageing conditions and the head space gas contents of cereal seed samples sealed in aluminum foil.

Materials and methods. Cereal seed samples of rye (Dańkowskie Złote and Warko), triticale (Magnat and Pronto), and wheat (Santa and Zorza) with different moisture contents (MC, 7, 10, and 13% (fwb)) were stored sealed in laminated, aluminum foil bags (hermetic storage) and/or over salt solutions in a periodically ventilated, glass desiccator ('open' storage) at 35°C. During storage, seed viability and moisture content were checked periodically. After 155 weeks, the head-space gas content of hermetically stored seed was assessed by GC/MS.

Viability results. The slowest decrease in viability was observed for wheat at 7% MC. The highest rate of aging was represented by triticale cultivars despite the MC. At 13% MC, all samples lost their viability after a few weeks.





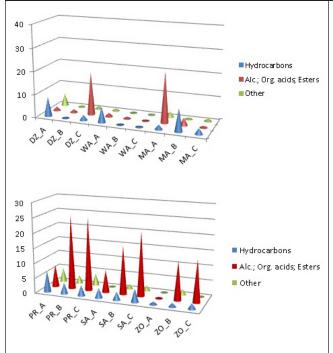


Fig. 2. The main groups of volatiles (a.u.) of head-space atmosphere of cereal seed samples hermetically stored for 155 weeks at 35°C at a moisture content of 0.07 (A), 0.10 (B), or 0.13 (C) gH₂O/gfw for Dańkowskie Złote (DZ) and Warko (WA) rye, Magnat (MA) and Pronto (PR) triticale, and Santa (SA) and Zorza (ZO) wheat.

Table 1. Seed moisture content at 0 time and after 155weeks of hermetic (bag) or 'open' (desiccator) storage.

0 L.

6 1.

		Time						
			155 days					
Сгор	Cultivar	0		Hermetic	Open			
Deve	D Złote	7		7	4			
Rye	Warko	11		10	9			
Triticala	Magnat	7		7	4			
Triticale	Pronto	10)	10	9			
Wheet	Santa	7		7	3			
Wheat	Zorza	10)	10	9			

Table 2. Total amount of accumulated volatiles (a.u.) after 155 weeks of hermetic seed storage at 35°C in relation to seed moisture content (*probably the result of microbial (fermentation) activity).

		Seed moisture content						
Crop	Cultivar	7%	10%	13%				
Dria	D Złote	15.53	2.36	22.25*				
Rye	Warko	10.47	1.33	1.14				
Triticale	Magnat	27.72	14.32	5.68				
Triticale	Pronto	20.41	31.46	33.09				
Wheat	Santa	10.80	19.30	27.78				
wheat	Zorza	1.40	16.30	17.80				

Seed with 7% MC were stored better when sealed in an hermetic container, but seed with a higher MC (10%) maintained their viability longer in 'open' storage (Fig 1, p. 44). The putative effect of varied metabolic activity due

to different seed MCs did not result in head-space content (Fig 2). The lower viability of seed at 7% MC and stored in an 'open' regime might be an effect of over-drying during storage to 3–4% (Table 1).

Head-space gas results. The most abundant of more than 63 gasses identified were alcohols, organic acids, esters, and hydrocarbons. Volatile aldehydes and/or ketones, putative products of lipid peroxidation, were hardly present (Fig 2). No volatiles specific to process of cereal seed aging were found. The total amount of volatile content increase was observed at higher seed MCs for longer lasting wheat and one triticale cultivar. In the case of rye and the second triticale cultivar, a low viable sample showed that less volatile products were accumulated (Table 2).

Conclusions. The results support recommendations for the optimal seed MC for hermetic long-term seed storage in the seed bank. A negative influence on seed longevity from over-dryingwas observed in the evaluated cereals. Hermetic storage did not result in deleterious volatile accumulation during seed storage.

ANNUAL WHEAT NEWSLETTER UNIVERSITY OF WROCLAW Plant Speciation Group, Institute of Experimental Biology, Przybyszewskiego 63-77, 51-148 Wroclaw, Poland.

Developmental variability of the aleurone layer in some members of the tribe Triticeae.

R. Kosina, P. Tomaszewska, and D. Zając.

An important role of noncellulosic polysaccharide aleurone cell walls in grain imbibition was evidenced in Avena fatua (Raju and Walther 1988). Polysaccharides are abundant in these walls, and they can hold a lot of water. Imbibition in the caryopsis also can be facilitated by the thick endosperm cell walls adjacent to an aleurone layer in *Brachypodium* distachyon. (Kosina and Jaroszewicz 2007). In wheat, endosperm cell walls are mainly composed of arabinoxylans and β -glucans (Philippe et al. 2006). Arabinoxylans dominate (70%) in the wall, whereas β -glucans amount to 20% (Shewry et al. 2012). Among cereals (wheat, rye, barley, and oat), differences have been detected in the amount of both groups of polysaccharides in cell walls of the aleurone layer and those in subaleurone endosperm (Dornez et al. 2011). Arabinoxylans are stored more in cell walls in wheat, but barley and oat are rich in β -glucans (Hands and Drea 2012).

Aleurone autofluorescence of starchy endosperm cell walls was examined under an epifluorescence microscope Olympus BX60 for some species of the tribe Triticeae and in cross sections of amphiploid caryopses. Seeds of 'wheat/ goatgrass' amphiploids were obtained from the Kyoto Germ-plasm Institute, and the Triticeae species were from Dr D. Dewey, Utah State University. Seeds were sown and maintained for many years by R. Kosina in his living grass collection.

In the caryopsis of a Triticum timopheevii subsp. timopheevii/Aegilops longissima amphiploid, a multilayered aleurone has developed locally (Fig. 1A). External and internal tangential aleurone walls show a blue fluorescence, evidence of no chemical difference between them. No change in fluorescence color or intensity is detected across the wall. The local development of groups of aleurone cells, similar to callus, confirms the mosaic pattern of the aleurone layer (endosperm) arrangement (Kosina 2007). The same walls were observed in the unilayered aleurone in Leymus racemosus (Fig. 1B). However, here the polysaccharides are synthesized in a great amount and the tangential walls are distinctly thicker. Mosaics of the aleurone layer can be expressed in the form of a group of very narrow cells, sometimes disappearing almost completely (see Fig. 1C in a ,T. turgidum subsp. dicoccoides/Ae. tauschii' amphiploid. In the callus-like aleurone layer, the development of polyploid cells also is observed (Fig. 1D for a lateral part of the caryopsis of L. racemosus). In these examples, wall fluorescence is uniform.

Sometimes, the mosaics of aleurone/endosperm tissue are composed of proteinaceous and starchy cells (Kosina 2007; Kosina and Tomaszewska

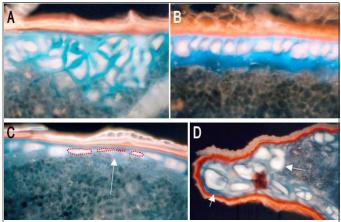


Fig. 1. Developmental events in the aleurone layer. A – amplification of aleurone cells with thick hemicellulosic walls, as in an irregular callus, in a Triticum timopheevii/ Aegilops longissima amphiploid; B – unilayered aleurone cells with thick tangential walls in Leymus racemosus; C – disappearance of the aleurone layer into small narrow cells (arrow) in an T. turgidum subsp. dicoccum/Ae. tauschii amphiploid; and D - polyploidization of aleurone cells in the lateral parts of the caryopsis in L. racemosus (arrows). A blue fluorescence of cell walls was documented on cross sections of ripe caryopses.

2010; Kosina and Zając 2010). Such a development is more often noted in plants of hybrid origin and less so in pure species. In Elymus canadensis (Fig. 2A, p. 47), a single starch cell is formed between the light aleurone cells. The wall of this cell shows the same pattern of fluorescence as is seen in a proteinaceous aleurone. The phenotype of the walls is the same, but the phenotype of the stored assimilates, protein versus starch, is completely different. The second example presents a different phenomenon (Fig. 2B, p. 47); the very thin walls of two starchy cells penetrating the aleurone layer do not express any fluorescence.

Two main conclusions can be drawn:

- The aleurone layer can disappear locally and look like a lighter dot of starchy cells. Such a development differs from the 'autonomous development' of cells with stored starch grains between aleurone cells.
- 2. The two main components of the starchy cell located within an aleurone layer, a cell wall and a protoplast with stored starch grains, are controlled by various genetic backgrounds.

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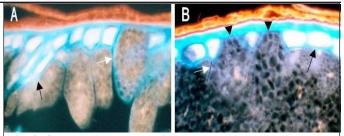


Fig. 2. Starchy phenotypes of aleurone cells expressing various cell wall phenotypes. A – a cell with an aleurone cell wall phenotype in *Elymus canadensis* (white arrow); B – two cells with starchy endosperm cell wall phenotypes (black arrowheads). The black arrow(s) shows the blue phenotype of an aleurone cell wall and the white arrow the thin, dark cell wall of a starch endosperm phenotype in a *Triticum timopheevii / Aegilops umbellulata* amphiploid. Caryopsis cross-section, autofluorescence.

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Polymorphism of starch granules in the endosperm of some species and amphiploids of the Triticeae L. tribe.

R. Kosina, P. Tomaszewska, and D. Zając.

Kosina (2009) attributed variations in the microstructure of grass caryopses to the clonal development of endosperm tissue. He described the nature of the tissue in a free nuclear stage as a complex body composed of subsyncytial units, i.e., groups of nuclei of different origin. As a result, for instance in *Avena strigosa*, adjacent cells of the endosperm synthesized starch granules of different sizes. However, starch synthesis can differ in two adjacent regions of a single cellular space, the central part versus external, and cells expressing such a nature created a single clone, e.g., in *A. brevis*. The morphology and size of starch granules also depends on the distance between tissues conducting assimilates, i.e., a vascular bundle and a transfer nucellar projection and pigment strand and a region of endosperm where the starch is stored. Smaller starch granules are synthesized in parts of a caryopsis more distant from the conducting tissues, as proved in *Bromus secalinus*. The amylopectin-poor starch was detected by a Lugol's reaction or imaging in a polarized light. The amylopectin-poor mutations of single starch granules were found in a '*T. turgidum* subsp. *dicoccum/Ae. tauschii*' amphiploid and in *B. secalinus*. An amylopectin/amylose-poor mutant with tiny starch granules was detected in *B. racemosus*.

The size of starch granules is species-specific in the genus *Avena* (Kosina 2007). The same situation was discovered in the genus *Hordeum* (Baum and Bailey 1987). A bimodal size for starch granules was noted for barley, rye, and wheat, but is unimodal in millet, rice, and triticale (Tester et al. 2004).

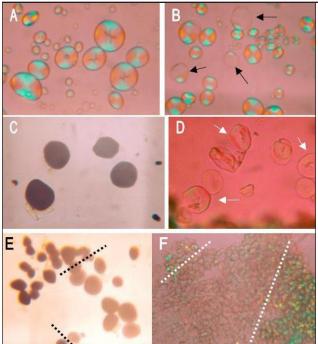


Fig. 3. Variation in starch granule reaction in polarized light and Lugol's solution. A - bimodally sized, amylopectin-rich starch granules in Triticum timopheevii subsp. timopheevii presenting a distinct 'polarizing reaction'; B – the same as in A for Leymus racemosus, but three granules present a very poor polarizing reaction (arrows); C - a strong Lugol's reaction for amylopectinrich starch in Aegilops umbellulata; D - a negative Lugol's reaction for amylopectin-poor granules in an Ae. umbellulata starch mutant; E – two types of Lugol's reaction for an amylopectin-rich (dark) pool of granules and an amylopectin-poor pool (lighter, separated by dotted lines) in L. racemosus; and F – a pool of amylopectin-poor granules with a weak polarizing reaction (between the dotted white lines) and a second with a contrasting reaction (outside the dotted lines) in a 'L. multicaulis/L. karataviensis' amphiploid.

large granules express a low amylopectin content seen in the form of poor coloring of outer parts of the granule. We also detected an amylopectin-free type without polarizing colors in *Ae. umbellulata* (Fig. 3D), whereas the normal type has darkly stained granules with Lugol's solution. The amylopectin-free trait in goatgrass is plant specific. A similar pool of amylopectin-free granules is found in an '*L. multicaulis/L. karataviensis*' (Fig. 3F) amphiploid, whereas an amylose-low pool is noted in *L. racemosus* (Fig. 3E).

Other examples of starch granule polymorphism are provided (Fig. 4). In a '*Triticum timopheevii* subsp. *timopheevii/Aegilops longissima*' amphiploid, the colors of polarization (amylopectin amount) are distinct and uniform (Fig. 4A); however, starch granules sometimes express stronger colors (Fig. 4B, more amylopectin). A different

Changes in the size of starch granules were described by Klemsdal et al. (1986) in the Risø high-lysine, barley mutants. Granules were small and caryopses poorly filled by endosperm tissue. Other starch mutations, Risø17 and Notch-2, were studied by Burton et al. (2002). These mutants synthesize phytoglycogen and several starch ganules develop in their plastids. In ripe caryopses, starch granules are composite. In addition, Patron et al. (2002) described some cultivars in waxy barley with low expressed levels of amylose in the starch granules or with starch free of amylose. The low-amylose cultivars have more amylose in the granules of the outer cells of the endosperm than in the central part of this tissue. The level of amylose depends on the activity of granule-bound starch synthase I (GBSSI). The low- or free-amylose types probably are of Chinese origin. Satoh et al. (2003) induced six low-amylose mutants in japonica rice using N-methyl-N-nitrosourea. All mutants were of the *waxy* type. The lowered synthesis of amylose did not change the development of normal chains of amylopectin. Waxy mutants expressing lower GBSSI activity also were obtained in A. strigosa (Verhoeven et al. 2004). In potato, starch granules with low GBSSI activity are not stained by Lugol's iodine (Edwards et al. 2002).

We stained starch granules with Lugol's solution. Nonstained starch granules also were observed under a polarizing Amplival microscope. Granules with high amounts of amylopectin stained with Lugol's iodine were dark brown, and had distinct red and blue color in a polarizing microscope. Such colors are noted for '*T. timopheevii* subsp. *timopheevii*' (Fig. 3A) and *L. racemosus* (Fig. 3B). Their granule pools are bimodal. In *L. racemosus*, several

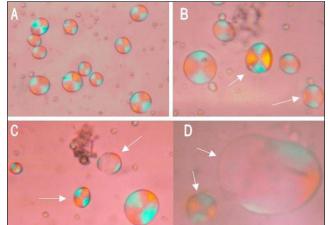


Fig. 4. The 'polarizing reaction' of starch. A – a positive reaction for amylopectin-rich granules and B – a more variable reaction, strong versus weak, in a '*Triticum timopheevii subsp. timopheevii/Aegilops longissima*' amphiploid; C – the same as in B for a '*T. turgidum* subsp. *carthlicum/Ae. tauschii*' amphiploid; and D – normal and giant granules presenting very poor reaction in an '*Elymus canadensis/Pseudoroegneria libanotica*' amphiploid.

level of amylopectin synthesis is detected among starch granules in a '*T. turgidum* subsp. *carthlicum/Aegilops tauschii* amphiploid (Fig. 4C, p. 48). A giant starch granule in an '*Elymus canadensis/Pseudoroegneria libanotica*' amphiploid expresses only weak a polarization reaction in outer parts (Fig. 4D, p. 48).

In conclusion, amylopectin- or amylose-low amounts in Triticeae are cell-, plant- or species-specific. Detecting natural starch mutations among accessions in the Triticeae collection is possible.

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Changes in the pericarp in Triticum sinskajae and T. timopheevii subsp. timopheevii under environmental stress.

R. Kosina.

The developing caryopsis of wheat is covered by a thick, parenchymatous pericarp. Many starch grains are in the cells of the outer layers (Simmonds and O'Brien 1981; Kosina 2014). The inner epidermis and hypodermis of the pericarp change into tube cells and cross cells, respectively (Morrison 1976). The fleshy pericarp is green and actively assimilates CO₂. Xiong et al. (2013) proved that the development and physiological role of different parts of the common wheat pericarp is cultivar-specific. The wheat pericarp is changed by apoptosis, which starts near the brush on the fourth day after fertilization (Young and Gallie 1999). At this time, the endosperm is enlarging. In unthreshable wheats, the parenchymatous pericarp is reduced in a ripe caryopsis to the outer epidermis and inner cross and tube cells (Kosina 1991, 1995). Similar changes are noted for an unthreshable oat, *Avena fatua* (Morrison and Dushnicky 1982).

Two wheats, *T. sinskajae* (AA), a diploid, free-threshing mutant from *T. monococcum* subsp. *monococcum*, and *T. timopheevii* subsp. *timopheevii* (AAGG), an unthreshable tetraploid species, were used in a starvation experiment. Plants of both wheats were cultivated in a greenhouse in pots filled with sand and on small plots in the field. In the greenhouse, plants were watered poorly. During the development of caryopsis, temperatures reached more than 60°C in the insolated room. In the field, plants were sown in soil of moderate fertility and were regularly watered. The development of the outer part of the caryopsis pericarp and inner layer of cross cells was examined under a microscope on a cross section of the middle part of the caryopsis.

In more favorable field conditions (Figs. 5A and 6A), the outer epidermis of the pericarp is thicker, with better preserved cell lumina in free-threshing *T. sinskajae* than it is in unthreshable *T. timopheevii* subsp. *timopheevii*. The same difference has been noted between *T. timopheevii* subsp. *timopheevii* and its threshable mutant, *T. militinae* Zhuk. & Migush. (Kosina 1995). The inner cross cells are well preserved in both wheats, but in *T. timopheevii* subsp. *timopheevii* they are thicker. One should remember that here species of different ploidy levels, 2n versus 4n, are compared. In starva-

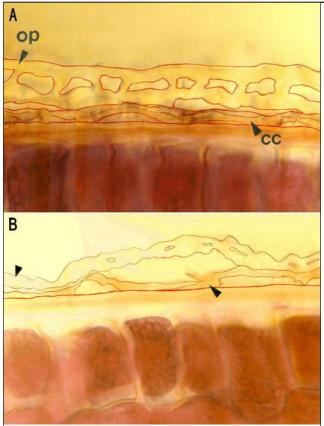


Fig. 5. The covering layers of a *Triticum sinskajae* caryopsis. A – field cultivation and B– stress cultivation in a greenhouse (op = outer pericarp and cc = cross cells; layers are indicated by arrowheads).

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tion conditions, high temperatures, poor sandy soil and deficiency of water (Fig. 5B and 6B), pericarp tissues in T. sinskajae are thin and cell lumina disappear. A very strange change is seen in pericarp of *T. timopheevii* subsp. timopheevii. This unthreshable wheat has a thick outer pericarp epidermis with well preserved cell lumina, and the epidermis is not collapsed. The cross cells are collapsed. This difference between both wheats in terms of their reaction to stress conditions seems difficult to explain. In Fig. 6B, the pericarp and nucellar tissue cover a dark layer of aleurone with cells not fully filled by protein bodies. Such a picture suggests poor endosperm development. Between both wheats, the possibility of ovary development within 'a floral cavity' is limited by the level of sclerification of glumellae, lemma and palea, and their pressure against ovary tissues. Under starvation conditions, endosperm develops badly and leaves free space for pericarp. Surprisingly, pericarp epidermis is less stressed in T. timopheevii subsp. timopheevii.

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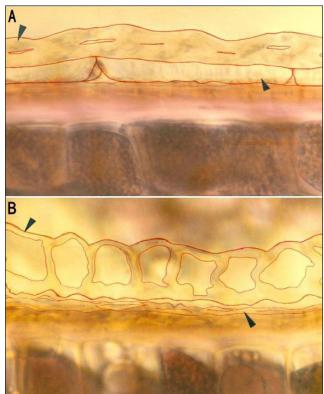


Fig. 6. The covering layers of a *Triticum timopheevii* subsp. *timopheevii* caryopsis. A – field cultivation and B – stress cultivation in a greenhouse. Outer epidermis of pericarp and underlying cross cells are indicated by arrowheads.

ANNUAL WHEAT NEWSLETTER On the glumeless form of Agropyron pectiniforme Roem. et Schult.

R. Kosina.

The inheritance of many traits is complex, however, morphological variations in plants are often under the control of only a few genes (Gottlieb 1984). Expression of these genes does not induce abnormal development, but their activity is shown in pleiotropic effects. The study of morphological deviation in the development of the grass inflorescence has mainly been on artificial mutants. Different mutagens have been applied. Cummings et al. (1978) used ethyl methanesulfonate (EMS) to induce morphological mutations in oats. They obtained mutations related to inflorescence bracts, inter alia, a semiglumeless form. A palealess mutant was described in rice (Luo et al. 2005). The palea was considered a homologous leaf to sepals in eudicot plants, but the lemma is recognized as a different organ. Expression of the Os-MADS22 gene in transgenic Oryza sativa results in the anomalous development of the palea and glume (Sentoku et al. 2005). Any change in the number of mutated organs is called a meristic mutation, which was described by Bossinger et al. (1992) within a barley spike composed of phytomers. The meristic addition of spikelets in Brachypodium distachyon is under the control of the MORE SPIKELETS1 gene (Derbyshire and Byrne 2013). An increase in the number of spikelets also was noted in mutants of Lolium multiflorum (Jauhar 1993). The change of flowers into spikelets was discovered by Ceynowa-Giełdon (1997) in Festuca polesica. She interpreted new spikelet bracts as lemmas, however, a microscopic examination proved their nature as glumes (Kosina 1998). This natural mutation shows a complex nature, homeotic and meristic. New glumes are homologous to lemmas. The mutation in *Festuca polesica* increases the potential for assimilation by adding new green organs in the inflorescence. The fertility of the plant is not reduced, therefore, this form can be active in the speciation process (Kosina 1999).

A meristic glumeless mutant of Agropyron pectiniforme (Fig. 7A) was found on the edge of a cultivated field in the Sudety Mountains, in southwest Poland. The plant was gathered before blooming. The flowers have three, well developed, long anthers, approximately 6 mm. Such long anthers are typical for an allogamous breeding system. The lack of glumes in all spikelets is a meristic defect of the spike. About 10 spikelets in the lower part of spike are underdeveloped. Additional flowers developed in the upper part of spike on the overgrown rachillae of spikelets. In Triticum jakubzineri (T. turgidum), four glumes develop at the base of each spikelet (Dorofeev 1987). This wheat also expresses a meristic mutation, but it is a reverse mutation compared to that in A. pectiniforme (Kosina 1998). The examined plant of A. pectiniforme has a smaller surface of assimilation and lower pollen grain production because of underdeveloped lower spikelets and a lack of glumes. The selective advantage of the population also would be lower (Kosina 2015).

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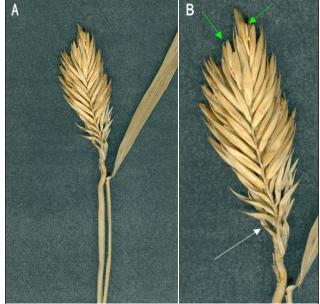


Fig. 7. Morphology of a glumeless spike in Agropyron pectiniforme. A - a general view and B - details of underdeveloped spikelets in the lower part of the spike (white arrow) and overgrown spikelets in the upper part (green arrows).

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On the spirodistichous form of Lophopyrum elongatum (Host) Á. Löve.

R. Kosina.

At least one nullisomic 3D plant with a spike expressing a compact arrangement of spikelets in the upper part and a few loose spikelets in the lower part can be recognized within the Sears' nullisomic series of Chinese Spring wheat (Schulz-Schaeffer 1980). Similar types, called 'squarehead', were exemplified by Mac Key (1966) in a hybrid progeny of 'Triticum aestivum subsp. aestivum/T. aestivum subsp. macha' and 'T. aestivum subsp. aestivum/T. aestivum subsp. vavilovii'. The Q factor (gene) is responsible for a free-threshing feature and square spikes (Mac Key 1964; Simons et al.

2006). This genetic control is closely related to other simple morphological inheritance patterns, which were exemplified by Gottlieb (1984). The Q gene exhibits dosage effects on spike compactness, but modifiers regulate its pleiotropic influence on the development of square spikes. In transgenic wheats, a high expression of the Q gene, due to its dosage, was detected (Faris et al. 2005). The gene was localized on chromosome 5A in T. aestivum (Jantasuriyarat et al. 2004). The QQ genotype was detected in T. turgidum subsps. carthlicum, polonicum, dicoccum, and durum. In these subspecies, dense compact spikes were described (Farris et al. 2005). Species with compact spikes also are known in diploid wheat diploids (T. sinskajae), in AAGG tetraploids (T. militinae), and in hexaploids (T. aestivum, subsps. compactum and sphaerococcum) (Dorofeev 1987; Goncharov 2002). Wheats with compact spikes, such as T. vulgare antiquorum, also were identified in fossil materials (Schiemann 1932).

A spontaneous, spirodistichous mutant of Lophopyrum elongatum found in the grass collection of R. Kosina shows a gross spike morphology similar to that mentioned above. The lower part of its spike is distichous (Fig. 8A). In some spikes, three spikelets are developed at each rachis segment, above the distichous part. In the short upper part, a spiral phyllotaxis is expressed (Fig. 8B). Flowers of L. elongatum have well-developed anthers, ~4–5 mm long, including in the spiral part of the spike. Spikelets are very densely packed in this section, and the morphology of glumes and glumellae are changed (Kosina 1998). Pollen grains often are reduced and no seeds are formed in the upper part (Kosina 1999, 2015). Lodicules are anomalous and flowers behave as cleistogamic (Kosina et al. 2012). Triticum aestivum subsp. compactum with square heads and QQ gene formulae also can lose the possibility of flower chasmogamy due to lodiculae mutation (Kosina and Tomaszewska 2012). In the hybrid progeny 'Triticum/L. elongatum, no compact heads or similar parts were described by Tsitsin (Tsitsin 1978).



Fig. 8. Morphology of a spirodistichous spike in Lophopyrum elongatum. A – a general view (arrows indicate a distichous part of a spike and an upper part with a spiral phyllotaxis) and B - details of the spiral arrangement of spikelets.

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Variability of germination in Brachypodium distachyon and B. sylvaticum evaluated with a variance-covariance matrix.

R. Kosina.

Various coefficients of similarity or dissimilarity are useful to describe numerical relationships among plant operational taxonomic units (OTUs) (Sneath and Sokal 1973). The coefficients are measures of taxonomic distances. Correlation coefficients are some examples. Most often, arithmetic means of the characters are used to calculate the difference between any pair of OTUs. An average taxonomic distance (ATD) based on character data is applied in biology (Rohlf 1994). The ATD is a generalized Euclidean distance (Sneath and Sokal 1973). The ATD was used to set OTUs belonging to two species of the genus *Brachypodium*, an annual autogamic *B. distachyon* (Bd) and perennial allogamic *B. sylvaticum* (Bs), in an ordination space by means of non-metric multidimensional scaling (Kosina and Jaroszewicz 2007). OTUs were described by germination data and arranged in two- or three-dimensional diagrams. Accessions of *B. distachyon* are scattered widely, whereas those of *B. sylvaticum* create a compact cluster. In the *x* and *y* ordinants, the points of OTUs are highly correlated. One conclusion is such that interaccessional variation in the autogamic species is larger than that between allogamic populations.

Sneath and Sokal (1973) pointed out that the weighting of data is important during the clustering process, because clusters are either less or more distinct and can be of different shape. Rohlf (1970) proposed some weighting by means of a generalized distance function, where the variance-covariance matrix (var-cov) of *n* variables is used. Rohlf's measure takes into account size and shape trends existing in each cluster. These trends change when adding successive OTUs into the cluster. A difference between clusters can be easily illustrated by a difference between, e.g., hyperellipsoid and hyperspheroid. Within two such geometric clouds of OTUs, correlations and covariances between OTUs will be different. The var-cov method was applied to germination data according to Rohlf's approach (Rohlf 1994). The eigenvalues and eigenvectors are calculated from the var-cov matrix (Rohlf 1970). Nonmetric multidimensional scaling was used to arrange OTUs into an ordination space (Figs. 9 and 10, p. 54). They are visually different from the results obtained with the application of ATD (Kosina and Jaroszewicz 2007). The OTUs belonging to *B. distachyon* create a compact cloud in the center, three Bd accessions are more distant from the center. Accessions of *B. sylvaticum* are located outwards (Fig. 9, p. 54). The distribution of OTUs on the *x*-*y* axes do not have any significant correlation (Fig. 10, p. 54). In fact, the relationships between Bd and Bs accessions are similar to the situation pertaining when ATD was applied. The main difference is shown by the reverse compactedness of Bs versus Bd OTUs. Looking at the variance–covariance

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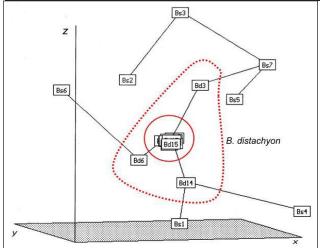
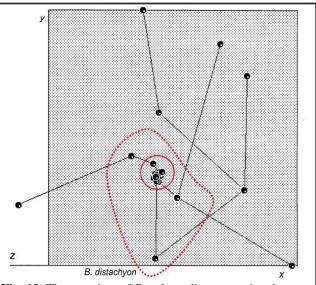


Fig. 9. Minimum spanning tree of accessions (operational taxonomic units (OTUs)) of *Brachypodium distachyon* (Bd, in the center of diagram) and *B. sylvaticum* (Bs)located around it. The tree was constructed after calculation of the variance-covariance matrix and the use of non-metric multidimensional scaling. The OTUs are scattered along three ordination axes (x, y, z).



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Fig. 10. The top view of *Brachypodium* operational taxonomic unit scattered on the plane of the x, y axes (the same diagram and description as in Fig. 9).

matrix, it is remarkable that Bd OTUs plotted in the center of diagrams are characterized by greater variances and covariances of the examined germination traits and in outer Bs accessions these values are smaller. The above statement

means that each examined caryopsis of *B*. *distachyon* is different from another. A normal occurrance when the progeny of an autogamic species is a set of many homozygous lines. Both kinds of results not only are visually different but biologically, they are consistent with each other.

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Annuality-perenniality and dormancy in the genus Brachypodium.

R. Kosina and P. Tomaszewska.

We know a lot about the germination of grass diaspores. Within the grass family, one can distinguish two extreme phenotypes related to breeding system, autogamic versus allogamic, with many intermediate types. Related to life habit, annual versus perennial, with some intermediates. Cereals from the Triticeae tribe are mostly annuals, but their mating system can be different, for instance, in autogamic wheat and allogamic rye. Wild grasses seem to be more differentiated. We will consider the relationships within a wild genus *Brachypodium*, which comprises annuals and perennials, auto- and allogamic and self-compatible and self-incompatible types. Dormancy, a life history component, is not well elucidated in the grass life habit.

In *Brachypodium*, the annual *B. distachyon* essentially expresses autogamy, however, in suitable weather conditions, can be chasmogamic and capable of cross-pollination (Kosina and Kłyk 2011; Kosina and Tomaszewska 2012; Kosina and Tomaszewska 2014b). Other species are perennials and self-incompatible, but *B. sylvaticum* is self-compatible facultatively (Khan and Stace 1999; Kłyk 2005). Differences in the germination potential between cereals and annualperennial species of *Brachypodium* are created by the level of dormancy, caryopsis microstructure, and assimilate storage pattern. In general, annuals are nondormant or less dormant versus dormant perennials. However, examples of the annual *Avena fatua* with fewer or more dormant diaspores and wild goatgrasses and diploid wheats expressing dormancy polymorphism in diaspores, contradict the above general assumption. Annual and perennial species of *Brachypodium* store assimilates in the form of endosperm starch and protein and, in addition, a large amount in the form of cell wall hemicellulosic compounds (Jaroszewicz et al. 2012; Kosina and Jaroszewicz 2007; Kosina and Kamińska 2013a and 2013b). In cereals, starch and protein are the main storage substances. Germination is more facilitated in *Brachypodium* due to the capillary potential of its coleorhizal hairs, than is the case in cereals (Kosina and Tomaszewska 2014a). Dormancy-germination behavior exhibits a large variation in *Brachypodium* (Kosina and Tomaszewska 2014c).

A question arises: What are the relationships between the dormancy pattern and life habit in the genus Brachypodium? Germination tests were performed for annual, spring, and winter accessions of B. distachyon of different geographic origin (Australia, Italy, Iran, Iraq, and Turkey) and perennials B. pinnatum, B. phoenicoides, B. rupestre, and B. sylvaticum. Accessions, evaluated by several germination traits and numerical methods (Rohlf 1994), were set into an ordination space using a nonmetric, multidimensional scaling. An interpretation of a two-dimensional (x and y axes of the ordination space) diagram (Fig. 11) was conducted, and regression parameters were calculated for a set of operational taxonomic units (OTUs) (Fig. 12). The arrangement of OTUs along the x and y axes is not random and seems to be highly correlated (Fig. 11). The variation in regression is highly significant, and the regression line has a slope close to zero (Fig. 12). The correlation coefficient is highly significant (r = 0.89). The results prove that dormancy is highly correlated with perennial habit, whereas nondormant types mostly are annual.

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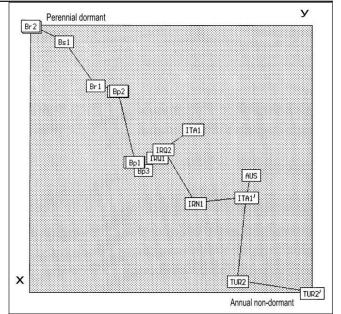


Fig. 11. The top view of the minimum spanning tree of annual and non-dormant accessions (operational taxonomic units, OTUs) of *Brachypodium distachyon* and perennial dormant species. The tree was constructed after calculating the matrix of average taxonomic distances and the use of non-metric multidimensional scaling. The OTUs are scattered along two ordination axes (x, y) (AUS = Australia, ITA = Italy, IRN = Iran, IRQ = Iraq, and TUR = Turkey).

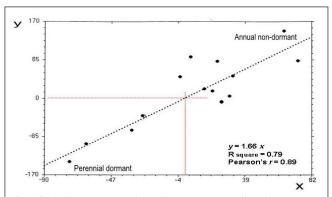


Fig. 12. A linear regression diagram presenting the relationship between dormancy and annual versus a perennial habit in the genus *Brachypodium*. The zero point is indicated by red lines. The *x* and *y* regression axes present values of *x* and *y* ordination axes.

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Mosaics in the aleurone layer in some members of Triticeae L.

R. Kosina.

Plant development through cell lineages is commonly accepted. The lineages are well recognized in roots or a leaf epidermis (Lyndon 1990). Some kinds of cell lineages can be observed in the grass endosperm. The endosperm is a very variable tissue. Multipolar anaphases and telophases are its cytogenetic phenomenon. Such a cytogenetic behavior also was noted in root mitoses, for instance, in Bromus secalinus (Skowrońska 2005), but is especially frequent in the triticale (*xTriticosecale*) endosperm (Kaltsikes et al. 1975). Multiple telophases or nuclei connected by chromatin threads are present in triticale. In the Avena amphiploids, such cytogenetics gives nuclei of various ploidy levels. Surprisingly, numerous nuclei are diploid, not triploid (Tomaszewska and Kosina 2015). Programmed cell death is another phenomenon that occurs during endosperm development (Young and Gallie 2000), however, this can relate not only to starchy cells but also to many defective nuclei at the free-nucleolar stage (Kosina and Tomaszewska 2013). This elimination of many nuclei results in isolation of the remaining, which differ from each other. In the later stages of endosperm development, large units (endospermal domains) of isolated cells are distinguished by thick cell wall ingrowths. Ivanovskaja (1983) presented such isolated groups of nuclei for 'Triticum aestivum subsp. aestivum/Leymus arenarius F, hybrids. Subsyncytial nuclear units of antipodal or a central embryo sac origin (Kosina 1992, 1996) are created by the same endospermal events. The clonal architecture of the grass endosperm was described by Kosina (1992, 2012) and, due to many earlier cytogenetic disorders, the clones can be different and observed in the form of mosaics (Kosina 2007; Kosina et al. 2013a and 2013b). Some clones can be highly polyploid (Kosina et al. 2013b).

The following examples show various mosaics/domains in the aleurone layer in some species and amphiploids of the Triticeae tribe. The aleurone

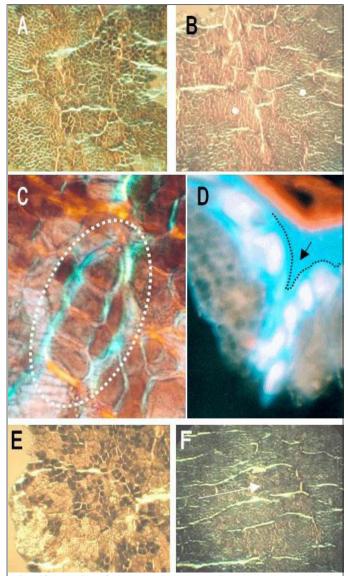


Fig. 13. Details of aleurone layer mosaics. A, large domains in the aleurone layer in Triticum turgidum subsp. turanicum bordered by thick light lines of nucellar and aleurone cell wall ingrowths; B, the same domains as in A in a 'T. turgidum subsp. dicoccoides/Aegilops tauschii' amphiploid (two types of polarizing color domains are marked by white dots); C, a small clone-domain of aleurone cells bordered by their thick non-cellulosic walls in a 'T. turgidum subsp. turanicum/ Ae. tauschii' amphiploid; D, details of nucellar (arrow) and aleurone cell wall ingrowths in *Elymus canadensis*, the border between both types of walls is marked by a dotted line; E, partly bordered domains in a 'Triticum turgidum subsp. turancium/Ae. tauschii' amphiploid that are composed of dark aleurone cells and lighter starchy cells; and F, domains with directionally ordered borders in a 'T. turgidum subsp. dicoccoides/Ae. tauschii amphiploid.

domains are separated by thick light lines, which are cell walls seen in a polarizing microscope (Fig. 13A, p. 56). These lines are created in regions of the aleurone layer having different colors (Fig. 13B, p. 56). These colors are a polarizing effect of the cell walls, indicating that aleurone cells are arranged differently in the layer. The thick aleurone wall can separate a group of cells of common origin, a clone (Fig. 13C, p. 56). The light borders of domains are created not only by an intrusive growth into starchy endosperm of thick-walled aleurone cell (Kosina et al. 2013b), but also by ingrowths of the thick walls of the nucellar epidermis (Fig. 13D, p. 56). Light borders can limit groups of aleurone cells with protein, but a mosaic of aleurone-protein and aleurone-starch cells also can be separated (Fig. 13E, p. 56). For cell characteristics, aleurone-protein versus aleurone-starch, see a report on variability of the aleurone layer (Kosina et al). The original development of an aleurone layer in which domainal borders are directional is noted for a dorsal surface of caryopsis (Fig. 13F, p. 56). Such an arrangement of borders is related to the I- or T-type of cell division by anticlinal walls. This developmental problem was discussed by Barlow (1991).

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External pressure on a dorsal surface of caryopsis changes the development of wheat endosperm.

R. Kosina.

The active cells inside the apical meristems of plants are isodiametric and their divisions are not regular (Lyndon 1990). The tree cambium is composed of two types of cells, parenchyma-like initials in the rays and axially elongated initials between the young differentiating elements of the xylem and phloem. The elongated initials are arranged orderly in the form of tangential strips. This order was examined by Steeves and Sussex (1989) and Lyndon (1990) and proved that pressure caused by expanding xylem and external phloem and other secondary tissues is important for an orderly cytokineses. In the cambium isolated from a tree, elongated initials start to divide like in a callus, but when external pressure is applied, cells divide tangentially to a pressed surface. The youngest endosperm tissue is located at the embryo sac wall, and the last tangential or anticlinal cytokineses occur there, giving an aleurone layer. Such divisions create regular endosperm cell clones (Kosina 1992, 2012). Thus, we justify the aleurone layer as an 'endosperm cambium'. The

cambial architecture of the aleurone layer is found in many different grasses (Mares et al. 1977; Simmonds and O'Brien 1981; Fineran et al. 1982).

Kosina (1989) reported an experiment with artificial pressure used against the endosperm cambium in several grasses. A spheroidal seed of clover was placed between a young, green pericarp and the lemma before cellularization of the endosperm. Pressure caused by the seed was maintained until maturity of the grass diaspore. Results for one of the examined grasses, Triticum turgidum subsp. turanicum are presented (Fig. 14). The distinct amplification of aleurone cells is visible beneath and around the pressure point (Fig. 14A). New tangential divisions occurr in smaller larger groups of aleurone cells (Fig. 14B). Locally, single cells with thick walls can be isolated and induced into an original development; the spherical cell shape and its larger size suggests that polyploidization occurred here (Fig. 14C). Pressure also caused starch cells of endosperm not to develop, and aleurone cells from the dorsal part were connected with those from a crease region (Fig. 14D).

In conclusion, external pressure induced the following changes:

- 1. multiplication of the aleurone cells is due to increased tangential cytokineses,
- 2. multiplication of the aleurone cells by divisions is typical for callus, and
- 3. anomalous, poor development of starchy endosperm beneath the pressure point

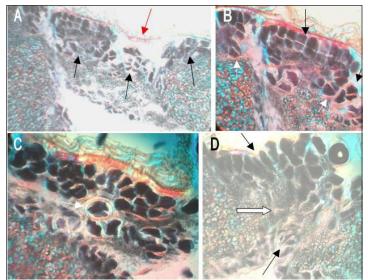


Fig. 14. Microstructure of *Triticum turgidum* subsp. *turanicum* changed by artificial pressure. A, a red arrow shows the point of the clover seed setting and black arrows indicate abundant amplification of aleurone cells; B, black and white arrows show amplification of periclinal (tangential) aleurone cell divisions; C, a white arrow indicates a polyploidized, callus-like, aleurone cell with a thick wall; and D, upper, dorsal aleurone cells and ventral ones in the bottom (black arrows) are connected (white arrow) in the area of pressure influence.

and, in consequence, connecting both aleurone layers, dorsal and ventral.

These results confirm experiments with tree cambium (Steeves and Sussex 1989; Lyndon 1990) and justify use of the term 'endosperm cambium'.

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Variation of winterhardiness in Brachypodium distachyon (2).

R. Kosina.

Brachypodium distachyon expresses wide variation in terms of flowering and vernalization time. Schwartz et al. (2010) mainly identified spring and winter forms within a set of diploid and polyploid accessions of various geographical origin. Polyploid accessions from Spain appear to be intermediate between spring and winter types. The vernalization period of

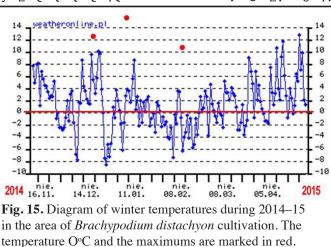
4°C for 3-week-old seedlings ranged from 2 to 6 weeks. In addition, Manzaneda et al. (2011) proved that, under drought stress, B. distachyon polyploids are more efficient than diploids in the use of water. Winter and heat survival in Avena sativa and A. byzantina varieties seem to be positively correlated (Levitt 1972). Tolerance for freezing and drought stresses are correlated, both via water stress. Supposedly, the same is true for B. dis*tachyon*, and the polyploid types will be more tolerant. However, Li et al. (2012) discovered that B. distachyon lacks genes for fructan synthesis and accumulation during cold stress. In this reaction, B. distachyon differs from that of other Pooideae grasses and both are components of freezing tolerance variation in the Poaceae family. Colton-Gagnon et al. (2014) presented contradictory data on fructan synthesis in *B*. *distachyon* treated by freezing stress. The authors also described some intermediate forms between spring and winter diploids of B. distachyon. The species requirements for vernalization in low temperatures showed a great variation (Woods et al. 2014).

To know precisely the winter hardiness in *B*. *distachyon*, new data are presented. After the summer of 2014, six accessions grew vegetatively into the winter of 2014–15; ITA3 (Italy), ITA3s (a selection from ITA3), TUR2 (Turkey), TUR2s (a selection from TUR2), BGR2 (Bulgaria), and BGR2s (a selection from BGR2). The plants were protected from severe frost by fleece, however, the winter of 2014-15 was especially mild. Minimum temperatures were a little lower than –8°C and were interrupted by periods of higher temperatures. The highest temperatures occurred on 20 December (14°C), 10 January (16°C), and 15 February (11°C) (see Fig. 15).

An increased vegetative growth and loose tuft habit were noted accession ITA3. The ITA3 plants develop prostrately rooted shoots and additional axillary tillers, such as in ITA1 (Fig. 16A and Kosina and Tomaszewska 2014a). Other accessions growing in as short, dense tufts, such as TUR2s, BGR2, and BGR2s, died during the winter (Fig. 16A, B). Only the accession TUR2 overwintered in lateral parts of the tuft (Fig. 16C). Several accessions resowed from falling diaspores. Seedlings of the IRQ accession not protected by fleece overwintered very well (see Fig. 16D). All overwintered forms headed on 15 May, but some differences were observed in the rate of this process (Fig. 17). The experiment concerning the wintering of all accessions of *B*. *distachyon* will be continued during winter 2015–16.

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According to *weatheronline.pl*.



Fig. 16. Accessions of *B. distachyon* of various geographical origin in a wintering experiment. Clumps of ITA3 (Italy, A) and BGR2 (Bulgaria, B) that died. A partly overwintered (yellow arrows) clump of TUR2 (Turkey, C). Overwintered, self-sowing seedling (yellow arrows) of the IRQ accession (Iraq, D). A blue, plastic bottle cap is included for size comparison.



Fig. 17. Plants of *B. distachyon* at heading stage (yellow arrows) after overwintering in 2014–15. A, TUR2 (Turkey) and B, FRAs, a selection from FRA (France). A blue plastic bottle cap is included for size comparison.

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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 Toulaikov St., Saratov, 410010, Russian Federation.

The influence of a translocation with the combination Lr19+Lr25 on grain productivity and bread-making quality in the spring bread wheat cultivar Dobrynya.

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

At the Agricultural Research Institute for the South-East Regions (ARISER), NILs based on the Saratov-bred, spring bread wheat cultivar Dobrynya and carrying translocations with the combination Lr19+Lr25 were produced and studied. The data from 2012–14 indicate that the interaction of these trans-

Table 1. Grain productivity and gluten values of near-isogenic lines (NILs) of the spring bread wheat cultivar Dobrynya, average for 2012–14. Gluten strength was evaluated by using the gluten deformation index.

	Grain yield	Gluten value		
NIL	(kg/ha)	Content (%) Strengt		
Dobrynya (Lr19)	3,164	38.03	71	
Dobrynya (<i>Lr19+Lr25</i>)	3,323	38.87	76	
LSD	NS	NS	NS	

Table 2. Bread-making qualities of near-isogenic lines (NILs) and spring bread wheat cultivar Dobrynya (average for 2012–14).

	Physical tra	it of dough ((alveograph)	Bre	ad-making qua	lity
	Dough extensibility		Flour strength	Loaf volume		
NIL	(P)	P/L	(W)	(cm ³)	Porosity	Crumb color
Dobrynya (Lr19)	142.3	2.33	368.7	847	4.9	yellow
Dobrynya (<i>Lr19+Lr25</i>)	126.3	1.83	351.0	920	4.9	yellow
LSD	NS	NS	NS	50	NS	

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Table 3. The reaction of powdery mildew, leaf rust grain productivity, grain protein content, and gluten deformation index, bread-making qualities of cultivars and near-

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locations has a neutral influence on grain yield (Table 1, p. 60). However, the influence of the translocation on grain yield in different years was ambiguous. During this period, leaf rust epidemics were observed twice (2013 and 2014) and drought conditions once (2012). Grain productivity significantly increased during the two leaf rust epidemics in NILs with Lr19+Lr25 (3,238 in 2013 and 5,012 kg/ha in 2014) and Dobrynya (2,988 in 2013 and 4,451 kg/ha in 2014) and was significantly reduced under drought conditions in the NILs (1,718 kg/ha) and Dobrynya (2,054 kg/ ha). The main limiting factor for the use of translocations from Secale cereale in wheat breeding is the influence on bread-making quality. In the Dobrynya NILs, the Lr19+Lr25 translocations did not influence gluten values. Dough extensibility (P) and strength of flour (W) were not significantly lower in the NILs with Lr19+Lr25 compared with those of Dobrynya. For bread-making qualities, the NILs have a loaf volume significantly higher but porosity equal to that of Dobrynya (Table 2, p. 60). Thus, the Lr19+Lr25 translocations had positive effects on resistance to disease, but reduced drought resistance and grain productivity in 2012. Grain yield increased in 2013 and 2014, years with leaf rust epidemics. For bread-making quality, the NILs with Lr19+Lr25 translocations were evaluated as good or excellent.

The use of Triticum turgidum subsp. durum as valuable source of genes for improving spring bread wheat.

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

In the laboratory of Genetics and Cytology at ARISER, we produced a number of introgression lines with genetic material from *T. turgidum* subsp. *durum* cultivars Saratovskaya Zolotistaya, Zolotaya volna, Taro1, and Yazi10 with the aim of enlargement the genetic diversity of the gene pool of spring wheat. During prebreeding studies in 2014, these introgression lines were studied for their agronomic value. We noted that 2014 was most favorable for spring bread wheat and for many pathogens, which allowed us to objectively evaluate them for disease resistance, grain productivity, and quality.

All introgression lines were resistant to leaf rust and powdery mildew (Table 3). In some cases, the introgression lines were better in comparison with the standard cultivars for grain yield

isogenic lines (NILs).	(NILs).)		4					-			V
					Gluter	Gluten value	Physica	Physical trait of dough (alveograph)	dough	Bread-	Bread-making	S L
							Dough		Flour	Loaf	2	6
NIL or		Powedery		Grain yield	Content		extensibility		strength	volume		τ
cultivar	Pedigree	mildew	Leaf rust	(kg/ha)	(%)	Strength	(P)	P/L	(W)	(cm^3)	Porosity	τ
Favorit		0	0	4,441	28.8	67	66	1.8	190	820	4.8	E
NIL 202	Saratovskaya Zolotistaya / Favorit // Favorit /3/ Favorit	0	0	4,496	29.5	59	165	3.1	347	740	4.6	R
L503		1	3	4,361	31.0	0 <i>L</i>	99	1.0	150	06 <i>L</i>	5.0	
NIL 573	L503 / Taro1*2 // L503	1	0	3,733	30.7	72	165	3.0	307	770	4.6	
Belyanka		1	0	4,900	30.0	68	77	1.0	196	700	4.6	
NIL 345	Belyanka / Taro1*2 // Belyanka	3	0	4,926	22.6	53	93	1.9	164	069	4.5	
Dobrynya		1	3	3,974	41.5	82	165	3.0	327	840	5.0	
NIL 293	Dobrynya / Zolotaya volna // Dobrynya /3/ Dobrynya	0	0	4,290	30.8	62	165	3.0	379	860	5.0	/ 0
NIL 216	Dobrynya*4 / Nik	0	3	4,228	29.7	65	141	3.5	255	830	5.0	L.
L505		1	3	4,150	26.4	58	165	2.5	497	780	4.8	
NIL 214	L505 / Yazi 10 // L505 /3/ L505	1	0	3,895	32.5	69	165	3.0	386	700	4.6	6 1.

and quality, some were not significantly different, and decreased in others. In NIL 573, from a cross between the cultivars L503 with Taro1, grain yield significantly decreased compared with the parental recipient cultivar, but in NIL 345, where Belyanka was crosse with Taro1, the grain yields were nearly similar (Table 3, p. 61). These lines were different in gluten content and strength of gluten; NIL 573 did not differ from L503, but those for NIL 345 were lower than those of Belyanka. In NIL 573, dough extensibility and strength of flour were were significantly higher than that of cultivar L503, whereas in NIL 345, they were slightly different from those of Belyanka. Similar data were obtained in other lines obtained from crossing with durum wheat cultivars. Dough extensibility and strength of flour were significantly higher in NIL 202 than in Favorit, lower in NIL 216 than Dobrynya, and similar in NIL 293 and Dobrynya. In NIL 214, dough extensibility was equal to that of L505, but flour strength was lower (Table 3, p. 61). These studies show that grain yield and quality in introgression lines of spring wheat *using T. turgidum* subsp. *durum* is largely determined by the cross combination. We plan to continue studying the introgression lines carrying genetic material from *T. turgidum* subsp. *durum*.

The influence of translocations $T7DS \cdot 7DL - 7Ae \# 1L + T1BL \cdot 1R \# 1S$ and a 6D (6Agⁱ) substitution on callusogenesis and regeneration in wheat plants.

E.M. Pankova, L.G. Kurasova, and Y.V. Lobachev.

Modern wheat biotechnology involves the use of somatic cell culture and tissues *in vitro*. Therefore, we studied the effect of T7DS·7DL–7Ae#1L + T1BL·1R#1S combination and A 6D (6Agⁱ) chromosome substitution on callus formation and plant regeneration of spring bread wheat. Substitution line 6D (6Agⁱ) has the gene combinations Lr19/Sr25 + Pm8/Sr31/Lr26/Yr9 and $Lr6Ag^i$. Two experiments using a set of two pairs of near-isogenic lines (NILs) L-503R (Lr19 + Lr26 translocations) and L-503S (Lr19 translocation), and L-400R (6D (6Agⁱ) substitution chromosome) and L-400S (normal 6D). Donor plants were grown in the field and greenhouse. In the first experiment, the ratio of the mass of callus after 20 days of culture (W20) to the weight of the explants (Wi) in the NILs L-503R and L-503S were significantly different; the NIL L-400R significantly exceeded those of NIL L-400S. The second experiment revealed significant differences in the W20/Wi for both NIL pairs. No differences in the ratio of the number of regenerates to the weight of callus after 20 days of culture in both NIL pairs were not observed in the all experiments. Thus, the specific effects of T7DS·7DL–7Ae#1L + T1BL·1R#1S translocation combination and the 6D (6Agⁱ) chromosome substitution on processes callusogenesis during culturing of somatic cells *in vitro* were found.

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Aluminum tolerance in spring triticale.

Species, and genotypes within species, are known to differ widely in their tolerance to aluminum. Aluminum (Al) toxicity primarily affects cell division in the root apex. the root meristem and zone of elongation are highly sensitive to Al and accumulate it very easily, resulting in root damage. This study evaluated the levels of aluminum tolerance in spring triticale varieties, using root regrowth to characterize Al tolerance.

Materials and methods. Sixteen cultivars of spring triticale were tested for Al tolerance. We used a method based on root activity exposure to solutions with aluminum (Aniol and Gustafson, 1984; Ma et al., 2000; Matos et al., 2005; Fontecha et al., 2007), with modifications.

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Seeds were germinated at 20°C in a 10^{-4} M CaSO₄ solution. Seedlings with a root length of 1.0–1.5 mm were placed in plastic cups in 250 mL of a 10^{-4} M CaSO₄ solution and grown 48 h (Fig. 1), which was replaced daily. Five seedlings were placed in each cup, with three replications. The CaSO₄ olution was replaced with one containing either 10, 20, or 40 mg AlCl₃·6H₂O/L for 24 h. Roots were stained in a 0.15% Eriochrome (black) solution. Plants were grown for 48 h and root regrowth was measured. Plants that maintained the ability to regrow roots were observed (Fig. 2). Groups of Al tolerance were separated according Butnaru et al. (1998).

Results and discussion. The spring triticale varieties were classified as highly tolerant, tolerant, medium tolerant, and intolerant according to their root regrowth after an Al stress.

- **Highly tolerant** (root regrowth on solution without Al after 24 h in a solution with Al concentrations of 10, 20, or 40 mg/L): Ulyana, Yarilo, Meksika 38, Meksica 51, Legalo, Presto/Tesmo, Dublet, Lana, and 131/7.
- **Tolerant** (root regrowth in a solution without Al after 24 h in a solution with Al concentration 10 or 20 mg/L): Gabo, Wanad, and Hlebodar Harkovskij.

Medium tolerant (root regrowth in solution without Al after 24 h in a solution with an Al concentration 10 mg/L): Grebeshok and Activo.Intolerant (no root regrowth): Sandro, Abaco, and Grego.

We supposed that cereals differ in response to Al in decreasing order: rye, triticale, wheat. In some of our experiments with acid soils, triticale has Al tolerance, which

is not confirmed in experiments using only one characteristic. A comparison in the decrease in yield of spring triticale and spring wheat, which were grown in pots with a soil application of 6 mg AlCl₃/kg of soil, was made (Fig. 3). We propose that the mechanisms of Al tolerance differ for triticale and wheat. The level of decrease was lower, even for the highly tolerant spring triticales Yarilo and Legalo. Tolerance was higher in spring wheat.

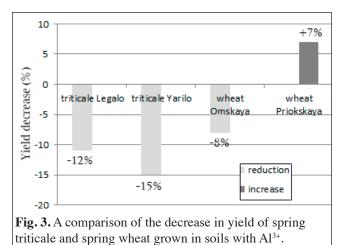
Conclusion. These results indicate that a single test for Al tolerance is not sufficient for grouping spring triticale varieties. Aluminum tolerance has different mechanisms, which have complex determinations on growth and yield of triticale and wheat in stress conditions. To estimate Al tolerance in triticale and wheat, a complex investigation is necessary, which would include testing at different stages of plant development and growth until harvest.

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Fig. 2. Root regrowth after aluminum treatment.



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COLORADO

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Wheat breeding and genetics.

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The primary goals of the Colorado State University (CSU) Wheat Breeding and Genetics Program are to: a) develop improved hard red winter (HRW) and hard white winter (HWW) wheat cultivars and germplasm adapted for the diverse production conditions in Colorado and the west-central Great Plains, and b) conduct research to improve understanding of genetic and environmental factors that affect wheat yield and end-use quality.

Production conditions, cultivar distribution. Total Colorado winter wheat production in 2014 was estimated at 89.3 x 10⁶ bushels, a 101% increase from the 2013 crop and 30% higher than the 10-year average. Average grain yield at 38.0 bushels/acre was the highest since 2010, 40% higher than in 2013, and 20% higher than the 10-year average. The area harvested for grain was estimated at 2.35 x 10⁶ acres, up from 1.64 x 10⁶ acres in 2013.

Planted acreage estimates for the 2014 crop were as follows: Hatcher -25.2%; Byrd -14.8%; TAM 111 -5.4%; Snowmass -5.1%; Ripper -4.4%; Bill Brown -2.7%; TAM 112 -2.5%; Brawl CL Plus -2.3%; Prairie Red -2.2%; Prowers/Prowers 99 -2.2%; Settler CL -2.0%; Danby -1.4%; Winterhawk -1.4%; TAM 107 -1.3%; Jagger -1.1%; Bond CL -0.9%; Antero -0.6%; Goodstreak -0.6%; Above -0.5%; Denali -0.5%; Jagalene -0.5%; and Other/Unknown -22.4%.

Breeding program test sites. In summer 2014, we harvested breeding trials at 11 locations in eastern Colorado (Akron, Burlington, Dailey, Fort Collins-irrigated, Julesburg, Lamar, New Raymer, Orchard, Roggen, Walsh, and Yuma). In addition to the Colorado locations, we obtained data from the CSU Elite Trial at two locations in Kansas (Hays and Colby) and one location in Nebraska (Imperial, irrigated). Due to various production problems (i.e., drought or hail), trials at Arapahoe, Genoa, Sheridan Lake, and Healy, KS, were abandoned. Overall, the quality of the data was very good and very useful for line selection decisions in the breeding program.

The CSU Elite Trial at New Raymer was added in 2014 to evaluate resistance to wheat stem sawfly. In autumn 2014, we further expanded the range of our CSU Elite Trial testing with the addition of three trial locations, which makes a total of 21 Elite Trial locations in 2015. One of the new locations is planted under irrigation in collaboration with New Mexico State University at Farmington, NM, in order to help to build a partnership with Navajo Agricultural Products Industry (NAPI), who are interested to have cultivars adapted for their production conditions and end-use markets. The other two trials are planted in Montana (Fort Benton and Hardin, MT) under contract with Northern Seed LLC. In 2015, we adopted a new trial design for the CSU Elite Trial that involves partial-replication (*p-rep* trials) of experimental entries at a given location to allow greater numbers of entries to be included in the trial. Thus, the CSU Elite Trial is now a 100-entry trial instead of a 75-entry trial. Randomization of the *p-rep* trials is being done with codes developed using the *DiGGer* package (http://www.austatgen.org/software/) in the R programming language (codes available upon request).

In autumn 2014, we prepared over 19,000 yield trial plots for planting at 21 total trial locations in Colorado, Kansas, Nebraska, New Mexico, and Montana. At Fort Collins, we also planted over 30,000 F_4 headrows, about 1,000 early-generation (F_2 – F_3) populations (including 219 two-gene *Clearfield* populations), and about 1,100 new cross combinations in

autumn 2014 and early spring 2015. We continue to utilize a wide variety of diverse germplasm sources in our crossing program, including elite materials from other regional programs, new sources of leaf and stripe rust resistance, solid-stem cultivars from Montana State for wheat stem sawfly resistance, winter wheat lines introduced from Turkey and other areas of eastern Europe, and germplasm carrying various novel traits from our and other programs. Beginning in autumn 2014, we have started to utilize genomic selection predictions for identifying lines for inclusion in our crossing program.

New cultivar release. In autumn 2014, the hard white winter wheat experimental line CO09W293 (pedigree: KS01HW152-6/HV9W02-267W) was formally released by the Colorado Agricultural Experiment Station. CO09W293 (named **Sunshine**) will be marketed by the Colorado Wheat Research Foundation (CWRF) under the PlainsGold Brand and the CWRF-Ardent Mills Ultragrain Premium Program. In three years of testing in the CSU Elite Trial (28 location-years, 2012-2014), the dryland yield of Sunshine was 101% that of the trial average, compared to 105% for Byrd HRW, 103% for Antero HWW, 99% for Hatcher HRW, and 91% for Snowmass HWW. Sunshine has average test weight and straw strength, is moderately susceptible to stripe rust, and susceptible to leaf rust. End-use quality characteristics of Sunshine are excellent, although the dough-mixing strength of Sunshine is less than that of Snowmass and other lines in our program with Snowmass-type characteristics. Preharvest sprouting tolerance and polyphenol oxidase activity of Sunshine are both similar to those of Hatcher, Snowmass, and Antero.

Foundation and breeder seed increases. In autumn 2014, experimental line **CO11D174** was advanced for Foundation seed production to enable release as a new cultivar in autumn 2015. CO11D174 is a doubled-haploid (DH) HRWW from the cross 'TAM 112/Byrd' made in 2009. CO11D174 is similar to Byrd in many respects, being of medium height and maturity, has a medium-long coleoptile, and average straw strength and test weight. CO11D174 is moderately susceptible to stripe rust, susceptible to leaf rust and stem rust, susceptible to Hessian fly and all biotypes of Russian wheat aphid, and resistant to wheat soilborne mosaic virus and the wheat curl mite. Across 26 site-years in the CSU Elite Trial (2013 and 2014) and UVPT (2014), CO11D174 was the highest yielding entry tested, approximately 7% higher yielding than Byrd. In the 2014 Southern Regional Performance Nursery, CO11D174 also was the highest yielding entry. CO11D174 has shown good overall milling and baking properties in tests conducted in the CSU Wheat Quality Lab. Individual milling and baking properties of CO11D174 are very similar to those of Byrd, although CO11D174 has a slightly greater kernel weight (29.3 vs. 27.7 grams/1,000 kernels) and diameter (2.58 vs. 2.49 mm), a slightly lower flour yield (69.9 vs. 72.0%), and a slightly shorter mixograph mixing time (5.3 vs. 6.6 minutes). Tests conducted on CO11D174 in the 2014 Wheat Quality Council tests also suggest that CO11D174 has a higher water absorption than that of Byrd. A decision on the release of CO11D174 will be made after the 2015 harvest.

In autumn 2014, eight HRW and two HWW lines were advanced for Breeder seed production to enable Foundation seed production and potential release in 2016. All of the lines are being tested in the 2015 CSU Elite Trial and the 2015 CSU Variety Trials (UVPT and IVPT). All of the HRW lines (CO11D446, CO11D1174, CO11D1236, CO11D1298, CO11D1353, CO11D1397, CO11D1539, and CO11D1767) are DH lines lacking the *Clearfield* herbicide-tolerance traits and both of the HWW lines (CO11D1306W and CO11D1316W) are DH lines that lack the *Clearfield* traits and the gluten strength trait in Snowmass and Sunshine. A decision on retention and advancement to Foundation Seed production will be made after harvest in 2015.

Doubled-haploid breeding. Since 2010, the CWRF royalty funds and our partnership with Ardent Mills have provided for a significant expansion of experimental HRW and HWW line development through the use of DH breeding technology. We have used the DH services at Heartland Plant Innovations and Washington State University, and, since 2012, have been working to build our own DH capacity on the CSU campus. In December 2013, we moved into a newly renovated DH lab in the CSU Greenhouse (renovations funded by CSU and CWAC).

In 2014, our advanced yield nurseries consisted of lines developed using both DH and 'conventional' breeding technologies. These trials all were set up as partially replicated trials to allow greater numbers of entries to be included. The trials were divided roughly as follows: HWW DH lines mostly carrying the 'Snowmass trait' (253 lines, six locations), HRW DH lines mostly lacking the 'Snowmass trait' (305 lines, three locations), conventionally-derived and single-seed descent derived HRW and HWW lines mostly lacking the 'Snowmass trait' (248 lines, eight locations), and a group of two-gene, HRW and HWW *Clearfield* lines (37 lines, two locations). From this group of 843 lines, 70 lines (about 8.3%) were selected and advanced to the 2015 CSU Elite Trial. These 70 lines can be categorized roughly as follows: 20 HWW DH lines that carry the 'Snowmass trait', 41 'conventional' HRW, and nine two-gene HRW *Clearfield* lines. Of these two-gene *Clearfield* lines, four are two-gene, Byrd backcross-derived lines.

ANNUAL WHEAT NEWSLETTER

In 2014, we had approximately 3,314 new DHs at Fort Collins in short-rows for seed increase. The vast majority of these (3,086) had Snowmass as one of the parents of the cross and, thus, had the genetic possibility of carrying the dough strength trait from Snowmass. Based on visual observations of agronomic suitability and DNA marker information, approximately 1,028 of these lines were hand-harvested in July. Following seed processing, we selected 984 of these lines (about 32% of the total) for advancement to yield trials in 2015. These lines can be categorized roughly as follows: HWW DH lines mostly carrying the 'Snowmass trait' (244 lines, seven locations), HRW DH lines mostly lacking the 'Snowmass trait' (244 lines, four locations), and HWW DH lines lacking the 'Snowmass trait' and HRW lines carrying the 'Snowmass trait' (496 lines, one location).

DNA marker implementation. Our current emphasis in marker-assisted selection (MAS) is centered on two main areas. First, we now are conducting routine marker screening for a key set of markers on virtually all experimental lines developed in the breeding program. These include DHs that are under first year seed increase prior to selection and lines that have been selected from F_4 headrows and are in testing in our preliminary yield nurseries (PYNs). Second, we continue to utilize MAS for backcross transfer (introgression) of various traits from non-elite germplasm sources to elite breeding program germplasm. Products of these introgression efforts are then used in 'forward crosses' for transfer of the traits into a DH line development pipeline or the main breeding program pipeline.

In 2014, we conducted DNA marker tests on 5,917 different lines and plant selections. The markers used were for multiple disease/insect resistance, quality-related, herbicide tolerance, and TILLING-derived traits. Most of the markers that we are using are sequence-based (KASP assays), which has dramatically improved our efficiency (lower costs, greater speed) for routine MAS. Overall, the materials tested included 3,236 DH lines under first-year, seed increase and 1,360 lines tested in the 2014 PYNs. Marker screening of plants from which DHs are made can dramatically improve the frequency of desirable DHs obtained. The numbers of markers for all of these materials varied from one to seven and in total we generated over 24,100 data points on these materials to aid in selection.

In 2014, we conducted DNA marker tests for backcross introgression of various traits from non-elite germplasm to elite breeding program germplasm. Across our three most recent crossing cycles, we generated about 4,100 data points from nearly 1,800 individual plants. Target traits for these tests included: *Clearfield* herbicide tolerance; low polyphenol oxidase expression; stripe rust resistance, and several different TILLING-derived mutants. Most of the markers we are using for this are KASP markers, especially in the case of TILLING mutants, where we are well positioned to design novel KASP assays in-house.

In addition to the trait-specific ,DNA marker screening described above, we also continue to exploit next generation sequencing technologies (called genotyping by sequencing or GBS) in our breeding program. Our pipeline involves DNA extraction and sample preparation at CSU, outsourcing of the high-throughput DNA sequencing to the core facility at the University of Missouri, and then bioinformatics analysis both at CSU (by Harish Manmathan) and in collaboration with Kansas State University (by Jesse Poland) for generating the marker calls. For each of the GBS assays, we can obtain about 40,000 DNA markers spread across the entire wheat genome, at a cost of about \$14/line. Since we began using GBS, we have sequenced about 7,800 breeding/germplasm lines, generating over 300 million total data points (including missing data). We have successfully used the GBS marker data in genomic selection and genome-wide association analysis (GWAS) for preharvest sprouting tolerance and various wheat quality traits (Jessica Cooper Ph.D.) as well as other more complex breeding targets (yield and test weight) for selection and parent identification.

End-use quality evaluation. End-use quality evaluations are done annually on samples from a variety of different field trials and research studies. In 2014, 3,957 different samples went through our quality lab for one or more quality tests. From breeding trials in 2013, we conducted comprehensive milling and baking quality tests on five locations of the CSU Elite Trial and three locations of the Advanced Yield Nursery (including both DHs and conventionally derived lines) and small-scale quality analyses from two locations of the PYN. Our comprehensive testing of advanced generation materials includes the full spectrum of quality tests: NIR protein, single-kernel characterization system, mixographs, polyphenol oxidase, and Quadrumat Senior milling and pup-loaf baking tests. Testing of earlier generation materials generally involves only NIR protein, the single-kernel characterization system, and the mixographs. Our overall strategy in line evaluation is to properly characterize experimental lines in order to inform the line selection and seed increase decision-making processes.

Comprehensive milling and baking quality evaluations are done annually on selected locations of the state dryland (UVPT) and irrigated (IVPT) variety trials. From trials in 2013, grain samples were collected from five dryland

(UVPT) variety trial locations (Akron, Julesburg, Orchard, Roggen, and Yuma) and two irrigated (IVPT) variety trial locations (Fort Collins and Haxtun). Preliminary, small-scale, quality analyses were done to determine suitability of the samples for full-scale analyses. In this process of sample selection, four of the dryland locations (Akron, Julesburg, Roggen, and Yuma) were excluded from analyses beyond protein content with the primary problem being elevated protein values far above the level conductive for meaningful dough mixing and baking quality evaluations. All of the data were reported in the booklet *Making Better Decisions*. The data also are used to develop and update the milling and baking quality scores that are reported in the Variety Characteristics Table in *Making Better Decisions*. Other variety-trial related activities from trials in 2013 include NIR protein on 83 samples from the Collaborative On-Farm Testing program and 74 samples from the western Colorado trials at Hayden and Yellow Jacket.

From trials in 2013, we determined NIR protein content from every plot of six locations (1,800 samples) of our Advanced Doubled-haploid Nursery (AYND). From trials in 2014, we are doing NIR protein on every plot of five locations (750 samples) of the CSU Elite Trial. Our objective is to begin to use 'grain protein deviation' (protein content adjusted for grain yield) as a measure of nitrogen use efficiency (NUE) and develop genomic selection prediction models for NUE selection in the breeding program. This research forms the basis of Sue Latshaw's Ph.D. dissertation, which she hopes to complete in spring 2016.

From trials in 2013, we evaluated 750 samples from a two-year study to evaluate the effect of different glutenin allele combinations on agronomic properties and end-use quality. This research was part of Jessica Cooper's PhD dissertation (successfully completed in November 2014), along with genomic selection model development for preharvest sprouting tolerance and various end-use quality traits.

Russian wheat aphid resistance. Our basic objectives with Russian wheat aphid (RWA) resistance are to transfer different resistance traits to our germplasm and, ultimately, develop resistant cultivars. Due to development of multiple new RWA biotypes, generally lower RWA incidence in recent years, and relatively inexpensive chemical control options, RWA resistance has, over time, become a less critical breeding objective in our program. Because 'nature abhors a vacuum' (according to Aristotle), the wheat stem sawfly now has become a major insect pest in Colorado and a potentially serious cereal aphid called *Sipha maydis* was recently found in New Mexico and western Colorado. Given these realities, we will continue to address all insect pests that affect wheat in Colorado for which there are reasonable opportunities for host–plant resistance. All of these efforts are done in very close collaboration with Frank Peairs and his team.

Over the last few years, we have developed and tested many experimental lines carrying RWA biotype 2 resistance. None of the lines have been yield-competitive with our best cultivars (Byrd HRW or Antero HWW) and, thus, none have been advanced toward release. In order to move the 'RWA yield curve' forward a bit more effectively, we have begun to generate a limited of number of DH lines from crosses with different sources of the *Dn7* resistance gene.

The first group of these DHs was a set that was planted in our Advanced Yield Nurseries in 2014. Among 30 DHs derived from a cross with CO08RWA060 (Yuma-type Dn7 carrier), 17 were resistant to RWA biotype 2, and 13 were susceptible in greenhouse seedling screening tests. These reactions were confirmed with a DNA marker linked to Dn7. Of the resistant lines, only one HRW line (CO12D1380, pedigree: Snowmass/CO08RWA060//CO05W111) was selected and advanced to the 2015 CSU Elite Trial. This line performed very well in 2014, yielding second among 305 DHs in our HRW DH trial. In addition to this line, we had six conventionally derived lines in the 2014 Advanced Yield Nursery and 29 lines in the PYN with RWA resistance in the pedigree. Several of these lines showed good resistance to RWA biotype 2 in greenhouse screening, but none showed adequate merit for advancement to testing in 2015.

In 2015, we have a set of 22 DHs in Advanced Yield Nurseries, also derived from the CO08RWA060 resistance source. Four of these were resistant to RWA biotype 2 and 18 were susceptible in greenhouse screening tests. DNA marker analysis is currently being done on these lines to confirm the presence/absence of Dn7. We also have a group of 30 DHs in first year seed increase and 91 PYN lines that carry Dn7 in the pedigree. We are currently conducting DNA marker screening on these lines to inform selection decisions in summer 2015.

We have completed backcrossing of RWA biotype 2 resistance from CI2401 into Yuma and a modified version of Dn7 (without the rye secalin proteins) into Bill Brown. These materials already have been used in new crosses and are currently under seed purification to enable release as germplasm in 2015–16. These materials may be useful for future biotype monitoring.

In addition to RWA, we also are aggressively pursuing wheat stem sawfly (WSS) resistance as a breeding objective. With one month of salary support from our program, Terri Randolph (Frank Peairs' team) coordinated solid stem evaluations of segregating populations at Fort Collins. We also have generated a group of 300 DHs from crosses with Byrd and Antero and the solid-stemmed Montana cultivar Bearpaw. We have completed DNA marker analysis for WSSassociated markers in these DHs and are hopeful that some of the DHs will be advanced to yield trials in 2016. In 2014, we added a field site near New Raymer for evaluation of wheat WSS response, and we believe that we have some form of non solid-stem resistance in our germplasm. One DH line (CO11D1397, pedigree: CO050337-2/Byrd) showed very good yield at New Raymer and other locations, low WSS damage, and low larvae counts in the stubble after harvest. This line is in the 2015 UVPT and IVPT and is under Breeder seed increase for potential Foundation seed production and release in 2016.

Personnel updates. CSU wheat breeder Scott Haley completed a six-month sabbatical leave in Europe from December 2013 to May 2014. The focus of the sabbatical was to learn new ideas and new techniques at the interface of crop genomics and wheat breeding. In December 2014, Ph.D. student Sue Latshaw accepted a position in wheat breeding with Bayer CropScience in Lincoln, NE, and will work to complete her Ph.D. in spring 2015. In November 2014, Ph.D. student Jessica Cooper successfully completed her degree program, focusing on genomic selection for end-use quality traits (including preharvest sprouting tolerance), and accepted a position in canola breeding with Cargill in Fort Collins. Our Ph.D. student Craig Beil completed his first year in our program in summer 2014 conducting research to leverage next-generation sequencing technologies (i.e., genotyping by sequencing) to more efficiently exploit winter wheat germplasm from the CIMMYT–ICARDA International Winter Wheat Improvement Program based in Turkey. Craig is currently spending three months with CIMMYT in Mexico (February to May 2015) participating in their international training program. Craig is only the 5th U.S. trainee to participate in this program since the 1960s. In autumn 2014, Ben Conway joined our program (co-advised by Pat Byrne) to work on a Ph.D. focusing on research to improve genomic selection models in wheat using climatological and other covariates. Ben joined us following completion of an M.S. degree in wheat breeding at the University of Maryland.

<u>KANSAS</u>

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Chemical properties of soil with winter cover crops.

Oliver W. Freeman and M.B. Kirkham.

In Kansas, winter cover crops have a new interest with the development of summer crops for biofuel. When a crop is harvested for bioenergy, the residue is removed leaving the soil prone to erosion during the winter fallow period. Winter cover crops may allow maximum biomass harvest by protecting the soil from wind and water erosion. Therefore, the objective of the research reported by Freeman (2014) was to determine the effect of two winter cover crops on the growth of two biofuel crops, corn (*Zea mays* L.) and forage sorghum [*Sorghum bicolor* (L.) Moench] in a corn–forage sorghum rotation. The two rotations, established in 2009, were continuous forage sorghum and corn–forage sorghum. In the corn–forage sorghum rotation, the 2009 plots with corn grew forage sorghum in 2010 and corn in 2011; the 2009 plots with forage sorghum in 2011. The two cover crops were a legume, Austrian winter pea (*Pisum sativum* var. *arvense* Poir.), and winter wheat. Control plots were fallowed. The experiment was done for two years in Manhattan and Tribune, KS, with harvests of the winter cover crops in the springs of 2011 and 2012. Two levels of nitrogen were added to the soil: 0 and 101 kg/ha N. The main results for both locations were 1) nitrogen increased yield of both corn and sorghum. 2) growth of the winter cover crops did not decrease the yield of the summer crops. and 3) winter wheat produced more biomass than Austrian winter pea. The Austrian pea winter killed in the second year of

the study at Manhattan, KS. The results showed that winter wheat is a better winter cover crop than Austrian winter pea, because of its ability to grow well during the off-season of the bioenergy crops and to provide soil cover during winter.

In the study of Freeman (2014), soil data were not reported, although soil was sampled. Here we report the soil data for Manhattan, KS. Soil samples were taken in the autumn of 2010 after harvest of the forage sorghum and corn and at the time of the planting of the cover crops. Soil was sampled again in the spring of 2011 after the cover crops were harvested and before the corn and sorghum were planted. The soil was analyzed for four chemical characteristics (pH, organic matter, nitrogen, and carbon) using standard methods practiced in the Soil Testing Laboratory of Kansas State University, Manhattan, KS.

Table 1. Properties of a silt loam soil at Manhattan, KS, before two winter cover crops were planted in the autumn of 2010 and after their harvest in the spring of 2011. The two cover crops were winter wheat and Austrian winter pea. Plots also were fallowed during the winter. The summer crops were forage sorghum and corn, and they were grown in two rotations established in 2009: continuous forage sorghum and corn-forage sorghum. In the corn-forage sorghum rotation, the 2009 plots with corn grew forage sorghum in 2010 and corn in 2011; the 2009 plots with forage sorghum grew corn in 2010 and forage sorghum in 2012. Half the plots were fertilized with 101 kg/ha nitrogen and half the plots received no fertilizer nitrogen. The values are the means and standard deviations of four replications.

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		/inter cover c	·		inter cover cr	
Soil property	Wheat	Pea	Fallow	Wheat	Pea	Fallow
AT COVER CROP PLANTING IN AUTUM	IN 2010 IN THE	FORAGE SORGH	UM-FORAGE SOR	GHUM ROTATION		,
рН	6.03 <u>+</u> 0.19	6.08 <u>+</u> 0.29	6.10 <u>+</u> 0.23	6.33 <u>+</u> 0.19	6.00 <u>+</u> 0.37	6.13 <u>+</u> 0.39
Organic matter, %	1.48 <u>+</u> 0.05	1.33 <u>+</u> 0.26	1.25 <u>+</u> 0.41	1.55 <u>+</u> 0.13	1.30 <u>+</u> 0.37	1.33 <u>+</u> 0.15
Nitrogen, %	0.10 <u>+</u> 0.01	0.09 <u>+</u> 0.02	0.08 <u>+</u> 0.02	0.10 <u>+</u> 0.02	0.09 <u>+</u> 0.02	0.09 <u>+</u> -0.02
Carbon, %	0.95 <u>+</u> 0.16	0.79 <u>+</u> 0.14	0.72 <u>+</u> 0.16	0.94 <u>+</u> 0.17	0.78 <u>+</u> 0.16	0.80 <u>+</u> 0.12
AT COVER CROP PLANTING IN FALL 2	010 in corn-fo	ORAGE SORGHUN	M ROTATION AFTE	ER SORGHUM HAR	VEST	
pH	6.08 <u>+</u> 0.38	5.85 <u>+</u> 0.36	6.20 <u>+</u> 0.28	6.10 <u>+</u> 0.26	6.08 <u>+</u> 0.39	6.00 <u>+</u> 0.35
Organic matter, %	1.03 <u>+</u> 0.49	1.03 <u>+</u> 0.28	1.10 <u>+</u> 0.29	1.05 <u>+</u> 0.47	1.03 <u>+</u> 2.38	1.05 <u>+</u> 0.27
Nitrogen, %	0.08 <u>+</u> 0.03	0.08 <u>+</u> 0.03	0.09 <u>+</u> 0.02	0.08 <u>+</u> 0.03	0.07 <u>+</u> 0.02	0.08 <u>+</u> 0.02
Carbon, %	0.66 <u>+</u> 0.23	0.62 <u>+</u> 0.16	0.65 <u>+</u> 0.12	0.62 <u>+</u> 0.21	0.57 <u>+</u> 0.14	0.62 <u>+</u> 0.13
AT COVER CROP PLANTING IN AUTUM	in 2010 in cor	N-FORAGE SOR	GHUM ROTATION .	AFTER CORN HAR	VEST	
pH	5.83 <u>+</u> 0.16	6.08 <u>+</u> 0.28	6.00 <u>+</u> 0.25	6.10 <u>+</u> 0.08	6.10 <u>+</u> 0.29	6.08 <u>+</u> 0.31
Organic matter, %	1.15 <u>+</u> 0.35	1.08 <u>+</u> 0.33	1.13 <u>+</u> 0.43	1.05 <u>+</u> 0.19	1.20 <u>+</u> 0.55	1.00 <u>+</u> 0.39
Nitrogen, %	0.08±0.02	0.09 <u>+</u> 0.03	0.09 <u>+</u> 0.01	0.09 <u>+</u> 0.02	0.09 <u>+</u> 0.02	0.08 <u>+</u> 0.02
Carbon, %	0.66 <u>+</u> 0.28	0.65 <u>+</u> 0.21	0.71 <u>+</u> 0.18	0.71 <u>+</u> 0.70	0.68 <u>+</u> 0.22	0.64 <u>+</u> 0.19
AFTER COVER CROP HARVEST IN SPRI	ng 20 11 in fof	RAGE SORGHUM-	-FORAGE SORGHU	UM ROTATION		
pH	6.08 <u>+</u> 0.30	5.85 <u>+</u> 0.49	6.13 <u>+</u> 0.34	5.95 <u>+</u> 0.45	5.90 <u>+</u> 0.35	6.18 <u>+</u> 0.15
Organic matter, %	1.38 <u>+</u> 0.25	1.15 <u>+</u> 0.21	1.40 <u>+</u> 0.24	1.23 <u>+</u> 0.15	0.98 <u>+</u> 0.49	1.30 <u>+</u> 0.27
Nitrogen, %	0.08 <u>+</u> 0.01	0.07 <u>+</u> 0.01	0.08 <u>+</u> 0.01	0.07 <u>+</u> 0.01	0.06 <u>+</u> 0.01	0.07 <u>+</u> 0.01
Carbon, %	0.93 <u>+</u> 0.14	0.81 <u>+</u> 0.11	0.91 <u>+</u> 0.05	0.82 <u>+</u> 0.10	0.71 <u>+</u> 0.18	0.88 <u>+</u> 0.10
AFTER COVER CROP HARVEST IN SPRI	ng 2011 in coe	RN-FORAGE SOR	GHUM ROTATION	BEFORE SORGHU	M PLANTING	
pH	6.15 <u>+</u> 0.17	5.88 <u>+</u> 0.10	5.98 <u>+</u> 0.17	6.25 <u>+</u> 0.13	5.88 <u>+</u> 0.36	6.08 <u>+</u> 0.30
Organic matter, %	0.95 <u>+</u> 0.48	0.93 <u>+</u> 0.22	1.15 <u>+</u> 0.31	0.93 <u>+</u> 0.49	0.98 <u>+</u> 0.26	1.03 <u>+</u> 0.46
Nitrogen, %	0.06 <u>+</u> 0.03	0.06 <u>+</u> 0.02	0.07 <u>+</u> 0.02	0.06 <u>+</u> 0.03	0.06 <u>+</u> 0.02	0.06 <u>+</u> 0.02
Carbon, %	0.72 <u>+</u> 0.28	0.65 <u>+</u> 0.15	0.74 <u>+</u> 0.27	0.71 <u>+</u> 0.28	0.67 <u>+</u> 0.19	0.70 <u>+</u> 0.24
AFTER COVER CROP HARVEST IN SPRI	ng 2011 in coe	RN-FORAGE SOR	GHUM ROTATION	BEFORE CORN PI	LANTING	
рН	6.05 <u>+</u> 0.24	6.15 <u>+</u> 0.35	6.84 <u>+</u> 0.29	6.03 <u>+</u> 0.38	6.05 <u>+</u> 0.24	6.15 <u>+</u> 0.10
Organic matter, %	0.83 <u>+</u> 0.26	0.90 <u>+</u> 0.34	0.88 <u>+</u> 0.21	0.78 <u>+</u> 0.28	0.88 <u>+</u> 0.34	0.91 <u>+</u> 0.26
Nitrogen, %	0.09 <u>+</u> 0.02	0.09 <u>+</u> 0.03	0.09 <u>+</u> 0.02	0.09 <u>+</u> 0.02	0.09 <u>+</u> 0.02	0.08 <u>+</u> 0.02
Carbon, %	0.65 <u>+</u> 0.22	0.66 <u>+</u> 0.25	0.59 <u>+</u> 0.18	0.60 <u>+</u> 0.14	0.62 <u>+</u> 0.18	0.62 <u>+0</u> .21

The soil data provided information about the change in soil properties after a winter season with the cover crops (Table 1, p. 69). The pH, organic matter, nitrogen, and carbon were not changed by the presence of either of the cover crops. Values before planting of the cover crops were similar to those after their harvest. Nitrogen in the soil was not increased by the presence of the peas. The results showed that there is no advantage of increased nitrogen in the soil, if winter pea is a cover crop. They reinforced the fact that the winter cover crop in Manhattan, KS, should be wheat.

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KANSAS STATE UNIVERSITY

Wheat Genetics Resource Center, Department of Plant Pathology, Department of Agronomy, and the USDA–ARS Hard Red Winter Wheat Genetic Research Unit, Throckmorton Plant Sciences Center, Manhattan, KS 66506-5501, USA.

Mining novel genetic diversity in Aegilops tauschii, the D-genome progenitor of hexaploid wheat.

Narinder Singh, Sunish K. Sehgal (South Dakota State University, Brookings), Duane L. Wilson, W. Jon Raupp, Bikram S. Gill, and Jesse Poland.

Wheat production is threatened by depleting resources, increasing cost of production and climate change. An estimated 60% increase in wheat production is needed by 2050 to feed the projected population of 9 billion. Hexaploid wheat, like many other crops, has undergone bottlenecks during polyploidization and domestication resulting in narrow genetic base. *Aegilops tauschii* the D-genome progenitor of bread wheat, has remained genetically diverse and is an excellent source for broadening the genetic base of wheat. With this vision, we assessed the diversity in the *Ae. tauschii* collection at the Wheat Genetics Resource Center at Kansas State University and developed PowerCore and MiniCore sets. We genotyped 551 accessions representing the world collection by genotyping-by-sequencing (GBS). More than 120K SNPs were discovered using TASSEL pipeline. SNPs with less than 50% missing data were filtered, and a random subset of 15K SNPs was selected to identify a PowerCore consisting of 144 accessions retaining most of the genetic diversity and maintaining frequency of alleles in core set similar to the entire collection. The PowerCore was optimized based on genetic distance to represent the major clusters of phylogenetic tree. A MiniCore set of 52 accessions was selected from the PowerCore set to represent all the major clusters in the phylogenetic tree. The MiniCore set of 52 accessions will be crossed to elite wheat cultivars to produce wheat–*Ae. tauschii* amphiploids. These amphiploids will be selfed and back-crossed to elite wheat lines to enhance the diversity of bread wheat.

In addition, the *Ae. tauschii* accessions were evaluated for a second year at the Rocky Ford Research Area, Manhattan, KS, for field resistance to leaf and strip rust and barley yellow dwarf virus (Table 1, pp. 72-81). The lines also were evaluated for heading date. Field data was recorded on two dates. Virus infection was rated as symptoms on visible as chlorosis, necrosis of the leaf tips and leaves, or purpling of the leaves. Hessian fly and seedling and adultplant stripe rust reactions were scored on greenhouse-grown plants.

The Wheat Genetics Resource Center Genebank and the rapid curation of germplasm Collections using Genotyping-by-Sequencing.

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

The main mission of the WGRC, collecting, conserving, and utilizing germplasm in wheat improvement for sustainable production, broadens the crop genetic base assuring future advances in breeding. The WGRC genebank contains passport and evaluation data on \sim 3,800 wheat species accessions and, in addition, houses \sim 3,400 cytogenetic stocks.

In wheat, accessions from genebanks and individuals have been widely circulated for the last century. Historically, each genebank has used their own accession identification numbers, often resulting in the loss of globally unique identifiers, cross-referenced collection information, or passport data. Thus, once an accession travels from genebank to genebank, the ability to discern duplicates is confounded. In this context, much effort is given at the WGRC to crossreference our accessions with those of other wheat gene banks.

Recognizing the importance of identifying duplicity and cross-referencing collections, we used genotyping-bysequencing (GBS) to ascertain the genetic diversity in our collection of 568 *Aegilops tauschii* accessions and compare it to an undocumented collection. After de novo SNP calling using the TASSEL pipeline, removing duplicate tags, and SNP filtering for missing data, 14k SNPs were mapped on wheat D genome. Using allele matching accounting for a ~1% sequencing error (>99% match), we could identify accessions with similar, yet incomplete, passport data as possible duplicates. Of 551 *Ae. tauschii* accessions assayed, 402 were unique, representing a 27% duplication. We also were able to match 118 unidentified accessions from the genebank at Punjab Agricultural University as the same accession represented the WGRC collection. We currently are using this same approach to characterize and curate our collection of over 900 tetraploid wheats.

With a rapid and cost-effective tool to study genetic diversity, giving a consistent characterization of genetic and phenotypic diversity in wheat germplasm GBS will be important in the genetic curation of accessions within and between collection(s). With such information across global collections, it becomes possible identify the truly unique accessions across all of our gene banks, enabling more targeted access to genetic diversity.

Detection of adult-plant resistance to Puccinia triticina in native wheat species, transfer, and mapping in wheat.

Bhanu Kalia, Jesse Poland, and Bikram S. Gill; Robert L. Bowden and Erena Edae, USDA–ARS, Manhattan; and Ravi P. Singh, CIMMYT, Mexico.

Resistance to wheat rusts may be race-specific and subject to boom and bust cycles, or race-nonspecific or adult-plant resistance (APR), which is associated with durability. We evaluated *Aegilops tauschii*, one of the diploid ancestors of wheat, for APR to *P. triticina*. The *Ae. tauschii* populations in Caspian Iran and eastern Afghanistan commonly exhibited APR, suggesting that APR may be an important defense in nature against leaf rust. We transfered APR to leaf rust from *Ae. tauschii* (TA2474) to wheat through production of synthetic-hexaploid wheat (SHW), but expression was suppressed in the progeny. To unlock the expression of APR, a population of 261 recombinant inbred lines (RILs) was developed from a cross of SHW with the cultivar WL711. The RILs were phenotyped for maximum disease severity at Manhattan, KS, in 2013–14 and at CIMMYT, Mexico, in 2013. Genotyping-by-sequencing (GBS) detected QTL associated with APR and was contributed by both the parents. Two major QTL from WL711 were mapped on chromosome 1BL, explaining 11–24% of the phenotypic variance across environments; two additional QTL were mapped on 5AL and 6BL. SHW-derived QTL for APR were mapped on 1AL, 1BS, 2DS, 2DL, and 5DL. The results demonstrate complex genetic

 $\frac{A \ N \ N \ U \ \lambda \ L \ W \ H \ \varepsilon \ \lambda \ T \ N \ \varepsilon \ W \ S \ L \ \varepsilon \ T \ T \ \varepsilon \ R \qquad \lor \ O \ L \ 6 \ 1 \ control and evolution of APR. The novel APR genes and their linked GBS-based ,SNP markers are potentially useful for the second seco$ durable control of leaf rust in wheat.

ID / accession	Country of	Leaf	rust		Strip	e rust		BY	DV	Hessian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June	fly	date
Triumph 64	Check	50MS	_	30MS	_			Н	_		27 May
Newton	Check	30M		15MS	_		_	Н	_		21 May
Fuller	Check	70S	_	25MS	_		_	Н	_		8 May
Everest	Check	20M	_	10MS	_		_	Н	_		8 May
Kingbird	Check	_	_	_	_		5R 5	_	_		
Morocco	Check	_	_	_	_	8 10	70S ⁵		_		_
Karl 92	Check									S	
Carol	Check									S	
Caldwell	Check									S	
WGRC1 (<i>H13</i>)	Check									R	
(inter (inte)		20MR	20MR	30MS	30MS			L	L		13 May
TA1585	Turkey	10MR	25MR	30M	30M	56	20MS ³	M	M	S	14 May
		5MR	25MR	20M	20M		201010	M	M		15 May
		5R	10R	30MS	30MS			M	M		26 May
TA1586	Turkey	10R	15MR	20M	20M	56	40MS ³	M	M	S	27 May
1111200	Turney	5MR	20MR	20MR	20MR	-	101010	M	M		18 May
		70S	705	30MS	30MS			H	H		27 May
TA1592	Turkey	60MS	705	30MS		5 6	40MS ³	H	H	S	16 May
1A1372	Turkey	60MS		30MS			401015	H	H		17 May
		WINTER KI		501015				11	11		17 Widy
TA1604	Afghanistan	70S		20MS	1	4 ⁵	60MS ³	Н	Н	S	16 May
1/1004	Arginallistali	WINTER KI		201015			001015	11	11		10 Widy
		10MR	10MR	5R	5MR			L	M		14 May
TA1606	Afghanistan	10101K	30MR	5R 5R	5MR	4 ²	5R ²	M	H	S	13 May
1A1000	Arginallistali	WINTER KI		л	JIVIK		JK	191	11		15 Widy
		10MS	10MS	30M	40MS			Н	Н		15 May
TA1620	Afghanistan	30M	35M	30M	30MS	5 6	20M ²	H	H	s	12 May
1A1020	Arginanistan	30MS	55101	40MS	301013	- 5	20101	M	H		12 May
		50MS	50MS	10M	20MS			M	H		29 May
TA1621	Georgia	50MS	50MS	20M	20MS	5 ⁴	5R 5	M	M	S	29 May 28 May
1A1021	Georgia	30MS	30MS	20MS	20MS		JK	H	H		1-Jun
		10M	30M	40MS	40MS			H	H		12 May
TA1629	Afghanistan	20MS		40MS	-	3 5	50S ³	H	H	S	12 May 10 May
111027	7 Hgnamstan	20MG	30M	10MR	15M		505	H	H		13 May
		25MS	50101	30MS				H	H		11 May
TA1631	Afghanistan	30MS		40MS		4 6	50S ³	H	H	S	9 May
1/11031		25MS		30MS			200	H	H		10 May
		20MR	 20MR	25R				L	L		24 May
TA1642	Iran	15R	25MR	5R	10MR	36	1R ³	L	M	R	16 May
1/11072	IIall	5MR	20MR	1R	5MR		11	L	M		16 May
	1	JIVIN	201111		JIVIN	I			141		10 101ay

ID / accession	Country of	Leaf	rust		Stripe	e rust		BY	DV	Hessian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June	fly	date
		10R	15MR	20MR	20MR			L	L		14 May
TA1644	Iran	10R	25MR	5R	15MR	36	1R ³	M	M	R	13 May
		10MR	30MR	5MR	20MR			M	M	1	12 May
		15MR	20MR	25MR	25MR			L	M		22 May
TA1645	Iran	10MR	_	5MR		36	15R ³	M	Н	R	16 May
		10M	15M	1R	20MR			L	Н	1	15 May
		WINTER KI									
TA1655	Afghanistan	20MS	_	40MS	-	55	70S ³	Н	Н	s	11 May
	0	WINTER KI				1			1		
		20M	_	20MS	_			Н	Н		22 May
TA1657	Afghanistan	30MS	_	40MS		35	30M ³	Н	Н	s	10 May
	8	40M	_	25MS	_	1		Н	Н		10 May
		20R	30MS	10R	10MR			L	L		14 May
TA1662	Azerbaijan	15M	30M	10MR	20M	2 4	5R ³	М	М	s	28 May
		WINTER KI			1	1			1		
		20R	20MR	15R	15MR			L	L		22 May
TA1664	Azerbaijan	10MR	25M	15MR	15MR	36	5MR ³	L	M	R	15 May
	l	1R	20M	5R	20MS		01111	H	H		14 May
		WINTER KI									
TA1667	Azerbaijan	10M	25M	5MR	15R	36	20MS ³	М	Н	R	30 May
		30M	30M	20MR	20M			M	M	1	18 May
		30R	30M	30MR	30MR			M	M		24 May
TA1668	Azerbaijan	10MR	30MS	5R	20MR	36	10MR ³	M	M	R	16 May
		30M	30M	5MR	25M			M	M	1	22 May
		1R	_	5R	_			М	Н		22 May
TA1670	Azerbaijan	1R	5R	5R	5R	45	20MR ³	L	L	R	16 May
	5	1R	20MR	5R	10MR	1		L	М	-	16 May
		20M	40MS	10MR	20MS			М	М		26 May
TA1679	Azerbaijan	40MS	50MS	20MR	20M	66	10M ³	L	М	s	30 May
	5	50MS	50MS	20M	20M	1		М	М	1	1-Jur
		30M	30M	10MR	15MR			L	L		28 May
TA1680	Azerbaijan	15MR	25MR	10MR	10MR	3 ²	20MR ²	М	М	R	28 May
	5	10M	30M	5MR	20MR	1		L	М	1	30 May
		40MS	40MS	10MR	10MR			М	М		27 May
TA1681	Azerbaijan	30M	30M	5R	25M	46	10MR ³	Н	Н	s	22 May
	5	40MS	50MS	5MR	20MR	1		Н	Н	1	17 May
		20M	10MR	5MR	10MR			М	М		15 May
TA1690	Afghanistan	20M	20M	5MR	25M	46	10R ²	М	Н	R	16 May
		30MS	30MS	10MR	25M	1		L	М	1	17 May
		20MR	20MR	10R	10MR			L	L		13 May
TA1691	Unknown	1R	20MR	5R	5MR	4 ⁵	20MR ³	L	М	4/7	15 May
		10MR	20MR	1R	5MR	1		L	M	1	15 May
		60S	_	50MS				Н	Н		12 May
TA1697	Unknown	20M	_	60MS		4 ⁵	25MS ³	Н	Н	s	12 May
		20M	_	40MS		1		Н	H	1	13 May
	1		1	101115	1					1	10 1.14

ID / accession	Country of	Leaf	-		Stripe	e rust		BY	DV	Hossian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June	fly	date
		50MS	_	20MS	_			Н	Н		11 May
TA1698	Russian	40MS	_	20MS	_	5 ⁴	10M ³	Н	Н	4/14	10 May
	Federation	60MS	_	20MS	_			Н	Н	1	11 May
		60S	_	30MS	_			Н	Н		12 May
TA1704	Tajikistan	30MS	_	30MS	_	5 ⁵	20MS ³	Н	Н	S	12 May
	5	WINTER KII	LLED		1	1			1		
		20MR	20M	10R	10MR			М	M		12 May
TA1707	Unknown	WINTER KII			1	4 ¹	30R ²		1	5/6	
	-	WINTER KII								1	
		40MS	_	40MS	_			Н	Н		10 May
TA1708	Unknown	30MS	_	40MS		4 6	40MS ³	Н	Н	s	10 May
		40MS		25MS			101115	Н	Н		10 May
		5R	10M	1R	5MR			M	M		22 May
TA1713	Turkey	30M	30M	15MR	20M	4 6	20MS ³	M	M	R	31 May
1111/15	Turkey	25M	40MS	15MR	20M		201010	M	M		31 May
		5MR	20MR	30M	40MS			H	H		14 May
TA2370	Unknown	5R	30MR	5R	15MR	86	60MS ³	H	H	S	13 May
1A2370	UIKIIOWII	10MR	20MR	40M	50M	0	001013	H	H		13 May 12 May
		50MS		40MS	1				Н		1
TA2377	Inon	40MS			_	6 ⁶	35MS ³	H	Н	S	11 May
IA2577	Iran			50MS		0-	33113	H		3	12 May
		40MS		40MS				Н	Н		13 May
TA 2204	D 1 · /	WINTER KII				6.6	403.403				
TA2384	Pakistan	WINTER KII			-	66	40MS ³			S	
		WINTER KII	1	50140	1			II	TT		10 M
Th 2207		5MR	—	50MS		4.6	20140.3	H	H	0/14	10 May
TA2387	Afghanistan	20MS		60MS		4 ⁶	20MS ³	H	H	3/14	10 May
		25MS	—	30MS				H	H		10 May
		30MS	—	50MS	—			H	H		10 May
TA2388	Afghanistan	20MS	—	40MS		7 4	50MS ³	Н	Н	S	11 May
		20MR	30MR	10MR	20MR			M	Н		10 May
		10MS		60MS				Н	Н	-	14 May
TA2395	Afghanistan	40MS		50S		7 5	60S ³	Н	Н	S	12 May
		40MS		50MS				Н	Н		12 May
		1R	15MR	1R	10MR			L	L		2-Jun
TA2369	Afghanistan	5R	20MR	10R	10MR	36	15MR ³	L	M	R	1-Jun
		1R	25MR	5R	15MR			L	М		1-Jun
		35MS		1R				Н	Н		13 May
TA2401	Afghanistan	40MS		5MR		3 ²	30M ²	Н	Н	S	15 May
		30MS		20MS				Н	Н		14 May
		40MS		5R				Н	Н		10 May
TA2407	Afghanistan	20MS	_	40MS	_	7 ³	20M 1	Н	Н] S	10 May
		25MS	_	10MS				Н	Н		13 May
		40MS	_	30MS	_			Н	Н		10 May
TA2412	Afghanistan	40MS	_	10M	_	4 ⁵	15MR ³	Н	Н	S	9 May
		40MS	_	10M	_	1		Н	Н	1	10 May
									1		

ID / accession	Country of	Leaf	rust		Stripe	e rust		BY	DV	Hessian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June		date
		50MS		30MS				Н	H		10 May
TA2413	Afghanistan	705		25MS	_	5 5	30MR ³	Н	Н	s	10 May
1112113	1 inginamotan	WINTER KII		201110			Sound		- 11		10 1014
		10M	_	50MS	_			Н	Н		9 May
TA2420	Afghanistan	40MS		40MS	_	56	60MS ³	Н	Н	s	9 May
	1 inginum sound	WINTER KII	LED	101110	I		001110				, indi
		30M	_	25MS	_			Н	Н		10 May
TA2424	Afghanistan	30MS	_	25MS	_	56	40MS ²	Н	Н	s	9 May
		WINTER KII	LLED	1	1				1		
		20M	_	10MS	_			Н	Н		9 May
TA2433	Afghanistan	15MR	_	5R		46	70MS ³	Н	Н	s	11 May
		5MR	_	20M	_			Н	Н	1	11 May
		WINTER KII	LLED	1	1				1		
TA2434	Afghanistan	25MS	_	40MS	_	86	20M ²	Н	Н	s	9 May
		50MS	_	40MS	_			Н	Н	1	9 May
		10MS	_	40MS				Н	Н		9 May
TA2437	Afghanistan	30MS	_	50MS	_	76	60S ³	Н	Н	s	9 May
		25MS	_	60S	_			Н	Н	1	9 May
		WINTER KII	LLED						1		
TA2442	Afghanistan	30M	_	20MS	_	35	15M ²	Н	Н	s	10 May
	0	WINTER KII	LED		1				1		
		20MS	30MS	15MR	15MR			Н	Н		13 May
TA2448	Iran	30M	30M	10MR	15M	4 ³	0	Н	Н	s	13 May
		10M	30M	5R	20M			М	Н	-	14 May
		WINTER KII		1	1				1		
TA2450	Iran	10R	20MR	5MR	5MR	46	1R ³	L	M	s	16 May
		1R	20MR	5R	5R			L	L	1	18 May
		15R	15MR	20M	20M			L	L		14 May
TA2455	Iran	5R	25MR	1R	20MR	4 6	1R ³	М	Н	8/6	15 May
		5R	20MR	1R	10MR			L	М	1	23 May
		10R	10R	5R	5R			Н	Н		14 May
TA2457	Iran	5R	30MR	5R	15MR	56	1R ³	М	Н	R	15 May
		1R	10MR	5R	15MR			М	М		22 May
		10MR	_	5R	_			М	Н		14 May
TA2458	Iran	WINTER KII	LLED			4 ⁵	20MS ³			s	
		1R	20MR	1R	15MR			L	Н	-	21 May
		15MR	15MR	5R	5R			М	М		15 May
TA2459	Iran	25MR	30M	15MR	15MR	46	20MR ³	М	Н	s	22 May
		5MR	25MR	5MR	10MR			М	Н	1	16 May
		5MR	25M	5R	15MR			L	М		15 May
TA2460	Iran	10MR	15M	1R	5MR	2 ²	_	L	М	2/10	17 May
		10MR	20M	1R	5MR	1		L		1	17 May
		25MS	30MS	5R	15MR			М	М		28 May
TA2461	Iran	30MS	40MS	15M	25M	46	20MR ³	М	М	s	28 May
		20MS	50MS	15M	15MS	1		М	М	1	22 May
	1									1	

ID / accession	Country of	Leaf	rust		Strip	e rust		BY	DV	Hassian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June	fly	date
		30MR	30M	10MR	20MR			M	H		15 May
TA2464	Iran	10MR	30MR	5MR	20M	5 5	15MR ³	М	Н	S	17 May
		_	_	_				_	_	-	15 May
		WINTER KII	LLED		1				1		
TA2468	Iran	1MR	15MR	5MR	10MR	55	5R ³	L	L	R	2-Jun
		_	_	_	_			_	_		16 May
		WINTER KII	LED	1					,		
TA2469	Iran	20MR	30MR	5R	20MR	46	15R ³	М	Н	R	15 May
		5R	30MR	1R	20MR			L	М	1	12 May
		20M	30MS	5R	15M			М	М		14 May
TA2471	Iran	15MR	15M	5R	20M	56	10R ³	L	М	S	15 May
		5M	40M	5R	15MS			L	М	1	16 May
		WINTER KII	LED						,		
TA2472	Iran	WINTER KII				4 6	10R ³			R	
		1R	20MR	1R	5MR			L	L	1	18 May
		30MR	30MR	5MR	10MR			М	М		15 May
TA2474	Iran	20MR	20MR	10MR	15MR	36	40R ³	М	Н	R	14 May
		5M	30M	1R	15MR			М	Н	1	14 May
		20M	25M	10MR	15MR			М	Н		13 May
TA2479	Iran	20M	30MS	10M	15MS	26	5R ³	М	Н	S	15 May
		10MS	25MS	1R	15MR			М	Н		16 May
		15MR	30MR	10R	25MR			Н	Н		15 May
TA2482	Iran	5R	20MR	30M	30MS	46	60MS ³	Н	Н	S	16 May
		5MR	_	25MS	_			Н	Н	-	16 May
		15MS	30MS	10R	25MS			М	М		30 May
TA2484	Iran	30MS	30MS	20MS	25MS	4 ⁵	0	М	М	S	1-Jun
		30M	30M	1R	20M			L	М	1	17 May
		40MS	_	20M				Н	Н		12 May
TA2488	Iran	205		20MS	_	4 ⁵	30S ³	Н	Н	S	14 May
		70S	_	20MS				Н	Н		18 May
		50S	_	15MS	_			M	Н		15 May
TA2491	Iran	40MS		20MS	_	46	20M ³	Н	Н	S	15 May
		60MS	_	20MS	_			М	Н	-	16 May
		30MR	30MR	20MR	20MR			М	М		15 May
TA2496	Iran	10MR	20M	5MR	15MR	3 ³	1R ³	М	Н	S	15 May
		5MR	30MR	5MR	20MR	-		L	М		16 May
		40MS	_	40MS	_			Н	Н		27 May
TA2502	Turkey	60MS	_	30MS	_	3 ³	50MS ³	Н	Н	S	17 May
		40MS	_	30MS	_			Н	H		17 May
		50MS	_	40MS	_			M	Н		29 May
TA2510	Turkey	70MS	_	30MS	_	66	40MS ³	Н	Н	S	24 May
		30M	30M	20M	30M	1		Н	H		18 May
		60S	_	30MS	_			Н	Н		26 May
TA2512	Iran	50MS	50MS	5R	30MS	46	30MS	M	H	s	17 May
		50MS	_	40MS	_			H	Н		25 May
	1	1 201110			l	L				1	IIII

ID / accession	Country of	Leaf	rust		Stripe	e rust		BY	DV	Hossian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June	fly	date
		10MR	30M	5MR	25M			Н	Н		15 May
TA2516	Iran	60MS	_	10MR	_	56	20MS ³	Н	Н	s	16 May
		40MS	_	10MR	_		201010	Н	H		17 May
		70S		25M				Н	Н		15 May
TA2521	Iran	50MS		40MS	_	56	50MS ³	Н	Н	s	14 May
		30MS		40MS				Н	Н	-	16 May
		20M	20M	10MR	15M			М	Н		15 May
TA2525	Iran	20M	30M	15M	25M	46	10R ³	М	Н	s	15 May
		10MS	30MS	1MR	25M			М	М		16 May
		WINTER KII							1		
TA2530	Iran	5MR	20MR	1R	15MR	4 ³	5R ³	L	М	s	14 May
		10MR	30MR	5MR	20MR			М	Н		12 May
		40MS	_	40MS	_			М	Н		13 May
TA2536	Afghanistan	40MS	_	20M	_	4 ³	50S ³	Н	Н	s	13 May
		25MS	_	30MS	_			Н	Н	1	11 May
		40MS	_	20MS	_			Н	Н		14 May
TA2538	Afghanistan	20M	25MS	20MS	30MS	4 ⁵	30MS ³	М	Н	1_	12 May
		40MS	_	40MS	_			М	Н	1	12 May
		20MR	20M	15MR	20M			М	Н		16 May
TA2539	Afghanistan	40MS	40MS	20MS	20MS	46	30MS ³	Н	Н	1_	16 May
		20MS	_	40MS	_			М	Н	1	15 May
		60MS	_	40MS	_			Н	Н		14 May
TA2540	Afghanistan	60MS	_	30MS	_	3 5	40MS ³	Н	Н	s	15 May
		60MS	_	30MS	_			М	Н	1	14 May
		30MS	30MS	20MR	20MR			М	Н		16 May
TA2544	Afghanistan	10M	30M	15MS	25MS	4 ⁵	50MS ³	М	Н	s	15 May
		10MR	30MS	20M	25MS			М	Н	-	16 May
		30M	_	40MS	_			Н	Н		12 May
TA2556	Afghanistan	60MS	_	30MS	_	4 ⁵	70MS ³	М	Н	s	14 May
		70S	_	20MS	_			Н	Н]	15 May
		5R	20MR	15MR	15MR			М	L		29 May
TA2561	Azerbaijan	10R	30MR	5R	25MR	4 ⁵	30M ³	М	М	R	31 May
		WINTER KII	LED							1	
		30MS	60S	15MR	20MS			М	L		30 May
TA2564	Azerbaijan	15MS	40MS	5R	15M	46	10MR ³	М	М	S	30 May
		20MS	25MS	15MS	20MS			L	L		22 May
		20MR	20M	5MR	15M			М	L		30 May
TA2565	Azerbaijan	5R	25MR	5MR	10MR	4 ⁵	0	L	L	R	1-Jun
		WINTER KII	LED								
		10MR	_	60MS				Н	Н		15 May
TA2569	Armenia	5R	30MR	20M	30M	56	50MS ³	Н	Н	S	15 May
		1R	25MR	5R	20M			Н	Н		18 May
		60MS	_	25MS	_			Н	Н		16 May
TA2575	Armenia	40MS	_	30MS		4 4	30MS ³	Н	Н	S	16 May
		70MS	_	20MS				Н	Н		17 May
		*	•		•			•			. ,

ID / accession	Country of	Leaf	rust		Stripe	e rust		BY	DV	Hessian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June		date
		60MS	_	10M	_			Н	Н		15 May
TA2581	Georgia	20M	30M	10M	15M	4 6	30S ³	Н	Н	s	14 May
	8	50MS	30MS	20MS	20MS	1		Н	Н	1	18 May
		60MS	_	40M	_			Н	Н		14 May
TA10069	Afghanistan	40MS		30MS		3 6	40S ³	Н	Н	S	15 May
		50MS	_	40MS			.05	Н	H		17 May
		60MS		30MS				Н	Н		24 May
TA10080	Armenia	10MS	_	50MS		3 4	30MS ³	Н	Н	s	15 May
		60MS	_	20MS	_	1		Н	Н	1	17 May
		20MR	30M	20MR	20MR			M	Н		13 May
TA10087	Azerbaijan	20M	30M	10M	20M	4 6	30M ³	M	Н	R	15 May
	1 ILoroaljan	10MS	_	5M		1 .	00101	L	Н		17 May
		20MR	20MR	5R	10MR			M	Н		13 May
TA10088	Azerbaijan	5R	30MR	1R	10MR	4 ³	20M ³	M	Н	S	13 May
	line	5MR	30M	5MR	15MR		20101	M	Н		14 May
		20M	40MS	5R	5MR			M	M		30 May
TA10089	Azerbaijan	1R	20M	5R	5R	3 5	5R ³	L	L	S	2-Jun
	1 III of Carjan	5MR	40MS	1R	15M		510	M	M		29 May
		5R	15MR	15MR	20MR			M	M		31 May
TA10090	Azerbaijan	10MR	25MR	1MR	15MR	3 5	25MR ³	L	L	s	31 May
11110070	1 izer burgun	10R	5R	1R	5R	1	2510110	L	L		2-Jun
		30MS	35MS	15MS	20MS			M	M		29 May
TA10104	Georgia	10MR	30M	5MR	25M	2 6	70S ³	M	M	s	30 May
millionon	Georgia	30MS	30M	5M	20MS	1 -	100	M	M		1-Jun
		10R	20MR	5R	15MR			M	M		30 May
TA10105	Georgia	10MR	25MR	5MR	10MR	2 ²	50S ²	M	M	s	22 May
11110105	Georgia						505				18 May
		30MS		40MS				Н	Н		9 May
TA10108	Tajikistan	WINTER KII	LED	101010		7 5	50S ³			s	> Widy
11110100	Tujikistan	WINTER KI				- '	500				
		70S		20MS	_			M	Н		14 May
TA10113	Turkmenistan	705		20MS		74	50S ³	H	H	S	10 May
IAIUIIJ	Turkinemstan	50MS		20M3		- '	505	H	H		14 May
		40MS		40MS				Н	H		14 May 15 May
TA10115	Turkmenistan	20MS		40MS		64	20MS ³	H	H	S	13 May
11110115	Turkinemstan	15MS		40MS			201010	H	H		15 May
		20M		30M	30M			H	H		13 May
TA10116	Turkmenistan	10M	30M	20M	25M	3 ²	30M ³	H	H	S	14 May
11110110	I ul Kinchistall	5R	35MR	10R	20MR	1	50141	H	H		14 May
		20M	20M	5MR	15MR			M	M		28 May
TA10124	Uzbekistan	15R	30MR	10R	15MR	3 5	20R ³	M	M	S	13 May
1/11/124	ULUCKIStall	5R	25MR	10K	15MK		201	M	M		22 May
		5R 5R	30MS	15MR	15MR			M	M		31 May
TA10130	Armenia	5R	20M	13MK	5MR	4 6	40MR ³	L	L	R	1-Jun
1710130		25MS	25MS	1R 1R	15MR			L	L		2-Jun
		231413	20110	11	IJIVIN	<u> </u>					∠-Juli

ID / accession	Country of	Leaf	rust		Stripe	e rust		BY	DV	Hossian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June		date
		20MS	40MS	30MS	30MS			M	Н		29 May
TA10132	Armenia	20MS	30MS	10MS	25MS	66	40MS ³	M	Н	s	16 May
		30MS	25MS	10MS	15MR		101110	L	M		22 May
		20M	30M	5MR	20MR			M	L		16 May
TA10136	PR China	15MR	25MR	5R	10R	5 ¹	25MS ²	M	M	s	24 May
	-	5MR	30MR	1R	20MR			М	М	-	16 May
		5M	_	60S	_			Н	Н		10 May
TA10140	PR China	5M	_	15MS	_	66	40M ²	Н	Н	s	10 May
		5MR		70S	_			Н	Н	1	12 May
	G : 4 1	1R	25MR	30MS	35MS			L	Н		11 May
TA10142	Syrian Arab	1R	_	40MS	_	56	30M ³	М	Н	R	9 May
	Republic	1R	25M	40MS	40MS			L	Н		11 May
		25MS	_	30MS	_			Н	Н		11 May
TA10145	Syrian Arab	40MS	_	20MS	_	56	60MS ³	Н	Н	s	10 May
	Republic	30MS	_	10MS	_	1		Н	Н	-	9 May
		5MR	_	15MR	_			Н	Н		9 May
TA10156	Tajikistan	30MS	_	20MS	_	2 6	30MR ³	Н	Н	s	10 May
		15MS	_	10R	_			Н	Н	1	9 May
		25MS	_	30MS	_			Н	Н		11 May
TA10158	Tajikistan	30MS	_	30MS	_	3 ³	10MR ³	Н	Н	S	10 May
		30MS	_	40MS	_			Н	Н	1	12 May
		20MR	30MR	15M	15M			Н	Н		12 May
TA10160	Turkmenistan	10M	20M	20M	30M	5 ⁵	40MS ³	Н	Н	S	11 May
		10M	_	25MS	_			Н	Н		11 May
		20MR	25MR	15MR	15MR			Н	Н		11 May
TA10168	Turkmenistan	20M		15MS		6 ³	20M ³	Н	Н	S	10 May
		1R	30M	1R	20MR			М	Н		13 May
		WINTER KII	LLED								
TA10172	Turkmenistan	WINTER KII	LED			2 5	50MS ²			S	
		10MR		30MS				Н	Н		12 May
		5MR		60S				М	Н		9 May
TA10174	Turkmenistan	WINTER KII	LED			6 ⁵	50MS ²			S	
		10MR		50MS				Н	Н		10 May
		WINTER KII	LED								
TA10176	Turkmenistan	20M	30MS	20M	30M	6 ⁶	60MS ³	Н	Н	S	13 May
		10MS		30MS				Н	Н		13 May
		10MR	30MR	5M	20MR			M	Н		11 May
TA10177	Turkmenistan	10MR	30MR	5MR	15M	6 ⁴	40M ³	M	Н	S	11 May
		25M	20M	20M	20M			Н	Н		12 May
		WINTER KII	LLED							_	
TA10185	Turkmenistan	WINTER KII	LLED	1	1	7 ⁶	40MS ³			S	
		5M		1R				М			13 May
		20MR	35MR	15R	15MR			Н	Н	1	16 May
TA10187	Turkmenistan	WINTER KII		1	1	2 4	10R ³			S	
		5MR	25MR	5MR	15MR			М	Н		18 May

ID / accession	Country of	Leaf			Stripe			BY		Hossian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	1		date
number		5MR	- June	50MS		8		H	H		13 May
TA10192	Uzbekistan	10MR		30MS		6 ⁵	40S ³	H	H	s	13 May
11110172	OZOCKIStali	30M		40MS			105	H	H		13 May 12 May
		30M	40MS	25M	30M			M	H		30 May
TA10197	Uzbekistan	30MS	40MS	20MS	20MS	3 ³	25MS ³	H	H	S	17 May
million	OZOCKIStali	60MS	40MS	25MS	25M		251410	M	H		28 May
		40MR	40MS	30MR	30M			M	H		16 May
TA10210	Uzbekistan	WINTER KI		501011	50101	2 4	10MR ³	111	11	s	10 Widy
11110210	OZOCKIStali	30MR	_	10MR	_		101011	Н	Н		17 May
		20M		40MS				H	H		11 May
TA10211	Uzbekistan	25MS		40MS		3 5	50MS ³	H	H	s	9 May
11110211	OZOCKIstali	20MS		30MS			501015	H	H		12 May
		20M3	20M	5MR	15MR			M	M		29 May
TA10292	Tajikistan	20M	35M	1MR	10MR	56	20MS ³	H	H	s	27 May
11110252	Tajikistan	10MR	30M	5MR	15MR		201010	H	H		30 May
		WINTER KI	1	510110	151011				- 11		50 May
TA10296	Tajikistan	50MS		20MS	_	26	15M ²	Н	Н	s	10 May
11110290	Tajikistan	20MS		25MS			1511	H	H		10 May 11 May
		WINTER KII	LED	251415				11	11		11 Widy
TA10303	Tajikistan	30MS		40MS	_	2 ³	50MS ³	M	Н	S	14 May
IA10505	Tajikistan	20MS		25MS			501015	H	H		14 May 12 May
		40MS	505	30M	30M			H	H		22 May
TA10308	Tajikistan	20MS	305	30M	30M	4 6	30MS ³	H	H	S	16 May
IA10500	Tajikistan	30M	30M	40MS	20MR		501015	H	H		22 May
		30MS	40MS	20M	20M			H	- 11		16 May
TA10309	Tajikistan	30MS	30MS	25MS	25MS	16	40MS ³	M	Н	S	16 May
1110505	Tajikistan	WINTER KI		251415	231410		401010	111	11		10 Widy
		WINTER KI		_	_				_		12 May
TA10316	Tajikistan	30MS		50MS		36	40M ³	Н	Н	S	10 May
1410510	Tajikistan	40MS		30MS			-10141	H	H		10 May 12 May
		40MS		20M				H	H		12 May
TA10323	Tajikistan	40MS		10MS		36	15M ³	M	H	S	10 May
1410525	Tajikistan	40MS		20MS			1.5111	H	H		13 May
		60MS		40MS				H	H		13 May
TA10327	Tajikistan	30MS		20M		7 4	40MS ³	M	H	S	13 May
IA10527	Tajikistan	30M	30MS	10MR	20M	- '	401015	H	H		15 May
		50MS		20MS				Н	Н		10 May
TA10330	Tajikistan	60S		20MS		1 2	30MS ²	H	H	S	9 May
IA10550	Tajikistan	30MS		30MS	—		301015	Н	Н	3	13 May
		50MS		10MR	 15MR			L	М		13 May 14 May
TA10417	Unknown	10MR	25M	5R	15MR	4 ⁶	10MR ³	L	M	15/2	-
1/1041/		10MR	30M	5MR	20MR	4 ⁻	TOMIK	M	H	1.3/2	13 May
				20M							18 May
TA 10019	Gaaraia	5R	20MR	20M 20M	20MS	4 ⁶	50MS ³	M u	H	- c	15 May
TA10918	Georgia	10M	35M		20M	4 [°]	201012	H	H	S	17 May
		10MR	30MR	5R	15MR			M	Н		16 May

ID / accession	Country of	Leaf	rust		Stripe	e rust		BY	DV	Hessian	Heading
number	origin	27 May	8 June	27 May	8 June	Seedling	Adult	27 May	8 June		date
		10R	15MR	20M	20M			M	M		30 May
TA10921	Georgia	1R	20MR	20M	20M	4 ⁵	60MS ³	M	M	R	28 May
	l	5MR	20MR	1R	20MR	1 .	001110	M	M		30 May
		10MR	10MR	15MR	15MR			Н	H		16 May
TA10922	Georgia	5R	20MR	1R	5MR	6 ⁵	30MS ³	M	M	s	17 May
	l	10MR	30MR	5MR	25MR		201110	H	H		17 May
		1R	5R	5R	5R			L	L		15 May
TA10923	Georgia	5R	20MR	1R	5R	4 ⁵	5R ³	L	L	4/8	22 May
	8	1R	15MR	1R	5R			L	L	1	2-Jun
		10R	10R	5R	10R			L	L		1-Jun
TA10926	Georgia	5MR	15MR	20M	30M	4 6	20M ³	L	L	R	29 May
11110920	Georgia	20M	20MS	25M	25M	1 '	20111	M	M		1-Jun
		10M	30M	10MR	15MR			M	M		31 May
TA10929	Georgia	10MR	25MS	1R	20MS	4 ⁵	20MS ³	M	M	10/3	30 May
11110727	Georgia	40MS	40MS	20MS	20MS		201010	M	M	10/5	31 May
		30M		5MR				M	_		16 May
TA10930	Georgia	10M	20M	1R	15MR	56	30M ³	L	L	R	30 May
1110950	Georgia	40MS	40MS	20MS	20MS		50111	L	L		17 May
		WINTER KI		201010	2010						17 Iviay
TA10940	Azerbaijan	20MS	20MS	5R	10MR	36	20MR ²	L	M	R	1-Jun
11110710	1 izer burjun	10MR	30MS	1R	5MR		2010110	L	L		2-Jun
		10MR	35MR	15MR	15MR			M	M		15 May
TA10943	Azerbaijan	20M	30M	5MR	15MR	36	35M ²	L	M	s	16 May
1110715	1 izerourjun	10R	35MR	5R	15MR		55111	M	H		18 May
		WINTER KI		bit	TOTAL						10 1014
TA10944	Azerbaijan	40M	50M	20MS	20MS	35	15MR ³	M	M	s	1-Jun
	1 izer burjun	5MR	30MR	1R	20MB		1510110	L	M		1-Jun
		WINTER KI	•		201011				101		1 Juli
TA10949	Azerbaijan	5R	10MR	1R	5MR	56	25M ²	L	M	s	18 May
11110747	/ izerbarjan	5R 5R	30MR	5R	15MR		25141	L	M		29 May
		WINTER KI		511	151011			L	141		25 Widy
TA10952	Azerbaijan	10MS	15MS	5MR	20MS	15	20MR ³	L	М	5/7	22 May
1110952	/ izerbarjan	WINTER KI		Juix	201010		201011		111	5/1	22 Iviay
		10M		60S	_			Н	Н		16 May
TA10954	Azerbaijan	10MR	25MR	30M	30M	7 5	40MS ³	Н	H	8/3	16 May
1110754	/ izerbarjan	15M		30MS		- '	401010	H	H	0,5	17 May
		50MS		40MS				H	H		16 May
TA10957	Azerbaijan	30MS	30MS	20MS	20MS	6 ³	70S ³	H	H	2/10	10 May
1110757		40MS	-	30MS	-		/05	H	H		17 May
		40MS		40MS				H	H		17 May
TA10960	Azerbaijan	60MS		30MS		6 ⁶	30MS ³	H	H	9/2	15 May
1/10/00	Azerbaijan	40MS		25MS			201012	Н	Н	- 7/2	13 May 14 May
		401013	_	231013	_	I]		п	п		14 May

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KANSAS WHEAT 1990 Kimball Avenue, Manhattan, KS 66502, USA.

Despite drought and disease, Kansas' 2015 yields higher than average.

Marsha Boswell and Julie Debes.

In 2014, total Kansas wheat production was 246.4 x 10⁶ bushels, down 26% from the 2013 crop and the lowest in 25 years (1989). Yield was 28 bu/acre, 10 bushels below 2013 and the lowest since 1995.

After the record low 2014 wheat harvest, the 2015 crop was not shaping up much better. Autumn planting started with persistent dry conditions across the state. A delayed, fall crop harvest set planting back even further. Then, over Veterans Day weekend in November, Kansas' state climatologist Mary Knapp explained that temperatures sank into the teens, causing some of the wheat crop to enter dormancy without sufficient root development. Jim Shroyer, K-State Research and Extension crop production specialist (retired), explained in November that the cold weather affected both wheat with excessive topgrowth and wheat that showed drought-stressed symptoms.

Winter brought a roller coaster of warm and cold spells, according to Knapp, and dry soil continued to limit development in many areas. The USDA National Agricultural Statistics Service (NASS) reported on 5 January that the winter wheat condition was rated 2% very poor, 7% poor, 42% fair, 45% good, and 4% excellent.

In late April, freezing temperatures hit the state, particular in south-central Kansas. Knapp explained that although these freezes were not particularly cold, the wheat crop was flowering and particularly vulnerable. By 27 April, the condition of winter wheat condition rated 11% very poor, 20% poor, 43% fair, 24% good, and 2% excellent. Winter wheat jointed was at 78%, ahead of 54% in 2014, and the five-year average of 68%. Headed wheat was at 18%, ahead of 4% in 2014, but near the 16% average.

Then the rain started to fall. The annual Hard Winter Wheat Tour was joined by rain as it moved across the state 47 May, 2015, taking measurements and making predictions. The official tour projection for total production numbers of hard red winter wheat to be harvested in Kansas was 288.5×10^6 bushels.

In May, just as the grain was filling, farmers across the state saw heavy rains. Knapp attributed the rains, in part, to moisture from the Gulf of Mexico mixing with cold fronts moving across the state that "opened a fire hose pointed north." According to the Kansas Weather Data Library, Kansas received 188% more moisture than normal in May, averaging 7.73 inches statewide.

By the end of May, the U.S. Drought Monitor listed just 6% of Kansas in moderate drought and 67% of the state as drought-free. However, wet soil, Knapp explained, helped create the right climatic conditions for thunderstorms to build and stay over a small geographic area. She added that these types of weather patterns also are conducive to creating hail, which severely damaged wheat in western Kansas, particularly in Kearney, Finney, and Haskell counties.

Rain also brought disease, stripe rust, leaf rust, and Fusarium head blight. On the annual Hard Red Winter Wheat Tour, Aaron Harries, Kansas Wheat vice president for operations and research, reported seeing stripe rust "in nearly every field we visited." In addition to stripe rust, head blight, and wheat streak mosaic, wheat head smut was found in the state for the first time in decades, initially detected in a field demonstration plot in Rooks County and confirmed by laboratory result during regular and on-going disease survey work. Additional survey teams scouted for the disease, locating it in several other locations. Wheat flag smut has potential yield and trade implications, but presents no human or animal health concerns, and has no impact on grain quality.

Despite the weather and its related effects, the wheat continued to fill and the combines started to roll; later and slower than normal but with better end results than in previous years for many farmers. Kansas farmer Chris Tanner's wheat near Norton did not have a good year, damaged by spring freeze, resurrected with May rainfall, and stricken with stripe rust. "The wheat was about two days from dying of drought when we hit the wet spell," Tanner said. "Then the rust came in bad when the flag leaf was fully emerged."

ANNUAL WHEAT NEWSLETTER

Luckily, Tanner made the decision to apply fungicide to his crop. His wheat yielded between 30 and 50 bu/acre with test weights of 59 to 62 pounds/bu, in contrast to producers who did not spray and ended the harvest season with yields ranging from 15 to 20 bu/acre with test weights of 46 to 55 pounds/bu.

In its June report, the USDA–NASS upped their forecast to 314.5×10^6 bushels in production; a 28% increase from the last year's drought-plagued crop. By 12 August, the USDA–NASS increased that projection, forecasting Kansas wheat production at 334 x 10⁶ bushels, up 36% from last year's crop. Yield is forecast at 38 bu/acre, 10 bushels above 2014.

As planting season approaches, Kansas wheat farmers are being encouraged to select wheat cultivars with high resistance to fungal diseases as well as to apply fungicides to seed before drilling wheat this season. According to Jeff Vogel, the Plant Protection and Weed Control program manager for the Kansas Department of Agriculture, "Research has shown that the use of certified seed combined with fungicide seed treatments, is highly effective in preventing the spread of disease." He noted that producers and seedsmen should follow proper protocols to ensure that a thorough and even application of fungicide is made to the seed to ensure a high level of product effectiveness.

After years of drought conditions, farmers can reasonably expect more of that moisture to continue, thanks to the official El Niño pattern declared in April, according to Knapp, who also said if the El Niño pattern persists, most of Kansas will continue to receive more moisture throughout the rest of summer and into the winter, which would be good news for the 2016 Kansas wheat crop.

MINNESOTA

CEREAL DISEASE LABORATORY, USDA–ARS University of Minnesota, 1551 Lindig St., St. Paul, MN 55108, USA. <u>www.ars.usda.gov/mwa/cdl</u>

J. A. Kolmer, Y. Jin, M.E. Hughes, S.W. Gale, and L.A. Wanschura.

Wheat rusts in the United States in 2014.

Small grain development and spring fieldwork in the Great Plains and to the east was generally delayed due to the unusually cool late winter and early spring weather. Ongoing drought conditions in many areas of the central and southern Plains were a significant constraint to small grain production and greatly limited development of rust diseases. Drought and freeze damage in early spring in the southern U.S. may have delayed rust development and spread in the spring. Significant rainfall occurred in many areas to the east in mid-June to early July. The widespread rain hampered winter wheat harvest in the South and limited fieldwork in other areas. In the Pacific Northwest, small grain development was somewhat ahead of the 10-year averages. Hot, dry weather dominated California and the Pacific Northwest areas.

Wheat stem rust (caused by *Puccinia graminis* **f. sp.** *tritici)***.** Wheat stem rust was not widespread or severe in the U.S. in 2014. It only was reported in nursery locations this season in Texas, Louisiana, Arkansas, Nebraska, Kansas, South Dakota, Minnesota, and Wisconsin. Wheat stem rust was first reported on 7 April at Weslaco in extreme southern Texas. Race QFCSC was the most commonly identified wheat stem rust race in 2014 and in recent years.

Rio Grande Valley, Texas. Wheat stem rust was found in sentinel plots of Morocco, Panola, Siouxland, and Line E at Weslaco in extreme southern Texas on 7 April 7. Severities ranged from <1% on Siouxland (stem rust pustules were found only on leaves) to 5% on Morocco with incidences from 10% on Siouxland to 90% on Morocco. Line E and Morocco were fully headed, whereas Panola and Siouxland did not completely vernalize. In previous years, barley, emmer, and triticale were used more commonly in windbreaks for watermelon, currently more sorghum or sorghum–Sudangrass is used. This was the first report of wheat stem rust in the U.S. in 2014.

Arkansas. Stem rust was found in late-maturing plots at Kibler and Fayetteville in northwestern Arkansas in early June, but was not reported elsewhere in the state in 2014. Generally, rust (leaf, stripe, and stem) was found at lower levels than any of the last 26 years.

Nebraska. Stem rust was found on two lines (at hard dough stage) in a wheat nursery at Lincoln in southeastern Nebraska on 13 June. Wheat stem rust was not reported in commercial fields in the state in 2014.

Kansas. Wheat stem rust at 100% incidence and approaching 30% severity was found in plots near Manhattan in northeastern Kansas in late June. Based on the samples, stem rust appears to have been in the plots for some time. Wheat stem rust was not reported in commercial fields in the state in 2014 and did not impact yields.

Wisconsin. On 26 June, stem rust was found on five plants in a single plot at Arlington in south-central Wisconsin. Stem rust was not found in any other plots at the location. Stem rust was not found at any other site in the state in 2014.

South Dakota. Trace levels of wheat stem rust were found in plots of the cultivar Rubidoux in Brookings County in eastern South Dakota in the second week of July.

Minnesota. On 10 July, trace to moderate levels of wheat stem rust were found in plots of the susceptible spring wheat cultivar Baart at Lamberton in southwestern Minnesota.

North Dakota. Wheat stem rust was found at trace levels on the susceptible spring cultivar Baart in plots at Langdon in the northeastern part of the state in early August.

Wheat stem rust map. Please visit: http://www.ars.usda.gov/Main/docs.htm?docid=9757.

Wheat Leaf Rust (caused by *Puccinia triticina)*. Leaf rust was at very low levels in the central Great Plains in 2014 due to drought and very dry conditions. As a result, wheat leaf rust inoculum for areas north and east was very limited. The cool spring delayed leaf rust development in many areas. In the Southeast and mid-Atlantic areas, wheat leaf rust was more widespread but generally at low levels, with the exception of higher severities noted on the cultivar Shirley at some locations. By late June, leaf rust had appeared at low levels in South Dakota, Minnesota, Wisconsin, and Michigan. The number and frequency of virulence phenotypes and number and frequency of isolates virulent to the 20 wheat lines with single resistance genes for leaf rust resistance, respectively, is reported (Tables 1 (pages 86-87) and Table 2 (p. 87)). An estimated national winter wheat loss of 0.1%, a trace spring wheat loss, and a 0% durum wheat loss were due leaf rust in 2014 (see Tables 3 (page 88) and 4 (page 89)).

Texas. Wheat leaf rust was slowly developing in plots at Castroville in early March and, by late March, it was uniformly distributed in the lower canopy and mid-canopy of winter wheat spreader rows in nurseries at Castroville and Wharton, respectively. Warm temperatures and rains created conditions favorable for rust spread. In the second week of April, wheat leaf rust was moving into the flag leaves of susceptible wheat in irrigated plots at Castroville. At Beeville, where there were both winter and spring wheat plots, leaf rust increased on TAM 112 (*Lr39/Lr41*) and in the spreader rows. Leaf rust developed on TAM 112 and in the spreader rows at College Station.

In a survey of north-central Texas in late March and early April, no rust was found in commercial fields, and rust had not been seen by consultants and extension agents in the areas. Typically, wheat leaf rust is found by this time in north-central Texas. Low levels of leaf rust were reported 30 miles south of Dallas. Some cultivars with leaf rust were Greer (Lr39/Lr41, Lr34, and Lr37), WB Cedar (Lr14a and Lr37) and Coronado (Lr1, Lr10, and Lr14a). Most of the wheat was fully headed.

Ten of the 11 lines in plots at Weslaco in extreme southern Texas had wheat leaf rust the second week of April; Panola (*Lr11*) was the lone exception. Severities were 3-40% with incidences from 20-90%. TAM 112 (*Lr39/Lr41*) was rated at 15S, whereas Jagalene (*Lr24*) was 60S on the flag leaves.

A rust survey covering the southern half of Texas to Baton Rogue in southeastern Louisiana was conducted between 30 April and 5 May. Winter wheat fields along a west to east transect extending from Uvalde, TX, to Baton Rouge, LA, varied from milk to soft-dough stage. Of the 11 fields sampled, leaf rust was found in all but one. Most of leaf rust

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 Table 1. Number and frequency (%) of virulence phenotypes of Puccinia triticina in the United States in 2014 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.

Pheno-		LA,	GA, NC, ,VA	r	NΥ	IL, I	N, WI	Т	X	К	S		, ND, D	То	otal
type	Virulences	#	%	#	%	#	%	#	%	#	%	#	%	#	%
MBDSB	1,3,17,B,10,14a	0	0	0	0	0	0	1	1.2	0	0	0	0	1	0.3
MBDSD	1,3,17,B,10,14a,39	0	0	0	0	0	0	16	19.5	0	0	4	3.5	20	5.3
MBPNB	1,3,3ka,17,30,B,14a	0	0	0	0	1	3.1	0	0	0	0	0	0	1	0.3
MBPSB	1,3,3ka,17,30,B,10,14a	0	0	0	0	0	0	0	0	3	33.3	3	2.6	6	1.6
MBPSD	1,3,3ka,17,30,B,10,14a,39	0	0	0	0	0	0	2	2.4	0	0	0	0	2	0.5
MBPTB	1,3,3ka,17,30,B,10,14a,18	0	0	0	0	0	0	0	0	1	11.1	0	0	1	0.3
MBTNB	1,3,3ka,11,17,30,B,14a	36	28.1	4	28.6	17	53.1	0	0	1	11.1	16	13.9	74	19.5
MCDSB	1,3,26,17,B,10,14a	0	0	0	0	0	0	3	3.7	0	0	0	0	3	0.8
MCDSD	1,3,26,17,B,10,14a,39	0	0	0	0	0	0	8	9.8	0	0	0	0	8	2.1
MCPSB	1,3,26,3ka,17,30,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
MCPSD	1,3,26,3ka,17,30,B,10,14a,39	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
MCTNB	1,3,26,3ka,11,17,30,B,14a	11	8.6	4	28.6	6	18.8	0	0	0	0	2	1.7	23	6.1
MDDSB	1,3,24,17,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
MDTSB	1,3,24,3ka,11,17,30,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
MFDSB	1,3,24,26,17,B,10,14a	0	0	0	0	0	0	0	0	3	33.3	1	0.9	4	1.1
MFNQB	1,3,24,26,3ka,17,B,10	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
MFNSB	1,3,24,26,3ka,17,B,10,14a	0	0	0	0	0	0	2	2.4	0	0	1	0.9	3	0.8
MFPSB	1,3,24,26,3ka,17,30,B,10,14a	4	3.1	0	0	0	0	1	1.2	0	0	2	1.7	7	1.8
MFTSB	1,3,24,26,3ka,11,17,30,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
MLDSD	1,3,9,17,B,10,14a,39	0	0	0	0	0	0	5	6.1	0	0	5	4.3	10	2.6
MLPSD	1,3,9,3ka,17,30,B,10,14a,39	0	0	0	0	0	0	7	8.5	1	11.1	5	4.3	13	3.4
MMDSD	1,3,9,26,17,B,10,14a,39	0	0	0	0	0	0	1	1.2	0	0	1	0.9	2	0.5
MMPSD	1,3,9,26,3ka,17,30,B,10,14a,39	2	1.6	0	0	0	0	7	8.5	0	0	0	0	9	2.4
PBDGJ	1,2c,3,17,10,28,39	3	2.3	0	0	0	0	0	0	0	0	1	0.9	4	1.1
PBDQJ PBDSJ	1,2c,3,17,B,10,28,39	0	0	0	0	0	0	2	2.4	0	0	0	0	2	0.5
PLDDJ	1,2c,3,17,B,10,14a,28,39 1,2c,3,9,17,14a,28,39	0	0	0	0	0	0	1	1.2	0	0	0	0	1	0.3
PNDGJ	1,2c,3,9,24,17,10,28,39	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
TBBGJ	1,2a,2c,3,10,28,39	0	0	0	0	0	0	6	7.3	0	0	0	0.5	6	1.6
TBBGS	1,2a,2c,3,10,21,28,39	1	0.8	0	0	0	0	1	1.2	0	0	42	36.5	44	11.6
TBHTB	1,2a,2c,3,11,30,B,10,14a,18	0	0	1	7.1	0	0	0	0	0	0	0	0	1	0.3
TBJGS	1,2a,2c,3,11,17,10,21,28,39	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
TBJSB	1,2a,2c,3,11,17,B,10,14a	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TBRJG	1,2a,2c,3,3ka,11,30,10,14a,28	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	11	8.6	0	0	0	0	0	0	0	0	0	0	11	2.9
TBTNB	1,2a,2c,3,3ka,11,17,30,B,14a	3	2.3	0	0	0	0	0	0	0	0	0	0	3	0.8
TBTSB	1,2a,2c,3,3ka,11,17,30,B,10,14a	0	0	2	14.3	0	0	0	0	0	0	0	0	2	0.5
TCJSB	1,2a,2c,3,26,11,17,B,10,14a	3	2.3	0	0	0	0	0	0	0	0	0	0	3	0.8
TCLJG	1,2a,2c,3,26,3ka,10,14a,28	0	0	0	0	0	0	1	1.2	0	0	0	0	1	0.3
TCRKG	1,2a,2c,3,26,3ka,11,30,10,1 4a,18,28	43	33.6	0	0	0	0	0	0	0	0	0	0	43	11.3
TCSQB	1,2a,2c,3,26,3ka,11,17,B,10	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TCTNB	1,2a,2c,3,26,3ka,11,17,30,B,14a	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TCTQB	1,2a,2c,3,26,3ka,11,17,30,B,10	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TCTSB	1,2a,2c,3,26,3ka,11,17,30,B,10 ,14a	0	0	1	7.1	0	0	0	0	0	0	3	2.6	4	1.1
TDBGJ	1,2a,2c,3,24,10,28,39	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
TDBGQ	1,2a,2c,3,24,10,21,28	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TDBJQ	1,2a,2c,3,24,10,14a,21,28	0	0	0	0	0	0	0	0	0	0	1	0.9	1	0.3
TDCHG	1,2a,2c,3,24,30,10,18,28	1	0.8	0	0	0	0	0	0	0	0	0	0	1	0.3
TLBGJ	1,2a,2c,3,9,10,28,39	0	0	0	0	0	0	1	1.2	0	0	0	0	1	0.3

Table 1. Number and frequency (%) of virulence phenotypes of Puccinia triticina in the United States in 2014 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

2,11,2,17																
Pheno-		LA,	AR, GA, LA, NC, TN, VA		2,		IL, IN, WI		TX		KS		MN, ND, SD		Total	
type	Virulences	#	%	#	%	#	%	#	%	#	%	#	%	#	%	
TNBGJ	1,2a,2c,3,9,24,10,28,39	0	0	0	0	4	12.5	12	14.6	0	0	3	2.6	19	5	
TNBJJ	1,2a,2c,3,9,24,10,14a,28,39	0	0	0	0	0	0	3	3.7	0	0	8	7	11	2.9	
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,1 4a,28,39	4	3.1	0	0	0	0	0	0	0	0	0	0	4	1.1	
TPBGJ	1,2a,2c,3,9,24,26,10,28,39	0	0	0	0	0	0	1	1.2	0	0	0	0	1	0.3	
TPBJJ	1,2a,2c,3,9,24,26,10,14a,28,39	0	0	0	0	2	6.3	0	0	0	0	1	0.9	3	0.8	
Total		128	1	4		32		82		9		115		380		

Table 2. Number and frequency (%) of isolates of Puccinia triticina in the United States in 2014 virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance			NY IL, IN, WI		TX		KS		MN, ND, SD		Total			
gene	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lrl	128	100.0	14	100.0	32	100.0	82	100.0	9	100.0	115	100.0	380	100.0
Lr2a	72	56.3	6	42.9	8	25.0	25	30.5	0	0.0	67	58.3	178	46.8
Lr2c	75	58.6	6	42.9	8	25.0	29	35.4	0	0.0	69	60.0	187	49.2
Lr3	128	100.0	14	100.0	32	100.0	82	100.0	9	100.0	115	100.0	380	100.0
Lr9	6	4.7	0	0.0	6	18.8	38	46.3	1	11.1	24	20.9	75	19.7
Lr16	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Lr24	10	7.8	2	14.3	8	25.0	19	23.2	3	33.3	30	26.1	72	18.9
Lr26	66	51.6	7	50.0	10	31.3	24	29.3	3	33.3	22	19.1	132	34.7
Lr3ka	118	92.2	13	92.9	26	81.3	20	24.4	6	66.7	44	38.3	227	59.7
Lr11	116	90.6	14	100.0	25	78.1	0	0.0	1	11.1	31	27.0	187	49.2
Lr17	66	51.6	13	92.9	26	81.3	57	69.5	9	100.0	59	51.3	230	60.5
Lr30	118	92.2	14	100.0	26	81.3	17	20.7	6	66.7	42	36.5	223	58.7
LrB	63	49.2	14	100.0	26	81.3	56	68.3	9	100.0	56	48.7	224	58.9
Lr10	77	60.2	6	42.9	8	25.0	81	98.8	8	88.9	97	84.3	277	72.9
Lr14a	120	93.8	14	100.0	28	87.5	59	72.0	9	100.0	65	56.5	295	77.6
Lr18	55	43.0	1	7.1	0	0.0	0	0.0	1	11.1	0	0.0	57	15.0
Lr21	2	1.6	0	0.0	0	0.0	1	1.2	0	0.0	44	38.3	47	12.4
Lr28	65	50.8	0	0.0	6	18.8	29	35.4	0	0.0	59	51.3	159	41.8
Lr39	10	7.8	0	0.0	6	18.8	74	90.2	1	11.1	74	64.3	165	43.4
Lr42	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Total	123		14		32		82		9		115		380	

samples had low severities (10–20%) and were taken from the edges of otherwise disease-free fields. However, samples obtained from Zavala and Bastrop counties in Texas had a high disease severity (50-80%) and prevalence (100%).

Louisiana. Wheat leaf rust was present at low incidence and severity in an early planted Baton Rouge nursery on 18 March. Due to the cool winter and spring wheat leaf rust occurred late in the season and at lower levels than is typical in Louisiana. Leaf rust in plots developed in grain-illing stages and did reach higher levels in late April and early May as the plants approached physiological maturity, but yield impact was minor.

Mississippi. Trace levels of wheat leaf rust were reported in Greenwood in the eastern Delta region in late April. As in Louisiana and Alabama, a very cool spring likely significantly delayed wheat leaf rust development.

Alabama. Leaf rust was found at trace levels in the state in 2014. The very cool spring likely impacted rust development.

Oklahoma. Other than the low levels of leaf rust found in one irrigated wheat field in central Oklahoma in early May and a single leaf rust pustule observed in late March, rust was not reported in the state in 2014. Drought conditions in the state, coupled with high temperatures and wind, were not conducive for wheat or rust development. Seventy-eight percent of the winter wheat crop was rated poor to very poor. Many fields were not harvested, however, irrigated fields in the panhandle had better yield potential and a few dryland fields appeared to have some yield potential.

Kansas. Persistent drought and high temperatures were not conducive for wheat or rust development in the state this season. Other than low levels of wheat leaf rust observed in plots in northeastern Kansas in late May, wheat leaf rust was not reported in the state. Winter wheat production in the state was forecasted to be down 26% from last year's crop and the lowest in 25 years. Yield was estimated at 28 bu/acre; 10 bushels below last year and the lowest since 1995.

	1,000	Yields in	Production	stimate). Losses due to:								
	acres	bushels	in 1,000	Stem rust		Le	af rust	Stripe rust				
State	harvested	per acre	of bushels	%	1,000 bu	%	1,000 bu	%	1,000 bu			
AL	225	69.0	15,525	0	0	0.0	0	0.0	0			
AZ	7	100.0	700	_	_	_	_					
AR	395	63.0	24,885	0	0	0.0	0	0.0	0			
CA	180	80.0	14,400	0	0	0.0	0	1.0	145			
СО	2,350	38.0	89,300	0	0	0.0	0	Т	Т			
DE	75	72.0	5,400	0	0	0.0	0	0.0	0			
FL	10	39.0	390	_	_	_	_					
GA	230	49.0	11,270	0	0	Т	Т	Т	Т			
ID	730	80.0	58,400	0	0	0.0	0	3.0	1,806			
IL	670	67.0	44,890	0	0	Т	Т	Т	Т			
IN	335	76.0	25,460	Т	Т	1	257	1.0	257			
IA	15	49.0	735	_	_	_	_					
KS*	8,800	28.0	246,400	Т	Т	Т	Т	0.0	0			
KY	510	71.0	36,210	0	0	Т	Т	0.0	0			
LA	150	62.0	9,300	0	0	1.0	94	Т	Т			
MD	250	70.0	17,500	_	_	_	_	_	_			
MI	485	74.0	35,890	0	0	2.0	732	0.0	0			
MN	32	49.0	1,568	0	0	0.0	0	0.0	0			
MS	215	58.0	12,470	0	0	Т	Т	2.0	254			
MO	740	58.0	42,920	0	0	Т	Т	Т	Т			
MT	2,240	41.0	91,840	0	0	0.0	0	Т	Т			
NE	1,450	49.0	71,050	0	0	Т	Т	0.0	0			
NV	9	110.0	990	_								
NJ	25	53.0	1,325	_		_						
NM	105	28.0	2,940	_								
NY	95	63.0	5,985	Т	Т	Т	Т	Т	Т			
NC	770	58.0	44,660	0	0	1.0	451	0.0	0			
ND	555	49.0	27,195	0	0	0.0	0	0.0	0			
OH	545	74.0	40,330	0	0	Т	Т	0.0	0			
OK	2,800	17.0	47,600	0	0	0.0	0	0.0	0			
OR	740	55.0	40,700	0	0	Т	Т	Т	Т			
PA	150	65.0	9,750	—								
SC	220	52.0	11,440	—								
SD	1,080	55.0	59,400	Т	Т	Т	Т	Т	Т			
TN	475	66.0	31,350	0	0	Т	Т	Т	Т			
TX	2,250	30.0	67,500	_								
UT	109	50.0	5,450	_								
VA	260	68.0	17,680	0	0	Т	Т	0.0	0			
WA	1,640	52.0	85,280	0	0	0.0	0	Т	Т			
WV	7	64.0	448	_								
WI	250	65.0	16,250	Т	Т	1.0	164	Т	Т			
WY	125	38.0	4,750	—								
U.S. % loss				Т		0.1		0.2				
U.S. total	32,304	42.6	1,377,526		Т		1,699		2,463			

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

SPRING WHEAT												
	1,000	Yields in	Production			Losses	s due to:					
	acres	bushels	in 1,000	Ste	Stem rust		af rust	Stripe rust				
State	harvested	per acre	of bushels	%	1,000 bu	%	1,000 bu	%	1,000 bu			
CA	NA	NA	NA	0	0	0.0	0	0.0	0			
CO	8	64.0	512	—	—	_	—	—	—			
ID	455	76.0	34,580	0	0	0.0	0	6.0	2,207			
MN	1,180	55.0	64,900	0	0	0.0	0	0.0	0			
MT	2,990	36.0	107,640	0	0	0.0	0	Т	Т			
NV	1	60.0	60	—	—	_	—	_	—			
NY	NA	NA	NA	Т	Т	Т	Т	Т	Т			
ND	6,190	47.5	294,025	0	0	1.0	2,940	0.0	0			
OR	78	48.0	3,744	0	0	Т	Т	Т	Т			
SD	1,280	56.0	71,680	Т	Т	Т	Т	Т	Т			
UT	8	54.0	432	—	—	_	—	—	—			
WA	610	38.0	23,180	0	0	0.0	0	Т	Т			
U.S. % loss				Т		0.5		0.4				
U.S. total *	12,800	46.9	600,753		Т		2,940		2,207			
			DURUM	1 WHEA	Т							
	1,000	Yields in	Production			Losses	s due to:					
	acres	bushels	in 1,000	Ste	m rust	Lea	af rust	Stripe rust				
State	harvested	per acre	of bushels	%	1,000 bu	%	1,000 bu	%	1,000 bu			
AZ	72	111.0	7,992	—	—		—	_	—			
CA	35	105.0	3,675	0	0	0	0	0	0			
ID	11	67.0	737	0	0	0	0	3	23			
MT	430	32.0	13,760	0	0	0	0	0	0			
ND	820	37.5	30,750	0	0	0	0	0	0			
SD	4	45.0	180	—			_		_			
U.S. % loss				0		0		0.04				
U.S. total *	1,372	41.6	57,094		0.0		0.0		23			

Nebraska. In late May, a few pustules of wheat leaf rust were observed in Nuckolls County and also in Clay County in south-central Nebraska. These were the first confirmed reports of wheat leaf rust in the state in 2014. Only two pustules of leaf rust were found in a survey of fields in south-central and southeastern areas of the state on 4 June. The fields surveyed were virtually disease free. A majority of the fields in the south-central area were severely drought stressed. The wheat was at soft to hard dough stage. On June 10, wheat leaf rust, at trace to low incidence with severities up to 30% on flag leaves, was found in plots at Lincoln in southeastern Nebraska. No rusts were observed in a survey of southwestern Nebraska and the southern and northern Panhandle during 17-19 June. Most fields were stressed due to a lack of moisture. Wheat ranged from milk to hard dough.

Very little, if any, rust inoculum was observed to the south in Kansas and Oklahoma, where drought conditions were severe. The lack of inoculum to the south, coupled with dry conditions in the state, created conditions unfavorable for rust development in the state in 2014.

Arkansas. Fresh, wheat leaf rust pustules were found on volunteer wheat at the experiment station at Marianna in the east-central part of the state on 20 March. No cereal rusts were found in plots throughout the state (Stuttgart, Marianna, Newport, Keiser, Fayetteville, and Kibler) during the second week of April. Wheat in the state ranged from Feekes 6 to Feekes 9. Traces of wheat leaf rust were observed on the cultivar Havoc at Marianna and Newport in eastern Arkansas in the fourth week of May. Hot, dry ,and windy conditions during May were not conducive for rust development.

There was less rust in Arkansas than in any of the previous 26 years. Leaf rust generally developed just prior to maturity and likely did not cause any yield loss.

Georgia. Wheat leaf rust was widespread in a very early planted (2 months earlier than normal recommendations) wheat plot in a nursery at Plains in southwestern Georgia on 2 April. Although leaf rust is usually found in this area, the severity level was high for this early in the season. Leaf rust also was found on the lower leaves of the most susceptible lines in another nursery 300 yards away. Wheat leaf rust had developed to severe levels on many lines in plots at Plains in southwestern Georgia by the third week in May. Plots of Shirley (postulated to have Lr26 and Lr18) had higher levels of leaf rust than seen in previous years. Leaf rust was found in only a few commercial fields this season. The widespread use of fungicides and a long, cool spring impacted wheat leaf rust development in the state.

South Carolina. Leaf rust had developed rapidly in areas of northern South Carolina by the second week of May.

North Carolina. In eastern North Carolina, leaf rust continued to increase in plots at Kinston, whereas at Ayden, leaf rust was just beginning to appear the third week of May. Conditions in early May were conducive for leaf rust development. Plots of Shirley in North Carolina also had higher levels of leaf rust severity than in past years.

In tests at the USDA-ARS Cereal Disease Laboratory, DG Shirley had a high infection type to leaf rust race TCRKG, which is virulent to Lr18 and Lr26. Marker data indicated the presence of the T1B·1R translocation in DG Shirley, indicating the presence of Lr26. DG Shirley has been postulated to also have Lr18 based on seedling leaf rust tests. In 2014, virulence to Lr26 was at 51.6% and virulence to Lr18 was at 43.0% of the southeastern population.

Wheat leaf rust was at low to moderate levels in commercial fields in the Coastal Plain and Tidewater areas and heavy in the nurseries at Kinston and Plymouth in eastern North Carolina in 2014. An estimated 1% statewide loss in winter wheat was due to leaf rust in 2014.

Virginia. A headrow in a nursery at Warsaw in eastern Virginia had low leaf rust incidence and low severity the third week of May. At Blacksburg in western Virginia low levels of wheat leaf rust were found in plots on 6 June.

Kentucky. Wheat leaf rust was widespread, but generally at low severity levels, in western Kentucky by late May. Most infections were found on the F-1 and F-2 leaves and occasionally on flag leaves. Wheat was at grain-filling stages.

Tennessee. Wheat leaf rust was found in plots at Jackson in western Tennessee in early June. Wheat in the state was generally disease free in spring 2014.

Illinois. Wheat leaf rust was found in a few plots at the Brownstown Research Farm in Fayette County in south-central Illinois on 6 June. No rust was found in surveys of Saline, Gallatin, White, Wayne, and Clay Counties in southern Illinois the week of 2 June. Wheat leaf rust at high incidence and severity was found on some cultivars in plots in Champaign County in east-central Illinois in mid-June. Rust developed too late in the season to cause yield reductions.

Michigan. Wheat leaf rust, at low severity in the lower canopy, was found in a nursery at Mason in south-central Michigan on 5 June. Wheat had finished flowering with earliest lines at milk growth stage. Wheat leaf rust was widespread across the state by mid-June. By crop maturity, flag leaf severities had reached 10% or more in fields not treated with fungicides.

New York. No cereal rusts were found on visits to fields and plots in eastern and central New York the fourth week of June.

Minnesota. A single pustule of wheat leaf rust was found in a winter wheat nursery at St. Paul in southeastern Minnesota on 18 June. By late June, the rust was found at low levels in the nursery. Heavy rains were common in Minnesota the previous weeks with many areas receiving record precipitation totals. On 10 July, wheat leaf rust was observed at trace levels in plots of spring wheat in southern Minnesota. In a plot of Marshall wheat (Lr2a, Lr10 and Lr34), heavy leaf rust infections were found. Plots of winter wheat had light to heavy leaf rust infections.

In early August, leaf rust was present at high severity in plots of susceptible wheat in west-central Minnesota. Plots of cultivars and breeding lines varied between trace levels of leaf rust to high severity. Cultivars with Lr21 had higher leaf rust levels compared to most other cultivars. Most wheat fields in west-central Minnesota were close to complete maturity, however a number of fields still had green flag leaves. Leaf rust was present at low to moderate levels in wheat fields that still had green leaves. Leaf rust had not yet been found in northwestern Minnesota by 5 August.

Wisconsin. On 26 June, leaf rust was found in several winter wheat plots in a nursery in south-central Wisconsin. Many plots had 100% incidence with 10% flag leaf severities. Wheat was approaching dough stage. Trace levels of leaf rust were observed in fields and plots in northeastern Wisconsin the second week of July. Leaf rust severities of 20% were found on flag leaves at early dough stage in unsprayed winter wheat fields along the Lake Michigan in northeastern Wisconsin in early August. Wheat leaf rust was observed on several cultivars in wheat growing areas of Wisconsin in 2014. Flag leaf severities were 10% or less and the rust generally did not appear until late in the growing season. An estimated 1% loss statewide was due to leaf rust in winter wheat in 2014.

South Dakota. Leaf rust, at low incidence and severity, was found in a winter wheat nursery at Brookings in eastern South Dakota in late June, which was the first report of wheat leaf rust in the state in 2014. Leaf rust was still at low levels in winter wheat plots in Brookings County in eastern South Dakota the second week of July. Low levels of leaf rust were found in adjacent spring wheat plots.

North Dakota. Wheat leaf rust, at low levels with severities between 5 and 10%, was found on the lowest leaves in plots at Fargo in eastern North Dakota on 2 July. Wheat leaf rust was found in one winter wheat plot at Minot in north-central North Dakota the third week of July.

Wheat leaf rust was present at varying levels across central and eastern North Dakota during the second week of August. In central North Dakota, susceptible wheat cultivars in plots had high leaf rust severities, whereas resistant cultivars and breeding lines had low to moderate severities. In northeastern North Dakota, susceptible cultivars in plots had moderate severity and resistant cultivars generally had low levels of rust. Cultivars such as Faller, Prosper, and Barlow with Lr21 had more leaf rust compared to other cultivars. Many wheat fields in eastern and central North Dakota were still very green the second week of August.

Wellington County, Ontario, Canada. A few pustules of wheat leaf rust were observed in variety plots in the Palmerston area in southern Ontario on 18 June. This report was the first for wheat leaf rust in the province in 2014. Winter wheat was in the grain-filling stage. The extreme winter caused significant damage to the winter wheat crop resulting in about 10% of the crop being replanted or reseded.

The 2013 wheat leaf rust observation map can be found at: <u>http://www.ars.usda.gov/Main/docs.htm?docid=9757</u>.

Lr gene postulations of current soft red winter, hard red winter, and hard red spring wheat cultivars are available in a searchable database at: <u>http://160.94.131.160/fmi/iwp/cgi?-db=Lr%20gene%20postulations&-loadframes</u>.

Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*, *Pst*). Wheat stripe rust was not generally as widespread in 2014 as in 2013 or as severe as 2012. Drought conditions in the Central Plains limited rust development there. Stripe rust disease pressure generally was light in most areas of the Pacific Northwest, where dry, warm conditions were common. Nationally, an estimated 0.2% loss in winter wheat was to stripe rust (see Tables 3 and 4).

South Texas. Wheat stripe rust was found in the middle of a nursery field at Castroville in South Texas on 7 March. The wheat was at Feekes stages 7–9. Conditions were conducive for further development and the rust spread throughout the irrigated field and reached 60S on flag leaves of some lines by 26 March and 70S on the susceptible cultivar Patton by 9 April. Wheat leaf rust was competing with stripe rust on the upper leaves and, with the warmer temperatures, stripe rust development stopped. The stripe rust population in the plots did not appear to have Yr17 virulence.

Low levels of stripe rust were reported in commercial fields as far north as 30 miles south of Dallas and areas to the south in early April. In a survey of north-central Texas in late March and early April, no rusts were found in commercial fields and consultants and extension agents in the areas had no reports of rust.

Louisiana. Low levels of stripe rust (<1% severity and prevalence) were observed on GACT7, a susceptible cultivar, in plots at Alexandria in central Louisiana in late March. Stripe rust at low incidence and severity also was observed in plots at Crowley in southwestern Louisiana. Traces of stripe rust had been found around the state by early April. High stripe rust severities were found in a single family of wheat headrows in plots at Baton Rogue in early April. The stripe rust had apparently been present for some time, but had not spread beyond the one family. Generally, the nursery had very little disease pressure. Wheat maturity was about 10 days behind the 10-year average.

Mississippi. A few stripe rust infected leaves were found on volunteer plants under a rainout shelter in Stoneville in the Delta region the last week of April. Most of the stripe rust had formed telia due to the warmer temperatures. As of3 May, stripe rust had not been confirmed in commercial fields or nurseries anywhere in the state.

Arkansas. A small wheat stripe rust hot spot was found in a plot of a known susceptible cultivar at Marianna in eastern Arkansas on 30 April. This report was the first for stripe rust in the state in 2014. A few scattered reports of stripe rust in the state were made during the season, but there was no further development.

Kansas. A large stripe rust focus was found in plots of 2137 near Manhattan in northeastern Kansas in late May. The spread from the foci center suggested the stripe rust infection developed 3–6 weeks prior. Most wheat at the location was at milk stage. Stripe rust did not develop to any extent due to the warmer temperatures. Persistent drought and high temperatures in the state were not conducive for wheat or rust development in 2014.

South Dakota. Trace levels of wheat stripe rust were found in winter wheat plots at Brookings in eastern South Dakota on 10 July. This report was the first for stripe rust in the state in 2014. No significant further development was observed.

North Dakota. Stripe rust was found in a commercial field south of Minot in north-central North Dakota and also on a few leaves in one plot at Fargo in eastern North Dakota the third week of July. Wheat stripe was present at very low incidence at a trace level in various cultivars in plots at Langdon in northeastern North Dakota the second week of August. Stripe rust did not develop to significant levels in the state.

Colorado. Stripe rust, at low levels, was found in two commercial fields in Weld County in eastern Colorado in early June. Stripe rust developed to severe levels in Fort Collins along the Front Range of Colorado, but there was minimal infection in eastern Colorado in 2014.

Wisconsin. Several small stripe rust foci were found in plots at Arlington in south central Wisconsin on 27 June. Incidence and severity were at very low levels. This finding contrasts to the 2012 and 2013 seasons, when stripe rust was found at high incidence and severity in plots at this point in the season. Stripe rust was not reported in other nurseries or in commercial fields in the state in 2014.

Virginia. One small wheat stripe rust foci was found in nursery headrows at Warsaw in eastern Virginia on 3 June. Stripe rust was not reported elsewhere in the state.

Oregon. Stripe rust was found in plots near Corvallis in western Oregon in late March. Wheat stripe rust was reported on the soft white winter wheat cultivars Goetze, Kaseberg, Sy Ovation,, and Tubbs 06 in north and south areas of the Willamette Valley in early April. Stripe rust appears to have overwintered in the valley. Stripe rust disease pressure was low in the western part of the state the third week of May, however, hot spots were observed in several fields.

In eastern Oregon, stripe rust hot spots were observed in the Hermiston and Pendelton-Ruggs nurseries, whereas trace amounts were found in the Milton–Freewater nursery in early May. Stripe rust also was found in a commercial field in Sherman County in early May. Low levels of stripe rust were observed in three commercial winter wheat fields in Umatilla County in northeastern Oregon on 22 May.

Washington and Idaho. Stripe rust was found on a solitary lower leaf of a susceptible check in a nursery at Walla Walla in southeastern Washington on 23 April. On revisiting a field in Grant County in eas-central Washington, which was heavily infected with stripe rust in November 2013, no stripe rust could be found in late April. Generally, stripe rust disease pressure was low in eastern Washington in late April.

Very low levels of stripe rust were found in three commercial fields north of Walla Walla in southeastern Washington on 22 May. No stripe rust was found in fields visited south of Walla Walla. Two stripe rust lesions were found in a commercial wheat field in Columbia County in southeastern Washington. No rust was found in commercial fields visited in Whitman, Benton, and Franklin Counties in southeastern Washington. Winter wheat ranged from Feekes 7 to 10.5, whereas spring wheat was at Feekes 2–6. Generally, stripe rust disease pressure was low in eastern Washington in late May. As is typical, stripe rust severities up to 30% were observed on susceptible cultivars in nurseries at Mount Vernon in northwestern Washington the first week of April.

Stripe rust was found in a field of the soft white winter wheat cultivar Brundage in the Hazleton area of south central Idaho in late May. The stripe rust was mostly confined to flag leaves, and the wheat was just beginning to head. Stripe rust was readily found on Brundage in 2013, growers continue to plant the cultivar due to the high-yield potential. One pustule of stripe rust was found in a nursery near Moscow in northwestern Idaho on 21 May.

In areas of eastern and southern Idaho, stripe rust was found, but only the soft white winter wheat cultivars Brundage and WB 470 in late June and early July. Stripe rust was not found on the most susceptible spring wheat lines in the nursery at Idaho Falls nor in the spring wheat nurseries at Rupert and Aberdeen in southeastern Idaho in late June. By early July, stripe rust was found on the cultivar WB936 west of Idaho Falls. Warming temperatures limited stripe rust development.

In an early July, a survey of fields in the Palouse region of Washington and Idaho (Whitman and Spokane Counties in eastern Washington and Latah County in northwestern Idaho) found stripe rust in only one winter wheat field in Whitman County and one winter wheat field in Spokane County. One or two small hot spots (<1 foot diameter) with mixed resistant and susceptible reactions were found in the fields. Stripe rust was found in about 60% of the spring wheat fields in Whitman County and about 40% in Latah and Spokane Counties. When found in the spring wheat fields, the incidence was less than 1%. An estimated statewide loss of 3% in winter wheat was due to stripe rust in Idaho and a trace loss in Washington in 2014.

Montana. Wheat stripe rust was found on the cultivar Yellowstone in the Hardin area south central Montana in late May.

Alberta, Canada. Low to moderate levels of wheat stripe were found in commercial winter wheat fields and plots in the Beaverlodge area in west-central Alberta in early July.

Wheat stripe rust map. Please visit: http://www.ars.usda.gov/Main/docs.htm?docid=9757.

The 2014 stripe rust observation map can be found at: <u>http://www.ars.usda.gov/SP2UserFiles/ad_hoc/36400500Cerealrus</u> tbulletins/2012wstr.pdf.

MONTANA

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2014 Spring Wheat Program.

Luther Talbert, Nancy Blake, Jamie Sherman, Hwa-Young Heo, Jay Kalous, Andrea Varella, and Afaf Nasseer.

Approximately 3.05×10^6 acres $(1.24 \times 10^6$ hectares) of hard red spring wheat were seeded in 2014. The season was excellent up until an extended period of rain near crop maturity, which caused sprouting problems in a large portion of the spring wheat crop. For spring wheat, 2.99×10^6 acres $(1.21 \times 10^6$ hectares) were harvested with an average yield of 36 bu/acre (2,419 kg/ha). Total harvested production was 107.6 x 10⁶ bushels (2.93 x 10⁶ metric tons). Leading spring wheat cultivars in Montana were Vida, Reeder, Choteau, and Mott. Vida, Choteau, and Mott all have some resistance to the wheat stem sawfly. A new cultivar named Duclair was grown on approximately 70,000 acres (28,350 hectares) in 2014. Major agronomic objectives for the program remain excellent yield potential in the harsh Montana environments

and resistance to the wheat stem sawfly. End-use quality targets for all cultivars remain excellent bread-making properties, including selection for high grain protein, strong gluten, good water absorption, and large loaf volume.

Release of Egan hard red spring wheat.

The hard red spring cultivar **Egan**, with resistance to the orange wheat blossom midge (OWBM), was released in 2014 for impacted areas in western Montana. Egan, tested experimentally as CAP400, has the pedigree '(McNeal*5/Glupro)*2/3/(Reeder/BW-277, CAP19)//Choteau'. Egan also has a high grain protein gene introduced from the cultivar GluPro and, as such, has grain protein levels approximately 1 percentage point higher than other cultivars. Egan should be grown in a blend with an OWBM-susceptible cultivar (90% Egan : 10% susceptible) to lessen the possibility that the OWBM will overcome the resistance.

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Association analysis of stem solidness and wheat stem sawfly (Cephus cinctus Norton) resistance in a panel of North American spring wheat germplasm.

A.C. Varella, D.K. Weaver, J.D. Sherman, N.K. Blake, H-Y. Heo, J. Kalous, S. Chao, M.L. Hofland, J.M. Martin, K.D. Kephart, and L.E. Talbert.

The wheat stem sawfly historically is a pest of major economic importance in wheat in the Northern Great Plains of North America. Limitations constraining traditional control measures have driven pest management efforts towards resistance breeding, so a better characterization of resistance genes will provide additional tools for breeders. An association mapping analysis for stem solidness and wheat stem sawfly resistance was conducted using a set of 244 elite spring wheat lines from 10 North American breeding programs. All lines were genotyped using the wheat 90K iSelect SNP assay and 25,728 polymorphic markers were detected. Field data were collected in three environments during four years of trials. Early and late stem solidness were shown to be associated with the solid stem QTL on chromosome 3B, but variation for early solidness also was affected by chromosomal regions on 1B and 5D. Despite the original expectation of having a single haplotype conferring solidness on the 3B locus, two lines from CIMMYT had haplotypes that differed from that of Rescue, the first solid-stemmed line developed in North America, which may indicate a different origin of the solid stem alleles in these lines. Previously identified QTL for resistance were confirmed, including QTL for heading date and stem cutting on chromosomes 1B and 4A, respectively. Potential sources of a novel resistance mechanism causing larval mortality were identified among the panel lines. Larval mortality was associated with QTL on chromosomes 2A, 3A, and 5B. Favorable alleles for stem solidness and other resistance traits are available within North American wheat germplasm. Thus, improvements in wheat stem sawfly management may be obtained using alleles that already exist in elite germplasm.

Publication.

Varella AC, Weaver DK, Sherman JD, Blake NK, Heo H-Y, Kalous J, Chao S, Hofland ML, Martin JM, Kephart KD, and Talbert LE. 2015. Association analysis of stem solidness and wheat stem sawfly resistance in a panel of North American spring wheat germplasm. Crop Sci [in press].

Impact of the D genome and quantitative trait loci on quantitative traits in a spring durum by spring bread wheat cross.

J. Kalous, J. Martin, J. Sherman, H-Y. Heo, N. Blake, S. Lanning, J. Eckhoff, S. Chao, E. Akhunov, and L. Talbert.

Tetraploid durum and hexaploid bread wheat diverged roughly 9,000 years ago creating two distinct gene pools. The unequal number of genomes between durum and bread wheat created a barrier inhibiting genetic flow, however, both species were cultivated in similar environments with similar production objectives.

Lanning et al. (2008) identified the cross between hexaploid Choteau and tetraploid Mountrail as producing a significantly high number of fertile hexaploid and tetraploid offspring. In this study, 205 'Choteau/Mountrail' recombinant inbred lines consisting of both hexaploid and tetraploid spring wheat were evaluated in Bozeman, and Sidney, MT, in 2012 and 2013, for a number of agronomic and end-use quality traits. Major QTL controlling seed size were identified on chromosomes 3B and 7A, with the positive allele originating in Mountrail. Additional positive alleles were identified in Mountrail that may prove valuable for introgression into spring bread wheat germplasm.

Reference.

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Publication.

Kalous J, Martin J, Sherman J, Heo H-Y, Blake N, Lanning S, Eckhoff J, Chao S, Akhunov E, and Talbert L. 2015. Impact of the D genome and quantitative trait loci on quantitative traits in a spring durum by spring bread wheat cross. Theor Appl Genet [in press].

2014 Winter Wheat Program.

Phil Bruckner, Jim Berg, Ron Ramsfield, and David May.

The winter wheat acreage for 2014 harvested in Montana was 2.24 x10⁶ acres (0.91 x 10⁶ hectares), averaging 41 bu/ acre (2,755 kg/ha) with a total production of 91.8 x 20⁶ bushels (2.50 x 10⁶ metric tons). Leading cultivars were Yel-lowstone (19.8%), Judee (11.4%), Decade (10.5%), and Genou (6.6%). The winter wheat program emphasizes on-farm productivity characteristics and quality characteristics to compete in a global market place. Specific objectives include productivity, adaptation (cold tolerance, maturity, and stress tolerance), pest resistance (wheat stem sawfly, wheat streak mosaic virus, and stem rust), and dual-purpose end-use quality. End-use quality goals are high grain protein and gluten strength, high flour extraction and low ash content, good dough mixing and bread-baking quality, and superior noo-dle color and textural characteristics. Results from the 2014 Montana Winter Wheat Variety Test can viewed at http:// plantsciences.montana.edu/crops/index.html

Release of Northern hard red winter wheat.

Northern hard red winter wheat has been approved for release in autumn 2015. Northern (previously tested under the experimental designation, MT0978) derives from a composite of two topcrosses made to the same 1999 F_1 population: '00X248, MT9982 (Yellowstone sib)//MTW0072/NW97151', and '00X249, MTW0047//MTW0072/NW97151'. Northern is an awned, white-glumed, hollow-stem, semi-dwarf hard red winter wheat. Northern has medium-late maturity, 169 days to heading from 1 January, similar to Yellowstone . Northern is semi-dwarf (*Rht1*) and medium-short (31.9 inches,

n=56), similar to Jagalene and Decade and shorter than Colter and Yellowstone. Northern is resistant to the prevalent races of stem rust including Ug99 and stripe rust, but susceptible to leaf rust. In 56 location-years of testing in the Montana Winter Wheat Intrastate and Off-station Nurseries, the average yield of Northern (70.8 bu/acre) was similar to that of Yellowstone, Colter, and Jagalene, but greater than those of CDC Falcon, Decade, and Jerry. The test weight of Northern (59.8 lb/bu, n=56) is below that of Jagalene and similar to those of CDC Falcon, Colter, Decade, and Yellowstone. Grain protein content of Northern is medium to high, higher than those of CDC Falcon, Jagalene, and Yellowstone.

Based on experimental milling using a Brabender Automat Mill, the flour yield of Northern is medium to high with relatively high flour ash content and high flour protein. Northern has medium dough-mixing characteristics with moderate water absorption and a relatively short mixing time. Baking qualities of Northern are acceptable, with good loaf volume, similar to that of Yellowstone and other check cultivars. Northern has relatively low polyphenol oxidase (*PPO-A1b*) activity and average to good Asian noodle brightness (L24) and color stability. Northern carries the 2* subunit at the *Glu-A1* locus, the 7+8 subunits at the *Glu-B1* locus, and the 5+10 subunits at the *Glu-D1* locus. Northern does not carry either the T1BL·1RS or T1AL·1RS translocation. Northern may have potential for tortilla utilization based on the 2012 crop Wheat Quality Council evaluations and further testing of 2014 samples at Texas A&M.

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Quantitative genetics, plant breeding, and small grain quality.

Jack Martin, Mike Giroux, Petrea Hofer, Alanna Schlosser, Andy Hogg, and Steve Hystad.

A small increase in amylose content may impact end product quality of wheat. The effect of elevated amylose content in durum wheat is not known. We surveyed 255 durum wheat accessions and found two genotypes that lacked the SGP-A1 protein. These genotypes were crossed to the cultivar Mountrail, an adapted durum genotype, to create populations segregating for the *SSIIa-Ab* null allele. Our goal was to determine the influence of allelic variation at the *SSIIa-A* locus on semolina properties and end-product quality using noodles as a test product. Amylose content increased 3% and cooked noodle firmness increased 2.8 g cm for the *SSIIa-Ab* class compared to the *SSIIa-Aa* class for the PI 330546 source but no change in either trait was detected between classes for the IG 86304 source. The *SSIIa-Ab* class had a 10% reduction in flour swelling compared to that of the *SSIIa-Aa* class for both crosses, Grain protein and semolina yield did not differ between *SSIIa-A* allelic classes within a cross. The different results for amylose content and noodle firmness between these sources may be because the two sources of the *SSIIa-Ab* null mutation contributed different linkages to the segregating populations. Results show that the *SSIIa-Ab* allele could be used to produce durum-based products that are slightly more firm in texture. However, the effect of the *SSIIa-Ab* allele may depend on the source.

Publication.

Martin JM, Hogg AC, Hofer P, Manthey FA, and Giroux MJ. 2014. Impacts of *SSIIa-A* null allele on durum wheat noodle quality. Cereal Chem 91:176-182.

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C.A. Griffey, W.E. Thomason, J.E. Seago, N.R. Carpenter, W.S. Brooks, S. Malla, E. Wright, L. Liu, and E. Hokanson (Virginia Tech, Blacksburg, VA), and R.M. Pitman, M.E. Vaughn, D. Dunaway, C. Barrack, M. Beahm, and R. Markham (Eastern Virginia Agricultural Research and Extension Center, Warsaw, VA).

2014 Wheat Production in the Commonwealth of Virginia.

Growing conditions. Temperatures in October 2013 were below the long-term average and, combined with rain showers, wheat planted acres were 10% behind the 5-yr average by the third week of October. Overall, temperatures in November were colder than normal as well and although topsoil moisture was mostly reported to be adequate, autumn growth was slowed. In mid-November, 78% of the intended wheat crop was seeded. Most of the state received adequate rainfall in December, but also experienced wide swings in temperatures. Many areas of the state received significant snow in January and nighttime lows below 0°F. February conditions were much the same, and small grain was rated as 68% in good or excellent condition with 24% fair. Continued wet and cool to cold weather hampered small grain progress, and the portion of the crop rated as good or excellent was reduced to 61%. Crop conditions for wheat improved in April. Major storm events delivered significant rainfall to many areas of Virginia in early May. By 12 May, 66% of the wheat crop was headed, compared with 74% on the same date in 2013. Temperatures that were in the high 80's and 90's resulted in a rapid increase in wheat heading to 84% by 19 May. Warm weather in mid-June hastened crop maturity, and 40% of the anticipated wheat crop was harvested by 22 June.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service (<u>http://</u> <u>quickstats.nass.usda.gov</u>), in the autumn of 2013, Virginia farmers planted 290,000 acres (117,450 ha) of wheat. The following spring, 260,000 acres (105,300 ha) were harvested. The average yield was 68 bu/acre (4,560 kg/ha), which was a 10% increase over the previous year. Overall, 17,680,000 bushels (481,603 metric ton) of wheat were produced in 2014.

Disease incidence and severity. Entries in Virginia's 2014 state wheat cultivar trials were rated (0 = no infection to 9)= severe infection) for disease severity at four diverse locations. The 116 entries in the 2014 trial had mean powdery mildew ratings that varied from 0 to 6 (mean of 1.6) in Virginia's southern Piedmont region (Nottoway County), 0 to 3 (mean of 0.8) in the southwestern region (Montgomery County), and from 0 to 2 (mean of 0.2) on the Eastern Shore (Accomack County). Barley/Cereal Yellow Dwarf Virus infection was moderate at the Eastern Shore site with ratings ranging from 0 to 4.5 (mean of 1.0). Leaf blotch also was prevalent in trials on the Eastern Shore with ratings ranging from 1 to 4 (mean of 1.5). Leaf rust was prevalent in several regions and was moderately severe at the southwestern test site with entry ratings ranging from 0 to 7 (mean of 2.5). Race surveys conducted by Dr. James Kolmer at the USDA-ARS Cereal Disease Lab on 21 isolates from three regions in Virginia identified seven races of leaf rust; only race MBTNB was common at two locations (Richmond and Montgomery Counties). Race TNRJJ also was identified from samples sent from Blacksburg, VA, in Montgomery County. Five additional races (TBJSB, TCJSB, TBRKG, TCRKG, and TCTNB) were identified on the Eastern Shore at Painter, VA. Stripe rust was prevalent and moderately severe in a headrow nursery of State Wheat Test entries at Blacksburg, VA, where race PSTv-100 (virulence for genes Yr2, Yr3a, Yr4a, Yr6, Yr7, Yr8, Yr9, Yr19, Yr20, Yr21, Yr22, Yr23, YrCle, YrSte, YrYam, YrPr1, YrPr2, and YrHVII) was artificially applied to susceptible borders in an adjoining stripe rust nursery. Stripe rust infection type scores (0 =resistant to 9 = susceptible) ranged from 0 to 9 (mean of 2.3) and rust severities ranged from 1 to 85% (mean of 19%). Naturally occurring stripe rust was noted on a few headrow plots in eastern Virginia at Warsaw (Richmond County). Samples sent to Dr. Xianming Chen at USDA-ARS in Pullman, WA, identified race PSTv-52 (virulence for Yr6, 7, 8, 9, 17, 27, 43, 44, and YrExp2).

State cultivar tests. Wheat trials were planted in 7-inch rows at Blackstone, Orange, Holland, Painter, and Shenandoah Valley. They were planted in 6-inch rows at Blacksburg. They were planted in 7.5-inch rows at the Warsaw no-till location. All no-till locations (Holland and Warsaw) and Shenandoah Valley were planted at 48 seeds/ft². All other locations were planted at 44 seeds/ft².

Selecting the best wheat cultivar is challenging but becomes easier with adequate information on performance over multiple environments. Tests conducted in recent years across Virginia have provided the opportunity to evaluate day length sensitivity, spring freeze damage, glume blotch, Fusarium head blight, and general plant health. Many newer wheat cultivars and lines performed well in all test environments.

The released cultivars that yielded significantly higher than the statewide mean in 2014 were Pioneer Brand 26R10, SS 8360, USG 3404, AgriMaxx 434, Shirley, Pioneer Brand 25R40, USG 3523, Pioneer Brand 26R20, USG 3251, AgriMAXX 413, AgriMAXX 427, Pioneer Brand 26R41, and SS 8412. Pioneer Brand 26R20 and SS 8412 also had test weights that were significantly higher than the overall test mean. The average yield of all lines tested in 2013–14 was 74 bu/acre (4972 kg/ha).

Pioneer Brand 26R10 had the highest two-year average yield at 84.7 bu/acre (5,691 kg/ha). The cultivars USG 3404, Pioneer Brand 26R41, Pioneer 25R40, USG 3251, AgriMaxx 434, USG 3523, Shirley, USG 3612, AgriMaxx 413, and SS 8340 all had grain yields significantly above the two-year (2013 and 2014) test mean of 76 bu/acre (5,106 kg/ha). Among these top yielding cultivars, SS 8340 also had an average test weight of 59.0 lbs/bu (759 kg/m³) that was significantly higher than the two-year mean of 57.8 lbs/bu (744 kg/m³) over all entries.

Producers who grow large acreages of wheat should plant two or more cultivars having significantly different maturity dates in order to ensure harvest of high-quality grain having high test weights and no sprouting. In Virginia, it is typical for sporadic or consistent rain showers to interrupt harvest. These wetting and drying cycles and subsequent harvest delays significantly reduce grain test weight and quality. Growers can circumvent this problem by planting cultivars that differ significantly in maturity. Early maturing cultivars often can be harvested first and prior to significant rain showers, and later maturing cultivars harvested subsequently will suffer less damage and losses in test weight and quality due to exposure to such a rain event.

Virginia Wheat Yield Contest results. The 2014 contest was conducted statewide, and the results are in Table 1. Congratulations to our winners!

Newly released cultivars. The soft red winter wheat cultivar **102015123**, derived from the cross 'Pioneer Brand 25R47 (PI 631473) / GA951079-2E31 (PI 644020)', was released by the Virginia Agriculture Experiment Station in 2014. This cultivar is a widely adapted, moderately early heading, wheat cultivar that has high grain yield potential, good milling and baking quality, and has performed well in soft red wheat production areas of the deep south and mid-Atlantic regions. With the possible exceptions of *Wheat Spindle Streak Mosaic Virus* and Hessian fly, cultivar 102015123 expresses moderate to high levels of resistance to diseases prevalent in the soft red wheat region, which include leaf, stripe, and stem rusts; powdery mildew; Fusarium head blight; *Septoria tritici* leaf blotch; *Stagonospora nodorum* glume and leaf blotch; *Barley and Cereal Yellow Dwarf Viruses*; and *Wheat Soil Borne Mosaic Virus*.

Table 1. 2014 Virginia Wheat Yield Contest results.										
Place	Grower	Farm	County	Yield (bu/acre)	Cultivar					
1st	L. Andrews	W.L. Andrews Farm	Essex	112.3	AgriMAXX 438					
2nd	Paul Davis	Davis Produce	New Kent	109.7	USG 3251					
3rd	Ronnie Russell	Corbin Hall Farm	Middlesex	107.7	Pioneer 26R10					
4th	Katie Crossman Myer	Laurel Spring Farm	Westmoreland	93.9	Pioneer 26R20					

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WASHINGTON

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Celiac-safe wheat genotypes: A dietary solution to the gluten-induced disorders.

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Wheat and derived products are elicitors of a number of frequent diet-induced health issues, including gluten intolerance, sensitivity, and allergy, collectively known as the 'gluten syndrome'. These disorders cumulatively affect more than 7.5% of the U.S. population (Rustgi 2013; Rosella et al. 2013). In particular, gluten intolerance or celiac disease alone affects more than 71 million individuals around the globe (i.e., $\sim 1\%$ of the world population), which makes it one of the most devastating disorders of the gastrointestinal tract (Bai et al. 2012). The seed storage proteins of wheat, in particular prolamins (i.e., gliadins and glutenins), are known to trigger this autoimmune condition. So far, 190 celiac-causing epitopes were identified from wheat prolamins, where origin of the 180 epitopes were tracked back to α/β -, γ -, and ω -gliadins and the remaining 10 to low- and high-molecular-weight glutenin subunits. Interestingly, out of these 10 epitopes from glutenins, the high molecular weight glutenins (HMWgs) contribute to only two epitopes, which have shown to elicit immune responses in relatively fewer cases (Comino et al. 2013). The HMW glutenins also are vital for the baking properties of common wheat. Furthermore, the low molecular weight glutenins (LMWgs) and gliadins have imbalanced amino acid profiles, with 15% proline and 35% glutamine, and a reduced content of the essential amino acids lysine, threonine, methionine, and histidine (Koehler and Wieser 2013). Parallel research also has demonstrated that gliadins and LMWgs are inessential for baking, because the flours derived from wheat deletion lines and transformants lacking one or more families of the gluten proteins baked into a normal bread loaf with characteristic organoleptic properties (van den Broeck et al. 2011; Gil-Humanes et al. 2014). Similarly, in vitro experiments with washed-out wheat flour residues mixed with recombinant HMWgs HMWDx5 and HMWDy10 baked into normal-looking bread loaves, which further supported the observations made with the wheat transformants and deletion lines (Wen et al. 2012 and references cited therein). Moreover, reduced-gluten, transgenic wheat lines exhibited improved nutritional properties, because their lysine content was significantly higher than that of normal flour due to the compensatory increase in the amount of lysine-rich proteins (Gil-Humanes et al. 2014).

Epigenetic elimination of immunogenic prolamins. Because HMWgs largely contribute to the baking properties of wheat, and are primarily non-immunogenic, we undertook a strategy to specifically eliminate LMWgs and gliadins from grains by endosperm-specific silencing of wheat *DEMETER (DME)* homoeologues. DME enzymes regulate transcriptional activation of the prolamin genes (except HMW glutenin genes) during endosperm development by demethylation of their promoters (Osorio et al. 2012; Wen et al. 2012). Under the auspices of NIH (National Institutes of Health) and

LSDF (Life Sciences Discovery Fund) funded research projects, we undertook cloning of wheat *DME* homoeologues, established connections between temporal expression of *DME* homoeologues and accumulation of specific prolamins, and transformed wheat cultivar Brundage 96 to express DME-targeting hairpin (hp) and artificial micro (ami) RNAs in the endosperm. Using this RNA interference-based approach, 401 candidate transformants were obtained (Rustgi et al. 2014). Of these 401 transformants, 333 were obtained through particle bombardment and 68 via microspore electroporation. Using protein gel electrophoresis and liquid chromatography, 19 viable wheat transformants showing the elimination of 45.2–76.4% immunogenic prolamins were identified. Protein profiling of these transformants exhibited elimination of specific prolamins and/or prolamin groups (Wen et al. 2012; Rustgi et al. 2014; Mejias et al. 2014). Differential silencing of three *DME* homoeologues in individual transformants due to variation in number and site of transgene integration(s), the *DME* site targeted by hp- and amiRNAs, and the level of conservation among *DME* homoeologues at the small interfering RNA targeted sites, explain the observed incomplete elimination of gluten proteins. This partial elimination of prolamins has motivated us to pyramid the effects of different transformants into a single plant to obtain genotypes completely devoid of celiac-causing prolamins. To achieve the desired objective, crossing of selected transformants after doubled haploidization is currently underway.

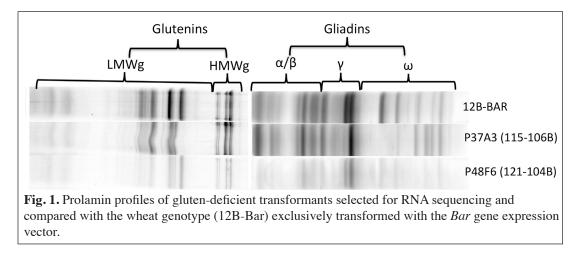
Determining the end-use quality of the gluten-deficient wheat transformants. In order to get the preliminary idea about the end-use quality of the selected wheat transformants, T_4 grains of these genotypes were used for detailed mixing and baking experiments at the Western Wheat Quality Laboratory in Pullman. In view of the importance of the physical properties of grain in determining end-use quality, a number of single-kernel parameters, such as grain hardness, grain weight, and grain size, were studied using the Single-Kernel Characterization System (SKCS). However, no major difference in the physical properties of the selected transformants and the untransformed control was observed. In order to get a deeper insight into the end-use quality of wheat transformants, other physical parameters, such as flour yield, break flour yield, flour ash content, and milling score, were recorded. For these parameters, the transformants exhibited subtle differences among themselves and with the control. Because most of the above-mentioned parameters are reflective of kernel hardness, and the literature suggests that it is not a sole determinative characteristic for bread-making properties, various other parameters that represent flour protein content and gluten strength were studied. Specifically, the SDS (sodium dodecyl sulfate)-sedimentation test and mixograph analyses, which are considered good indicators of bread-making quality, were studied in the selected transformants. The analyses suggested significant gluten strength in transformants P42G4, P32F2, P31D12, P48F6, P78E7, and P48F5 compared with that of the wild-type control, Brundage 96. Interestingly, different transformants exhibited higher scores for different mixograph parameters. Specifically, wheat transformant P31D12, which exhibited a 76.4% reduction in the amount of immunogenic gluten proteins (Wen et al. 2012), also showed the highest gluten strength. In addition to the mixing assay, a baking experiment also was performed with these transformants. In this experiment, the loaf volume of breads baked from the selected wheat transformants ranged from 775 cubic centimeter (CC) for P22H3 and P48F6 to 930 CC for P42G4, whereas the loaf volume of the untransformed control was 765 CC. Four transformants, P42G5, P42G4, P32F2, and P31D12, exhibited significantly high loaf volumes compared with that of the control. Collectively, these biochemical and baking experiments unambiguously suggested that these transformants exhibit physical properties similar to soft wheat genotypes, however, they posses the potential to be baked into breads somewhat similar to hard wheat genotypes.

Background effect of silencing wheat DEMETER homoeologues. To obtain detailed understanding of the global genomic changes taking place due to the silencing of the homoeologous wheat DME genes, a bi-partite approach was adapted, which involves phenotype charcterizing and transcript profiling of the selected wheat transformants. Due to limited availability of the T₂ grains, 3×12 ft. plots with 10 rows each were planted per genotype and four agronomical traits, grain number, grain weight, heading date, and anthesis date, were recorded. Because phenotypic data alone were inadequate for predicting the agronomical potential of the selected wheat transformants, we undertook transcript profiling of these transformants by RNA sequencing (RNA-seq). In this particular case, RNA-seq is expected to provide the information necessary for 'genomic selection', where prediction about a genotype's breeding value is made on the basis of understanding of its genomic constitution. In genomic selection, predictions about the breeding value of an uncharacterized genotype rely on a training set of plants, which is a collection of densely genotyped and precisely phenotyped individuals. To make it financially feasible, we modified this approach by undertaking sequencing of the grain transcriptome instead of the whole genome of the two selected wheat transformants, P37A3, which showed elimination of specific prolamins, and P48F6, which showed an over all reduction in the prolamin content, and compared their transcript profiles with that of the untransformed control and a genotype (12B-Bar) exclusively transformed with selectable marker gene (Bar) construct (Fig. 1). In this case, the two controls, i.e., the untransformed Brundage 96 and 12B-Bar, will serve as the training set, because great body of information about the phenotypic characteristics of Brundage 96 is already available. Transcript profile of 12B-Bar will help in separating out the effect of silencing wheat DME genes from

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that of the genetic transformation. The comparisons based on the transcriptomic data and magnitude of expression level differences between the selected wheat transformants and controls will give a fair idea about the performance of the two gluten-deficient transformants. Other advantages associated with this analysis are the precision and depth of information one receives in comparison to recording a few phenotypic traits. Because many genomic changes do not result in a visible phenotype, due to the masking effect of homoeologous and paralogous gene actions and/or genotype–environment interactions, their effects can be missed by the traditional phenotypic screens. Despite the fact that the methylation status of a gene and its transcriptional pattern are not perfectly correlated, we expect that this analysis will provide sufficient information about the epigenetic regulation of genes involved in endosperm development, which significantly contributes to grain yield. In order to study transcript profiles of the selected transformants and controls, RNA was extracted from 50–70%-filled grains and used for RNA-seq. For this purpose, cDNA libraries were prepared for each genotype and sequenced in-depth using Ion Torrent sequencing procedure. After removal of transcripts derived from the chloroplast and mitochondrial genes, the two controls, Brundage 96 and 12B-Bar, respectively, yielded 107.28 and 84.92 Mb of clean sequence. Simi-

larly, for the two selected transformants, P48F6, which exhibited a 77.8% reduction in immunogenic prolamins, and P37A3, which showed a 40.2% reduction in toxic gluten proteins, 93.95 and 74.75 Mb sequences,



respectively, were obtained (Fig. 1).

The analysis revealed at least 262 and 327 genes showing perturbed expression in P48F6 and P37A3 when respectively compared with 12B-Bar. However, the phenotypic screen performed earlier on these genotypes suggested close similarity among them. Plotting these differentially expressed (DE) genes using a homology search on the wheat chromosome assembles revealed that, in several cases, the number of DE genes does not correspond well with the total number of genes predicted for that chromosome or group of homoeologous chromosomes.

This biased distribution of differentially expressed genes in the wheat genome has prompted us to investigate if there is a location effect within each chromosome by virtually mapping differentially expressed genes onto the chromosome assemblies. In several instances, plotting the observed number of differentially expressed genes onto the chromosome axis with the expected number of differentially expressed genes revealed biased distribution. This analysis clearly showed that the DME targeted sites are nonrandomly distributed in the wheat genome. The preliminary data from *Arabidopsis* exhibited localized demethylation at >9,000 loci in the euchromatic regions (Ibarra et al. 2012). Whereas, the preliminary data presented here do not suggest that the magnitude of changes is similar in two plant species, this aspect warrants further investigation.

In order to demonstrate correspondence between gene methylation/demethylation and its transcription, 10 up and 10 down regulated genes showing maximum expression level differences were listed in each combination. Interestingly, the genes showing maximum expression level differences overlapped among different combinations, which further supported the idea that these observations are non-random. These highly up/down regulated genes currently are being tested for the endosperm-specific changes in DNA methylation pattern using bisulphite sequencing in two wheat transformants, P48F6 and P37A3. This analysis will throw further light on the role of DME during the grain development in small grain cereals. Acknowledgements. This work was supported by National Institutes of Health Grants GM080749-01A2 and 2R42DK072721-02, and Life Sciences Discovery Fund Grant 3143956.

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National Small Grains Collection activities.

H.E. Bockelman, Agronomist and Curator.

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

Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN): <u>http://www.ars-grin.gov/npgs</u>. 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. There were no PI assignments in *Aegilops* or *Secale* in the past year.

Table 1. Recent PI assignments in Triticum, X Triticosecale, Aegilops, and Secale.							
		Cultivar name or					
PI number	Taxonomy	identifier	Country	State/Province			
671987 PVPO	Triticum aestivum subsp. aestivum	Doublestop CL Plus	United States	Oklahoma			
671988 PVPO	Triticum aestivum subsp. aestivum	WB9507	United States	Illinois			
671989 PVPO	Triticum aestivum subsp. aestivum	WB1529	United States	Illinois			
671990 PVPO	Triticum aestivum subsp. aestivum	WB1604	United States	Illinois			
671991 PVPO	Triticum aestivum subsp. aestivum	WB6121	United States	Illinois			
671992 PVPO	Triticum aestivum subsp. aestivum	WB6341	United States	Illinois			
671993 PVPO	Triticum aestivum subsp. aestivum	WB6430	United States	Illinois			
671994 PVPO	Triticum aestivum subsp. aestivum	WB9668	United States	Illinois			
671995	Triticum aestivum subsp. aestivum	UC1113 + Hope FT-B1	United States	California			
671996	Triticum aestivum subsp. aestivum	UC1041 + Hope FT-B1	United States	California			
671997	Triticum aestivum subsp. aestivum	UC1041 Yr15+ GluD1d	United States	California			
671998	Triticum aestivum subsp. aestivum	UC1110 + Hope FT-B1	United States	California			
671999	Triticum aestivum subsp. aestivum	UC1110 + Yr15 + Yr5 + Yr17 + GluD1d + Gpc- B1 + Yr36	United States	California			
672000	Triticum aestivum subsp. aestivum	Kern + Hope FT-B1	United States	California			
672001	Triticum aestivum subsp. aestivum	Kern + Yr5 + Yr17 + GluD1d	United States	California			
672002	Triticum aestivum subsp. aestivum	Clear White + <i>vrn-B1</i> + Hope FT-B1	United States	California			
672003	Triticum aestivum subsp. aestivum	Clear White + vrn-B1	United States	California			
672004	Triticum aestivum subsp. aestivum	Clear White + Hope FT-B1	United States	California			
672005	Triticum aestivum subsp. aestivum	Clear White + $Yr17$ + Yr15	United States	California			
672072 PVPO	Triticum aestivum subsp. aestivum	LCS Iguacu	United States	Colorado			
672163 PVPO	Triticum aestivum subsp. aestivum	3120	United States	Georgia			
672164 PVPO	Triticum aestivum subsp. aestivum	Linkert	United States	Minnesota			
672165 PVPO	X Triticosecale spp.	Buxom	United States	Arizona			

A N N U A L W H E A T N E W S L E T T E R **Table 1.** Recent PI assignments in *Triticum, X Triticosecale, Aegilops,* and *Secale,*

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672540 JPRTriticum aestivum subsp. aestivumL699672556 PVPOTriticum aestivum subsp. aestivumMS Sting	China	Sichuan
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	ray United States	s Colorado
	United States	
672559 PVPO Triticum aestivum subsp. aestivum WB7390	United States	
672560 PVPO Triticum aestivum subsp. aestivum WB7618	United States	
672561 PVPO Triticum aestivum subsp. aestivum WB9112	United States	
672579 PVPO <i>Triticum aestivum</i> subsp. <i>aestivum</i> SY Lland		
672580 PVPO <i>Triticum aestivum</i> subsp. <i>aestivum</i> BC03212		
672581 PVPO <i>Triticum aestivum</i> subsp. <i>aestivum</i> SY Monu		
672582 PVPO Triticum aestivum subsp. aestivum SY Sky	United States	
672583 PVPO Triticum aestivum subsp. aestivum SY Cypr	i	
672584 PVPO Triticum aestivum subsp. aestivum SY Basa	ss United States	
672585 PVPO Triticum aestivum subsp. aestivum SY 547	i	
672586 PVPO Triticum aestivum subsp. aestivum SY Ingm	t United States	s Iowa
672587 PVPO Triticum aestivum subsp. aestivum HRS 336	t United States United States	
672588 PVPO Triticum aestivum subsp. aestivum HRS357	t United States United States ar United States	s Iowa

A N N U A L W H E A T N E W S L E T T E R **Table 1.** Recent PI assignments in *Triticum, X Triticosecale, Aegilons,* and *Secale.*

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Table 1. Recent PI assignments in Triticum, X Triticosecale, Aegilops, and Secale.							
PI number	Taxonomy	identifier	Country	State/Province			
672589 PVPO	X Triticosecale spp.	SY TF 131	United States	Iowa			
672590 PVPO	X Triticosecale spp.	SY TF 813	United States	Iowa			
672837	Triticum aestivum subsp. aestivum	Hahn 1RS ^{ww}	United States	California			
672838	Triticum aestivum subsp. aestivum	Hahn 1RS ^{WR}	United States	California			
672839	Triticum aestivum subsp. aestivum	Hahn 1RS ^{RW}	United States	California			
672996 JPR	Triticum turgidum	UC1308 2+12	United States	California			
672997 JPR	Triticum turgidum	UC 1171 2+12	United States	California			
672998 JPR	Triticum turgidum	UC 1113 Gpc 2+12	United States	California			
673013 PVPO	Triticum aestivum subsp. aestivum	W020016C1	United States	Iowa			
673014 PVPO	Triticum aestivum subsp. aestivum	W020175C1	United States	Iowa			
673015 PVPO	Triticum aestivum subsp. aestivum	W020314H3	United States	Iowa			
673016 PVPO	Triticum aestivum subsp. aestivum	W030033A1	United States	Iowa			
673017 PVPO	Triticum aestivum subsp. aestivum	W030065A1	United States	Iowa			
673018 PVPO	Triticum aestivum subsp. aestivum	W030154L1	United States	Iowa			
673019 PVPO	Triticum aestivum subsp. aestivum	W030189G1	United States	Iowa			
673020 PVPO	Triticum aestivum subsp. aestivum	W030240F1	United States	Iowa			
673021 PVPO	Triticum aestivum subsp. aestivum	W030377L1	United States	Iowa			
673022 PVPO	Triticum aestivum subsp. aestivum	W030396G1	United States	Iowa			
673023 PVPO	Triticum aestivum subsp. aestivum	W030410S2	United States	Iowa			
673024 PVPO	Triticum aestivum subsp. aestivum	W030578B1	United States	Iowa			
673086 PVPO	Triticum aestivum subsp. aestivum	LCS News	United States	Colorado			
673087 PVPO	Triticum aestivum subsp. aestivum	LCS Rews	United States	Colorado			
	1						
673088 PVPO	Triticum aestivum subsp. aestivum	W020307E1	United States China	Iowa			
673103 JPR	Triticum aestivum subsp. aestivum	ShunMai 1718		Shanxi			
673106 PVPO	Triticum turgidum subsp. durum	Joppa	United States	North Dakota			
673131 PVPO	Triticum aestivum subsp. aestivum	Redfield	United States	South Dakota			
673132 PVPO	Triticum aestivum subsp. aestivum	Rosalyn	United States	Oregon			
673133 PVPO	Triticum aestivum subsp. aestivum	Bobtail	United States	Oregon			
673134 PVPO	Triticum aestivum subsp. aestivum	Moats	Canada	Ontario			
673347 JPR	Triticum aestivum subsp. aestivum	ShunMai yyAh	China	Shanxi			
673352 PVPO	Triticum aestivum subsp. aestivum	Flourish	Canada	Alberta			
673410	Triticum aestivum subsp. aestivum	6x: GPC-A1 WT: GPC- D1 MT	United States	California			
673411	Triticum aestivum subsp. aestivum	6x: GPC-A1 MT: GPC- D1 WT	United States	California			
673412	Triticum aestivum subsp. aestivum	6x: GPC-A1 MT: GPC- D1 MT	United States	California			
673413	Triticum turgidum subsp. durum	4x: GPC-A1 WT: GPC- B2 MT	United States	California			
673414	Triticum turgidum subsp. durum	4x: GPC-A1 MT: GPC- B2 WT	United States	California			
673415	Triticum turgidum subsp. durum	4x: GPC-A1 MT: GPC- B2 MT	United States	California			
673416	Triticum aestivum subsp. aestivum	NX10MD2299	United States	Nebraska			
673417	Triticum aestivum subsp. aestivum	NX10MD2300	United States	Nebraska			
673418	Triticum aestivum subsp. aestivum	NX10MD2216	United States	Nebraska			
673419	Triticum aestivum subsp. aestivum	N10MD2020	United States	Nebraska			
673420	Triticum aestivum subsp. aestivum	N10MD2023	United States	Nebraska			
	Triticum aestivum subsp. aestivum	N02Y5149-13	United States	Nebraska			
D/34/1		1 1 1 0 4 1 2 1 7 2 1 2	Junea States	1 WOLUDING			
673421 673422	Triticum aestivum subsp. aestivum	N02Y5149-10	United States	Nebraska			

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	PI assignments in <i>Triticum</i> , <i>X Triticose</i>	Cultivar name or		
PI number	Taxonomy	identifier	Country	State/Province
673428 JPR	Triticum aestivum subsp. aestivum	102-51-2	United States	Montana
673429 JPR	Triticum aestivum subsp. aestivum	102-51-5	United States	Montana
673430 JPR	Triticum aestivum subsp. aestivum	103-51-4	United States	Montana
673431 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	302-52-3	United States	Montana
673432 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	302-52-9	United States	Montana
673433 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	303-56-12	United States	Montana
673434 JPR	Triticum aestivum subsp. aestivum	402-53-1	United States	Montana
673435 JPR	Triticum aestivum subsp. aestivum	402-53-4	United States	Montana
673436 JPR	Triticum aestivum subsp. aestivum	403-57-15	United States	Montana
673437 JPR	Triticum aestivum subsp. aestivum	502-55-11	United States	Montana
673438 JPR	Triticum aestivum subsp. aestivum	502-55-16	United States	Montana
673439 JPR	Triticum aestivum subsp. aestivum	503-51-1	United States	Montana
673440 JPR	Triticum aestivum subsp. aestivum	702-51-1	United States	Montana
673441 JPR	Triticum aestivum subsp. aestivum	702-51-4	United States	Montana
673442 JPR	Triticum aestivum subsp. aestivum	703-55-16	United States	Montana
673453 PVPO	Triticum aestivum subsp. aestivum	102015123	United States	Virginia
673943 PVPO	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Prestige	United States	Colorado
673944 PVPO	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Atomo	United States	Colorado
673945 PVPO	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Star	United States	Colorado
673946 PVPO	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Pro	United States	Colorado
674000	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	ProINTA Imperial	Argentia	Cordoba
		ProINTA Imperial NIL		
674001	Triticum aestivum subsp. aestivum	Glu-A3e	United States	California
674002	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL Glu-A3f	United States	California
674003	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
074003	Truicum destivum subsp: destivum	Glu-A3g	United States	Camornia
674004	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
074004	Trucum destivum subsp. destivum	Glu-B3a	United States	Camornia
674005	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
071005	Triteum destrum subsp. destrum	Glu-B3b_Buck Poncho	Office States	Cumorina
674006	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
071000	Triteum destrum subsp. destrum	<i>Glu-B3b</i> _RetaconINTA	Office States	Cumorina
674007	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
		Glu-B3g		
674008	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
	1	<i>Glu-B3i</i> _BuckManant.		-
674009	Triticum aestivum subsp. aestivum	ProINTA Imperial NIL	United States	California
(7410(IDD	-	<i>Glu-B3i_</i> NorkinChur.	TT : 10	0111
674106 JPR	X Triticosecale spp.	NF201	United States	Oklahoma
674161 PVPO	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	25R72	United States	Minnesota
674162 PVPO	Triticum aestivum subsp. aestivum	25R25	United States	Minnesota
674163PVPO	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	25R50	United States	Minnesota
674173 JPR	Triticum aestivum subsp. aestivum	SA 16486	South Africa	Free State
674174 JPR	Triticum aestivum subsp. aestivum	SA 16487	South Africa	Free State
674175 JPR	Triticum aestivum subsp. aestivum	SA 16488	South Africa	Free State
674176 JPR	Triticum aestivum subsp. aestivum	SA 16490	South Africa	Free State
674177 JPR	Triticum aestivum subsp. aestivum	SA 16491	South Africa	Free State
674178 JPR	Triticum aestivum subsp. aestivum	Ax1-E28H	United States	California
674179 JPR	Triticum aestivum subsp. aestivum	Ax1-F259C	United States	California
674180 JPR	Triticum aestivum subsp. aestivum	Ax1-F261B	United States	California

		Cultivar name or		
PI number	Taxonomy	identifier	Country	State/Province
674181 JPR	Triticum aestivum subsp. aestivum	Ax1-F80B	United States	California
674182 JPR	Triticum aestivum subsp. aestivum	Ax1-F83B	United States	California
674187 PVPO	Triticum aestivum subsp. aestivum	A030093P1	United States	Indiana
674188 PVPO	Triticum aestivum subsp. aestivum	W030258E2	United States	Indiana
674189 PVPO	Triticum aestivum subsp. aestivum	W040241D1	United States	Indiana
674190 PVPO	Triticum aestivum subsp. aestivum	W040278H1	United States	Indiana
674191 PVPO	Triticum aestivum subsp. aestivum	W040650E1	United States	Indiana
674192 PVPO	Triticum aestivum subsp. aestivum	4231598	United States	Illinois
674193 PVPO	Triticum aestivum subsp. aestivum	4240867	United States	Illinois
674194 PVPO	Triticum aestivum subsp. aestivum	WB1376CLP	United States	Illinois
674195 PVPO	Triticum aestivum subsp. aestivum	WB4614	United States	Illinois
674196 PVPO	Triticum aestivum subsp. aestivum	WB4623CLP	United States	Illinois
674197 PVPO	Triticum aestivum subsp. aestivum	26R94	United States	Georgia
674198 PVPO	Triticum aestivum subsp. aestivum	LX65E89	United States	Georgia
674340 PVPO	Triticum aestivum subsp. aestivum	AP08TS7124	United States	Iowa
674341 PVPO	Triticum aestivum subsp. aestivum	SY Valda	United States	Iowa
674342 PVPO	Triticum aestivum subsp. aestivum	WB7328	United States	Illinois
674343 PVPO	Triticum aestivum subsp. aestivum	WB 7417	United States	Illinois
674344 PVPO	Triticum aestivum subsp. aestivum	WB7589	United States	Illinois
674345 PVPO	Triticum aestivum subsp. aestivum	WB9377	United States	Illinois
674346 PVPO	Triticum aestivum subsp. aestivum	WB9411	United States	Illinois
674347 PVPO	Triticum aestivum subsp. aestivum	WB9653	United States	Illinois
674437 PVPO	X Triticosecale spp.	Wheatly	United States	Arizona
674514 PVPO	Triticum aestivum subsp. aestivum	TAM 305	United States	Texas
674720 JPR	Triticum aestivum subsp. aestivum	ND 816	United States	North Dakota
674721 JPR	Triticum aestivum subsp. aestivum	ND 817	United States	North Dakota
674738 PVPO	Triticum aestivum subsp. aestivum	HRS 3419	United States	Colorado
674739 PVPO	Triticum aestivum subsp. aestivum	Chevelle	United States	Colorado
674740 PVPO	Triticum aestivum subsp. aestivum	LCS Nitro	United States	Colorado
674741 PVPO	Triticum aestivum subsp. aestivum	Sunshine	United States	Colorado

A N N U A L W H E A T N E W S L E T T E R IV. 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 mosaci virus **WYMV** = wheat yellow mosaic virus *E. graminis* f.sp. *tritici* = *Erysiphe graminis* f.sp. *tritici* = the powdery mildew fungus *F. graminearum* = *Fusarium graminearum* = head scab fungus *F. nivale* = *Fusarium nivale* = snow mold fungus *H. avenae* = *Heterodera avenae* = cereal cyst nematode *P. graminis* = *Polymyxa graminis* = wheat soilborne mosaic virus vector *P. striiformis* **f.sp.** *tritici* = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus *P. triticina* = *Puccinia triticina* = *P. recondita* f.sp. *tritici* = leaf rust fungus **R. cerealis** = Rhizoctonia cerealis = sharp eyespot **R.** solani = Rhizoctonia solani = Rhizoctonia root rot *R. padi* = *Rhonpalosiphum padi* = bird cherry-oat aphid *S. tritici* = *Septorai tritici* = Septoria leaf spot fungus *S. graminearum* = *Schizaphus graminearum* = greenbug *St. nodorum* = *Stagonospora nodorum* = *Stagonospora glume blotch T. indica* = *Tilletia indica* = Karnal bunt fungus

SCIENTIFIC NAMES AND SYNONYMS OF GRASS SPECIES (NOTE: CLASSIFICATION ACCORDING TO VAN SLAGEREN, 1994):

A. strigosa = Avena strigosa Ae. cylindrica = Aegilops cylindrica = Triticum cylindricum Ae. geniculata = Aegilops geniculata = Aegilops ovata = Triticum ovatum Ae. longissima = Aegilops longissima = Triticum longissimum Ae. markgrafii = Aegilops markgrafii = Aegilops caudata = Triticum caudatum Ae. speltoides = Aegilops speltoides = Triticum speltoides Ae. tauschii = Aegilops tauschii = Aegilops squarrosa = Triticum tauschii Ae. triuncialis = Aegilops triuncialis = Triticum triunciale Ae. umbellulata = Aegilops umbellulata = Triticum umbellulatum Ae. peregrina = Aegilops peregrina = Aegilops variabilis = Triticum peregrinum Ae. searsii = Aegilops searsii = Triticum searsii Ae. ventricosa = Aegilops ventricosa = Triticum ventricosum D. villosum = Dasypyrum villosum = Haynaldia villosa *S. cereale* = *Secale cereale* = rye *T. aestivum* subsp. *aestivum* = *Triticum aestivum* = hexaploid, bread, or common wheat T. aestivum subsp. macha = Triticum macha *T. aestivum* subsp. *spelta* = *Triticum spelta* **T. militinae** = Triticum militinae *T. monococcum* subsp. *aegilopoides* = *Triticum* boeoticum T. timopheevii subsp. timopheevii = Triticum timopheevii T. timopheevii subsp. armeniacum = Triticum araraticum = T. araraticum *T. turgidum* subsp. *dicoccoides* = *Triticum dicoccoides* = wild emmer wheat

T. turgidum subsp. *durum* = *Triticum durum* = *durum*, pasta, or macaroni wheat *T. urartu* = *Triticum urartu Th. bessarabicum* = *Thinopyrum bassarabicum Th. elongatum* = *Thinopyrum elongatum* = *Agropyron elongatum Th. intermedium* = *Thinopyrum intermedium* = *Agropyron intermedium*

SCIENTIFIC JOURNALS AND PUBLICATIONS:

T. turgidum subsp. *dicoccum* = *Triticum dicoccum*

Agron Abstr = Agronomy Abstracts **Ann Wheat Newslet** = *Annual Wheat Newsletter* Aus J Agric Res = Australian Journal of Agricultural Research **Can J Plant Sci** = Canadian Journal of Plant Science **Cereal Chem** = *Cereal Chemistry* **Cereal Res Commun** = *Cereal Research Communications* **Curr Biol** = *Current Biology* **Eur J Plant Path** = European Journal of Plant Pathology **Funct Integ Genomics** = Functional Integrative Genomics Ind J Agric Sci = Indian Journal of Agricultural Science **Int J Plant Sci** = International Journal of Plant Science **J Agric Sci Technol** = Journal of Agricultural Science and Technology **J Cereal Sci** = Journal of Cereal Science **J Hered** = Journal of Heredity **J Phytopath** = *Journal of Phytopathology* **J Plant Phys** = Journal of Plant Physiology **Mol Gen Genet** = *Molecular and General Genetics* **Nat Genet** = *Nature Genetics* **PAG** = Plant and Animal Genome (abstracts from meetings) **Phytopath** = *Phytopathology* **Plant Breed** = *Plant Breeding* **Plant, Cell and Envir** = *Plant, Cell and Environment* **Plant Cell Rep** = *Plant Cell Reporter* **Plant Dis** = *Plant Disease* **Plant Physiol** = *Plant Physiology* **Proc Ind Acad Sci** = *Proceedings of the Indian Academy of Sciences* **Proc Natl Acad Sci USA** = Proceedings of the National Academy of Sciences USA Sci Agric Sinica = Scientia Agricultura Sinica **Theor Appl Genet** = *Theoretical and Applied Genetics* Wheat Inf Serv = Wheat Information Service

UNITS OF MEASUREMENT:

bp = base pairs **bu** = bushels **cM** = centimorgan **ha** = hectares **kDa** = kiloDaltons m^2 = square meters m^3 = cubic meters μ = micron **masl** = meters above sea level **me** = milli-equivalents **mL** = milliliters **mmt** = million metric tons **mt** = metric tons **Q** = quintals **T** = tons **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 $\mathbf{BW} = \text{bread wheat}$ **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 tagFAWWON = Facultative and Winter Wheat Observation Nursery GA = gibberellic acid**GIS** = geographic-information system **GM** = genetically modified **GRIN** = Germplasm Resources Information Network **HPLC** = high pressure liquid chromatography **HMW** = high-molecular weight (glutenins) **HRSW** = hard red spring wheat **HRRW** = hard red winter wheat **HWSW** = hard white spring wheat **HWWW** = hard white winter wheat **ISSR** = inter-simple sequence repeat **IT** = infection type **kD** = kilodalton **LMW** = low molecular weight (glutenins) **MAS** = marker-assisted selection **NSF** = National Science Foundation **NILs** = near-isogenic lines **NIR** = near infrared **NSW** = New South Wales, region of Australia **PAGE** = polyacrylamide gel electrophoresis **PCR** = polymerase chain reaction **PFGE** = pulsed-field gel electrophoresis **PMCs** = pollen mother cells **PNW** = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada) **PPO** = polyphenol oxidase **QTL** = quantative trait loci **RAPD** = random amplified polymorphic DNA **RCB** = randomized-complete block **RFLP** = restriction fragment length polymorphism **RILs** = recombinant inbred lines **RT-PCR** = real-time polymerase-chain reaction **SAMPL** = selective amplification of microsatellite polymorphic loci **SAUDPC** = standardized area under the disease progress curve **SCAR** = sequence-characterized amplified region **SDS-PAGE** = sodium dodecyl sulphate polyacrylamide gel electrophoresis

SE-HPLE = size-exclusion high-performance liquid chromatography
SH = synthetic hexaploid
SNP = single nucleotide polymorphism
SRPN = Southern Regional Performance Nursery
SRWW = soft red winter wheat
SRSW = soft red spring wheat
STMA = sequence tagges microsatellite site
SWWW = soft white winter wheat
SSD = single-seed descent
SSR = simple-sequence repeat
STS = sequence-tagged site
TKW = 1,000-kernel weight
UESRWWN = Uniform Experimental Soft Red Winter Wheat Nursery
VIGS = virus-induced gene silencing

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ANNUAL WHEAT NEWSLETTER VII. VOLUME 62 MANUSCRIPT GUIDELINES.

The required format for Volume 62 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 44–61 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Use Microsoft WordTM 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 <u>jraupp@k-state.edu</u>.

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The Annual Wheat Newsletter also will continue to be available (Vol. 37–61) through the Internet on Grain-Genes, the USDA–ARS Wheat Database at <u>http://wheat.pw.usda.gov/ggpages/awn/</u>.