ANNUAL WHEAT NEWSLETTER

Volume 63

Contribution no. 18-097-B from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

ANNUAL WHEAT NEWSLETTER

Volume 63

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

1 September, 2017.

Contribution no. 18-097-B from the Kansas Agricultural Experiment Station, Kansas State University, Manhattan.

TABLE OF CONTENTS

IN DEDICATION TO
DR. SHIVCHARAN SINGH MAAN

Dr. S.S. Maan, a world renowned wheat geneticist, born 11 January, 1926, in Karnal, Punjab, India passed away on 1 November, 2016, at home in Davis, California, while in the care of his wife Ranjit Kaur and daughter Ajit Kaur.

After receiving his B.S. degree in Botany from Punjab University in 1948. He studied at Kansas State University, Manhattan, obtaining an M.S. degree in 1958 and a Ph.D. in 1961. While working as a postdoctoral fellow at the University of Nebraska, Lincoln (1961–63), he made a seminal discovery of a genetic system for producing hybrid wheat. He would then devote his life to hybrid wheat research as a faculty member at North Dakota State University, Fargo, from 1964 until his retirement in 2000.

Dr. Maan was a deep thinker and his discoveries and vision for hybrid wheat were ahead of their time, only now attracting huge interest from industry and academia. Currently, hundreds of millions of dollars are being spent working with materials that Dr. Maan developed to realize the dream of hybrid wheat. The genetic stocks and breeding lines that Dr. Maan and his collaborator Karl Lucken developed underpin hybrid wheat programs around the world, helping to increase wheat yield so that we may be able to feed 9.5 billion people by 2050. Dr. Maan trained many graduate students and postdoctoral fellows, collaborated with many scientists around the world, and published over 100 research papers. For his outstanding research achievements, Dr. Maan was honored as Fellow of the Crop and Agronomy Societies of America and received the Crop Science Research award in 1980. He was awarded the first Distinguished Professorship at North Dakota State University among many other awards and recognitions.

He is survived by his wife of 61 years, Ranjit Kaur Maan, his son Paul Singh Maan, and his daughter Dr. Ajit Kaur Maan, and his grandchildren Sohni Shivan Maan-Davie and Simrin Ruchi Maan-Davie.

I. WHEAT WORKER'S CODE OF ETHICS

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

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

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

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

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

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

ITEMS FROM AZERBAIJAN

GENETIC RESOURCES INSTITUTE
Azerbaijan National Academy of Science, Baku, Azerbaijan.

Evaluating genetic diversity of durum and bread wheat genotypes using Next-generation Sequencing.

Mehraj Abbasov, Zeynal Akparov, Khanbala Rustamov, Sevda Babayeva, Vusala Izzatullayeva, Fatma Sheykzamanova, Sveta Rzayeva, and Elchin Hajiyev; Robert L. Bowden (USDA–ARS Hard Winter Wheat Genetics Research Unit, Manhattan, KS 66506 USA); W. John Raupp and Bikram S. Gill (Wheat Genetics Resource Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506 USA); and Sunish Sehgal (Department of Agronomy, Horticulture & Plant Science, South Dakota State University, Brookings, SD 57007, USA).

The bread wheat (2n=6x=42) genome, 17 GB size and 124,201 genes, is considered to be one of the largest and the most complex genomes among crop plant species and also is a polyploid consisting of three different subgenomes (AABBDD). Both *de novo* and re-sequencing are extremely complicated processes and require detailed bioinformatic data analyses. Genotyping-by-sequencing (GBS) is based on simplifying the complexity of genomes using restriction enzymes with no requirement for a reference genome for detecting SNPs. We used GBS for genotyping durum wheat (*T. turgidum*, 2n=4x=28, genomes AABB) and bread wheat accessions. We genotyped 82 durum wheat accessions belonging to 13 botanical varieties, mainly from Azerbaijan. We identified 1,058 SNPs with less that 50% missing data and studied the genetic variability in 71 accessions of *Triticum turgidum* subsp. *durum*. A dendrogram was constructed that classified genotypes from the same botanical varieties into congenial clusters. Improved varieties of Azerbaijani origin were genetically close, in contrast with the relatively different U.S. durum cultivar Langdon.

Introduction. Azerbaijan has unique diversity of populations of *Aegilops* and wild barley (*Hordeum vulgare* subsp. *spontaneum* (C.Koch) Thell.), which are the progenitors and wild relatives of cultivated wheat and barley (Aliyev et al. 2007, 2008). Wheat and barley are considered main food and feed crops worldwide, thus the subject of many investigations. Until recently, most genetic investigations is used biomorphologic, protein marker, or molecular markers (Babayeva et al. 2009; Izzatullayeva et al. 2014; Hajiyev et al. 2015). With the advent of Next-generation Sequencing (NGS) technologies a new era has begun in genomics; genome sequencing is easier, more accessible, and effective. Development and application of NGS has provided many opportunities in molecular marker development, transcriptome investigations, and phylogenetic and ecological studies. A number of research centers created Next-generation sequencers. Currently, widely used NGS systems include the Roche/454 FLX, the Illumina/Solexa Genome Analyzer, the Applied Biosystems SOLiDTM, the Ion Torrent, and the PacBio. Using these devices, in the last decade, many herbaceous and woody plant (nuclear) genomes were sequenced. *Arabidopsis thaliana* was the first plant species with the whole nuclear genome sequenced (The Arabidopsis Genome Initiative 2000). Later, the genomes of two rice varieties, Japonica and Indica, were sequenced by Goff et al. (2002) and Yu et al. (2002). Recently, more than 50 different plant species have been sequenced, including genomes of two of the *Prunus* subfamilies of the *Rosaceae*, plum (Japanese apricot, *Prunus mume*; 280 Mb; Zhang et al. 2012) and peach (*Prunus persica*; 265 Mb; Verde et al. 2013); *Aegilops* (Jia et al. 2013); and bread wheat (Brenchley et al. 2012).

Genome analysis of wheat and barley using new, modern technologies has created new opportunities for breeding. Different assumptions about the origin of the bread wheat genomes have been put forward. Recent studies have shown that A and B genome arose about 7 x 10^9 years ago from the same origin. The D genome arose from A and B genome after 1–2.7 x 10^9 years. Through sequencing of all three genomes, the genome size of bread wheat is 17 GB and includes 124,201 genes.

Plant material. This study used 83 durum and 100 bread wheat lines belonging to 29 botanical varieties, mainly from Azerbaijan and Central Asia (Figs. 1 and 2).

DNA extraction and GBS. Young leaves for each accession were collected and lyophilized for DNA extraction according to the CTAB procedure described by Doyle and Doyle (1987). The GBS libraries were constructed in 95-plex and genomic DNA was co-digested with restriction enzymes *Pst*I (CTGCAG) and *Msp*I (CCGG). Barcoded adapters were ligated to individual samples. Samples were pooled by plate into libraries and PCR-amplified. Each 95-plex library was sequenced to 100 bp on a single lane of an Illumina HiSeq 2500. Sequence results were analyzed using the UNEAK GBS pipeline, which is part of the TASSEL 3.0 bioinformatics analysis package.

GBS and SNP discovery. We genotyped 102 accessions of *T. aestivum* using GBS, however 20 accessions had sequence data < 30 % of the SNPs and were removed from the analysis. In total, 897 SNPs were identified and 411 SNPs had genotype information ≥50% individuals. The data analysis obtained from GBS of *T. aestivum* is being processed.

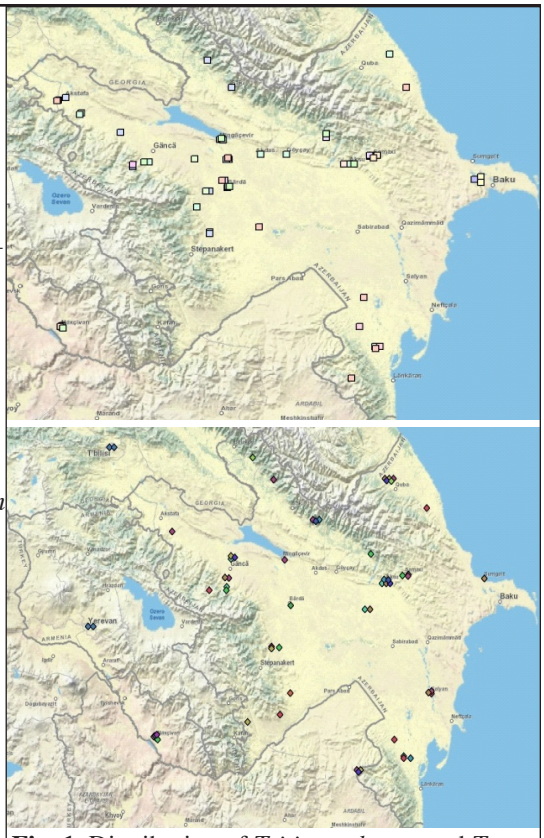

Fig. 1. Distribution of *Triticum durum* and *T. aestivum* accessions from Azerbaijan. Each square represents a durum (top) and each diamond represents a wheat (bottom) accession placed on the map according to latitude and longitude.

From the GBS analysis of 83 durum wheat accessions, we identified 1,058 SNPs with <50% missing data and studied the genetic variability in 71 accessions of *T. turgidum* subsp. *durum*. A dendrogram was constructed that classified genotypes into eight clusters (Fig. 3, p. 5). Most of the improved varieties of Azerbaijan origin were genetically close and fell into the same subclusters within cluster 1 and cluster 8, indicating that these cultivars share alleles. Sharg and Jafari were the closest related cultivars. Sadigov-Baykishi (2015) reported a 100% similarity among these two improved varieties and both are var. *horanoleucurum*. In contrast, the U.S. durum cultivar Langdon was relatively different from the local varieties. Of the 13 botanical varieties, the most similarity was within var. *leucurum*, followed by var. *hordeiforme* and var. *leucomelan,* which formed separate groups with minimal distance between. Cluster 3 was comprised of only one genotype, var. *melanopus* from the Nakhchivan region, indicating the distinct nature of this accession.

Fig. 2. Distribution of wheat accessions from Azerbaijan and Central Asia. Each square represents a durum and each diamond represents a wheat accession placed on the map according to latitude and longitude.

Acknowledgment. Mehraj Abbasov thanks the USDA and the Borlaug family for funding a Norman Borlaug International Agricultural Science and Technology Fellowship.

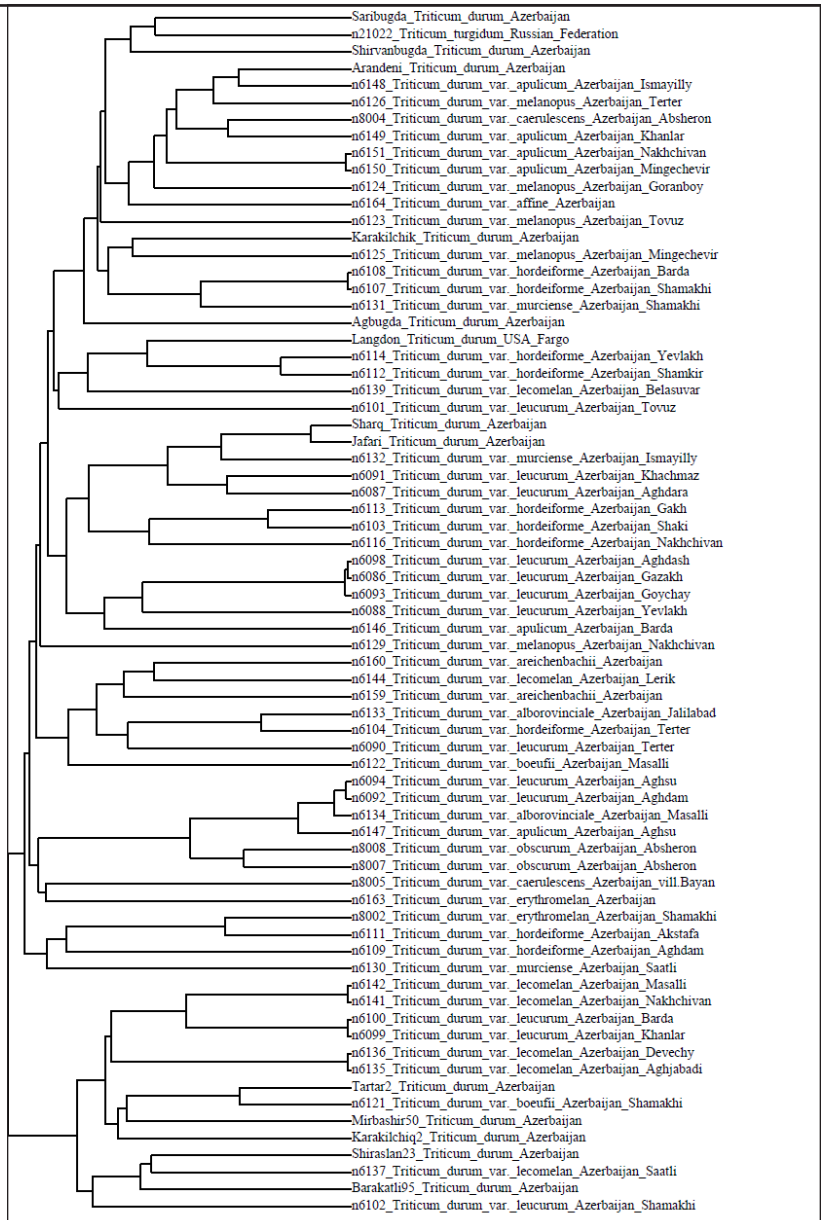

Fig. 3. Grouping of durum wheat accessions based on genotyping-by-sequencing data.

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ITEMS FROM BRAZIL

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

Wheat in Brazil – 2016 crop year.

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

In 2016, the Brazilian wheat production was a little bit higher than 6 x 10^6 tons (Conab 2017), 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 91.2% 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 very favorable to wheat in 2016. However, the commercialization of production was not easy, because of the price payed to the producers.

Table 1. Cultivated area, total production and grain yield of wheat in Brazil in 2015 (* estimated value in March, 2017 (source: CONAB. 2017).

Region	Area (ha x 1,000)	Production (t x 1,000)*	Grain yield (kg/ha)*
North	—	—	—
Northeast	3.0	18.0	6,000
West-central	32.9	120.3	3,657
Southeast	161.1	459.4	2,852
South	1,921.4	6,129.1	3,190
Brazil [total]	**2,118.8**	**6,729.8**	**3,175**

Reference.

CONAB. 2017. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Disponível em: http://www.conab.gov.br/conabweb/index.php?PAG=131 (In Spanish).

Performance of wheat cultivars in the state of Rio Grande do Sul, Brazil, in 2015.

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

The Brazilian Commission of Wheat and Triticale Research (BCWTR) annually conducts the State Test of Wheat Cultivars in the Rio Grande do Sul state (STWC–RS). This work evaluates wheat cultivar grain yield performance of the STWC–RS in 2015. The grain yield performance of 30 wheat cultivars (Ametista, BRS 327, BRS 331, BRS Marcante, BRS Parrudo, BRS Reponte, CD 1440, CD 1805, Celebra, Esporão, Estrela Atria, Jadeíte, LG Oro, LG Prisma, Marfim, Mirante, ORS Vintecinco, Quartzo, TBIO Alvorada, TBIO Iguaçu, TBIO Itaipu, TBIO Mestre, TBIO Pioneiro, TBIO Sintonia, TBIO Sinuelo, TBIO Tibagi, TBIO Toruk, TEC 10, TEC Frontale, and Topazio) was studied in 12 environments (Coxilha, Cruz Alta, Passo Fundo, Sertão, Vacaria, Augusto Pestana, Eldorado do Sul, Ijuí, Santo Augusto, São Borja, São Luiz Gonzaga, and Três de Maio), in the state of Rio Grande do Sul in 2015. The experiments were carried out in a randomized block design with three or four repetitions. Each plot consisted of five rows, 5-m long with a 0.2-m spacing between rows; the plant density was about 330 plants/m^2. Grain yield data (kg/ha) were subjected to individual analysis of variance (for each environment) and grouped analysis of variance (for all environments). The grouped analysis of variance employed the mixed model (fixed cultivar effect and randomized environment effect). The grain yield performance of wheat cultivars was evaluated by analyzing 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 the ability to respond positively to improvement of favorable environments. The general average of STWC–RS in 2015 was 3,428 kg/ha. The experiment conducted in Cruz Alta had the highest average grain yield; 4,582 kg/ha. The maximum grain yield was 5,566 kg/ha in Cruz Alta. a Celebra cultivar. Cultivars TBIO Mestre, Topazio, BRS Marcante, LG Prisma, and TBIO Sinuelo had adaptability and stability in favorable environments (environments with average grain yield higher than the general average). Cultivars ORS Vintecinco, LG Prisma, TBIO Mestre, Ametista and Estrela Atria had adaptability and stability in unfavorable environments (environments with average of wheat grain yield lower than the general average). In general, averaged over all environments, cultivars TBIO Mestre (3,801 kg/ha), LG Prisma (3,766 kg/ha), Topazio (3,709 kg/ha), ORS Vintecinco (3,701 kg/ha), and BRS Marcante (3,708 kg/ha) came closest to the ideal cultivar.

Reference.

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

Wheat crop in the state of Rio Grande do Sul, Brazil, in 2015.

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. This study analyzed the wheat crop in Rio Grande do Sul in 2015. In 2015, Rio Grande do Sul harvested 874,362 ha of wheat (35.4% of the total area harvested in Brazil), producing 1,391,829 tons of wheat (25.3% of the Brazilian production), with an average of grain yield of 1,592 kg/ha (636 kg/ha below the Brazilian average of 2,228 kg/ha).

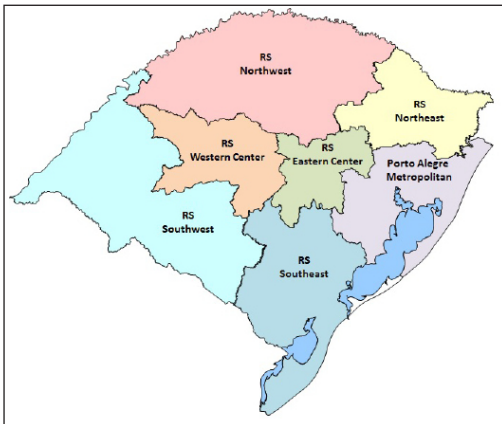

Fig. 1. Mesoregions in the state of Rio Grande do Sul, Brazil.

Among the geographical mesoregions of the Rio Grande do Sul state (Fig. 1, p. 6), the RS Northwest mesoregion harvested the largest wheat area, 691,613 ha (79.1% of the cropped area in the state), and had the largest production, 1,061,648 tons of grain (76.3% of state production) (Table 2). However, the average of grain yield obtained in this mesoregion was the third highest of the state; 1,535 kg/ha (57 kg/ha below the state average) (Table 2). The RS Northeast mesoregion harvested 41,651 ha of wheat (4.8 % of the cropped area in the state), produced 102,266 tons of wheat grain (7.3 % of state production), and had the highest average grain yield in the state; 2,455 kg/ha (863 kg/ha above the state average) (Table 2). The wheat crop in Rio Grande do Sul in 2015 had unfavorable weather conditions, with a late frost and an excess of rain in the spring. In Passo Fundo, in the RS Northwest mesoregion, for example, it rained a total of 673.1 mm in the months of September, October and November. Consequently, the average wheat grain yield in 2015 was very low in Rio Grande do Sul. Comparing the wheat crop data with the results of the STWC–RS in 2015, we observed an average grain yield of commercial crops 1,836 kg/ha, below the STWC-RS average of 3,428 kg/ha.

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 2015 (Source: IBGE. 2017).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	691,613	79.1	1,061,648	76.3	1,535
RS Northeast	41,651	4.8	102,266	7.3	2,455
RS Western Center	60,586	6.9	83,600	6.0	1,380
RS Eastern Center	12,627	1.4	18,907	1.4	1,497
Porto Alegre Metropolitan	2,253	0.3	2,394	0.2	1,063
RS Southwest	54,312	6.2	108,808	7.8	2,003
RS Southeast	11,320	1.3	14,206	1.0	1,255
Rio Grande do Sul State	874,362	100.0	1,391,829	100.0	1,592

Reference.

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ITEMS FROM GERMANY

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

A. Börner, M. Agacka-Mołdoch, D.Z. Alomari, M.G. Cardelli, A.M. Castro, Yu.V. Chesnokov, A.K. Chistyakova, M. Dell' Arciprete, J.I. Dietz, K. Eggert, Fauzia, G.S. Gerard, D. Giménez, K. Jończyk, U. Lohwasser, G. Lori, I. Malbrán, E.V. Morozova, Q.H. Muqaddasi, M. Nagel, S.V. Osipova, H.M. Pardi, A.E. Perelló, L. Perello, A.V. Permyakov, M.D. Permyakova, T.A. Pshenichnikova, M.A. Rehman Arif, M.S. Röder, S.V. Rudakov, A.S. Rudakova, E.G. Rudikovskaya, A.V. Rudikovsky, L. Saldúa, M. Schierenbeck, U. Skomra, L.V. Shchukina, S. Shokat, M.R. Simón, A.V. Simonov, R. Tarawneh, J.P. Uranga, M.E. Vicente, N. von Wirén, M. Yanniccari, and Chr. D. Zanke.

Genome-wide analysis of resistance to eyespot disease in European winter wheat.

Eyespot (also called Strawbreaker) is a common and serious fungal disease of winter wheat caused by the necrotrophic fungi *Oculimacula yallundae* and *O. acuformis* (former name *Pseudocercosporella herpotrichoides*). A genome-wide association study for eyespot was performed with 732 microsatellite markers (SSR) and 7,761 mapped single-nucleotide

polymorphism (SNP) markers derived from the 90K iSELECT wheat array using a panel of 168 European winter wheat cultivars and three spring wheat cultivars and phenotypic evaluation of eyespot in field tests in three environments. Best linear unbiased estimations (BLUEs) were calculated across all trials and ranged from 1.20 (most resistant) to 5.73 (most susceptible) with an average value of 4.24 and a heritability of $h^2 = 0.91$. A total of 108 SSR and 235 SNP marker-trait associations (MTAs) were identified by considering associations with a $-\log_{10}$ (P-value) ≥ 3.0. Significant MTAs for eyespot-score-BLUEs were found on chromosomes 1D, 2A, 2D, 3D, 5A, 5D, 6A, 7A, and 7D for the SSR markers and chromosomes 1B, 2A, 2B, 2D, 3B, and 7D for the SNP markers. For 18 cultivars (10.5%), a highly resistant phenotype was detected that was linked to the presence of the resistance gene *Pch1* on chromosome 7D. The identification of genotypes with recombination events in the introgressed genomic segment from *Aegilops ventricosa* harboring the *Pch1* resistance gene on chromosome 7DL allowed the fine-mapping of this gene using additional SNP markers, and a potential candidate gene *Traes_7DL_973A33763* coding for a CC–NBS–LRR class protein was identified.

Genetic dissection of anther extrusion in elite European winter wheat.

Efficient, hybrid wheat breeding largely depends on high rates of cross-pollination which can be ensured by high anther extrusion (AE). Here, we report the AE capacity and elucidate its genetics in 514 elite European winter wheat cultivars via genome-wide association studies (GWAS). We observed a wide range of variation among genotypes and a high heritability (0.80) for AE. The whole panel was genotyped with the 35k Affymetrix and 90k iSELECT SNP arrays plus *Ppd-D1, Rht-B1, and Rht-D1* candidate markers. The GWAS revealed 51 MTAs on chromosomes 1A, 1B, 2A, 4D, and 5B, with *Rht-D1* (4D) being the most significant marker. Division of the whole panel, according to the *Rht-D1* genotype, resulted in 212 and 294 cultivars containing the *Rht-D1a* and *Rht-D1b* alleles, respectively. The GWAS performed on these subpanels detected novel MTAs on chromosomes 2D, 3B, and 6A with increased phenotypic variance imparted by individual markers. Our study shows that AE is a highly quantitative trait and wild-type *Rht-D1* greatly improves AE. Moreover, linkage disequilibrium analyses revealed the AE-candidate genomic regions. Understanding the genetics of AE and utilizing the linked markers in breeding programs can help to enhance cross-pollination for the better exploitation of heterosis in wheat.

Genome-wide association mapping of minerals in wheat grains: a potential for wheat quality improvement.

Wheat is one of the most essential and planted crops worldwide and its products are a main source of food and dietary energy for most of the global population. However, billions of people are suffering from nutrient deficiency, food insecurity, and hidden hunger, especially for the mineral elements Fe, Zn, Ca, and Mg. On the other hand, wheat grain contains low amounts of these minerals. Therefore, our focus is to improve the quality of wheat by increasing the mineral element concentration values in the edible parts (wheat grain), which is an important issue and a strong challenge for human dietary consumption and nutritive value. Using traditional remedies, such as food fortification, supplements, and fertilizer strategy, work as a short-term remedy and are not effective to meet daily needs, especially in developing countries where people consume cereals as their staple food. Certainly, we need a long-term with low-cost methodology to face this kind of problem and, at the same time, provide essential macro and micronutrients for suffering people. Crop biofortification (i.e., genetic biofortification) as one plant breeding strategy for the nutrient deficiency problem, offers a sustainable solution for developing mineral dense crop cultivars. Our work explores the genetic variation of macro- and micronutrients concentration in the grain among 353 of European wheat cultivars (339 winter and 14 spring wheats), and identifys QTL associated with these traits by using a GWAS in order to detect candidate genes for Fe and Zn and some other mineral elements, such as Ca, K, Mg, Mn, P, and S. To this end, GWAS was performed using SNP (90k ILLUMINA and 35k Affymetrix chips) and SSR markers with the application of mixed linear models for two field experiments (2015 and 2016). Preliminary results have confirmed that there is genetic variation in mineral content between the genotypes, which is controlled by a number of associated loci with positive and negative effects. The output show some shared associations between 2015, 2016, and BLUEs. Further validation of these associations is required to reveal the candidate gene(s) of the targeted traits.

Genetic mapping of germination and termite tolerance under drought stress in durum wheat.

An attempt was made to map loci regarding germination and termite tolerance under drought stress under field conditions in a set of 114 recombinant inbred durum wheat lines (RILs) at the NIAB, Pakistan, in 2016–17. The population was developed by making a cross between a drought tolerant cultivar Omrabi5 (O5) with a heat and salt tolerant cultivar Belikh2 (B2) at ICARDA, Syria. The genetic map, constructed at IPK-Gatersleben using 265 markers, was available for genetic mapping. Seeds of 104 RILs were successfully regenerated in the 2015–16 season at the NIAB fields, Pakistan. The regenerated population was grown on 1 November, 2016, in 2-m rows with 9 inches distance between at 5 g seed/line. One set was tested under control conditions and two were tested under drought stress. Irrigation was applied 14 days after sowing to the control, whereas the stress treatments were kept free of any irrigation. Germination data were recorded 3 weeks after planting. Termite infection in drought replicates happened naturally, because drought favors termite attack. Data for termite resistance were recorded on 12 January, 2017, using a visual scale of 0–4, where 0 = no damaged/infected plants, 0.5 = 12.5% plants damaged/infected, 1 = 25% plants damaged/infected, 1.5 = 37.5% plants damaged/infected, 2 = 50% plants damaged/infected, 2.5 = 62.5% plants damaged/infected, 3 = 75% plants damaged/infected, 3.5 = 87.5% plants damaged/infected, and 4 = 100% plants damaged/infected.

Mean germination under control (Gr) ranged between 50% and 100%, with a mean value of 81.86±9.6%. Germination under drought (GrD) reduced the mean to 72.16±9.6% and ranged between 47.5% and 92.5%. Relative germination in drought (RGrD) ranged from 66.7% to 100%, where the mean value was 88.38±8.1%. The mean value of termite tolerance (TT) was 1.37±0.6 and ranged from 0.5 to 3. Genetic mapping, using QTL cartographer v2.5, revealed a total of seven (five major (with $R^2 > 0.1$) and two minor (with $R^2 < 0.09$)) QTL. There were three QTL (one minor and two major QTL) for Gr; two were detected on chromosome 5A (onw associated with marker *Xbarc342* at 73.7 cM with LOD score of 2.51 and $R^2 = 0.086$ contributed by O5 and the other associated with marker *Xgwm1171b* at 171.8 cM with LOD score of 3.6 and $R^2 = 0.18$ contributed by B2) and one on 6B (associated with marker *Xbarc178* at 147.1 cM with LOD score of 3.03 and $R^2 = 0.12$ contributed by B2). For GrD, one minor QTL was observed on chromosome 6B (associated with marker *Xbarc247* at 149.9 cM with LOD score of 2.56 and $R^2 = 0.09$ contributed by B2). Two major QTL were discovered for RGrD on chromosomes 2A (associated with marker *Xgwm1256* at 179.9 cM with LOD score of 2.73 and $R^2 = 0.11$ contributed by O5) and 4B (associated with marker *Xgwm736b* at 140.2 cM with LOD score of 3.2 and $R^2 = 0.11$ contributed by O5). In the end, there was one major QTL for TT that was observed on chromosome 5B (associated with marker *Xgwm1043* at 140.2 cM with LOD score of 3.7 and $R^2 = 0.15$ contributed by B2). This study will be extended to genetic mapping of yield and yield related traits under field conditions in future.

Induction of tolerance to Fusarium head blight.

Fusarium graminerarum (*Fg*) infests a wide range of hosts, including wheat, corn, and barley, producing yield losses, deterioration of the quality, and grain contamination with mycotoxins, which constitute a risk to human and animal health. Few sources of Fusarium head blight (FHB) resistance have been reported, and several resulted in a lack of tolerance when these lines were tested with local populations of *Fg*.

For 8 years, several wheat recombinant and dihaploid populations were tested against a wide range of *Fg* strains in Argentina. We identified lines with SAR and ISR types of tolerance activated by the spray with plant hormones. In the last year, we assessed if the pretreatment with gibberellic acid (GA) and jasmonic acid (J) elicited inducible defences against *Fg*. Two experimental lines (M and P) and a commercial cultivar (ACA 315) were used. The trials were performed in two localities, La Plata and Tres Arroyos, Argentian, with a complete factorial design in blocks with three replicates for every treatment.

At anthesis, spikes of every wheat line or cultivar were sprayed with water (control plants (C)), GA (10^{-4} M), or J (10^{-4} M). After 48 h, half of the pretreated spikes were inoculated with *Fg*. Such a technique helps to highlight the mechanism of resistance to spread of the pathogen (Type-II mechanism). The following treatments were recorded: control-*Fg*, gibberellic-*Fg*, jasmonic-*Fg*. At harvest, spikes were maintained at room temperature until these were manually hacked. Total grain number (GT), the damaged grain (GD), and the 1,000-kernel weight (TKW) were recorded. An ANOVA included the assessment of genotype, treatment, locality, and the interactions. The mean analysis showed the gibberellic-*Fg* treatment significantly increased the total number of grains in both experimental lines compared with the controls and the plants treated with jasmonic acid. Experimental line M produced a higher number of GT compared to that of the commercial cultivar ACA 315; when both were treated with J these wheats presented similar GTs. The number

of GD was reduced under the J treatment in line M, compared to the rest of inoculated treatments (C-*Fg* and G-*Fg*). ACA 315 showed a low number of GD when infested compared with their controls. The TKW was significantly lower in ACA315 J and J-*Fg* treatments. Locality influenced the TKW, with the highest values obtained in Tres Arroyos, in the experimental line P, when plants were treated with G and inoculated (G-*Fg*). This value was significantly higher compared with the rest of the treatments at both localities. Treatment with hormones could induce Type-II FHB tolerance in wheat lines carrying this mechanism of resistance.

Isoenzyme profiles of grain esterases in hexaploid wheat.

Esterases represent a large group of enzymes that catalyze cleavage of multiple-ester bonds. In general, esterases are divided into four types: cholinesterases (most frequently, these are identified using ordinary electrophoretic analysis), acetylesterases, arylesterases, and carboxyl esterases. Plant carboxyl esterases catalyze conversion of the esters into bioactive acids and alcohols, thereby playing a key role in many biological processes. Lack of epistatic interactions and a co-dominant nature of inheritance of the esterase isozymes makes them meaningful for quick and accessible investigation of the processes of biochemical adaptation to environmental changes. Such a marker, which is convenient for solution of practical problems of selection, can be used as a tool that can speed up and simplify the selection of significant material. Our aim was to estimate the isoenzyme profile of esterases isolated from mature seed and, to ascertain using such a biochemical marker, the polymorphism among samples of promising breeding material of hexaploid wheat. Ripe seed from following wheat cultivars were used as samples: Zlata, Lyubava, Agatha, Lisa (spring wheat), and Mera (winter wheat) (originated from the Moscow Agricultural Research Institute «Nemchinovka», Moscow District, Russian Federation); lines AFI91 and AFI177 (spring wheat) (originated from the Agrophysical Research Institute–AFI, St. Petersburg, Russian Federation); and RILs 7, 10, 29, 32, 44, 47, 57, 83, 88, 89, and 115 of the ITMI mapping population (spring wheat). The seeds were ground in a porcelain mortar and the flour sieved. Enzymes were extracted from the flour and subjected to vertical native electrophoresis using 4% concentrating and 8% separating polyacrylamide gels. Molecular weight markers were Page Ruler Prestained Protein Ladder (Thermo Scientific, Lithuania). After electrophoresis, gels were treated with a reagent for a nonspecific esterase and scanned. The individual electrophoretic profile of each sample was estimated. Heterozygosity and its dispersion were calculated.

The esterase complex in the wheat seed studied was represented by 10 isoforms. Between nine and ten isoforms of various electrophoretic mobility were identified in cultivars Zlata, Lyubava, Agatha, Lisa, and Mera, seven were found in line AFI91, eight in AFI177, and from seven to ten in the ITMI RILs. All samples were characterized by the presence of esterases isoforms *Est-8*, *Est-9*, and *Est-10*. Heterogeneity was found only in the qualitative and quantitative composition of esterases with a greater molecular weight, *Est-1*, *Est-2*, *Est-3*, *Est-4*, *Est-5*, *Est-6*, and *Est-7*. Each cultivar among the 18 had a genotype different from that in the other samples. The average heterozygosity (H) of samples within ten loci encoding esterase isoforms was 0.924; the dispersion of heterozygosity for all the samples studied was $\mathrm{Var}(H) = 0.0004$. As a result of the analyses, the most promising breeding parental forms are cultivars Zlata and Mera and lines AFI91, AFI177, ITMI7, ITMI44, ITMI83, and ITMI115. Because of the existence of ten isoforms in hexaploid wheat, the esterases might represent a convenient biochemical marker suitable for examination of samples of the hexaploid wheat at physiological, biochemical, and genetic levels.

Studies on drought stress in spring wheat using genome-wide association mapping.

As a result of climate change, drought severity is expected to increase in the future, which will limit the global production of different crops. Bread wheat is one of the most important crops worldwide facing drought that will result in yield loses. Today, tolerance against abiotic stress is an important goal in wheat breeding. Identification of wheat genotypes that tolerate drought conditions and detect QTL for drought stress were the aims of a study using 111 spring wheat genebank accessions from 27 countries and genotyped with the 15k chip. Drought stress was applied by chemical desiccation using potassium iodide (KI, 0.5% w/v). KI was applied 14 days after anthesis to simulate drought in two subsequent years. The accessions were evaluated for a number of morphological and agronomical traits, such as plant height, spike length, grain number, and 1,000-kernel weight. Genome-wide association mapping studies were performed to reveal significant marker-trait associations under drought and control conditions. The analysis showed that chemical desiccation had a strong impact on yield parameters and significant differences between the genotypes. Genome-wide association mapping analysis revealed major marker-trait associations on different chromosomes.

Genome-wide association mapping of genetic factors controlling Pyrenophora spp. resistance in spring wheat.

Tan spot (*Pyrenophora tritici-repentis* (Died.) Drechs. (anamorph *Drechslera tritici-repentis* (Died.) Shoem.)) is one of the most important wheat diseases. *Pyrenophora teres* Drechs. (anamorph Drechslera teres Sacc. Shoemaker) is a barley pathogen, but some studies conclude that it may attack also wheat. Association mapping analysis was performed in a population of spring wheats to determine the location of the resistance to both pathogens. Field experiments were carried out at the Experimental Station J. Hirschhorn, Faculty of Agriculture and Forestry Sciences, UNLP, Argentina, during 2 years using a split-plot design with two replications. The main plots were two isolates of *P. tritici-repentis* (LH and G) and two isolates of *P. teres* (Pt1 and Pt2). Subplots were a population of 110 wheat genotypes. The severity of both diseases was evaluated at seedling (GS14) and adult stages (GS49) and data were analyzed by ANOVA. The wheat population was genotyped using 2,132 DArT markers. All genotypes were affected by both *Drechslera* species. The average severity for both diseases in seedlings was 36.02% and 15.14% in 2014 and 2015, respectively. Twenty-two markers associated with resistance to *P. tritici-repentis* in seedlings were detected, two to LH, 18 to G, and two to both isolates. Furthermore, 12 markers associated with seedling resistance to *P. teres* were found, three to Pt1 and nine to Pt2. The markers associated with the *P. tritici-repentis* isolates were different from the markers associated with the *P. teres* isolates. The average severity for both diseases at the adult stage was 67.25% and 74.95% in 2014 and 2015, respectively. Fifty markers associated with adult-plant resistance to *P. tritici-repentis* were detected, 20 to LH, 12 to G, and 18 to both isolates. In addition, 62 markers associated with adult-plant resistance to *P. teres* were found, 22 to Pt1, 19 to Pt2, and 21 to both isolates. From these markers, 35e were associated with adult-plant resistance to both species. Only two markers (located on chromosomes 2A and 3A) were associated with resistance in seedlings and at the adult stage. Identifying genotypes with a high percentage of favorable alleles may be useful as parents in breeding programs.

Genome-wide association mapping for yield and yield components in spring wheat.

The molecular localization of genes controlling yield has a large importance in order to perform marker-assisted selection for accelerating genetic gain in wheat. A 2-year field experiment was carried out at the Experimental Station J. Hirschhorn, Faculty of Agriculture and Forestry Sciences, Argentina. Yield and its components were evaluated in a spring wheat core collection of 110 accessions from 27 countries. The wheat population was genotyped using 2,132 DARt markers. The 'year x genotype' interaction showed significant differences for the number of heads/m^2 (NH), kernel number/heads (KNH), 1,000-kernel weight (TKW), kernels/m^2 (K), and yield. Ninteen molecular markers were related to KNH (1 on chromosome 1A; 2 on 1B; 5 on 2A; 3 on 2D; 1 on 4A; 2 on 5B; 2 on 6A; 1 on 6B; 1 on 7B; 1 on 7D); 11 to NH (4 on 1A; 1 on 1B; 1 on 2A; 1 on 3A; 1 on 4B; 1 on 5A; 2 on 6B); 6 to TKW (2 on 3D; 2 on 4A; 2 on 7B); 12 to K (2 on 2A; 1 on 2D; 1 on 3B; 1 on 4B; 1 on 5B; 4 on 6A; 1 on 7A and 1 on 7B); and 14 to yield (2 on 1A; 1 on 2A; 1 on 2D; 3 on 3B; 1 on 4D; 1 on 5B; 1 on 6A; 2 on 6B; 1 on 7A; 1 on 7B). Molecular markers associated to more than one trait also were identified: 3 to KNH-K; 2 to K-yield; 1 to NH-K; 1 to KNH-yield; 1 to NH-yield and 2 with three traits (KNH, K, and yield).

Genome-wide association mapping of grain yield components and grain quality traits in winter wheat.

Wheat cultivars with high yield and an appropriate end-use quality are the primary objective of all breeding programs around the world. An association mapping approach has the power to detect the genetic basis of complex traits with low heritability, such as yield and its components. Genetic analysis of peduncle length (PL), spike length (SL), spike weight (SW), grain number/spike (GN), spike weight (SW), spike fertility (SF), grain weight/spike (GW), spike index (SI), 1,000-kernel weight (TKW), spikelets/spike (SS), number of fertile spikelets/spike (FSS), grain number/fertile spikelets (GFS), protein content (PR), and sedimentation value (SD) through a GWAS was performed using phenotypic data from a field test in three environments of a panel of 96 winter wheat accessions. The complete collection was genotyped with 874 polymorphic DArT markers and significant MTAs were identified using both mixed linear and general linear models based on the average phenotypic value for each environment. In all cases, only MTAs significant ($P < 0.01$) in at least two of the three environments and in both models were considered. Altogether, 215 MTAs associated to 141 DArT markers were identified. Of the total, 68 were trait-specific markers, whereas the other 73 were associated with at least two traits. PL showed the highest number of MTAs (26), followed by SL (23), SW (20), SS (18), SI (16), SD (15), PR (13),

GN and TKW (each 8), SF (10), GW and FSS (each 9), and GFS (8). Nineteen chromosomes (except 3D and 6D) were involved in the MTAs. The highest number of MTAs were found on chromosome 2B (28), followed by 3A (22), 5B (20), 7B (19), 1A (16), 1B (15), 6B and 7A (each 14), 2D (13), 3B, 4A and 4B (each 8), 5A (10), 6A (11), 2A (3), and 4D, 5D and 7D (2 each). The phenotypic variation explained by significant DArT markers ranged from 4.3% in SW (wPt6005 on 1A) to 26.8% in SI (wPt5503 on 1D), indicating that the genetic basis was determined by several genetic factors with small to moderate effects. Although some significant markers were mapped on chromosome regions previously reported for the traits studied, others were found in regions where, to our knowledge, no previous evidence has been reported and, therefore, appear to be novel.

Analysis of stability of photosynthetic parameters in wheat D-genome introgression lines adapting to water deficit with different intensity.

The RILs developed from a cross between Chinese Spring (CS) and a synthetic hexaploid wheat (Synthetic 6x, Syn) were grown in the greenhouse of SIFIBR SB RAS and in the climatic chamber CLF Plant Master (CLF Plant Climatic GMBH, Wertingen, Germany) of SIFIBR SB RAS under two variants of water supply, optimal and water deficit. In both experiments, the soil–water deficit was maintained by a decrease in water supply by 50% compared to that of the optimum. The growing conditions differed in the air humidity; which was two-times lower in the greenhouse compared to that in the CLF PlantMaster. The water-deficient variant in the greenhouse was denoted as a severe drought and, in the climatic chamber, as a moderate drought. Shoot biomass, gas exchange parameters (LCi Photosynthesis System, ADC BioScientific Ltd., Hoddesdon, England) chlorophyll (Chl) fluorescence parameters (PAM-250 chlorophyll fluorometer (Heinz Walz GmbH, Effeltrich, Germany), and the content of photosynthetic pigments were measured in flag leaves at the shooting stage in all the experiments. The stress-resistance index of Fernandez (STI) was calculated for all the traits studied, and the RILs grouped by mean STI for biomass. In the greenhouse, group 1, with the STI for biomass < 0.2, included lines 1D-4, 2D-1.2, 2D-2, 2D-7, 2D-8, 2D-18, 5D-2, 5D-3, 5D- 5, 5D-6, 5D-7, 5D-8, 5D-9, 7D-5, and 7D-6. Group 2, with the STI for biomass > 0.4, included lines 1D-5, 1D-6, 1D-7, 2D-12, 3D-1, 3D-2, 3D-3, 3D-5, 3D-8, 6D- 1, 6D-3, 6D-6, 6D-10, 6D-11, 6D-12, 7D-3, 7D-4, 7D-10, and 7D-12. In the climatic chamber, group 3, with STI for biomass < 0.4, included lines 2D-6, 2D-12, 2D-14, 2D-17, 3D-8, 4D-2, 4D-4, 4D-5, 5D -3, 5D-5, 5D-6, 5D-7, and 5D-10. Group 4, with STI values for biomass > 0.7, included lines 1D-4, 1D-6, 2D-10, 2D-16, 2D-18, 3D-4.1, 3D-10, 7D-1a, 7D-1b, 7D-3, 7D-4, 7D-8, 7D-11, and 7D-12.

Under moderate drought conditions, lines with a high stability of shoot biomass (group 4) differed from group 3 ($P < 0.001$) by high stability of the chlorophylls and total carotenoid content, which indicates the effectiveness of carotenogenic response and physiological responses, similar to stay-green, when the destruction of the photosynthetic apparatus during drought-induced leaves aging is partially or completely prevented. Under severe drought conditions, the lines contrasting in their STI for biomass (groups 1 and 2) but did not differ in the stability of pigment content. In the greenhouse, the stability of shoot biomass correlated with the stability of transpiration rate and stomatal conductance, which resulted in higher efficiency of water usage in the group-2 lines with a high STI for biomass ($P < 0.05$). In the Plant Master climatic chamber, differences in the stability of shoot biomass were not determined by the stomatal effects.

The stability of F_V/F_M (maximum quantum yield of PS2 photochemistry), Y(II) (actual quantum yield of PS2 photochemistry), and NPQ (nonphotochemical quench of Chl fluorescence) did not differ in the groups contrasting in STI for biomass, regardless of the experimental conditions. Under severe drought conditions, lines with a low stability of shoot biomass (group 1) had higher ($P < 0.01$) STI for F_0 values (ground Chl fluorescence yield), which indicates a significant decrease in the efficiency of the transfer process of excitation energy in the light-harvesting antenna PS2 in these RILs. Under moderate drought conditions, lines with high stability of shoot biomass (group 4) were characterized by higher ($P < 0.0001$) STI for F_M (maximum Chl fluorescence), Ft (stationary Chl fluorescence), and F_V/F_0 (maximum quantum yield of PS2 photochemistry). Under severe drought conditions, lines with a higher stability of shoot biomass (group 2) were distinguished by a high ($P < 0.01$) STI for ETR (electron transport rate) and Lk (intensity of illumination, expressesing the beginning of photosynthetically active radiation saturation).

The results showed that changes in the studied photosynthetic parameters while adapting RILs to the water deficiency depend on the stress load degree; different protective mechanisms are effective under different conditions. A more detailed analysis of Chl fluorescence and JIP-test in leaves of RILs CS/Syn under the different conditions of water supply will let us choose parameters and resistance indices, most accurately reflecting the physiological state of wheat plants.

The development of super-soft lines of bread wheat.

Multiple polymorphism of genes in a single locus *Ha* of chromosome 5D determines the variability for endosperm structure of grain in bread wheat from mealy to hard and vitreous. Chromosomes 5A and 5B do not significantly affect the trait due to the deletion loss of homeoallelic loci in the tetraploid ancestor. On chromosome 5A of the hard-grain bread wheat Rodina (vitreousness more than 85%, particle size about 23 μm), the *Ha-Sp* locus was introgressed from *Ae. speltoides,* which resulted in grain softness of the obtained line 84/98^{w} (vitreousness about 50%, particle size about 11–15 μm). In this work, the *Ha* locus of Chinese Spring on chromosome 5D (vitreousness about 50-70%, particle size about 11–15 μm) and the introgressed locus *Ha-Sp* on chromosome 5A of the line 84/98^{w} were combined in one genotype. For a number of generations, selection was made among the 'Chinese Spring x 84/98^{w}' hybrids based on the endosperm characteristics grain vitreousness and flour particle size during milling. After 6–8 generations of self-pollination, the constant super-soft forms were isolated with a particle size of flour of about 10–11 μm and a vitreousness of much less than 50% with a stable manifestation of the traits under greenhouse and field conditions. These new forms of bread wheat may be used in the selection of wheat cultivars where flour will not need baking powders in the confectionery industry.

The influence of crop production systems on seed germination in winter wheat.

Experiments were performed at the Experimental Station in Osiny, Poland. Four winter wheat cultivars, Sailor, Jantarka, Arkadia, and Bamberka, were grown under four crop production systems, conventional (CON), conventional-monoculture (MONO), integrated (INT), and ecological (ECO). The CON (winter rape, winter wheat, and spring wheat) and MONO systems are conducted intensive crop production technologies that use pesticides and chemical fertilizers. In the MONO system, wheat was cultivated every year in the same field. In the INT system (potato, spring wheat, faba bean, and winter wheat), mineral fertilization was calculated on the basis of results obtained from soil and plant tests. Moreover, plant protection was applied based on a threshold of harmfullnes of agrophages. In the ECO system (potato, spring wheat, red clover with grass, oat + vetch mixture, and winter wheat + catch crop), synthetic crop protection chemicals and most mineral fertilizers are forbidden.

Germination tests were done in two replications of 50 seeds/cultivar and cultivation system. Seeds were germinated at a constant 20±2°C using a Jacobsen apparatus. Four germination-related traits were investigated by examining the seeds: total germination (%), normal germination (%), time to reach 50% of total germination (h), and the area under the curve after 150 hours of germination.

The production system had no influence on germination characters. However, the cultivars did have an effect, especially with respect to Bamberka. This cultivar did show the lowest percentage for total germination and normal germination independently from the production system. Also, the germination speed of Bamberka was reduced, especially under INT and CON conditions. A strong genetic component in Bamberka seems to affect germination independently from the growing conditions of the plants. No clear tendencies were observed For the other three cultivars.

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ITEMS FROM INDIA

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

Irradiation-induced resistance to yellow (stripe) rust in Indian wheat cultivars through mutation breeding.

G. Vishwakarma, Vikas, and B.K. Das; Satish Kumar, M.S. Saharan, Indu Sharma, and C.N. Mishra (ICAR–Inidan Institute of Wheat & Barley Research, Karnal, Haryana) and A. Saini (Moleuclar Biology Division, Bhabha Atomic Research Centre, Trombay, Mumbai-400085, India).

Wheat rusts (black rust, brown rust, and yellow rust) are the most devastating diseases of wheat crop with significant impact on yield. Among the three rust diseases, yellow or stripe rust (caused by *Puccinia striiformis*f.sp. *tritici*), is one of the major problems in the North Western Plain Zone (NWPZ) of India, which is known as the bread basket of India. Most of the recently released wheat cultivars have some level of susceptibility to the ever-evolving pathogen. New pathotypes have emerged in a short time, which have overcome resistance genes deployed in the popular high-yielding cultivars of this zone, posing a serious threat to wheat production in India. Conventional breeding methods for development of resistant genotypes can cause many recombination events thus leading to unwanted variability. Mutation breeding, on the other hand, can be useful as it may produce the desired variant without disturbing the agronomic background. In order to enhance the resistance in some high-yielding wheat cultivars grown in these areas, radiation-induced mutation breeding was initiated in the cultivar DBW 88. Gamma-ray irradiated M_1 population of DBW88 was raised at Trombay, Mumbai, India. Subsequently, the M_2 was raised at IIWBR Karnal, and putative mutants were advanced to M_3 at IIWBR regional station Dalang Maidan. Rigorous screening of these populations was by artificially creating the disease epiphytotics. Seventy-two lines were identified as having enhanced resistance to stripe rust and were advanced to the M_4 at IIWBR Karnal. Thirteen lines were resistant to stripe rust in the M_5. The selected lines will be further evaluated for their resistance to stripe rust in the M_6 generation. To further increase the level of resistance to yellow/stripe rust in the NWPZ, we generated a mutagenized population of two, high-yielding cultivars, HD2967 and WH1105, using gamma rays. The M_1 population was raised at IIWBR Karnal in *rabi* 2016–17 and, subsequently, the M_2 will be screened for resistant mutants.

Molecular characterization of an early maturing wheat mutant line in C-306 background using SSR markers.

G. Vishwakarma, Vikas, K. Suryavanshi, A.S. Shitre, and B.K. Das; A. Saini (Molecular Biology Division, Bhabha Atomic Research Centre, Trombay, Mumbai–400085, India); and D.A. Gadekar (Agricultural Research Station, Niphad, Maharashtra, India).

Under the IAEA–RCA project RAS/5/045, we developed an early maturing mutant in the wheat cultivar C-306 using gamma rays. The mutant is ~25 days earlier than the parent and has no yield penalty. The mutant also exhibits other traits similar to the parent cultivar, which, although an old cultivar and susceptible to rust, is still very popular among farmers for its end-use quality. An early maturing mutant in C-306 is an important stepping stone for strengthening the breeding efforts for improvement of this important cultivar, thus making it important to fully characterize this mutant. We

used SSR markers for the molecular characterization. After screening the parent and mutant with 297 SSR markers, 35 markers were found to be polymorphic. We will screen these polymorphic markers in a segregating F_2 population of the 'mutant x parent' cross. This information will be helpful in mapping the mutant loci to the closest possible marker, which in future will help in developing a tightly linked marker for the earliness trait.

Combining earliness with rust resistance in an early maturing wheat mutant.

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

An early-maturing mutant in the wheat cultivar C-306 is a significant improvement allowing wheat to escape terminal heat stress, which is one of the main reasons for loss in yield due to incomplete grain filling. To further improve biotic stress resistance in this mutant, we introduced rust resistance gene *Sr24*/*Lr24* from the near isogenic line HW-2004 (UC-306). *Sr24*/*Lr24* is an important rust-resistance gene widely deployed in Indian wheat cultivars, and it confers resistance to most of the Indian stem and leaf rust pathotypes. An F_2 population of this cross was phenotyped for earliness and rust resistance. The status of *Sr24*/*Lr24* in F_2 plants was confirmed by MAS using a SCAR marker. The F_3 lines were screened for true breeding nature for earliness and rust resistance. Selected lines will be stabilized in further filial generation and then forwarded for multi-location trials.

Marker-assisted, background selection in a backcross-derived wheat line.

G. Vishwakarma, Vikas, Jyothy Warrior, A.S. Shitre, and B.K. Das; A. Saini (Molecular Biology Division, Bhabha Atomic Research Centre, Trombay, Mumbai–400085, India); and D.A. Gadekar (Agricultural Research Station, Niphad, Maharashtra, India).

The wheat cultivar HD-2189, which is a popular in Peninsular zone (PZ) of India, was improved in our laboratory for resistance to rust diseases and chapat-making quality using backcross breeding. Genes for rust resistance (*Sr24*/*Lr24*) and high-molecular weight glutenin protein subunits 5+10 (*Glu-D1d*) was introduced from donor parent KS-3. Subsequently, backcross lines were screened for presence of these two traits using MAS (foreground selection). We used SSR markers to ascertain the recovery of recurrent parent (HD-2189). Parental polymorphism was screened using 297 SSR markers, out of which 33 were found to be polymorphic. These markers were then used to ascertain background genome recovery in two background-derived lines (TNIAW-1 and TNIAW-2) of the above-mentioned cross. All polymorphic markers showed the presence of recurrent parent type alleles in both backcross lines, ascertaining that genome of the recurrent parent was recovered. These lines will be taken forward for multi-location trials in the coming *rabi* season.

Validation and marker-assisted selection of Sr2 in Indian wheat cultivars.

G. Vishwakarma, A.S. Shitre, and B.K. Das; A. Saini and R. Sanyal (Molecular Biology Division, Bhabha Atomic Research Centre, Trombay, Mumbai–400085, India); and D.A. Gadekar (Agricultural Research Station, Niphad, Maharashtra, India).

Sr2 is an important, slow-rusting, stem rust resistance gene that confers partial resistance to nearly all races of stem rust. *Sr2* also is effective against the devastating pathotypes of Ug99 and its variants. Hence, incorporating the *Sr2* gene in modern wheat cultivars for achieving durable stem rust resistance is desirable. We validated SSR marker *Xgwm 533*, reported to be linked to the *Sr2* gene, in Indian wheat cultivars. All the wheat cultivars reported to have *Sr2* amplified a 120-bp band, whereas noncarriers of *Sr2* either gave a null, 155-bp band or some other high-molecular-weight products. Marker *Xgwm 533* was used for MAS for *Sr2* in important PZ wheat lines developed at the Agriculture Research Station, Niphad, India. Interestingly, we found that PBW-343 and TWM-97 (an Ug99-resistant mutant of PBW-343) amplified a 100-bp band instead of the 120-bp, as observed in other *Sr2* carriers. We are in the process of sequencing this allele and developing a SYBR-green dye, melt-curve-based, gel-free approach for screening for the presence/absence and type of *Sr2* alleles. This system could facilitate high-throughput (96-well or 384-well based), low-cost marker-assisted screening of populations for the desired trait, which would be beneficial for breeders and wheat researchers.

Validation of AFLP-based markers Sr24#12 and Sr24#50 in Indian wheat genotypes.

G. Vishwakarma and B.K. Das, and A. Saini (Molecular Biology Division, Bhabha Atomic Research Centre, Trombay, Mumbai–400085, India).

Sr24 is an important, major rust resistance gene, present in many Indian and global wheat cultivars, is located on chromosome 3DL and is tightly linked to *Lr24*. *Sr24* is being used widely by wheat breeders in crossing programs, necessitating a fast and accurate screening methods for this gene. Molecular markers reported for the gene include SSR marker BARC-71 and the AFLP-based markers Sr24#12 and Sr24#50. Sr24#12 is reported to be completely linked to *Sr24* gene. We validated this marker in Indian wheat genotypes (five carriers and five noncarriers of *Sr24*) and found that Sr24#12 amplifies a 500-bp fragment in all carriers of *Sr24* and a null band in noncarriers, which agrees with previously published reports. We are developing a SYBR-green dye-based, melt-curve assay that would help in gel-free screening for the *Sr24* rust resistance gene using the Sr24#12 marker. Similarly, Sr24#50 amplified a 200-bp fragment in all carriers of *Sr24* and a null band in noncarriers.

Biochemical and molecular characterization of polyphenol oxidase activity in wheat genotypes of the Peninsular Zone of India.

A.S. Shitre and B.K. Das; D.A. Gadekar (Agricultural Research Station, Niphad, Maharashtra, India); and N.R. Potdukhe and S.R. Bharad (Wheat Research Unit, Dr. PDKV, Akola, Maharashtra, India).

The consumer preference of any food depends upon its color, appearance, and test. For wheat, the color of the end-product, specifically noodles, pasta, chapati, and bread depend upon the color of the dough. Polyphenol oxidase (PPO) is responsible for the discoloration of the dough and ultimately that of the end-product.

We initiated a study to investigate PPO activity in Indian wheat genotypes by enzymatic assay and validating molecular markers for PPO. Anderson and Morris (2001) screened 100 wheat genotypes by enzymatic assay. The PPO activity is calculated at two time intervals (30 min and 120 min). At the 30-min interval, the highest activities reported were 180.04 au/min/g (LOK 1), 137.47 au/min/g (NI5439), and au/min/g 132.52(NI747-19), where the lowest PPO activities reported were 6.14 au/min/g (AKDW 2997-16), 6.86 au/min/g (AKDW-4791), and 8.82 (AKDW-4750) au/min/g. At the 120-min interval, the highest activities reported were 87.48 au/min/g (LOK 1), 63.45 au/min/g (NI747-19), and 57.61 au/min/g (MIAW1846) and the lowest PPO activities were 2.83 au/min/g (NI179), 4.79 au/min/g (AKDW4791), and 5.08 au/min/g (AKDW 2997-16). Genotypes showing the least PPO activity were durum genotypes. Low values of PPO activity will be confirmed by repeating the assay for those genotypes. The PPO activity in wheat is largely governed by two genes located on chromosomes 2A and 2D. Two dominant STS markers, PPO16 and PPO29, for the allele located on 2D, and co-dominant markers for PPO18 and PPO33, for the allele located on chromosome 2A, are being validated to correlate their linkage with enzymatically measured PPO activity.

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SHER-E-KASHMIR UNIVERSITY OF AGRICULTURAL SCIENCES AND TECHNOLOGY OF KASHMIR
Division of Genetics & Plant Breeding, Faculty of Agriculture, SKUAST–K Wadura Campus, Sopore–193201, Kashmir, India.
www.skuastkashmir.ac.in/

R.R. Mir, M.A. Khan, M. Ashraf Bhat, Sandhya Tyagi, Rahul Nelwadker, Tahir Yusuf, Safoora Shafi, Asma Hamid, Parvez Sofi, Kamaludin; and Bikram Singh (Division of Genetics & Plant Breeding, Faculty of Agriculture (FoA), SKUAST–Jammu, Chatha–18009, Jammu, India).

Molecular breeding for improvement of wheat in the Northern Hill Zone of Kashmir.

Breeding early maturing wheat cultivars. One of the most important wheat breeding objectives for our Kashmir region is for cultivars that fit in the rice–wheat crop rotation, which will ensure food security for the people in this region. Rice, the most stable food in the region, is grown from June to September. Following the rice crop harvest, efforts are made to sow a wheat crop in October with harvest by the end of May or early June. The main challenge is to vacate wheat fields by 10 June for rice cultivation. To make this rotation successful, we are screening a variety of wheat germplasm/nurseries received from national partners, such as the Indian Institute for Wheat and Barley Research (IIWBR), Karnal, Haryana, and from international institutes, such as the Borlaug Institute for South Asia (BISA) of CIMMYT. A set of six early maturing lines were identified from material provided by national partners, and a set of 25 early maturing lines were procured from BISA. The material was evaluated at two locations in Kashmir, including the Faculty of Agriculture, SKUAST–K, Wadura, Sopore (extreme northern Kashmir) and at the Mountain Research Centre for Field Crops (MRCFC), Khudwani, Anantnag (extreme southern Kashmir). These extra-early maturing lines are crossed in different combinations and F_1 seeds were obtained for ~140 cross combinations. The F_1 seed were planted in the greenhouse and F_1 plants are currently growing. Any F_2 seed obtained will be planted in the field in October to obtain an F_2 generation. In addition to 'spring × spring' crosses, 'spring × winter' genotypes also were crossed and F_1 plants are currently growing in the greenhouse. The F_2 seeds obtained will be planted again in field in October to obtain F_2 generation. Selection for early maturity will be made in the F2 generation and will be advanced for varietal development.

Breeding for quality/nutritional traits. One of the most important areas of wheat breeding is for cultivars with enhanced quality and nutritional traits. We have selected a set of 23 lines possessing high grain Fe, Zn, and protein content. Those lines were evaluated at two locations (SKUAST–Jammu and the MRCFC, Khudwani (SKUAST–K). Important lines with high Zn, Fe, and protein content were involved in a crossing program with extra-early maturing lines and stripe rust resistant lines. Approximately 100 crosses were made. The F_1 seeds were harvested and sown in pots under controlled conditions in a polyhouse at SKUAST–K. The F_2 seeds that will be obtained soon will be planted in the field in October to obtain an F_2 generation.

Evaluation of wheat germplasm under the All India Co-ordinated Research Program on Wheat. Being one of the funded centers, a set of 24 advanced breeding lines received under Initial Varietal Trails (IVTs) for the Northern Hill Zone were evaluated in four replications in a randomized, complete-block design for a variety of traits. A few very promising lines for yield, early maturity, and disease resistance were identified.

Genetic dissection for heat tolerance in wheat using multiple recombinant inbred line (RIL) mapping populations. This project is funded by the Department of Biotechnology, Government of India, New Delhi. Three bi-parental RIL mapping populations were developed and evaluated for two years (2015–16 and 2016–17) for heat tolerance-related traits such as flowering time, canopy temperature depression, 1,000-kernel weight, and grain yield at Pantnagar, Varanasi, and SKUAST–Jammu. In addition, genotyping work was divided among all centers with each center working on one mapping population. At SKUAST–Jammu, we used more than 119 SSR markers to study parental polymorphism, and the polymorphic markers will be used in genotyping of one RIL mapping population segregating for heat tolerance related traits at SKUAST–K.

We expect to identify a set of new major, stable QTL/genes. In addition, previously identified QTL/genes will be validated for use in molecular breeding programs aimed at enhancing heat tolerance of Indian bread wheat cultivars.

Identification and characterization of heat responsive miRNA-SSRs in wheat. This project is funded by SERB, DST, Government of India. We are trying for genome-wide identification and characterization of miRNA-SSRs for heat tolerance in wheat. In addition, diversity analysis for heat tolerance miRNA genes in wheat also will be conducted. This study represents an extensive identification of heat responsive, miRNA gene-based SSRs (miRNA-SSRs) that can distinguish more efficiently the heat tolerant and heat susceptible lines compared to genome-based SSR markers that currently are being used by the researchers. The miRNA-associated markers have a high potential of linkage. These identified miRNA-SSRs can then be used in a marker-assisted selection program for heat tolerance in wheat that will be a completely novel approach for crop improvement.

ITEMS FROM MEXICO

NATIONAL INSTITUTE FOR FORESTRY, AGRICULTURE, AND LIVESTOCK RESEARCH (INIFAP–CIRNO), CAMPO EXPERIMENTAL NORMAN E. BORLAUG
Apdo. Postal 155, km 12 Norman E. Borlaug, entre 800 y 900, Valle del Yaqui, Cd. Obregón, Sonora, México CP 85000.

Grain yield evaluation of advanced wheat lines adapted to stress, during the 2015–16 crop season.

Ivón Alejandra Rosas-Jáuregui, Guillermo Fuentes-Dávila, Carlos Antonio Ayón-Ibarra, Pedro Félix-Valencia, José Luis Félix-Fuentes, Miguel Alfonso Camacho-Casas, and Gabriela Chávez-Villalba.

Abstract. Forty-four advanced wheat lines of the 1'st Stress Adaptive Trait Yield Trial from CIMMYT and the durum wheat cultivar Movas C2009 were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station, in the Yaqui Valley, Sonora, México. Plots consisted of a 1-m long bed with two rows 0.80 m apart without replications and a seed density of 100 kg/ha. Maximum, minimum, and average daily temperature (°C), relative humidity, and rainfall were recorded during the crop season. Cold hours were determined as the temperature > 0.1°C to < 10°C that occured during a given hour. The variables evaluated were days-to-heading, 1,000-kernel weight (TKW, g), and grain yield/plot. The highest number of cold hours (261) accumulated during January, followed by February with 92, 62 in March, 24 in April, and 1 in May. The total number of accumulated cold hours was 440. The average heading of lines was 75 days. The average group height was 79 cm. The shortest line was REEDLING #1 at 70 cm; lines 'FRTL//ATTILA/3*BCN' and 'SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/ PASTOR' (line 30) showed heights of 90 and 89 cm, respectively. The average TKW of the group was 50 g. Line 'SOKOLL/WBLL1' had the highest TKW at 60 g, followed by seven lines that had a similar TKWs of 56 g. Four lines and the check showed the lowest TGW at 42 g. The average grain yield/plot was 349 g. Outstanding lines were REEDLING #1 (488g), 'SW94.2690/SUNCO' (471 g), and 'SOKOLL/ROLF07' (470 g).

Introduction. Thermal stress is generally defined as the temperature increase above a determined threshold for a period of time, enough to cause irreversible deleterious effects on development and growth of crops, in this way reducing their yield and or quality (Wahid et al. 2007). However, high temperatures have a complex effect on crops and the final result on yield and quality by the thermal stress will strongly depend on the characteristics of such a stress (i.e., severity, duration, and/or in combination with other stresses), the crop (phonologic stage when it occurs and species/genotype), and the interaction with other environmental factors (Savin 2010). On the other hand, high temperatures occur in all agricultural regions and is a common and universal stress so that, quite often, its effect is not taken into consideration. Wardalaw and Wrigley (1994) and Tewolde et al. (2006) calculated that yield reduction in winter cereals due to high temperatures during the grain-filling period may reach 10–15%. The probability that high temperatures occur in a given agricultural region depends on the sowing date, altitude, and the ocurrence of events of high temperatures. Naturally, when agricultural areas expand, it is probable that crops in these new areas experience stress levels, including thermally important ones. Even in the traditional agricultural zones, an increase in the occurrence of these thermal stresses is expected.

Table 1. Advanced bread wheat lines of the 1,st Stress Adaptive Trait Yield Trial (CIMMYT).

Line #	Pedigree and selection history
1	MOVAS C2009
2	SOKOLL/WBLL1 PTSS02Y00021S-099B 099Y-030ZTM-040SY-040M-18Y-0M-0SY-0B-0Y
3	SOKOLL/WBLL1 PTSS02Y00021S-099B-099Y-030ZTM-040SY-040M-9Y-0M-0SY-0B-0Y
4	PASTOR//HXL7573/2*BAU/3/WBLL1 PTSS02Y00023S-099B-099Y-030ZTM-040SY-040M-19Y-0M-0SY-0B-0Y
5	SOKOLL//W15.92/WBLL1 PTSS02B00088T-0TOPY-0B-0Y-0B-5Y-0M-0SY-0B-0Y
6	FRTL//ATTILA/3*BCN PTSS02Y00011S-099B-099Y-099B-0Y-0B-17Y-0ZTB-0SY-0B-0Y
7	OR791432/VEE#3.2//ATTILA/3*BCN PTSS02Y00013S-099B-099Y-099B-0Y-0B-8Y-0ZTB-0SY-0B-0Y
8	PUB94.15.1.12/WBLL1 PTSS02Y00027S-011Y-0B-0Y-0B-7Y-0M-0SY-0Y-0Y
9	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN PTSS02B00132T-0TOPY-0B-0Y-0B-39Y-0M-0SY-0Y-0Y
10	SOKOLL/WBLL1 PTSS02Y00021S-099B-099Y-099B-099Y-43B-0Y
11	SOKOLL/WBLL1 PTSS02Y00021S-099B-099Y-030ZTM-040SY-040M-5Y-0M-0SY-0B-0Y
12	SOKOLL/WBLL1 PTSS02Y00021S-099B-099Y-030ZTM-040SY-040M-21Y-0M-0SY-0Y-0Y
13	WBLL4//OAX93.24.35/WBLL1 PTSS02B00110T-0TOPY-0B-0Y-0B-24Y-0M-0SY-0Y-0Y
14	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/KAUZ//PRINIA/3/BAV92 CMSA05Y01011T-040M-040ZTP0Y-040ZTM-040SY-4ZTM-03Y-0B
15	PFAU/MILAN/5/CHEN/AEGILOPS TAUSCHII (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR CMSS02Y00613S-59Y-0M-099Y-5M-0WGY-0B
16	SLVS//ATTILA*2/M10 (MUTATED C-306) CMSA00M00164S-040P0M-13CRE-010M-010SY-7M-0Y-0SY-0Y-0Y
17	SOKOLL*2/TROST CMSA05Y01186T-040M-040ZTP0Y-040ZTM-040SY-32ZTM-02Y-0B
18	SOKOLL/ROLF07 CMSA04M00346S-040ZTP0Y-040ZTM-040SY-28ZTM-01Y-0B
19	SW94.2690/SUNCO CMSA01M00069S-040P0M-030ZTM-040SY-040M-1Y-0M-0SY-0Y-0Y
20	WHEAR//2*PRL/2*PASTOR CGSS03B00090T-099Y-099M-099Y-099M-17WGY-0B
21	CHEN/AE.SQ//2*OPATA/3/FINSI CMSA00M00128S
22	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1 PTSS02B00102T-0TOPY-0B-0Y-0B-11Y-0M-0SY-0B-0Y
23	SOKOLL/WBLL1 PTSS02Y00021S-099B-099Y-099B-099Y-234B-0Y
24	HGO94.9.1.37/2*NAVJ07 PTSA08M00008T-050Y-050ZTM-050Y-3ZTM-010Y-0B
25	CHEN/AE.SQ//2*WEAVER/3/BAV92/4/JARU/5/OLI2/SALMEJA/6/ CROC_1/AE.TAUSCHII (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2 PTSA08M00026T-050Y-050ZTM-050Y-8ZTM-010Y-0B
26	PASTOR//HXL7573/2*BAU/3/ATTILA/3*BCN/4/SOKOLL/3/PASTOR//HXL7573/2*BAU PTSA08M00041S-050ZTM-050Y-47ZTM-010Y-0B
27	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/ATTILA/PASTOR PTSA08M00044S-050ZTM-050Y-51ZTM-010Y-0B
28	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SRMA/TUI PTSA08M00045S-050ZTM-050Y-28ZTM-010Y-0B
29	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR PTSA08M00046S-050ZTM-050Y-80ZTM-010Y-0B
30	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR PTSA08M00046S-050ZTM-050Y-85ZTM-010Y-0B
31	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/ASTREB PTSA08M00047S-050ZTM-050Y-28ZTM-010Y-0B
32	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/MEX94.2.19//SOKOLL/WBLL1 PTSA08M00050S-050ZTM-050Y-51ZTM-010Y-0B
33	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/MEX94.2.19//SOKOLL/WBLL1PTSA08M00050S-050ZTM-050Y-56ZTM-010Y-0B

Table 1. Advanced bread wheat lines of the 1,st Stress Adaptive Trait Yield Trial (CIMMYT).

Line #	Pedigree and selection history
34	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/WBLL4//OAX93.24.35/WBLL1PTSA08M00051S-050ZTM-050Y-19ZTM-010Y-0B
35	SOKOLL/3/PASTOR//HXL7573/2*BAU/5/CROC_1/AE.TAUSCHII (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2 PTSA08M00052S-050ZTM-050Y-30ZTM-010Y-0B
36	PASTOR//HXL7573/2*BAU/3/ATTILA/3*BCN/4/SOKOLL/3/PASTOR//HXL7573/2*BAU PTSA08M00041S-050ZTM-050Y-111ZTM-010Y-0B
37	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR PTSA08M00046S-050ZTM-050Y-82ZTM-010Y-0B
38	WBLL4//OAX93.24.35/WBLL1/5/CROC_1/AE.TAUSCHII (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2 PTSA08M00070S-050ZTM-050Y-39ZTM-010Y-0B
39	PUB94.15.1.12/FRTL//92.001E7.32.5/SLVS PTSA08M00076S-050ZTM-050Y-48ZTM-010Y-0B
40	SOKOLL CMSS97M00316S-0P20M-0P20Y-43M-010Y
41	ROELFS F2007 CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B
42	WEEBILL1 CGSS95B00014T-099Y-099B-099Y-099B-35Y-0B-0B
43	KACHU #1 CMSS97M03912T-040Y-020Y-030M-020Y-040M-4Y-2M-0Y
44	BAJ #1 CGSS01Y00134S-099Y-099M-099M-13Y-0B
45	REEDLING #1 CMSS06Y00605T-099TOPM-099Y-099ZTM-099Y-099M-11WGY-0B

Most models predict that temperatures during the day and night will increase 1–4 ºC during the next few years. This is important because, in some crops, high night temperatures seem to be more damaging in reducing productivity than high temperatures during the day (Hall 1992). In winter crops sown in temperate zones, the temperature normally increases throughout the ontogeny of the crop. The fact that flowering of the crop must occur with the least or without a possible risk of frosts determines the sowing date for a given genotype, such that high temperatures generally occur during the grain-filling period. Therefore, high temperatures, along with a low hydric availability, are the abiotic stresses more common in winter cereals (Wardlaw and Wrigley 1994). Our objective was to identify wheat lines with a high yield potential under stress conditions.

Materials and Methods. Forty-four advanced wheat lines of the 1'st Stress Adaptive Trait Yield Trial from CIMMYT and the durum wheat cultivar Movas C2009 (Table 1, pp. 21-22) were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station, located in block 910 in the Yaqui Valley, Sonora, México, at 27°22'04.64" latitude north and 109°55'28.26" longitude west, 37 masl, with warm climate (BW (h)) and extreme heat according to Koppen's classification modified by García (1964). Plots consisted of a bed 1-m long with two rows 0.80 m apart without replications, and a seed density of 100 kg/ha. For management of the trial, the INIFAP technical recommendations were followed (Figueroa-López et al. 2011). Maximum, minimum, and average daily temperature (°C), relative humidity, and rainfall were recorded during the crop season. Cold hours were determined as the temperature > 0.1°C to < 10°C that occured during a given hour. The variables evaluated were days-to-heading, TKW (g), and grain yield/plot.

Results. Optimum sowing dates for this region, based on historical data, range from 15 November to 15 December. The highest number of cold hours (261) accumulated during January, followed by February with 92, 62 in March, 24 in April, and 1 in May. The total number of accumulated cold hours was 440, without considering 125 in December 2015, since sowing of the trial took place on 29 December. Annual productivity in an agricultural area may be explained greatly by the temperature fluctuation; knowledge of this factor may help to plan the most appropriate technologies in order to avoid risks and production losses or for better agronomic management. The average heading of the lines was 75 days; the highest difference, relative to the group average, was 5 days in line BAJ#1, which was the earliest (Fig. 1A, p. 23). The average group height was 79 cm; the shortest line was REEDLING #1 at 70 cm, and lines 'FRTL//ATTILA/3*BCN' and 'SOKOLL/3/ PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR' (line 30) were 90 and 89 cm, respectively. The height of the check was 75 cm, which was lower than the group average (Fig. 1B, p. 23). The average TKW of the group was 50 g; line 'SOKOLL/WBLL1' (line 12) was the highest at 60 g, followed by seven lines that had similar TKWs of 56 g. Four lines and the check had the lowest TGW at 42 g (Fig. 1C, p. 23). The average grain yield/plot was 349 g. Outstanding lines were REEDLING #1 (488 g), 'SW94.2690/SUNCO' (471 g), and 'SOKOLL/ROLF07' (470 g) (Fig. 1D, p. 23). The greatest difference in yield among lines was shown by 'SOKOLL/3/PASTOR//HXL7573/2*BAU/4/WBLL4// OAX93.24.35/WBLL1' at 188 g/plot and 'PUB94.15.1.12/FRTL//92.001E7.32.5/SLVS' at 236. Nineteen lines had a

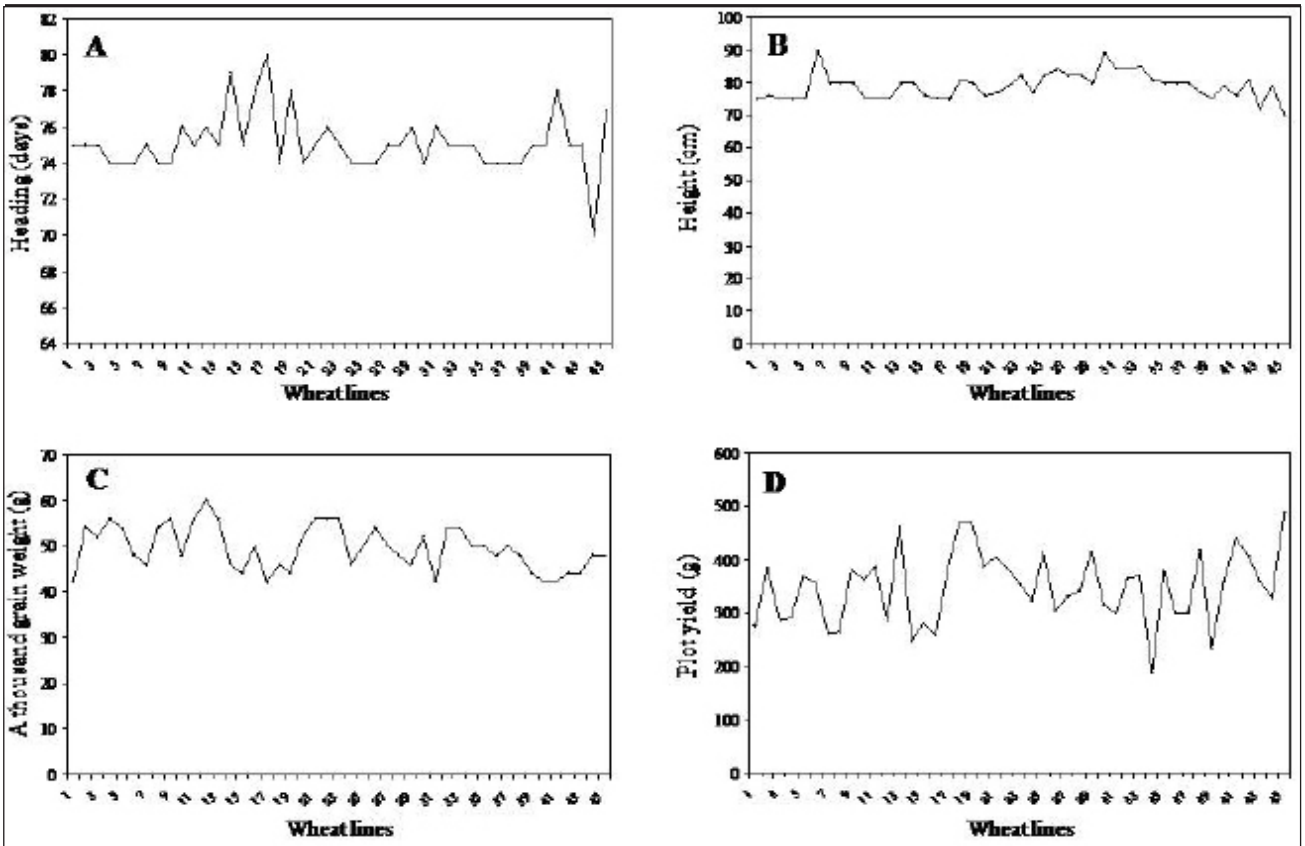

Fig. 1. Heading (A), height (B), 1,000-kernel weight (C), and plot yield (D) of 44 advanced bread wheat lines (see Table 1) from the 1'st Stress Adaptive Trait Yield Trial (CIMMYT) and durum cultivar Movas C2009 (1), durng the 2015–16 season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonory, Mexico.

grain yield above the 4-ton level, nine above the 5-ton level, and only REEDLING #1 above the 6-ton level. The commercial durum wheat cultivar Movas C2009 showed great sensitivity to heat and the shortage of cold hours because grain yield was 3.45 t.

Conclusion. Nine lines of the 1st Stress Adaptive Trait Yield Trial from CIMMYT showed grain yield above the 5-ton level in a late sowing date (29 December), with a shortage of cold hours (440 total) during the 2015–16 crop season. Line REEDLING #1 showed the highest grain yield (> 6 ton) and the lowest height (70 cm).

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Evaluation of yield components of durum wheat genotypes (Triticum turgidum spp. durum).

José Luis Félix-Fuentes, Guillermo Fuentes-Dávila, Rebeca Pinto-González, and Ivón Alejandra Rosas-Jáuregui.

Abstract. yield components of eight durum wheat cultivars and two advanced lines were evaluated under a randomized complete block experimental design with three replications, in a greenhose at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. The sowing date was 16 December, 2013, and the variables evaluated were grain yield, 1,000-kernel weight, grain weight/spike, grain/spike, spike length, aerial biomass weight, stem and spike weight, number of spikes, and harvest index. Regarding grain yield, the advanced lines 'CHEN_1/TEZ/3/GUIL// CIT71/CII/4/SORA/PLATA_12/5/STOT//ALTAR84/ALD/6/ SOMAT_3/PHAX_1//TILO_1/LOTUS_4/7/AJAIA_12/ F3LOCAL(SEL.ETHIO.135.85)// PLATA_13/4/CHEN_1/TEZ/3/GUIL//CIT71/CII/5/SORA/2*PLATA_12//SO-MAT_3' and 'CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/4/JUPAREC2001/5/CNDO/PRIMADUR// HAI-OU_17/3/ SNITAN/6/RISSA/GAN//POHO_1/3/PLATA_3//CREX/ALLA*2/4/ ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1' were statistically similar to that of cultivar CIRNO C2008, which was released for its high yield potential and occupies the largest area grown with wheat in southern Sonora. However, cultivars Quetchehueca Oro C2013 and Baroyeca Oro C2013 showed higher grain yield than that of cultivar CIRNO C2008.

Introduction. Wheat is one the most important crops in Mexico and occupies an area greater than 300,000 ha every year in the state of Sonora (SIAP 2014), which is the state with the highest wheat production in the country. Therefore, the wheat-breeding program in southern Sonora aims at generating material with outstanding plant traits, such as grain yield potential, number, and weight. The number of grain/m^2 is negatively related with grain weight. Slafer et al. (1996) reported that modern cultivars show a greater number of grain/m^2. Villaseñor and Espitia (2000) indicate that the increase in grain yield in new wheat genotypes is due to a greater number of grain/spike, and not to a greater grain weight, which suggests that in the future, a compensatory effect might be generated, where as the number of grains increases there will be lower amount of photoassimilates for each grain. Therefore, we evaluated variables highly related to wheat grain yield of genotypes, which represent new options for farmers in northwest Mexico.

Materials and Methods. This work was carried out in a greenhouse at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. Eight durum wheat commercial cultivars and two advanced lines (Table 2) were sown on 16 December, 2013, in 20-L pots (15 x 20 cm) with a mixture of 3:1 peat moss and perlite. The experimental design was a randomized complete block with three replications.,ANOVA was performed using the SAS System for Windows 9.0. Variables evaluated were grain yield, 1,000-kernel weight (TKW), grain weight/spike, grain/spike, spike length, aerial biomass weight, stem and spike weight, number of spikes, and harvest index. Data were recorded in g or in g/m^2 according to the variable evaluated.

Table 2. Durum wheat genotypes evaluated in the Yaqui Valley, Sonora, Mexico, during the 2013–14 crop season.

Cultivar/cross	Selection history
Atil C2001	CD91B1938-6M-030Y-030M-4Y-0M
CIRNO C2008	CGS02Y00004S-2F1-6Y-0B-1Y-0B
Sáwali Oro C2008	CDSS02Y00786T0TOPB-0Y-0M-2Y-0M-0Y
Patronato Oro C2008	CDSS02Y00390S-0Y-0M-8Y-0M
Movas C2009	CDSS02B00720S-0Y-0M-8Y-1M- 04Y-0B
Huatabampo Oro C2009	CDSS02B00562S-0Y-0M- 2Y-1M-04Y-0B
Quetchehueca Oro C2013	CDSS04B00367T-0TOPY-10Y-0M-4Y-0M-4Y-0B
Baroyeca Oro C2013	CDSS02B00643S-0Y-0M-1Y-4M-04Y-0B
CHEN_1/TEZ/3/GUIL//CIT71/CII/4/SORA/PLA-TA_12/5/STOT//ALTAR84/ALD/6/ SOMAT_3/ PHAX_1//TILO_1/LOTUS_4/7/AJAIA_12/ F3LOCAL(SEL.ETHIO.135.85)// PLATA_13/4/CHEN_1/ TEZ/3/GUIL//CIT71/CII/5/SORA/2*PLATA_12//SO-MAT_3	CDSS07B00086S-099Y-030M-13Y-4M-0Y
CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/4/JU-PAREC2001/5/CNDO/PRIMADUR// HAI-OU_17/3/ SNITAN/6/RISSA/GAN//POHO_1/3/PLATA_3//CREX/ ALLA*2/4/ ARMENT//SRN_3/NIGRIS_4/3/CANE-LO_9.1	CDSS07Y00184S-099Y-099M-12Y-1M-04Y-0B

Quetchehueca Oro C2013

Baroyeca Oro C2013

CIRNO C2008

Fig. 2. Commercial wheat cultivars.

Results. The ANOVA detected highly significant statistical differences among genotypes. Quetchehueca Oro C2013 (Fig. 2A) showed the highest grain yield (9.9 t/ha) followed by that of Baroyeca Oro C2013 (9.7 t/ha) (Fig. 2B, Table 2, p. 24). These cultivars were released for their high yield potential and resistance to leaf rust (Fuentes et al. 2014; Chávez Villalba et al. 2015). The grain yield of cultivar CIRNO C2008 averaged 350 kg lower than that of the advanced lines (Fig. 2C), although statistically similar. Cultivars Atil C2001 and Patronato Oro C2008 had the lowest grain yield with 7.3 and 7.4 t/ha, respectively. Durum wheat cultivars released previously to CIRNO C2008 do not have great yield potential, but those released later have great grain yield potential. We expect that they will reduce the pressure on CIRNO C2008, because it has shown susceptibility to yellow rust in some seasons. Previous research and historical data indicate that, within the management of the wheat crop in southern Sonora, sowing dates between 1 November to 15 December render the highest grain yield (INIFAP 2001). CIRNO C2008 had the highest TKW with 63.5 g, followed by that of Huatabampo Oro C2009 (61.2 g). Quetchehueca Oro C2013 and Baroyeca Oro C2013, the most recently released commercial durum cultivars, had 51.3 g and 48.1 g, respectively, and the advanced lines 'CHEN_1/TEZ/3/GUIL//...' and 'CNDO/PRIMADUR//...' had 58.2 g and 49.8 g, respectively. CIRNO C2008 had also the highest grain weight/spike R 3 g, followed by those of Movas C2009 (2.82 g) and Huatabampo Oro C2009 (2.81 g). Movas C2009 (57.4 g) and line 'CNDO/PRIMADUR...' (56.4 g) were statistically similar for the number of grain/spike. Althought Atil C2001 has a good number of grain/spike, this cultivar is affected by leaf rust, which reduces the size and grain weight. Atil C2001 showed the longest spikes with an average of 7.75 cm, and was statistically different from the other genotypes (Table 3). Quetchehueca Oro C2013 and Baroyeca Oro C2013 had the highest aerial biomass weight with 2006 g/m^2 and 1968, respectively (Table 4, p. 26). This characteristic is positively associated with grain yield. Foulkes et al. (2007) reported that, in early stages of plant development, a higher biomass gives a greater yield, while after the flowering stage, the higher the biomass the lower the yield, because as the biomass increases the assimilates available for grain filling diminish, which is related to the temperature. When high temperatures prevail, the plant closes the stomates in order to avoid loss of humidity and photosynthesis is reduced. The maximum daily temperature recorded at noon in the greenhouse during plant development was recorded (Fig. 3, p. 26). Baroyeca oro C2013 and Quetchehueca Oro C2013 showed the highest number of spikes with 529 and 505, respectively, whereas CIRNO C2008 had 423.

Table 3. Grain yield, 1,000-kernel weight (TKW), grain weight, number of grain/spike, and spike length of durum wheat genotypes evaluated in the Yaqui Valley, Sonora, Mexico, during the 2013–14 crop season. Genotypes followed by the same letter within the columns are statistically similar.

Cultivar	Grain yield (t/ha)	TKW (g)	Grain weight/ spike (g)	Grain/spike	Spike length (cm)
Atil C2001	7.3 c	44.4 d	2.39 b	53.2 ab	7.75 a
CIRNO C2008	8.8 abc	63.5 a	3.00 a	47.2 ab	6.47 bc
Sáwali Oro C2008	8.0 abc	48.9 d	2.24 b	51.0 ab	6.45 bc
Patronato Oro C2008	7.4 c	50.9 bcd	2.31 b	44.4 b	7.09 ab
Movas C2009	7.9 abc	49.0 cd	2.82 ab	57.4 a	7.00 abc
Huatabampo Oro C2009	7.5 bc	61.2 ab	2.81 ab	47.2 ab	6.73 bc
Quetchehueca Oro C2013	9.9 a	51.3 bcd	2.64 ab	51.6 ab	6.71 bc
Baroyeca Oro C2013	9.7 ab	48.1 cd	2.33 b	50.9 ab	6.98 bc
CHEN_1/TEZ/3/GUIL//...	9.3 abc	58.2 abc	2.71 ab	48.7 ab	6.13 c
CNDO/PRIMADUR//...	9.0 abc	49.8 bcd	2.68 ab	56.4 a	6.73 bc
Coefficient of variation	8.91	7.85	7.7	7.13	4.57

Table 4. Aerial biomass weight, stem weight, spike weight, number of spikes, and harvest index of durum wheat genotypes evaluated in the Yaqui Valley, Sonora, during the 2013–14 crop season. Genotypes followed by the same letter within the columns are statistically similar.

Cultivar/Cross	Aerial biomass weight/m² (g)	Stem weight// m² (g)	Spike weight/m² (g)	Spikes/m²	Harvest index
Atil C2001	1,582 c	604.3 cde	1,030 b	413 b	0.464 ab
CIRNO C2008	1,673 bc	578.3 e	1,127 ab	423 ab	0.530 ab
Sáwali Oro C2008	1,693 bc	662.3 bcde	1,050 b	481 ab	0.473 ab
Patronato Oro C2008	1,546 c	637.3 cde	1,004 b	481 ab	0.481 ab
Movas C2009	1,654 c	593.6 de	1,060 b	421 ab	0.481 ab
Huatabampo Oro C2009	1,804 abc	688.3 abcd	1,146 ab	453 ab	0.417 b
Quetchehueca Oro C2013	2,006 a	765.3 ab	1,264 a	505 ab	0.498 ab
Baroyeca Oro C2013	1,968 ab	792.6 a	1,245 a	529 a	0.495 ab
CHEN_1/TEZ/3/GUIL//...	1,824 abc	707.0 abc	1,185 ab	479 ab	0.510 ab
CNDO/PRIMADUR//...	1,703 bc	650.3 cde	1,122 ab	460 ab	0.531 a
Coefficient of variation	5.82	5.41	5.54	8.29	7.92

Conclusions. Under greenhouse conditions, the advanced lines 'CHEN_1/TEZ/3/GUIL// CIT71/CII/4/SORA/PLATA_12/5/STOT//ALTAR84/ALD/6/SOMAT_3/PHAX_1//TILO_1/LOTUS_4/7/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/4/ CHEN_1/TEZ/3/GUIL//CIT71/CII/5/SORA/2*PLATA_12//SOMAT_3' and 'CNDO/ PRIMADUR//HAI-OU_17/3/SNITAN/4/JUPAREC2001/5/CNDO/PRIMADUR//HAI-OU_17/3/SNITAN/6/RISSA/GAN//POHO_1/3/PLATA_3//CREX/ALLA*2/4/ARMENT// SRN_3/NIGRIS_4/3/CANELO_9.1' were statistically similar in grain yield to cultivar CIRNO C2008, which was released for its high yield potential and occupies the largest area grown with wheat in southern Sonora. Cultivars Quetchehueca Oro C2013 and Baroyeca Oro C2013 showed higher grain yield with 9.9 t/ha and 9.7 t/ha, respectively, than that of cultivar CIRNO C2008 (8.8 t/ha).

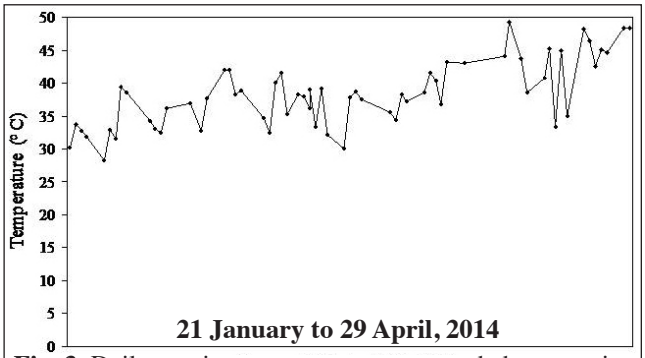

Fig. 3. Daily maximum temperatures recorded at noon in a greenhouse from 21 January to 29 April, 2014, where yield components of eitght commercial durum wheat cultivars and two advanced lines were evaluated at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

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Evaluation of bread wheats for grain yield and other parameters at two sowing dates with two and three complementary irrigations during the 2007–08 crop season.

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

Abstract. Commercial bread wheat cultivars Tacupeto F2001 and Kronstad F2004, and five advanced lines were evaluated for grain yield, test weight, protein, days-to-flowering, and days-to-maturity at two sowing dates (15 and 30 November, 2007) with two and three complementary irrigations, during the 2007–08 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. The experimental plots consisted of four beds with two 5-m rows with a seed density of 100 kg/ha under a randomized complete block design with three replications. The ANOVA was performed using the SAS System for Windows 9.0 and mean comparison with Tukey's test (α=0.01). All genotypes produced greater grain yield with three complementary irrigations in both sowing dates, and greater grain yield in the first than in the second sowing date. The 'ATTILA/PASTOR' line produced the highest grain yield at 6.9 t/ha in the first date with three complementary irrigations, and showed the highest test weight with 82.6 kg/hl. Cultivar Kronstad F2004 showed the highest protein content. The earliest genotype was 'TOBA97/PASTOR' with an average of 121 days. The 'CHEN/AE.SQ//2*OPATA/3/ BABAX/4/JARU' lline was 101 cm in height with a 6 cm difference with respect to 'ATTILA/PASTOR', which was the shortest.

Introduction. Currently, wheat is one of the most important cereals worldwide as staple food, assuming that the world population will double in the next decades and the worldwide demand will rise. Under this context, wheat production must increase along with higher grain yield per unit area and/or greater area cultivated. Implementing strategies in order to increase wheat production are part of a current global debate. One of the key aspects, determining how much it would be possible to express the genetic potential of a given cultivar, is to establish environmental limits that allow the expression of maximum yield, that is yield potential, so as to establish the gap between potential and actual yield. For that reason, working with advanced lines is necessary in order to evaluate the performance of the genetic material generated by the breeding programs. Therefore, genotypes must be stabilized in different environments (Solano et al. 1998) with two and three complementary irrigations. Our objective was to evaluate several bread wheats for grain yield, test weight, protein, days-to-flowering, and days-to-maturity in two sowing dates with two and three complementary irrigations.

Materials and Methods. The commercial bread wheat cultivars Tacupeto F2001 and Kronstad F2004 and five advanced lines (Table 5) were evaluated for grain yield, test weight, protein, days-to-flowering, and days-to-maturity at two sowing dates (15 and 30 November, 2007) with two and three complementary irrigations during the 2007–08 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, located in block 910 in the Yaqui Valley, Sonora, Mexico, at 27° 22'04.64" latitude north and 109° 55'28.26" longitude west, 37 masl, with warm climate (BW (h)) and extreme heat according to Koppen's classification modified by García (1988), in a heavy clay soil. Experimental plots consisted of four beds with two 5-m rows with a seed density of 100 kg/ha under a randomized complete block design with three replications. The ANOVA was performed using the SAS System for Windows 9.0 and mean comparison with Tukey's test (α=0.01). The agronomic management followed the recommendations of INIFAP for the region (Figueroa-López et al. 2011).

Table 5. Bread wheats evaluated during the 2007–08 crop season at the Norman E. Borlaug Experimental Station, in the Yaqui Valley, Sonora, Mexico.

Line	Genotype	Pedigree and selection history
1	TACUPETO F2001	CGSS95B00016F-099Y-099B-099Y-099B-15Y-0B
2	KRONSTAD F2004	CMSS92Y01425T-16Y-010M-010Y-010Y-1M-0Y-50EY-0Y
3	KAMB1*2/KUKUNA	CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B
4	ATTILA/PASTOR	CMSS97Y04045S-040Y-050M-040SY-030M-14SY-010M-0Y
5	TOBA97/PASTOR	CMSS97M05756S-040M-020Y-030M-015Y-3M-1Y-3M-0Y
6	CHEN/AE.SQ//2*OPATA/3/BABAX/4/JARU	CMSS99Y03521T-040M-040Y-040M-040SY-040M-5Y-010M
7	D67.2/P66.270//AE.TAUSCHII (320)/3/CUNNINGHAM	CMSS99M02230S-040M-040SY-6M-3Y-0M-10Y

Results. All genotypes had a greater grain yield with three complementary irrigations at both sowing dates (Fig. 4). At the first sowing date, the difference in grain yield between the three and two complementary irrigations ranged from 575 to 1,529 kg with an average of 1,064 kg. At the second date, the difference ranged from 667.5 to 1,138.3 kg, with an average of 958.3 kg. Similarly, all genotypes showed a greater grain yield at the first sowing date than in the second; the difference ranging from 295.7 to 705.7 kg. Grain yield of the genotypes with three complementary irrigations sown on 15 November had an average of 6.5 t/ha, and 5.4 with two irrigations (1.1 t/ha difference). Grain yield of the group with three irrigations sown on 30 November had an average of 5.8 t/ha and 4.8 with two irrigations (a 1.0 t/ha difference). Statistical differences were detected between the sowing dates and between complementary irrigations (Table 6). The 'ATTILA/PASTOR' line showed the highest grain yield at 6.9 t/ha at the first date with three complementary irrigations, followed by Tacupeto F2001 (6.6 t/ha), 'KAMBI*2/KUKUNA' (6.5 t/ha), and 'D67.2/P66.270//AE.TAUSCHII(320)/3/CUNNINGHAM' (6.4 t/ha). The same genotypes showed lower yields with two irrigations with a difference of 1.5, 1.0, 0.721, and 1.28 t/ha, respectively. The 'ATTILA/PASTOR' line, which was generated by the CIMMYT Wheat Program as tolerant to drought (Figueroa-López et al. 2007), showed a grain yield lower than those of Tacupeto F2001 and 'KAMB1*2/KUKUNA' with reduced irrigation, contrary to its performance during the 2005–06 crop season, although the difference with respect to 'KAMB1*2/KUKUNA' was 358 kg and 187 kg with Tacupeto F2001. A statistical difference was detected for test weight among the genotypes evaluated (Table 6). The 'ATTILA/PASTOR' line showed the highest test weight with 82.6 kg/hl. Genotypes with the lowest test weight were 'D67.2/P66.270//AE.TAUSCHII (320)/3/CUNNINGHAM' and 'CHEN/AE.TAU//2*OPATA/3/BABAX/4/JARU'. The cultivar Kronstad F2004 showed the highest protein content, whereas 'ATTILA/PASTOR' had the lowest, with an average of 12.9 kg with two complementary irrigations at both sowing dates. This agrees with the report by Ruvalcaba et al. (2007) who indicate that there is a negative correlation between grain yield and protein content. The earliest genotype was 'TOBA97/PASTOR' with an average of 121 days, whereas Kronstad F2004 and 'D67.2/P66.270//AE.TAUSCHII (320)/3/CUNNINGHAM' had an average of 127 days at both sowing dates with two and three complementary irrigations. The same behavior was observed with days-to-flowering, with a seven day difference. Statistical differences were detected among the height of the genotypes. 'CHEN/AE.TAU//2*OPATA/3/ BABAX/4/JARU' was 101 cm tall, with a 6-cm difference

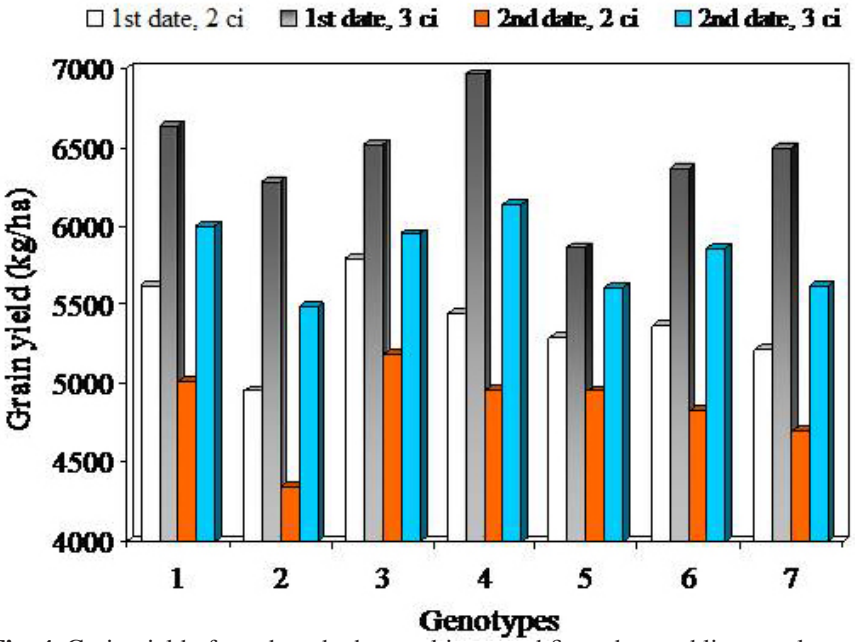

Fig. 4. Grain yield of two bread wheat cultivars and five advanced lines evaluated at two sowing dates and three complementary irrigations during the 2007–08 crop season at the Norman E. Borlang Experimental Station (1 = Tacupeto F2001, 2 = Kronstad F2004, 3 = KAMBI*2/KUKUNA, 4 = ATTILA/PASTOR, 5 = TOBA97/Pastor, 6 = CHEN/AE.TAU//2*OPATA/3/Babax/4/Jaru, and 7 = D67.2/P66.270/AE. TAUSCHII (320)/3/CUNNINGHAM

Table 6. Average of several parameters of two commercial bread wheat cultivars and five advanced lines sown in two dates and with two and three complementary irrigations, during the 2007–08 crop season, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. Columns with the same letter are statistically similar (Tukey's test, α=0.01).

Variable	Grain yield (kg/ha)	Test weight (kg/ha)	Protein (%)	Flowering (days)	Maturity (days)
15 November	5.9 a	82.14 b	13.47 b	84.2 a	126.8 a
30 November	5.3b	82.37 a	13.97 a	84.3 a	121.6 b
2 irrigations	5.1 b	81.76 b	14.36 a	83.83 b	123.16 b
3 irrigations	6.1 a	82.75 a	13.08 b	84.76 a	125.28 a

with respect to 'ATTILA/PASTOR', which was the shortest. The last three variables are affected by temperature during crop development (Fig. 5), and show important variation previous to flowering. Of the variables analyzed, only protein content was favored when two complementary irrigations were applied, which indicates that if quality is to be improved following the agronomic management recommended by INIFAP for the region, reducing irrigation is important. However, quality must have a significant cash value, so that wheat cultivated for that purpose is profitable.

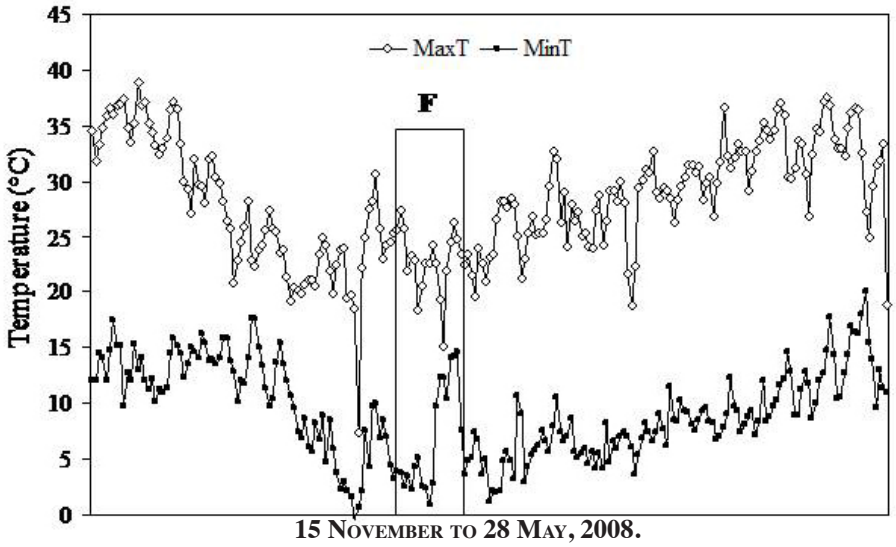

Fig. 5. Maximum and minimum temperatures during the 2007–08 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico (F = flowering stage at two sowing dates.

Conclusions. The application of three complementary irrigations has an important effect of increasing grain yield and decreasing protein content. The cost/benefit of using more or less water with a specific wheat cultivar must be analyzed based on the commercialization in the region.

All the genotypes we evaluated showed greater grain yield with three complementary irrigations than with two, at both sowing dates (15 and 30 November, 2007). All genotypes showed greater grain yield in the first than in the second sowing date, although the 'ATTILA/PASTOR' line showed the highest grain yield at the first and the second sowing dates with three complementary irrigations, but did not perform as a genotype tolerant to drought stress as its yield with reduced irrigation was lower than that of the other genotypes, which are not classified as drought tolerant.

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Reaction of elite advanced bread wheat lines to karnal bunt under artificial field inoculation, during the 2014–15 crop season.

Guillermo Fuentes-Dávila, Ravi P. Singh (CIMMYT Int, km 45 Carret. México-Veracruz, El Batán, Texcoco, Edo. de México CP 56130), Carlos Antonio Ayón-Ibarra, Ivón Alejandra Rosas-Jáuregui, Pedro Félix-Valencia, Miguel Alfonso Camacho-Casas, José Luis Félix-Fuentes, and Gabriela Chávez-Villalba.

Abstract. We evaluated 168 elite advanced bread wheat lines for resistance to Karnal bunt during the 2014–15 autumn–winter crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. Sowing dates were 19 and 29 November, and 8 December, 2014. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage in five heads from each line. Harvest was done manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. The range of infection for the first sowing date was 0 to 48.2%, with a mean of 12.7, 0–29.3% with a mean of 7.9 for the second sowing date, and 0–26.3 with a mean of 6.3 for the third sowing date. The average of the three highest percentage of infection of the susceptible check KBSUS 1 was 98.6%. Overall, for the three dates, 18 lines fell within the 0.1–2.5 infection category, 28 in the 2.6–5.0 category, 60 in the 5.1–10.0 category, and 62 in the 10.1–30 infection category. The highest percentage of infection in all dates was line 'CHYAK/PRL' in the first date with 48.2, followed by 'PICAFLOR #1/NELOKI' with 41.7%, also in the first date. Twelve lines consistently showed a percentage infection below 5%, and seven showed a percentage of infection below 2.5% in all dates.

Introduction. The most susceptible plant species to Karnal bunt is *Triticum aestivum*. Under artificial inoculation, some lines may show more than 50% infeted grain (Fuentes-Dávila et al. 1992; 1993). The causal agent of this disease is the fungus *Tilletia indica* (Mitra 1931) (syn. *Neovossia indica*). Although *T. indica* may affect durum wheat (*T. turgidum*) and triticale (X *Triticosecale*; Agarwal et al. 1977), the levels of infected grain are generally low. 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 can be 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. The objective of this work was to evaluate elite advanced bread wheat lines for resistance to Karnal bunt.

Materials and Methods. We evaluated 168 elite advanced bread wheat lines for resistance to Karnal bunt during the autumn–winter 2014–15 crop season in block 910 in a clay soil with pH 7.8, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. Sowing dates were 19 and 29 November, and 8 December, 2014, 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 (Fig. 6). After teliospore germination, fungal colonies were transferred and multiplied on potato-dextrose-agar. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage (Fig. 7) in five heads from each line. High relative humidity in the experimental area was provided by an automatic mist spray-irrigation system five times a day for 20 min each time. Harvest was done manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. Evaluated lines originated from the collaborative project between the International Maize and Wheat Improvement Center (CIMMYT) and the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP).

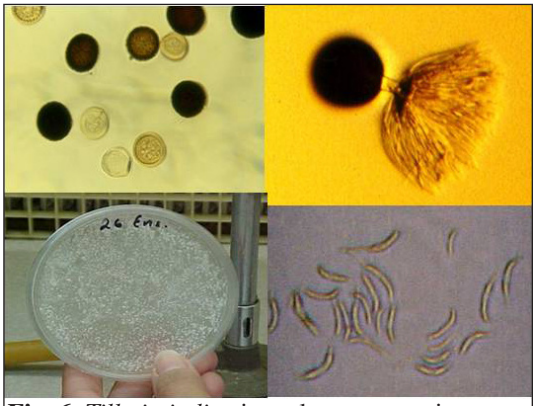

Fig. 6. *Tilletia indica* inoculum preparation.

Fig. 7. Artificial inoculation of wheat with *Tilletia indica* by boot injection.

Results. The range of infection for the first sowing date was 0 to 48.2%, with a mean of 12.7. One line did not have any infected grain (Fig. 8A, p. 31). For the first sowing date, 16 lines fell within the 0.1–2.5 infection category, 12 were 2.6–5.0, 43 were 5.1–10.0, 88 were 10.1–30 category, and eight had more than 30% infection (Fig.

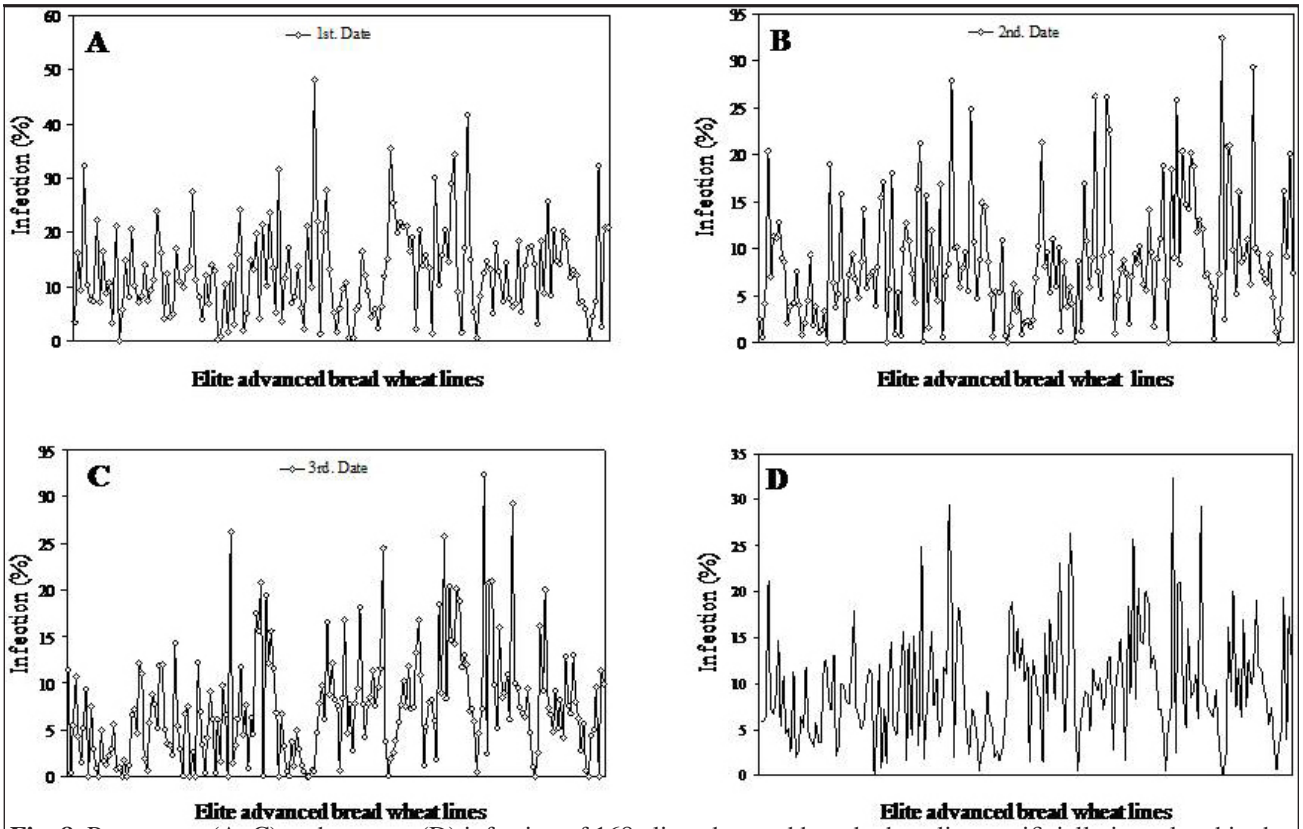

Fig. 8. Percentage (A–C) and average (D) infection of 168 elite advanced bread wheat lines artificially inoculated in the field with Tilletia indica at three dates (19 (A) and 29 (B) November, and 8 December (C), 2014) during the 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

9A, p. 32). The range of infection for the second sowing date was 0–29.3%, with a mean of 7.9. Eight lines did not have any infected grains (Fig. 8B). The overall results of the second sowing date were 26 lines within the 0.1–2.5 infection category, 21 within 2.6–5.0, 70 within 5.1–10.0, and 43 within 10.1–30 (Fig. 9B). For the third sowing date, the range of infection was 0–26.3 with a mean of 6.3; 16 lines did not have any infected grain (Fig. 8C). At the third sowing date, 29 lines fell within the 0.1–2.5 infection category, 29 within 2.6–5.0, 62 within 5.1–10.0, and 32 within 10.1–30 (Fig. 9C, p. 32). The average percent infection of the three dates is shown in Fig 8D. The average of the three highest percentage of infection of the susceptible check KBSUS 1 was 98.6%. For all three dates, 18 lines fell within the 0.1–2.5 infection category, 28 in the 2.6–5.0 category, 60 in the 5.1–10.0 category, and 62 in the 10.1–30 infection category (Fig. 9D, p. 32). Lines with less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). Twelve lines consistently showed a percentage of infection below 5% at all sowing dates (Table 7, p 32) and seven showed a percentage of infection below 2.5% (Table 8, p. 33). The highest percentage of infection at all dates was in line 'CHYAK/PRL' in the first date with 48.2, followed by 'PICAFLOR #1/NELOKI' with 41.7% also in the first date. The elite advanced bread wheat lines with resistance shown to *T. indica* may be prospects for release if attributes like resistance to rusts, yield and quality are met, in regions where Karnal bunt constitutes an economic constraint, as it has been in Mexico (Camacho et al. 1993; Valenzuela-Herrera et al. 2011), or be part of a resistant pool in a wheat-breeding program.

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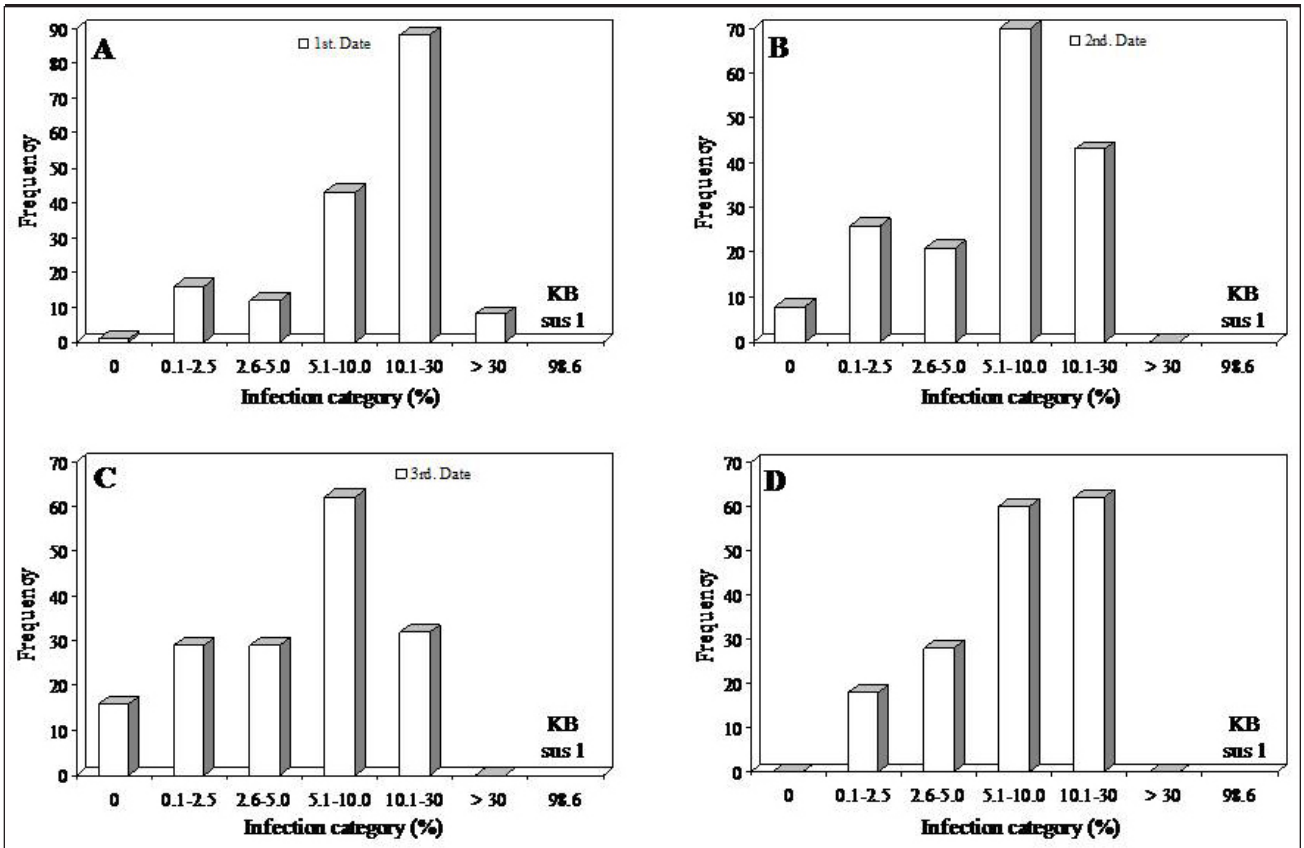

Fig. 9. Infection categories (%) of 168 elite advance bread wheat lines artificially inoculated in the field on three dates (19 (A) and 29 (B) November, and 8 December (C), 2014) during the 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. The level of infection of KBSUS1 is the mean of the three highest infection scores.

Table 7. Elite advanced bread wheat lines that consistently showed a percentage of infection with *Tilletia indica* below 5% planted at three dates after artificial field inoculation during the 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Line	Range of infection	Average
PICAFLOR #1/8/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/KUKUNA	0.0–3.1	1.2
TRCH/SRTU//KACHU/3/KINGBIRD #1	0.0–2.8	1.4
ROLF07/KINGBIRD #1//MUNAL #1	0.0–4.2	1.6
FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/KITE/6/KINGBIRD #1/7/FRANCOLIN #1	0.0–3.0	1.6
PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI	0.6–3.6	1.8
KACHU/2*MUNAL #1	0.0–3.9	1.9
LERKE/5/KAUZ/3/MYNA/VUL//BUC/FLK/4/MILAN/6/PROGRESO F2007/7/MUNAL/8/MUNAL #1	0.6–4.3	1.9
KIRITATI/2*WBLL1/8/SHA7//PRL/VEE#6/3/FASAN/4/HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA/9/PFAU/SERI.1B//AMAD*2/3/PBW343*2/KUKUNA	0.0–4.7	2.0
SOKOLL/WBLL1/4/D67.2/PARANA 66.270//AE.TAUSCHII (320)/3/CUNNINGHAM	0.0–4.5	2.1
BAJ #1*2/BECARD	0.0–4.2	2.5
PFAU/MILAN//TROST/3/MUNAL #1/4/PFAU/MILAN//TROST/3/PBW65/2*SERI.1B	0.0–4.6	3.0
MILAN//PRL/2*PASTOR/4/CROC_1/AE.TAUSCHII(213)//PGO/3/BAV92/5/PAURAQ	0.6–4.8	3.3

Table 8. Elite advanced bread wheat lines that consistently showed a percentage of infection with *Tilletia indica* below 2.5% at three sowing dates after artificial field inoculation during the 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Line	Range of infection	Average
KACHU/6/YAR/AE.TAUSCHII(783)/4/GOV/AZ//MUS/3/SARA/5/MYNA/ VUL//JUN	0.0–0.4	0.1
MUNAL #1/2*FRNCLN	0.0–0.8	0.4
MUNAL #1*2/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07	0.0–1.0	0.5
BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/MUNAL #1	0.0–1.1	0.5
PRL/2*PASTOR//SUNSTATE/3/GRACK	0.0–1.7	0.8
WHEAR/SOKOLL/4/PASTOR//MILAN/KAUZ/3/BAV92	0.7–2.2	1.3
PASTOR/3/VORONA/CNO79//KAUZ/4/MILAN/OTUS//ATTILA/3*BCN/5/ KINGBIRD #1/6/PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07	0.0–2.4	1.5

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Evaluation in the field of the International Spring Bread Wheat Screening Nursery during the 2015–16 crop season.

Guillermo Fuentes-Dávila, Ivón Alejandra Rosas-Jáuregui, Carlos Antonio Ayón-Ibarra, Pedro Félix-Valencia, José Luis Félix-Fuentes, Miguel Alfonso Camacho-Casas, and Gabriela Chávez-Villalba.

Abstract. Two hundred eighty-five lines from the 48th International Spring Bread Wheat Screening Nursery from CIMMYT were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station, in the Yaqui Valley, Sonora, México. Plots consisted of a 1-m long bed with two rows 0.80 m apart without replications and a seed density of 100 kg/ha. The variables evaluated were days-to-heading, height (cm), 1,000-kernel weight (g), and visual agronomic stand. The average heading of the lines was 75 days and the average group height was 77 cm. The shortest line was 'SNB// CMH79A.955/3*CNO79/3/ATTILA/4/CHEN/AEGILOPSTAUSCHII (TAUS)//BCN/3/2*KAUZ/5/KINGBIRD #1' at 65 cm and line 'BECARD*2/PFUNYE #1' had a height of 90 cm. The average 1,000-kernel weight of the group was 46 g; line 'WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/HUW234+LR34/ PRINIA//PBW343*2/KUKUNA/3/ ROLF07' had the highest weight at 59.8 g, followed by 'PRL/2*PASTOR//KACHU/3/TRCH/SRTU//KACHU' at 58.8 g. The best visual agronomic stand (score of 4) was assigned to lines 'KIRITATI/4/2* SERI.1B*2/3/KAUZ*2/BOW// KAUZ/5/WAXWING*2/KRONSTADF2004/6/ KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ' and 'CHWINK/ GRACKLE#1// FRNCLN', however, they were below for 1,000-kernel weight with 41.8 g and 44.1 g, respectively. The highest number of cold hours (261) accumulated during January, followed by 92 in February, 62 in March, 24 in April, and 1 in May. The total number of accumulated cold hours was 440.

Introduction. Wheat is one of the most important cereals worldwide, in production and consumption by humankind (Hoseney 1991). However, changing climatic conditions may not be adequate for agricultural purposes primarily because of temperature alterations. Fokar et al. (1998) indicate that heat stress is the main factor that causes a reduction in wheat

productivity due to high temperatures. Optimum temperatures for spring wheat development fluctuate between 8 and 25°C; however, breeding and selection have made wheat into a species with wider adaptation (INIFAP 2001), even when temperatures are not adequate for plant development. Yield and/or quality may be affected by thermal stress, which is defined as the temperature increase above a determined threshold for a period of time, enough to cause irreversible deleterious effects on development and growth of crops (Wahid et al. 2007). High temperatures have a complex effect on crops, and the final result on yield and quality by thermal stress will strongly depend on the characteristics of such a stress (i.e., severity, duration, and/or in combination with other stresses), the crop (phenologic stage when it occurs and species/genotype), and the interaction with other environmental factors (Savin 2010). Sowing date also is an important factor for productivity of any crop, because plant development at various growth stages is influenced positive or negatively by the prevailing weather conditions. In general, wheat yield will be drastically reduced if the sowing dates are not followed by the technical recommendations, based on the historical records of a given region (López 1991; Figueroa-López et al. 2011). In southern Sonora, heat waves during the wheat season have had negative effects on productivity, by causing flower abortion and/or sterility, affecting kernel development, and reducing final grain weight (Félix-Valencia and Fuentes-Dávila 2015). Theferore, experimental wheat germplasm should be subjected to heat stress in order to generate information and, consequently, selection of the materials better adapted to such conditions. The International Bread Wheat Screening Nursery (IBWSN), produced by the International Maize and Wheat Improvement Center, is designed to rapidly assess a large number of advanced generation (F_3–F_7) lines of spring bread wheat under 'mega-environment 1' (ME1), which represents diversity for a wide range of latitudes, climates, day length, fertility conditions, water management, and, most importantly, disease conditions. The distribution of these nurseries is deliberately biased toward the major spring wheat regions of the world where diseases of wheat are of high incidence. The IBWSN is distributed to 180 locations and contains from 300 to 450 entries (CIMMYT 2017). Our objective was to determine the preliminary performance of experimental germplasm from the 48th ISBWSN from CIMMYT under one date of late sowing.

Materials and Methods. Two hundred eighty-five advanced wheat lines from the 48th ISBWSN from CIMMYT were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station, located in block 910 in the Yaqui Valley, Sonora, México, at 27° 22'04.64" N and 109° 55'28.26" W, 37 masl, with warm climate (BW (h)) and extreme heat according to Koppen's classification modified by García (1988). Plots consisted of a 1-m long bed with two rows 0.80 m apart without replications and a seed density of 100 kg/ha. For management of the trial, INIFAP technical recommendations were followed (Figueroa-López et al. 2011). Maximum, minimum, and average daily temperature (°C) and relative humidity and rainfall were recorded during the crop season. Cold hours were determined as the temperature > 0.1°C to < 10°C that occur during a given hour. The variables evaluated were days-to-heading, height (cm), 1,000-kernel weight (g, TKW), and visual agronomic stand (on a scale from 1 (worst) to 5 (best)).

Results. Based on historical data, optimum sowing dates in southern Sonora are between 15 November to 15 December. The highest number of cold hours (261) accumulated during January, with 92 in February, 62 in March, 24 in April, and 1 in May. The total number of accumulated cold hours was 440, without considering 125 in December 2015, since sowing of the trial took place on 29 December. The average heading of the lines was 75 days; the highest difference in relation to the group average was 8 days in the line 'GRACKLE #1*2/KINGBIRD #1', which was the earliest (Fig. 10A, p. 35).

The average group height was 77 cm. The shortest line was 'SNB//CMH79A.955/3* CNO79/3/ATTILA/4/CHEN/AEGILOPSTAUSCHII(TAUS)//BCN/3/2*KAUZ/5/ KINGBIRD#1' at 65 cm, followed by lines 'BECARD*2/PFUNYE #1' (90 cm); 'SHA7//PRL/ VEE#6/3/FASAN/4/HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA/8/2*WHEAR/SOKOLL' (88 cm); and 'KACHU/3/PBW343*2/ KUKUNA//PBW343*2/KUKUNA', 'PBW343*2/KUKUNA//PBW343*2/KUKUNA/6/ WBLL1*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/KACHU', and 'PBW343*2/ KUKUNA//PBW343*2/KUKUNA/8/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/KUKUNA' at 87 cm (Fig. 10B, p. 35). The average TKW of the group was 46 g. Line 'WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/HUW234+LR34/ PRINIA//PBW343*2/KUKUNA/3/ROLF07' was the highest at 59.8 g, followed by 'PRL/2*PASTOR//KACHU/3/TRCH/SRTU//KACHU' with 58.8 g, 'FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/WHEAR/6/KINGBIRD#1/7/ FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/TNMU/6/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ' at 57.2 g, 'QUAIU #1*2/MUNAL #1' at 56.5 g, and 'PRL/2*PASTOR//WAXWING*2/KRONSTADF2004/4/PBW343*2/KUKUNA// KRONSTAD F2004/3/PBW343*2/KUKUNA' with 56.0 g. Line 'TC870344/GUI//TEMPORALERA M 87/AGR/3/2*WBLL1/4/HUW234+LR34/ PRINIA//PBW343*2/KUKUNA/3/ROLF07' showed the lowest TKW with 38.9 g (Fig. 10C, p. 35). The best visual agronomic stand (score 4) was assigned to lines 'KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/WAXWING*2/KRONSTAD F2004/6/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ'

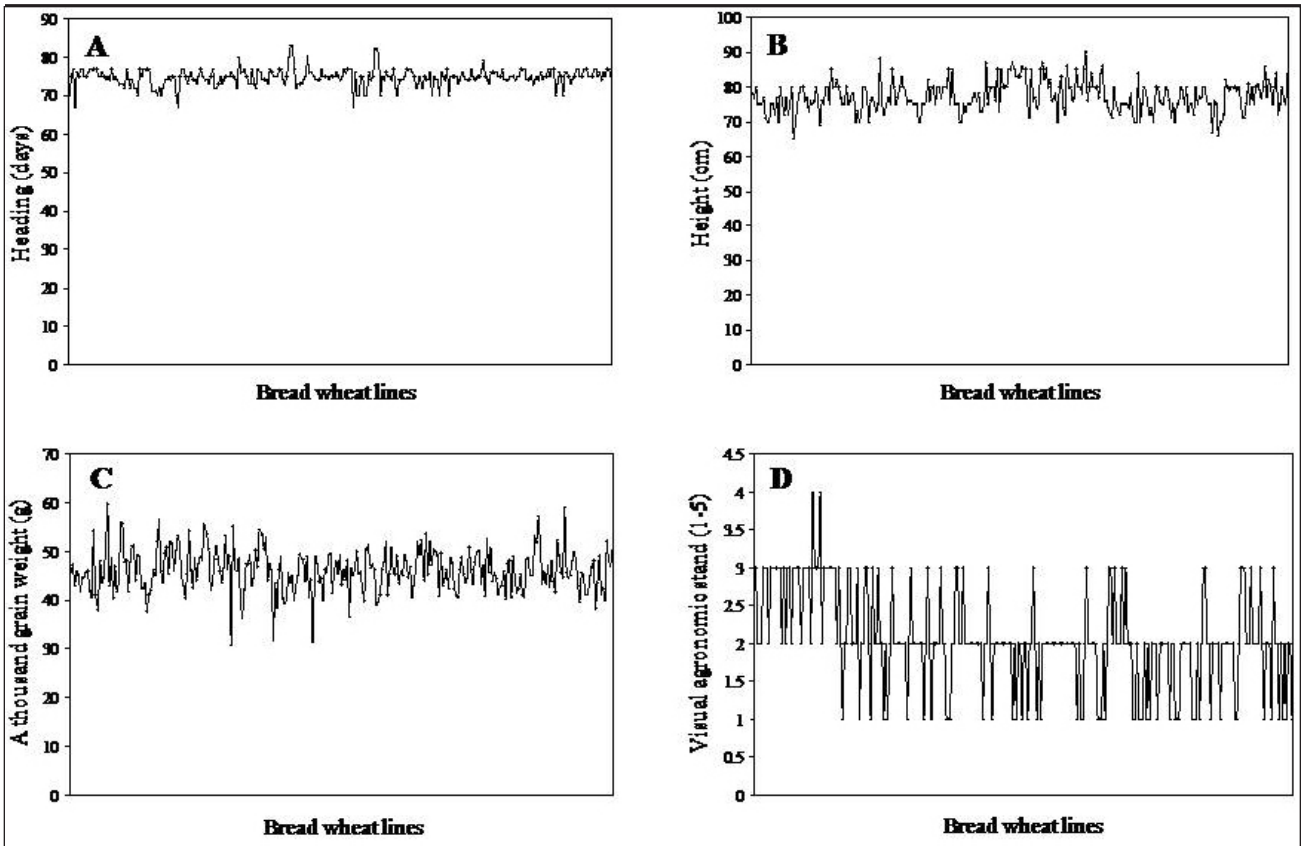

Fig. 10. Days-to-heading (A), height (B, cm), 1,000-kernel weight (C, g), and visual agronomic stand (D, scale 1 (worst)–5(best)) of 285 lines from the 48th International Spring Bread Wheat Screening Nursery from CIMMYT during the 2015–16 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

and 'CHWINK/ GRACKLE #1//FRNCLN' (Fig. 10D), however, they were below for TKW with 41.8 g and 44.1 g, respectively. None of the lines showed yellow or leaf rust infection during the season.

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Preliminary evaluation in the field of the 33rd Semi-Arid Wheat Screening Nursery during the 2015–16 crop season.

Ivón Alejandra Rosas-Jáuregui, Guillermo Fuentes-Dávila, Carlos Antonio Ayón-Ibarra, Pedro Félix-Valencia, José Luis Félix-Fuentes, Miguel Alfonso Camacho-Casas, and Gabriela Chávez-Villalba.

Abstract. We sowed 271 advanced bread wheat lines from the 33rd Semi-Arid Wheat Screening Nursery from CIMMYT on 29 December, 2015, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, México. Plots consisted of a 1-m bed with two rows 0.80 m apart without replications and a seed density of 100 kg/ha. The variables evaluated were days-to-heading, height, 1,000-kernel weight, and visual agronomic stand (on a scale from 1 to 5 as the best). The average heading of the lines was 74 days and the average height was 77 cm. Lines 'PREMIO/2*BAVIS' and '92.001E7.32.5/SLVS/5/NS-732/HER/3/PRL/SARA//TSI/VEE#5 /4/FRET2/6/SOKOLL/3/PASTOR// HXL7573/2*BAU' showed a height of 90 cm. The average 1,000-kernel weight of the group was 48 g. Line 'SUP152*2/ PFUNYE#1' had the greatest weight with 59.93 g. The best visual agronomic stand (score 4) was assigned to lines 'PRL/2*PASTOR' and 'KACHU/PRL'. None of the lines showed yellow or leaf rust infection during the season. Of the 271 lines, 32 had a 1,000-kernel weight equal to or greater than 53 g, although the average of the visual agronomic stand was 1.8. Lines 'PBW65/2*PASTOR' (line 1) and 'PICAFLOR#1/8/NG8201/ KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/ MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/ KUKUNA' (line 16) had the highest agronomic stand score with 3. The total number of accumulated cold hours during the crop season (after 29 December, 2015) was 440.

Introduction. Wheat is the cereal with the highest production worldwide, and one of the most important and stable components of the human diet due to its great nutritious value and the high carbohydrate (65–70%) and protein (12–13%) contents. Wheat is cultivated under both irrigated and rain-fed conditions. Water availability allows the wheat plant to yield close to its highest potential. In rain-fed regions, rainfall is concentrated during the winter months with hydric deficits in the spring and summer. The lack of water during plant growth and grain filling may be manifested in severe production losses. Because wheat is important for human consumption and has great genetic variability, breeding programs include it when developing improved genotypes for diverse environments. A fundamental part of this process is the evaluation of genotypes in comparative yield trials. However, the selection of superior genotypes is not that simple due to the interaction 'genotype x environment' (Basford and Cooper 1998). Determining yield potential and yield under stress of a given genotype is a way to evaluate its adaptation (Acevedo and Fereres 1993). Yield potential is defined as the yield produced by a given genotype under optimum conditions and the lack of biotic and abiotic stresses. Globally, CIMMYT wheat breeding recognizes 12 mega-environment (ME) wheat areas accordingly structured to address the respective germplasm needs (Rajaram et al. 1994). Six MEs pertain to spring wheat; ME (irrigated), ME2 (high rainfall), ME3 (acid soils), ME4 (low rainfall), ME5 (high temperature), and ME6 (high latitude). Three MEs are assigned to facultative wheats; ME7 (irrigated), ME8 (high rainfall), and M9 (semi-arid). Additionally, three MEs belong to the winter wheats; ME10 (irrigated), ME11 (high rainfall), and ME12 (semi-arid). The Semi-Arid Wheat Screening Nursery (SAWSN) is a single, replicate trial that contains diverse spring bread wheat germplasm adapted to low-rainfall, drought-prone, semi-arid environments typically receiving less than 500 mm of water available during the cropping cycle (CIMMYT 2017). The CIMMYT breeding approach attempts to combine high yield potential with drought resistance for ME4. The combination of water-use efficiency and water-responsive traits plus yield potential is important in drought environments where rainfall is frequently erratic across the years. When rains are significantly above average in certain years, the crop must respond appropriately (water responsive) with higher yields, while expressing resistance to the wider suite of diseases that appear under more favorable conditions. Biotic constrains considered include leaf, stem and yellow rusts; *Septoria* spp.; *Fusarium* spp.; *Pyrenophora tritici-repentis*; nematodes; and root rots distributed to 120 locations and containing 150–250 entries. Our objective was to determine the preliminary performance of experimental germplasm from the 33rd SAWSN under one date of late sowing.

Materials and Methods. The 271 advanced bread wheat lines from the 33rd SAWSN from CIMMYT were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station, located in block 910 in the Yaqui Valley, Sonora, México, at 27° 22'04.64" latitude north and 109° 55'28.26" longitude west, 37 masl, with warm climate (BW (h)) and extreme heat according to Koppen's classification modified by García (1988). Plots consisted of a 1-m bed with two rows 0.80 m apart without replications and a seed density of 100 kg/ha. For management of the trial, INIFAP technical recommendations were followed (Figueroa-López et al. 2011). Maximum, minimum, and average daily temperature (°C), relative humidity, and rainfall were recorded during the crop season. Cold hours were determined as the temperature > 0.1°C to < 10°C that occur during a given hour. The variables evaluated were days-to-heading, height (cm), 1,0000-kernel weight (TKW, g), and visual agronomic stand (on a scale from 1 to 5, with 5 as the best).

Table 9. Lines from the 33rd Semi-Arid Wheat Screening Nursery that had a 1,000-kernel weight greater than 53 g.

Line	Pedigree and selection history
1	PBW65/2*PASTOR CGSS97Y00036M-099TOPB-067Y-099M-099Y-099B-5Y-0B
2	QUAIU #1 CGSS01B00046T-099Y-099M-099M-099Y-099M-29Y-0B-12B-0Y
3	SHA7/VEE#5/5/VEE#8//JUP/BJY/3/F3.71/TRM/4/2*WEAVER/6/SKAUZ/PARUS//PARUS/7/DANPHE#1 CMSS09Y00360S-099Y-099M-099Y-5WGY-0B
4	TRCH*2//WHEAR/SOKOLL CMSS09Y00691T-099TOPM-099Y-099ZTM-099NJ-099NJ-23WGY-0B
5	PRL/2*PASTOR//WAXWING*2/KRONSTADF2004/4/PBW343*2/KUKUNA//KRONSTAD F2004/3/PBW343*2/KUKUNA CMSS09Y00695T-099TOPM-099Y-099ZTM-099NJ-099NJ-7WGY-0B
6	KACHU*2/BECARD CMSS09Y00815T-099TOPM-099Y-099ZTM-099NJ-099NJ-5WGY-0B
7	PRL/2*PASTOR//SUNSTATE/3/MUNAL#1/4/OTUS//PRL/2*PASTOR CMSS09Y00944T-099TOPM-099Y-099M-099Y-12WGY-0B
8	BERKUT//PBW343*2/TUKURU/3/KINGBIRD #1/4/KACHU CMSS09Y00953T-099TOPM-099Y-099ZTM-099NJ-099NJ-6WGY-0B
9	BABAX/LR42//BABAX/3/ER2000/4/KA/NAC//TRCH/5/SOKOLL/3/PASTOR//HXL7573/2*BAU CMSA09Y00387T-099B-050Y-050ZTM-0NJ-099NJ-1WGY-0B
10	BAVIS/4/TC870344/GUI//TEMPORALERA M 87/AGR/3/2*WBLL1 CMSA09Y00643S-050Y-050ZTM-0NJ-099NJ-8WGY-0B
11	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/MILAN/KAUZ//PRINIA/3/BAV92 CMSA09Y00817S-050Y-050ZTM-0NJ-099NJ-4WGY-0B
12	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/WBLL4//OAX93.24.35/WBLL1 PTSA09M00067S-050ZTM-050Y-2WGY-0B
13	WBLL1*2/BRAMBLING/5/BAV92//IRENA/KAUZ/3/HUITES/4/DOLL CMSS09B00289S-099ZTM-099NJ-099NJ-14WGY-0B
14	PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI/5/WHEAR/SOKOLL CMSS09B00506S-099ZTM-099NJ-099NJ-16WGY-0B
15	PAURAQ/6/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1 CMSS09B00531S-099ZTM-099NJ-099NJ-7WGY-0B
16	PICAFLOR #1/8/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/KUKUNA CMSS09B00613S-099ZTM-099NJ-099NJ-15WGY-0B
17	FRNCLN*2/KINGBIRD#1 CMSS09B00695T-099TOPY-099M-099Y-8WGY-0B
18	MUNAL #1*2/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07 CMSS09B00794T-099TOPY-099ZTM-099NJ-099NJ-7WGY-0B
19	SUP152*2/PFUNYE #1 CMSS09B00816T-099TOPY-099ZTM-099NJ-099NJ-21WGY-0B
20	SUP152*2/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ CMSS09B00818T-099TOPY-099ZTM-099NJ-099NJ-6WGY-0B
21	TC870344/GUI//TEMPORALERA M 87/AGR/3/2*WBLL1/4/2*BAVIS CMSA09M00166T-050Y-050ZTM-0NJ-099NJ-4WGY-0B
22	BAJ #1/5/ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE#5//ARIV92 CMSS10Y00029S-099Y-099M-12WGY-0B
23	ROLF07/YANAC//TACUPETO F2001/BRAMBLING/6/FRET2*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ*2/5/TUKURU CMSS10Y00417S-099Y-099M-10WGY-0B
24	FRET2*2/KUKUNA*2/4/BOW/URES//2*WEAVER/3/CROC_1/AE.TAUSCHII (213)//PGO/5/TRCH/SRTU//KACHU CMSS10Y00460S-099Y-099M-8WGY-0B
25	FRET2*2/KUKUNA*2/4/BOW/URES//2*WEAVER/3/CROC_1/AE.TAUSCHII (213)//PGO/5/TRCH/SRTU//KACHU CMSS10Y00460S-099Y-099M-12WGY-0B
26	FRET2/KIRITATI/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/PVN CMSS10Y00845T-099TOPM-099Y-099M-1WGY-0B
27	ROLF07/YANAC//TACUPETO F2001/BRAMBLING/4/WBLL1/KUKUNA//TACUPETO F2001/3/BAJ #1/5/WBLL1/KUKUNA//TACUPETO F2001/3/BAJ #1 CMSS10Y00973T-099TOPM-099Y-099M-15WGY-0B

Table 9. Lines from the 33rd Semi-Arid Wheat Screening Nursery that had a 1,000-kernel weight greater than 53 g.

Line	Pedigree and selection history
28	PFAU/MILAN/5/CHEN/AEGILOPS TAUSCHII(TAUS)//BCN/3/VEE#7/ BOW/4/PASTOR/6/CROC_1/AE.TAUSCHII (205)// BORL95/3/PRL/SARA//TSI/ VEE#5/4/FRET2/7/TRCH/SRTU//KACHU CMSS10Y01236T-099TOPM-099Y-099M-3WGY-0B
29	PFAU/MILAN/5/CHEN/AEGILOPS TAUSCHII (TAUS)//BCN/3/VEE#7/ BOW/4/PASTOR/8/2*SHA7//PRL/VEE#6/3/FASAN/4/ HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA CMSS10Y01238T-099TOPM-099Y-099M-5WGY-0B
30	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/4/EGA BONNIE ROCK CMSA10Y00272T-050M-050Y-050ZTM-11WGY-0B
31	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/4/GLADIUS CMSA10Y00274T-050M-050Y-050ZTM-17WGY-0B
32	KS82W418/SPN/3/CHEN/AE.SQ//2*OPATA/4/FRET2/5/2*SOKOLL/3/PASTOR//HXL7573/2*BAU CMSA10Y00307T-050M-050Y-050ZTM-2WGY-0B

Results. Thirty-two lines from the 33rd Semi-Arid Wheat Screening Nursery had a TKW greater than 53 g (Table 9, pp. 37-38). The average heading of the lines was 74 days. The highest difference relative to the group average was 8 days in lines 'SUP152/3/INQALAB 91*2/TUKURU//WHEAR' and 'TRCH/SRTU//KACHU*2/3/PVN', which were the earliest (Fig. 11A). The average group height was 77 cm. The shortest lines were 'WHEAR/KIRITATI/3/C80.1/3* BATAVIA//2*WBLL1/4/2*KACHU' and 'BAJ#1/6/WBLL1*2/4/YACO/PBW65/3/KAUZ *2/TRAP//KAUZ/5/KACHU #1' at 66 cm. Lines 'PREMIO/2*BAVIS' and '92.001E7.32.5/SLVS/5/NS-732/HER/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/SOKOLL/3/ PASTOR//HXL7573/2*BAU' had a height of 90 cm; 'BAV92/3/PRL/SARA//TSI/ VEE#5/4/WBLL1/5/CROC_1/AE.TAUSCHII(205)//BORL95/3/PRL/SARA//TSI/VEE #5/4/FRET2/6/NS-732/HER/3/PRL/SARA//TSI/VEE#5/4/FRET2' was 88 cm; and three lines, 'MELON//FILIN/MILAN/3/FILIN/4/PRINIA/PASTOR//HUITES/3/ MILAN/OTUS//ATTILA/3*BCN/5/MELON//FILIN/MILAN/3/FILIN', '92.001E7.32.5/ SLVS/5/NS-732/HER/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/SOKOLL/3/PASTOR// HXL7573/2*BAU', and 'SOKOLL/3/PASTOR//HXL7573/2*BAU/4/GLADIUS' were 85 cm (Fig. 11B). The average a TKW of the group was 48 g. Line 'SUP152*2/PFUNYE#1' showed the highest weight with 59.93 g, followed by 'MUNAL#1*2/4/HUW234+LR34/PRINIA//

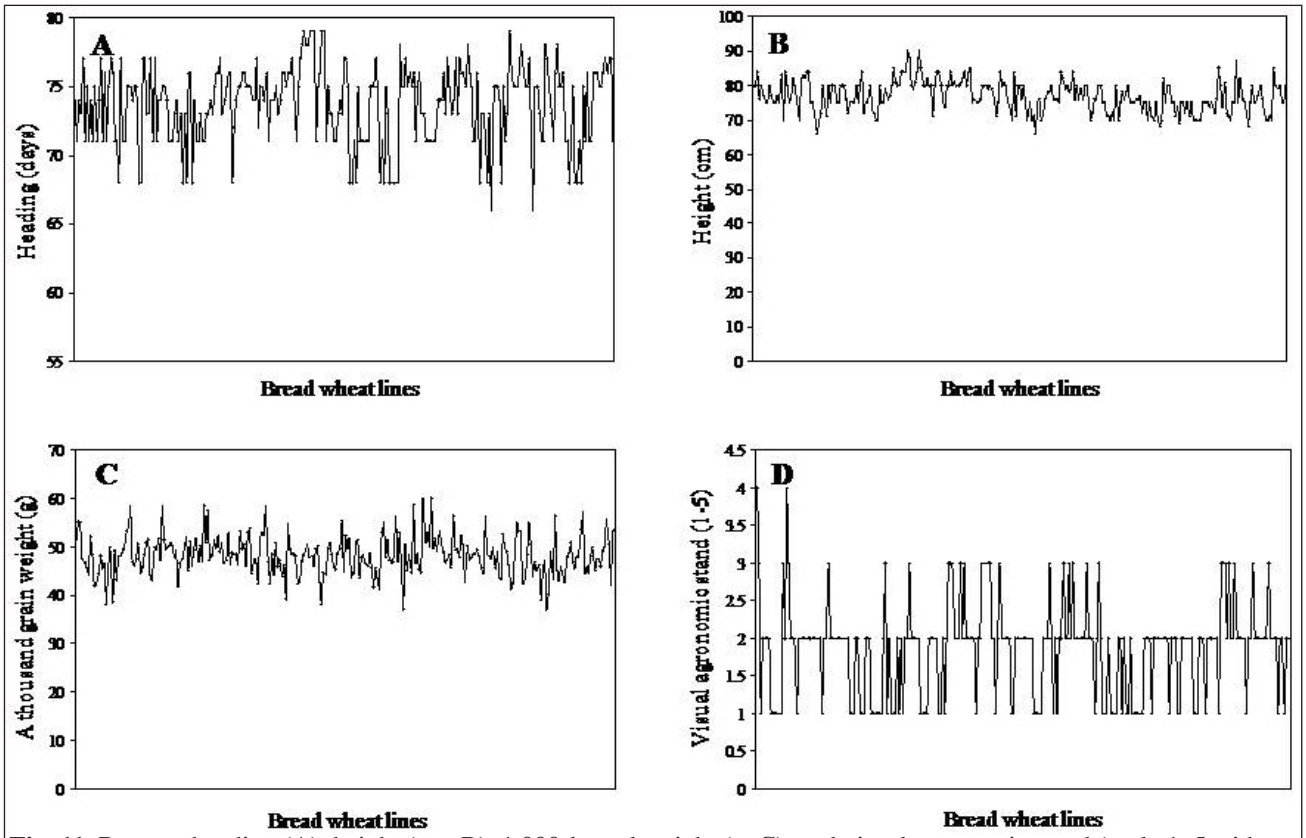

Fig. 11. Days-to-heading (A), height (cm, B), 1,000-kernel weight (g, C), and visual agronomic stand (scale 1–5 with 5 as the best) of 271 lines form the 33rd Semi-Arid Wheat Screening Nursery from CIMMYT during the 2015–16 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

PBW343*2/KUKUNA/3/ROLF07' with 59.86 g, 'FRNCLN*2/KINGBIRD#1' with 58.73 g, 'PRL/2*PASTOR//SUNSTATE/3/MUNAL#1/4/ OTUS//PRL/2*PASTOR' with 58.49 g, and 'KACHU*2/BECARD' with 58.29g. The TKW of those lines is greater than that of REEDLING #1 (50.76 g) and 'SUP152//PUB94.15.1.12/WBLL1' (PTSS09GH-B00014S-0SHB-099Y-15Y-020Y-0MXI) (44.85 g), which had grain yield/ha of 6.35 t and 5.98 t, respectively (Rosas-Jáuregui et al. 2016). Line 'MUTUS*2/KIRITATI' had the lowest TKW with 36.93 g (Fig. 11C, p. 38). The best visual agronomic stand (score 4) was assigned to lines 'PRL/2*PASTOR' and 'KACHU/PRL' (Fig. 11D, p. 38); the latter was below the average TKW weight at 37.98 g. None of the lines showed yellow or leaf rust infection during the season. Of the 271, 32 had a TKW equal to or greater than 53 g (Table 9, pp. 37-38, Fig. 12C), although the average of the visual agronomic stand was 1.8. Lines 'PBW65/2*PASTOR' (line 1) and 'PICAFLOR#1/8/NG8201/ KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/ KUKUNA' (line 16) had the highest agronomic stand score with 3 (Fig. 12D). The total number of accumulated cold hours during the crop season (after 29 December, 2015) was 440.

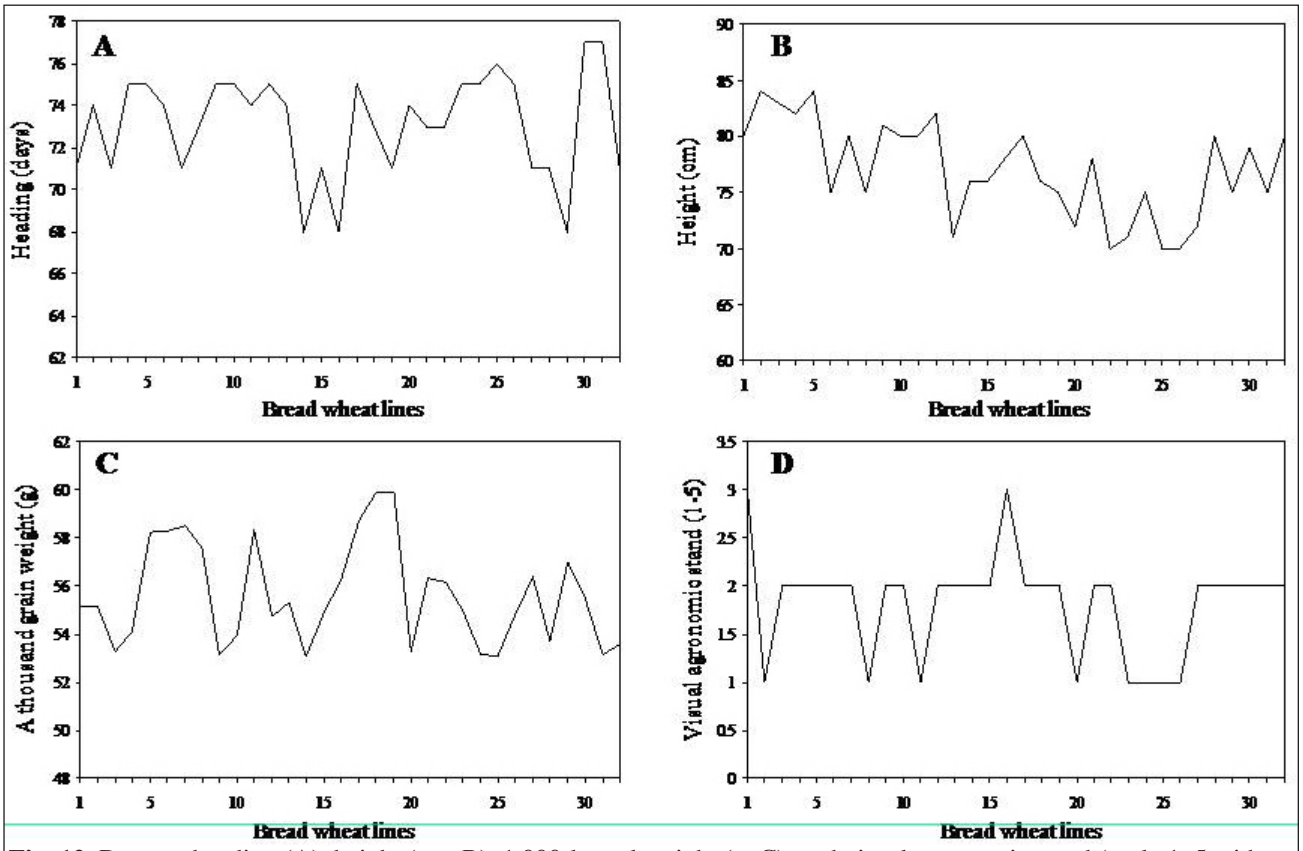

Fig. 12. Days-to-heading (A), height (cm, B), 1,000-kernel weight (g, C), and visual agronomic stand (scale 1–5 with 5 as the best) of 32 lines with a 1,000-kernel weight equal to or granter than 53 g from the 33rd Semi-Arid Wheat Screening Nursery form CIMMYT, during the 2015–16 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Conclusions. From the 33rd SAWSN, 220 lines have the potential for a grain yield greater than 5.5 t/ha under a late sowing (29 December) in the southern Sonora, and 62 have the potential for a grain yield greater than 6.0 t/ha.

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Percentage of Karnal bunt infection obtained after artificial field inoculation of different numbers of wheat spikes.

Guillermo Fuentes-Dávila.

Abstract. This work evaluated the effect of inoculating three, five, and ten wheat spikes in order to determine differences in the percentage of infection with Tilletia indica. Experiments were conducted at the Norman E. Borlaug Experimental Station, in the Yaqui Valley, Sonora, Mexico, during the 2000–01 and 2001–02 crop seasons. Plots consisted of 1-m beds with with two rows 0.80 m apart. For the first experiment, different bread wheat genotypes and inoculation dates were used for the study, whereas for the second, cultivar WL711 was used at different dates. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage. Harvest was done manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. The range of infection in the first crop season was 0– 59.2%, 0–84.3%, and 0–79.4% for ten, five, and three spikes, respectively; and the average was 18.5%, 23.3%, and 20.8%. However, there were no statistical differences. The frequency of occurrence when a given number of spikes showed a greater percentage of infection was as follows: 10 ≥ 5 = 20, 10 ≥ 3 = 23, 5 ≥ 3 = 26, 3 ≥ 10 = 25, and 3 ≥ 5 = 24. The range of infection in the second season was 0.5–54.8%, 0–79.4%, and 0–87.6% for ten, five, and three spikes, respectively; and the average was 19.3%, 20.3%, and 17.4%. However, there were no statistical differences. The frequency of occurrence when a given number of spikes showed a greater percentage of infection was as follows: 10 ≥ 5 = 20, 10 ≥ 3 = 22, 5 ≥ 3 = 21, 3 ≥ 10 = 12, and 3 ≥ 5 = 14.

Introduction. Karnal bunt caused by *Tilletia indica* Mitra (syn. *Neovossia indica* (Mitra) Mundkur), was first identified in India (Mitra 1931), and later in Mexico (Duran 1972), Pakistan (Munjal 1975), Nepal (Singh et al. 1989), Brazil (Da Luz et al. 1993), the United States of America (APHIS 1996), Iran (Torarbi et al. 1996), and the Republic of South Africa (Crous et al. 2001). More recently, the CIMMYT-blog/tag/karnal-bunt (CIMMYT 2011) indicates that "Karnal bunt has long been present in Afghanistan, with favorable climatic conditions promoting occasional outbreaks, and a recent survey by ARIA indicated that several popular wheat varieties are susceptible to the disease. It is particularly prevalent in the eastern region bordering Pakistan, which has emerged in recent years as an important seed-producing area within Afghanistan". Despite this, no public information is available regarding the history of Karnal bunt in that country, disease incidence, and the area affected. Teliospores of *T. indica* are resistant to extreme cold, heat, and chemical treatment (Smilanick et al. 1985), and can survive up to 3 (Bonde et al. 2004) to 4 years in field soil (Krishna and Singh 1982), making control difficult. Fairly good chemical control with fungicide applications during flowering can be accomplished (Salazar-Huerta et al. 1997). However, in northwest Mexico due to quarantine regulations (SARH 1987), this measure is still not profitable for commercial use.

Mitra (1935, 1937) believed that infection of the wheat plant occurred in the soil during the seedling stage, but Mundkur (1943a, 1943b) proved that infection takes place during anthesis, which was later corroborated by Bedi et al. (1949) using Moore's inoculation technique (Moore 1936). Since that time, artificial inoculation by injection started to be used in order to reproduce the disease and evaluate germplasm for resistance (Chona et al. 1961; Durán and Cromarty 1977; Aujla et al. 1980; Singh and Krishna 1982; Warham 1988; Fuentes-Dávila et al. 1993). Although this technique provides reliable results under the appropriate environment, the economic cost of this technique is based on the number of spikes to be inoculated and evaluated, which has to be done by hand since infected grains may be destroyed if me-

chanical threshing would be performed. Therefore, our objective was to evaluate the effect of inoculating three, five, and ten wheat spikes in order to determine differences in the percentage of infection with *T. indica*.

Materials and Methods. The experiments were conducted in two different crop seasons (2000–01 and 2001–02) at the Norman E. Borlaug Experimental Station, previously known as CIANO, located in the Yaqui Valley, Sonora, Mexico (27° 20´N, 105° 55´W, elevation 39 masl), in block 910 in a clay soil with pH 7.8. Plots consisted of 1-m beds with two rows 0.80 m apart without replications and a seed density of 100 kg/ha. For the first experiment, different bread wheat genotypes and inoculation dates (46 starting in January) were used, whereas for the second, cultivar WL711 was used on 34 different dates. Inoculations were by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage in three, five, and ten heads from each genotype. High relative humidity in the experimental area was provided by a T-bird sprinkler irrigation system five times a day for 20 min each time. Harvest was manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. The ANOVA was performed using the SAS System for Windows and mean comparison by Tukey's test (p = 0.05).

Results. For the first crop season, the range of infection was 0–59.2% (18.5% average) , 0–84.3% (23.3% average), and 0–79.4% (20.8% average), for ten, five, and three spikes, respectively (Fig. 13). However, there were no statistical differences. With very few exceptions, most genotypes showed similar reactions whether ten, five, or three spikes were inoculated. For example, on date 15, the genotype inoculated showed a susceptible reaction with 41.1%, 49.7%, and 47.5% infection in ten, five, and three spikes, respectively, while on date 40, the genotype inoculated showed a resistant reaction with 0.23%, 0%, and 0% infection in ten, five, and three spikes, respectively. The frequency of occurrence when a given number of spikes showed a greater percentage of infection was as follows: 10 ≥ 5 = 20, 10 ≥ 3 = 23, 5 ≥ 3 = 26, 3 ≥ 10 = 25, and 3 ≥ 5 = 24 (Fig. 14, p. 42). For the second crop season with cultivar WL711, the range of infection was 0.5–54.8%, 0–79.4%, and 0–87.6% for ten, five, and three spikes, respectively; and the average in the same order was 19.3%, 20.3%, and 17.4% (Fig. 15, p. 42). However, as in the previous crop season, there were no statistical differences. Despite using the same cultivar in this experiment, the reaction of the plant to the inoculation was quite diverse, because it is considered susceptible to *T. indica*, and the difference in the percentage of infection between numbers of spikes varied in a third of the total dates of inoculation. The frequency of occurrence when a given number of spikes showed a greater

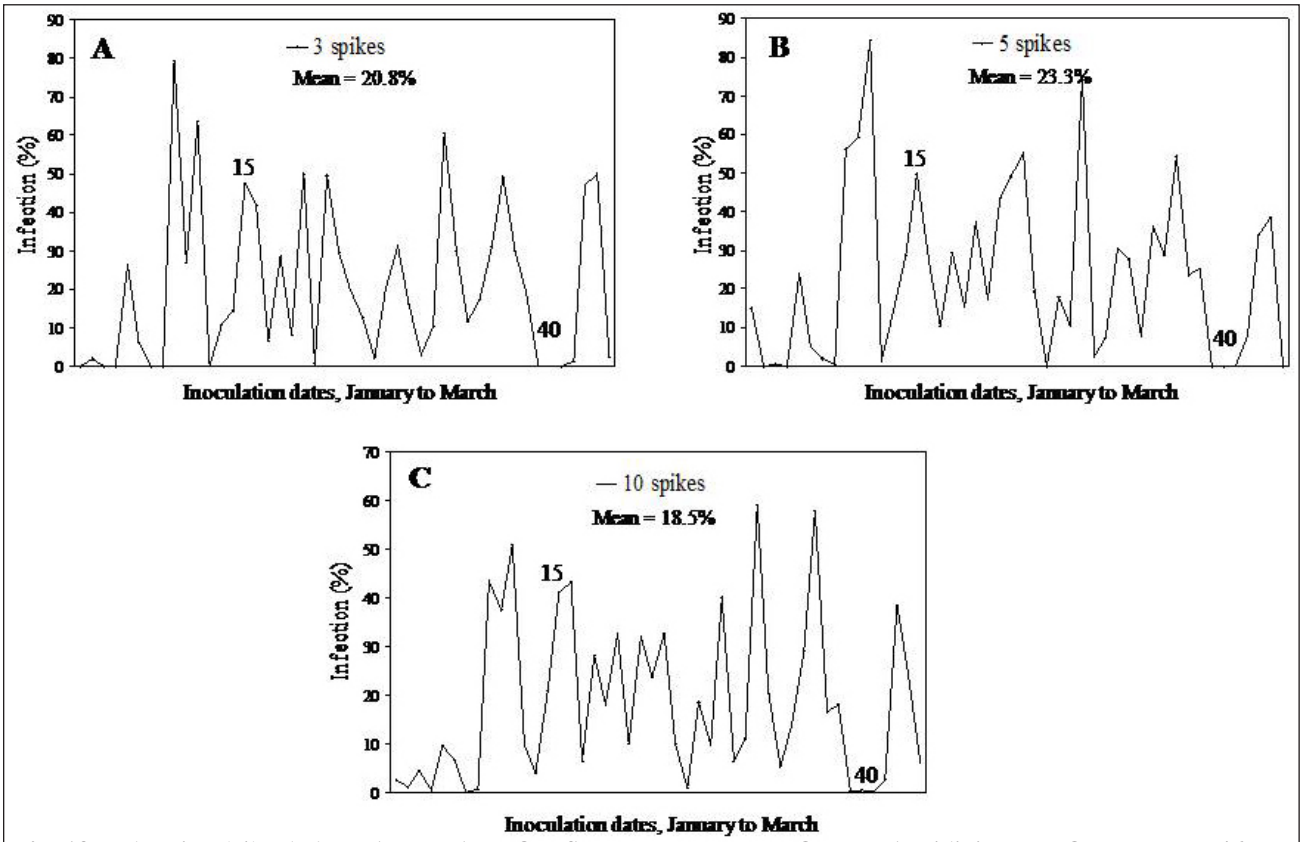

Fig. 13. Indwxrion (%) od qhwR APIKWA DEOM SIDDWEWNR FWNORYPWA eridixiLLY INOXULrws on 46 dates with *Tilletia indica* at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, during the 2000–01 crop season.

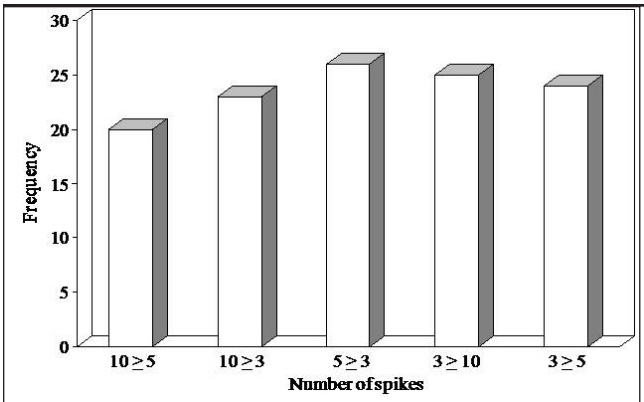

Fig. 14. Frequency of occurrence when a given number of spikes showed a greater percentage of infection from different genotypes artificially inoculated on 46 dates with *Tilletia indica* at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, during the 2000–01 crop seasosn.

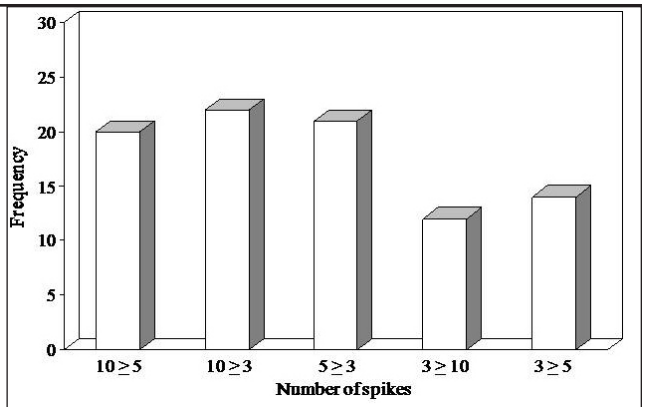

Fig. 16. Frequency of occurrence when a given number of spikes showed a greater percentage of infection from the bread wheat cultivar WL711 artificially inoculated on 34 dates with *Tilletia indica* at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, durng the 2001–02 crop season.

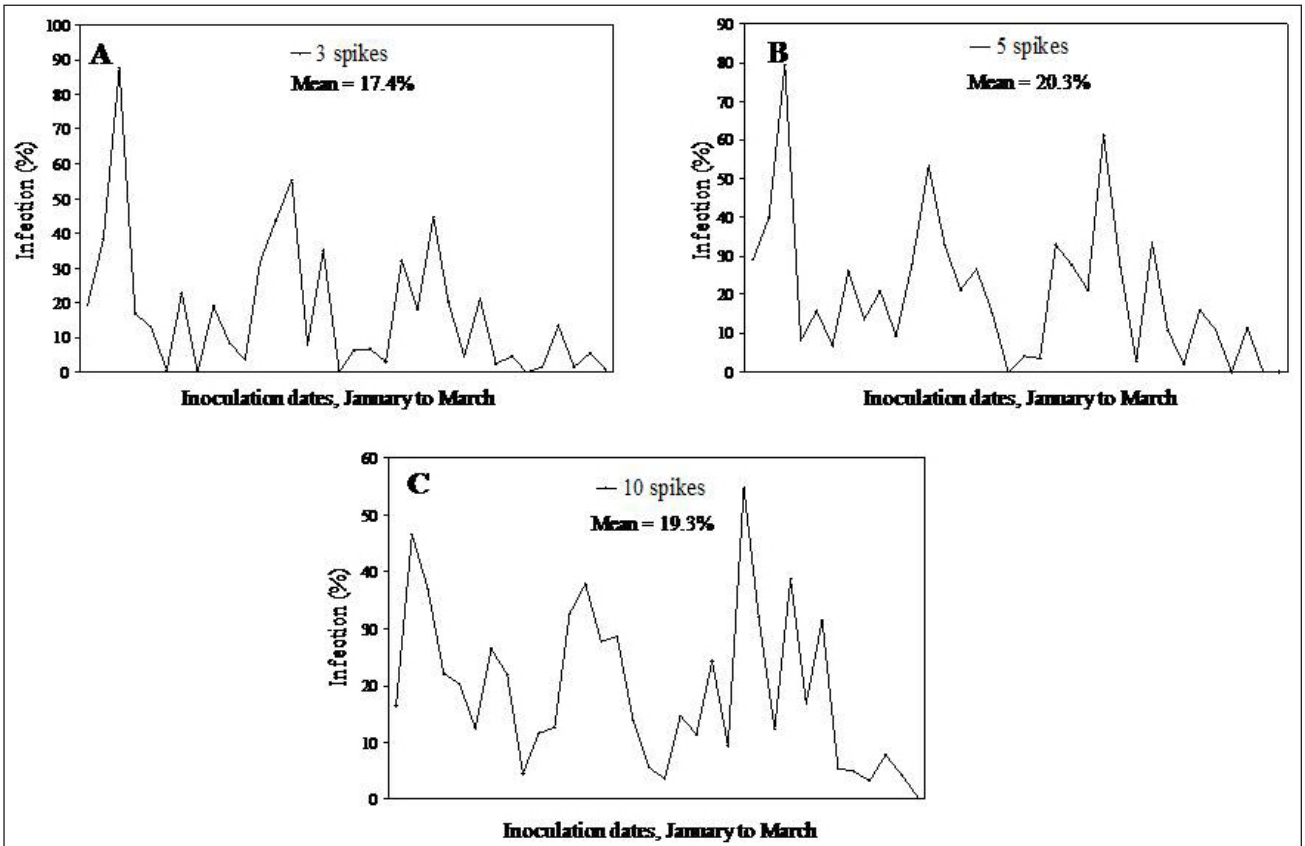

Fig. 15. Infection (%) of wheat spiked from the bread wheat culitvar WL711 artificially inoculated on 34 dates with *Tilletia indica* at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, during the 2001–02 crop season.

percentage of infection was as follows: 10 ≥ 5 = 20, 10 ≥ 3 = 22, 5 ≥ 3 = 21, 3 ≥ 10 = 12, and 3 > 5 = 14 (Fig. 16). The first three were similar, as in the first crop season, but the last two, when three spikes were inoculated, the frequency of occurrence with a higher percentage of infection was lower than those obtained when five or ten spikes were inoculated.

Conclusions. Results of experiments conducted during two crop seasons showed that inoculation of three, five, and ten spikes with *T. indica* rendered percentages of infection that were not statistically different. The highest percentage of

infection were obtained in both crop seasons when three and five spikes were inoculated. When fewer spikes are inoculated, infected grains will increase the percentage of infection than when ten spikes are inoculated.

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ITEMS FROM PAKISTAN

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NATIONAL AGRICULTURAL RESEARCH CENTER (NARC)
Crop Diseases Research Institute, Islamabad. Pakistan.

PAKISTAN AGRICULTURAL RESEARCH COUNCIL (PARC)
Islamabad. Pakistan.

The status of Karnal bunt in Pakistani wheat seed.

Monsif Ur Rehman and Muhammad Imtiaz (CIMMYT), Shahzad Asad and Anjum Munir (NARC), and Atiq Ur Rehman Rattu (PARC).

Abstract. Karnal/partial bunt (KB) caused by the fungus *Tilletia indica* is listed as a quarantine pest in many countries to avoid its dissemination through long distances via infected seed. Early detection of the pathogen is a crucial step in diagnosis and management programs. The washing test is considered more reliable than visual observation of grain to adequately identify and detect KB infection in the grains. CIMMYT Pakistan, in partnership with national wheat breeding programs, is collecting and testing Pakistan wheat germplasm nationally and internationally to identify rust resistance breeding parents. To ship seed outside Pakistan for testing at Njoro, Kenya, for stem rust adult plant reaction to the Ug99 lineage, a prerequisite is screening seed for KB infection. For this purpose, three sets of over 900 advanced wheat breading lines and cultivars from the 2013–14, 2014–15, and 2015–16 crop harvests were assembled and tested for KB infection using the washing test at the Crop Disease Research Institute, Islamabad. The test identified 42% of the samples from 2013–14, 76% from 2014–15, and 45% from 2015–16 were infected with KB. Out of the 40 National Uniform Wheat Yield Trial (NUWYT) (2014) lines tested, 17 were infected with KB, highlighting the presence of KB across Pakistan and an alarming situation for future wheat production and export.

Introduction. Wheat generally suffers from two major groups of diseases, rusts and smuts. Of the smut diseases, KB is one of the important disease of wheat in South Asia. Discovered on wheat grown near Karnal, India, in 1931 and since, KB has been found in many wheat-growing conutries, such as India, Pakistan, Iraq, Mexico, and Afghanistan. Hosts of KB include wheat, durum wheat, and triticale (Majumder et al. 2013). In Pakistan, KB was reported for the first time in 1971 in Sialkot, Gujranwala and Mardan districts, and soon spread throughout the Punjab with a prevalence in 23 districts with a frequency ranging from 0.32 to 3.50%. At present, KB exists in a majority of the wheat-growing areas in Pakistan with different frequencies. Twenty-one countries currently list KB as a quarantine pest and developed a plan to test wheat for KB spore contamination to make sure of disease-free seed. Contaminated wheat shipments for any purpose are not accepted, because KB spread mainly by planting infected seeds in a clean area (APHIS 2001). Yield losses resulting from KB are generally low but may reach up to 20–40% in highly susceptible cultivars where 90% of the grain is infected with KB. Definitely, the greatest impact of the disease for a country could be on grain exports. Although KB does not present a risk to human health, it does reduce flour quality as wheat containing more than 3% bunted kernels is considered unfit for human consumption. The fungus produces the chemical trimethylamine, which adversely affects the odor and palatability of whole meal and finished products. If flour contains KB spores, an unacceptable color is given to pasta products made from it. This study assessed KB spread in Pakistan and identified clean seed samples for shipment to Kenya.

Materials used. Baseline resistance study (BRS) sets were prepared by collecting wheat breeding lines and cultivars from national and provincial wheat-breeding programs. The sets were comprised of old and newly released wheat cultivars, advanced lines, and CIMMYT introduced germplasm. A total of 918 wheat genotypes in three BRS sets, i.e. 5th (435 entries), 6th (302 entries), and 7th BRS (181 entries), were used. The 5th BRS set was prepared from 2013–14, the 6th BRS from 2014–15, and the 7th BRS from the 2015–16 crop harvests. Fourteen institutes contributed samples for testing, including the Agriculture Research Institute, Sariab Quetta (ARI–Q); the Arid Zone Research Center, Quetta

(AZRC–Q), the Baluchistan Agricultural Research & Development Center, Quetta (BARDC–Q); the Barani Agricultural Research Institute, Chakwal (BARI–CWL); the Barani Agricultural Research Stations, Fateh Jang (BARS–FJ) and Kohat (BARS–KT); the Cereal Crop Research Institute, Pirsabak-Nowshera, Khyber Pakhtunkhwa (CCRI–KP); the National Agricultural Research Center, Islamabad (NARC–ISD); the National Institute for Biotechnology and Genetic Engineering, Faisalabad (NIBGE–FSD); the Nuclear Institute for Agriculture, Tandojam (NIA–TJ); the Nuclear Institute for Food and Agriculture, Peshawar, Khyber Pakhtunkhwa (NIFA–KP); the Regional Agricultural Rresearch Institute, Bahawalpur (RARI–BPR); the Wheat Research Institute, Faisalabad (WRI–FSD); and the Wheat Research Institute, Sakrand (WRI–SKD).

Karnal bunt testing procedure. Direct visual observation of dry seed for KB is regarded as insufficient for quarantine purposes due to the fact that a low level of infection might pass undetected, which can substantially contaminate healthy seed lots. Thus, a washing test method (Castro et al. 1994) was used to screen seed. The test can rapidly detect surface-borne teliospores of *T. indica* (Shetty et al. 1988). Between 10–20 g of wheat seed from each entry was put in separate flasks and the seed submerged in ~100 mL of deionized water and two to three drops of Tween-20 was added to the flask. The flasks were agitated on a shaker for 30 minutes at 200–250 rpm to obtain spore suspension. The water was filtered through a 50 watt man filter paper and the debris caught on the filter paper was observed under the stereo microscope for KB spores (Begum and Mathur 1989). Flasks were thoroughly washed and cleaned before reuse.

Results. CIMMYT–Pakistan and its national partners under a wheat productivity enhancement program for Pakistan is evaluating elite wheat germplasm nationally and internationally for stripe, leaf, and stem rusts resistance. Materials received from the national partners were the BRS. The 5th BRS was planned for adult-plant stem rust resistance screening at the CIMMYT-managed facility in Kenya during the 2015 wheat season. Similarly, a 6th BRS set was planted in Kenya in for off-season screening in 2016, and the 7th BRS was planting in Kenya during the normal screening season in 2017. As per the quarantine requirement, the seed must be free of KB prior to entering Kenya and, therefore, we tested the seed for KB before shipping. Using the washing method described above, a total of 918 entries were tested for KB at the Crop Diseases Research Institute (CDRI), Islamabad.

Of the total 435 entries tested, 252 (58%) were free of KB, whereas the remaining 183 were contaminated with KB spores in the 5th BRS set. In these 435 entries, 72% were from NARC–ISL, 69% from BARS–FJ, 47% from CCRI–KP, 42% from AZRC–Q, 34% from NIA–TJ, 33% from BARI–CWL, 31% from RARI–BPR, 25% from WRI–FSD, 20% from NIFA–PWR, and 15% from WRI–SKD were infected with KB (Fig. 1). In a previous study conducted by Haq et al. (2002), CCRI–KP was found to be almost free of KB, but the current 47% infected entries signifys the importance of KB spreading in to previously KB-free areas. Testing 40 lines included in the Pakistan NU-WYT for 2014–15 identified 17 (42%) KB-infected entries. These entries included AUR-08010, SKD-II, Pak-13, 99172, DN-102, NRL-1123, PR-111, PR-112, PR-106, 12266, 11098, 11138, V-12001, NR-429, FSD-08, NR-436, and NR-423. Two commercial cultivars, Dharabi-11 and Hamal-11, were infected with KB, which may have served as an inoculum source for KB spread in previously KB-free areas with the use of cultivars by farmers.

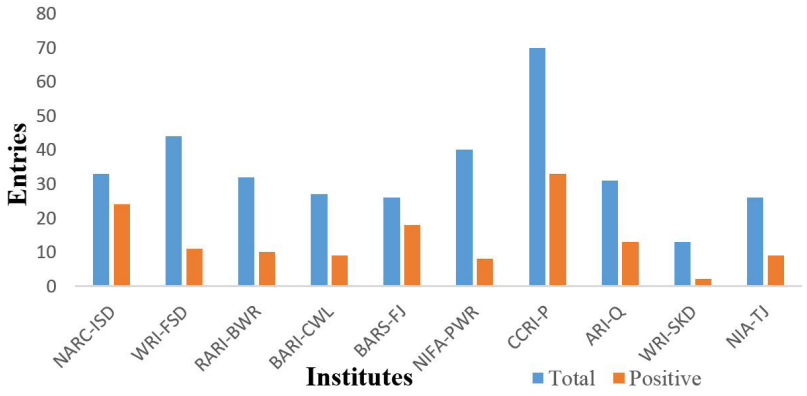

Fig. 1. Karnal bunt status in wheat across Pakistan in 2013–14: NARC-ISD (National Agricultural Research Center, Islamabad), WRI-FSD (Wheat Research Institute, Faisalabad), RARI-BPR (Regional Agricultural Research Institute, Bahawalpur), BARI-CWL (Barani Agricultural Research Station, Chakwal), BARS-FJ (Barani Agricultural Research Station, Fateh Jang), NIFA–PWR (Nuclear Institute for Food and Agriculture, Peshawar, Khyber Pakhtunkhwa), CCRI-P (Cereal Crop Research Institute, Pirsabak-Nowshera, Khyber Pakhtunkhwa), ARI-Q (Agriculture Research Institute, Sariab Quetta), WRI-SKD (Wheat Research Institute, Sakrand), and NIA-TJ (Nuclear Institute for Agriculture, Tandojam).

Similarly, testing of the materials included in the 6th BRS set identified a high overall infection (76%) of KB compared to 42% the previous year. The test also identified four commercial cultivars with grain bunt infection, including Mehran-89, Moomal-2002, TD-1, and Pakistan 2013. None of the seed samples from NARC and CCRI were found free of KB. Similarly, 97% of the samples from BARS–FJ, 85% from BARI–CWL, 75% from NIFA–KP, 73% from WRI–FSD, 57% from NIBGE, 53% from RARI–BPR, 45% from NIA–TJ, and 35% each from ARI–Q and WRI–SKD were KB infected (Fig. 2). Keeping this alarming situation for Pakistan in view for wheat in the future, CIMMYT in Pakistan is making efforts to provide KB Screening Nurseries to several national collaborators for testing and identifying genotypes with some degree of KB resistance. All the national partners were requested to put in their full efforts for providing KB clean seed for inclusion in the BRS set meant for testing outside the country. In this regard, partners were asked to adopt the following strategies:

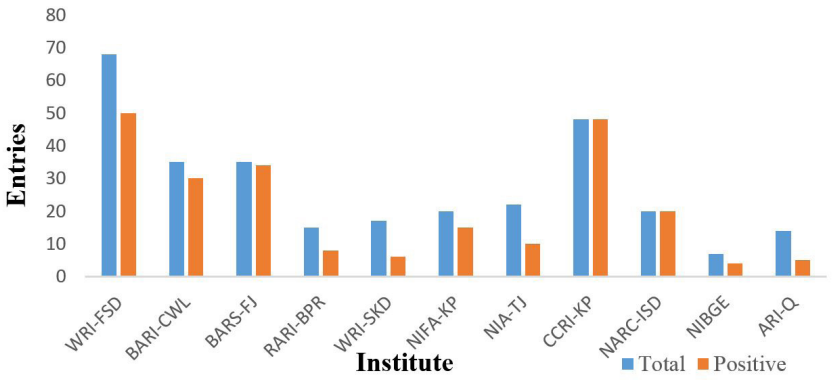

Fig. 2. Karnal bunt status in wheat across Pakistan in 2014–15: WRI-FSD (Wheat Research Institute, Faisalabad), BARI-CWL (Barani Agricultural Research Station, Chakwal), BARS-FJ (Barani Agricultural Research Station, Fateh Jang), RARI-BPR (Regional Agricultural Research Institute, Bahawalpur), WRI-SKD (Wheat Research Institute, Sakrand), NIFA–KP (Nuclear Institute for Food and Agriculture, Peshawar, Khyber Pakhtunkhwa), NIA-TJ (Nuclear Institute for Agriculture, Tandojam), CCRI-KP (Cereal Crop Research Institute, Pirsabak-Nowshera, Khyber Pakhtunkhwa), NARC-ISD (National Agricultural Research Center, Islamabad), NIBGE (National Institute for Biotechnology and Genetic Engineering Faisalabad), and ARI-Q (Agriculture Research Institute, Sariab Quetta).

— First, seed of entries planned for international screening obtained by planting in pots in controlled conditions.
— Second, protect by fungicide spray at proper stage and/or seed treatment to kill the seed-borne spores.
— Identify and collect seed from uninfected heads as some times infected heads produce symptoms in the field
— Use clean harvesting and processing machines and other equipment especially for breeding materials at advanced stages.
— Bag selected heads before grain formation and harvest separately.

Although it is a tedious job to get samples clean from a pathogen that is soil, seed, and air-borne, as the case with KB, continued progress with these strategies can curtail *Tilletia indica* inoculum load under field conditions. As a result, the overall percentage of infection in wheat samples that reached nearly 76% in 2014–15 was reduced to 45% in 2015–16 (Fig. 3) although infection at the source institutes was still present. Additionally, the delay in rain during the season for the last few years also could contribute to the increased KB infection because most of the cultivars and genotypes are susceptible to KB.

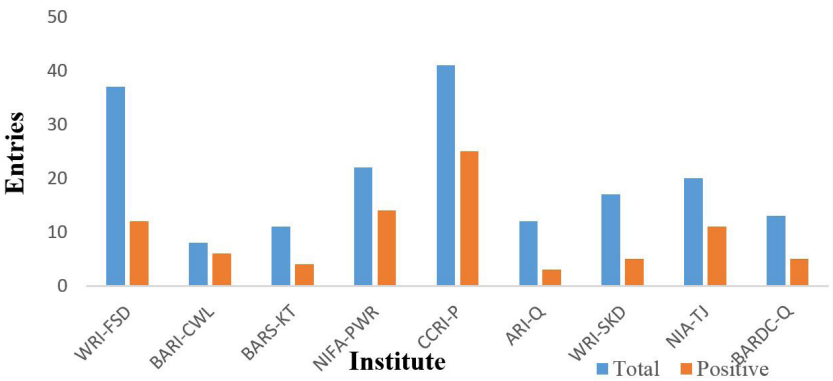

Fig. 3. Karnal bunt status in wheat across Pakistan in 2015–16: WRI-FSD (Wheat Research Institute, Faisalabad), BARI-CWL (Barani Agricultural Research Station, Chakwal), BARS–KT (Barani Agricultural Research Stations, Kohat), NIFA–PWR (Nuclear Institute for Food and Agriculture, Peshawar, Khyber Pakhtunkhwa), CCRI-P (Cereal Crop Research Institute, Pirsabak-Nowshera, Khyber Pakhtunkhwa), ARI-Q (Agriculture Research Institute, Sariab Quetta), WRI-SKD (Wheat Research Institute, Sakrand), NIA-TJ (Nuclear Institute for Agriculture, Tandojam), and BARDC–Q (Baluchistan Agricultural Research & Development Center, Quetta).

Conclusion.

The threat of KB is increasing, possibly due to delays in rain during the growing season, no control on

movement of seed in the country, and that most of the culitvars are susceptible. Thus, concerted efforts are needed to develop new KB-tolerant/resistant cultivars and promote management to control present and future spread of the disease if Pakistan plans to export wheat in the future. Additionally, seed corporations and seed companies should not get infected grain from affected areas so as to control spreading the disease, and KB should be a core breeding trait for the national breeding programs.

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NUCLEAR INSTITUTE FOR FOOD AND AGRICULTURE (NIFA)
Wheat Group, Plant Breeding and Genetics Division, P.O. Box 446, Tarnab, Peshawar, Pakistan.

Socio-economic impact and progress in wheat breeding.

Abdul Jabbar Khan, Fazle Subhan, Babar Manzoor Atta, Muhammad Irfaq Khan, Farooq-i-Azam, and Akhtar Ali.

Wheat, being the staple food crop, occupies strategic space in the agricultural policy and covers about 58% of the food crop area in Khyber Pakhtunkhwa (KP). The crop is grown in diversified agro-climatic zones, such as the Northwestern hilly tracts, the central irrigated/semi-irrigated plains, and southern mixed dry/hot areas in the province. Realizing these facts, NIFA wheat breeders are making concerted efforts for developing potential cultivars to meet the need of the farming communities for breaking the yield barriers coupled with tolerance to adverse climatic conditions.

High-yielding, disease resistant, and widely adopted cultivars of wheat developed at NIFA are continuously playing a role in boosting per acre yield coupled with upgrading the financial status of the farmers of KP. Each year, 10–15 metric tons of source seed is delivered to public/private seed multiplication agencies and progressive farmers of the province. Due to the combined efforts of the stakeholders, NIFA-released wheat cultivars are grown on 10–15% of the cultivatable area of the province. However, most of the seed proliferation occurs through informal distribution of seed among the neighboring farmers.

Consistent efforts are made to maintain seed purity, and a total of 9.7 tons of quality seed of NIFA-released wheat cultivars was produced during 2016, duly certified by the Federal Seed Certification and Registration Department. As per standard procedure, the seed was collected by provincial agricultural extension linked with selected progressive growers in KP. In the absence of a public sector seed industry, the availability of improved NIFA wheat cultivars to private seed companies will not only quickly proliferate the seed but also generate employment opportunities for the local farming communities.

The research endeavors of the Plant Breeding and Genetics Division culminated into the release of the improved wheat cultivar NIFA Aman, which was approved by the Variety Evaluation Committee of the Pakistan Agriculture Research Council (PARC), Islamabad, and the Technical Committee of the Khyber Pakhtunkhwa Seed Council during 2016 for general cultivation in the province. This cultivsrt is high-yielding, widely endowed with a high protein content, and possesses resistance against stripe, leaf, and stem rust. NIFA Aman will further fill a gap with its adaptation in a range of environments in Pakistan. Wheat diseases can have a wide impact, therefore, effective race non-specific germplasm was identified that will have visible economic benefits for growers. Two candidate wheat lines (CT-12176 and NRL-123) had higher yield and disease resistance in the national trials and were subjected to subsequent mandatory evaluation. Based on proving worth for higher yield and yield components in provincial multi-locational trials, two candidate lines, SRN-13121 and NRL-1206, were subjected to first year evaluation in the national trials for 2016–17.

Introducing, evaluating, and selecting wheat genotypes for higher yield and disease resistance under local environmental conditions.

Fazle Subhan, Babar Manzoor Atta, Muhammad Irfaq Khan, Abdul Jabbar Khan, Farooq-i-Azam, and Akhtar Ali.

The global exchange of wheat germplasm, in particular by CIMMYT and ICARDA through trial and observation nurseries to cooperating institutions, always plays a positive role for selecting desirable ideotypes by breeders. Our specific objective was to identify genotypes showing adaptation the the environmental conditions of Khyber Pakhtunkhwa.

Methodology. Trials received from CIMMYT and ICARDA were planted. The 36th Elite Spring Wheat Yield Trial was sown in two replications with a plot size of 9 m^2. Each entry was planted in six 5-m rows with a 30-cm row-to-row spacing. The 3rd Wheat Yield Consortium Trial was sown in two replications with a plot size of 6 m^2. Each entry was planted in four 5-m rows with a 30-cm row-to-row spacing. Frequent rains were recorded during the growing season. A total of 280 mm rainfall was recorded from mid-October 2015 to mid-May 2016. Maximum rainfall was recorded in March 2016 (82.8 mm) at anthesis. Fertilizer was applied as N–P–K at 100–60–30 kg/ha. The broad-spectrum herbicide Affinity (Isoproturon) was used at 2,000 g/ha to control weeds. Data regarding yield and other agronomic traits were recorded for individual entries on traits such as days-to-heading and maturity, plant height (cm), lodging (%), biological yield (kg/ha), grain yield (kg/ha), harvest index (%), and stripe and leaf rust.

Summary. The 36th ESWYT consisting of 50 genotypes (with two replications) was evaluated for yield performance and rust disease reaction with local check Bathoor-08. Of the 50 genotypes, 15 were selected for further evaluation and confirmation of the desired traits. The selected genotypes out yielded the check cultivar (4,457 kg/ha) with grain yield in the range of 4,499 to 5,706 kg/ha. Data of the top five selected entries is presented in Table 1 (p. 49). These genotypes have a higher harvest index coupled with good disease resistance.

The 3rd WYCT, consisting of 42 genotypes (with two replications), also was evaluated for yield performance and rust disease reaction with the local check Bathoor-08. Of the 42 genotypes, nine were selected for further evaluation and confirmation of their desired traits. The selected genotypes out yielded the check Bathoor-08 (4,911 kg/ha) by producing grain yields in the range of 5,262 to 6,578 kg/ha. The top high-yielding genotypes produced 16-34% higher grain yield with a comparatively taller plant stature than the check. These genotypes also expressed a desirable response to both stripe and leaf rust.

Expected results/output. The selected lines from the exotic yield trials will be further tested in advanced yield trials under normal and late-planting conditions at NIFA in the upcoming cropping season.

Evaluating exotic wheat germplasm for improved yield and disease resistance under international coordination.

Babar Manzoor Atta, Fazle Subhan, Muhammad Irfaq Khan, Abdul Jabbar Khan, Farooq-i-Azam, and Akhtar Ali.

Providing wheat germplasm through international collaboration is an asset for the cooperating institutes for selecting desirable plant types better suited to their climatic conditions. Our objective was to identify genotypes better adapted to the local environments of the province.

Table 1. Agronomic data of the top five wheat genotypes and a check from international yield trials.

#	Genotype	Days-to-heading	Days-to-maturity	Plant height (cm)	Lodging (%)	Grain yield (kg/ha)	Harvest index (%)	Stripe rust	Leaf rust
36TH ELITE SPRING WHEAT YIELD TRIAL									
1	106	110	154	97	0	5,706	39	0	0
2	118	112	154	104	25	5,081	35	Trace	0
3	135	117	156	106	0	4,998	37	0	0
4	107	113	155	95	0	4,915	35	Trace	0
5	127	113	154	97	0	4,457	32	5R	0
Check	Bathoor-08	117	155	100	140	4,457	32	10M	0
	P value	0.00	0.00	0.00	0.62	0.00	0.05	—	—
3RD WHEAT YIELD CONSORTIUM TRIAL									
1	5	116	156	106	45	6,578	46	0	0
2	34	116	155	113	0	6,402	42	5R	0
3	33	119	156	112	40	5,788	38	0	0
4	35	116	155	109	0	5,788	38	5R	0
5	22	117	155	109	0	5,701	39	5M	0
Check	Bathoor-08	114	153	100	25	4,911	32	5M	0
	P value	0.00	0.00	0.01	0.00	0.00	0.00	—	—

Methodology. Nurseries received from CIMMYT and ICARDA were planted in nonreplicated fashion based on an augmented statistical design. Each entry of the respective nursery was planted as two 2.5-m rows with a 30-cm row spacing. Other details are described earlier (Methodology, p. 48). Ninety superior (high-yielding, water-use efficient, and drought and disease resistant) wheat lines/cultivars were imported from Australia. The adaptation of these genotypes need to be tested in environmental conditions of the KP province to identify useful genotypes carrying genes for high yield and disease resistance. Eighty-five imported and 12 genotypes developed through hybridization in F_6 and F_7 generations were evaluated in a NIFA Observation Nursery with the local checks Fakhre Sarhad, Bathoor-08, and Pirsabak-13, and a susceptible check Morocco, grown in each block. Each of the 117 entries were planted as two 2.5-m rows with a 30-cm row spacing. Data regarding yield and other agronomic traits were recorded for individual entries on traits such as days-to-heading and maturity, plant height (cm), tillers (m^2), lodging (%), grain yield (kg/ha), and resistance to stripe rust, leaf rust, barley yellow dwarfvirus, and loose smut.

Summary. The International Bread Wheat Screening Nursery, consisting of 300 genotypes received from CIMMYT, Mexico, was evaluated with local check Bathoor-08. Based on plant type, yield performance, and disease reaction (*Yr* and *Lr*), 48 genotypes were selected. The selected genotypes out yielded the check Bathoor-08 (3,555–5,511 kg/ha) by producing grain yield in the range of 4,444–6,222 kg/ha. Data of the top five selected entries is presented (Table 2, p. 50). These genotypes have good plant stature (around 100 cm) coupled with zero lodging, improved harvest index, and disease resistance.

The Central and West Asia 16th Spring Bread Wheat Observation Nursery, consisting of 130 genotypes received from ICARDA, was evaluated with the local check Bathoor-08. Ten genotypes were selected based on plant type, yield performance, and rust reaction (*Yr* and *Lr*). The selected genotypes out-yielded the check Bathoor-08 (3,733 kg/ha) producing grain yields in the range of 3,733–4,711 kg/ha. The top yielding genotypes had a medium plant height with zero lodging, resistance to leaf rust, and acceptable resistance for stripe rust (Table 2, p. 50).

The 26th High Rainfall Wheat Screening Nursery, consisting of 117 genotypes received from CIMMYT, Mexico, was evaluated with local check Bathoor-08. Twenty-four genotypes were selected based on plant type, yield performance, and disease reaction (*Yr* and *Lr*). The selected genotypes out yielded the check Bathoor-08 (4,144–5,155 kg/ha) producing grain yield in the range of 4,444–5,777 kg/ha. The top five genotypes (Table 2, p. 50) had normal maturity, medium plant height, zero lodging, and good disease resistance.

In the NIFA Observation Nursery, 117 entries were evaluated including three commercial checks and the susceptible check Morocco. Based on plant type, yield performance, and disease reaction, we selected 27 genotypes. The list

Table 2. Agronomic data of the top five wheat genotypes and a check from three exotic trials.

#	Genotype	Days-to-heading	Days-to-maturity	Plant height (cm)	Lodging (%)	Grain yield (kg/ha)	Harvest index (%)	Stripe rust	Leaf rust
48TH INTERNATIONAL BREAD WHEAT SCREENING NURSERY									
1	1084	121	157	102	0	6,222	41	0	0
2	1198	114	156	102	0	6,222	41	5M	0
3	1298	113	154	100	0	5,777	42	5R	0
4	1197	118	156	100	0	5,777	40	0	0
5	1127	111	153	90	0	5,777	42	5M	0
Check	Bathoor-08	119	156	97	0	4,574	36	5M	0
CENTRAL AND WEST ASIA 16TH SPRING BREAD WHEAT OBSERVATION NURSERY									
1	100	115	153	97	0	4,711	42	10R	0
2	15	110	153	96	0	4,444	31	5M	0
3	21	115	154	90	0	4,000	30	5M	0
4	37	116	156	100	0	4,000	36	5R	0
5	57	118	155	96	0	4,000	28	5M	0
Check	Bathoor-08	116	153	98	0	3,733	31	10M	0
26TH HIGH RAINFALL WHEAT SCREENING NURSERY									
1	2076	116	155	100	0	5,777	37	0	0
2	2055	119	156	104	0	5,422	33	0	0
3	2054	120	156	101	0	5,155	33	10M	0
4	2004	116	154	92	0	4,888	31	0	0
5	2005	119	155	97	0	4,888	31	0	0
Check	Bathoor-08	117	154	95	0	4,800	33	5M	0

Table 3. List of the selected genotypes imported from Australia along with their parentage.

#	Genotype	Parentage
1	Australia-10	SOKOLL
2	Australia-26	MELON//FILIN/MILAN/3/FILIN
3	Australia-28	PBW343*2/KUKUNA//PBW343*2/KUKUNA
4	Australia-29	ASEEL-6
5	Australia-36	MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92
6	Australia-39	POTCH 93/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92
7	Australia-40	ACHTAR*3//KANZ/KS85-8-5/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92
8	Australia-41	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX
9	Australia-42	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX
10	Australia-43	ONIX//TACUPETO F2001*2/KUKUNA
11	Australia-44	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/KAUZ//PRINIA/3/BAV92
12	Australia-50	GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92
13	Australia-52	SOKOLL//TACUPETO F2001*2/KUKUNA
14	Australia-55	MILAN/KAUZ//PRINIA/3/BAV92/4/WBLL1*2/KUKUNA
15	Australia-56	ATTILA/BAV92//PASTOR/3/ATTILA*2/PBW65
16	Australia-58	ESDA/KKTS
17	Australia-60	PASTOR*2/BAV92/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
18	Australia-64	WBLL1/KUKUNA//TACUPETO F2001/5/WAXWING/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
19	Australia-66	TACUPETO F2001/BRAMBLING//KIRITATI
20	Australia-69	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES/7/CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/PASTOR

Table 3. List of the selected genotypes imported from Australia along with their parentage.

#	Genotype	Parentage
21	Australia-71	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA//TSI/VEE#5/4/CROC_1/ AE.TAUSCHII (224)//2*OPATA
22	Australia-75	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/PARUS/6/FRET2*2/KUKUNA
23	Australia-76	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
24	Australia-77	FRET2/KUKUNA//FRET2/3/YANAC/4/FRET2/KIRITATI
25	Australia-78	FRET2/KUKUNA//FRET2/3/PASTOR//HXL7573/2*BAU/5/FRET2*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ
26	Australia-80	SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
27	Shafaq x AS	Shafaq x Abdus Sattar-2002, F_7
28	Fakhre Sarhad	Local Check
29	Bathoor-08	Local Check
30	Pirsabak-13	Latest Check
31	Morocco	Susceptible Check

of the selected genotypes imported from Australia along with their parentage is presented (Table 3, p. 50-51). The agronomic data of the selected wheat genotypes and the checks in NIFA Observation Nursery is given in Table 4 (p. 52). The selected genotypes out yielded the latest check Pirsabak (4,657 kg/ha) producing grain yield in the range of 4,711–6,222 kg/ha. The highest yield was produced by Australia-78 (6,222 kg/ha), followed by Australia-10, -40, -43, and -77 (5,777 kg/ha), and check Bathoor-08 (5,342 kg/ha). The selected genotypes that yielded more than the Pirsbak-13 check also were good for disease resistance and other parameters. Maximum variability among the selected genotypes was for days-to-heading (107–118 days), plant height (95–114 cm), and tiller number (467–793). Barley yellow dwarf virus resistance in the selected lines was zero to low, resistant to leaf rust, and minimum reaction to stripe rust (up to 20R).

Expected results/output. The selected lines from the exotic yield nurseries will be further tested in preliminary yield trials under normal and late-planting conditions at NIFA during the next year.

Table 4. Agronomic data of selected wheat genotypes and the checks from NIFA Observation Nursery (a barley yellow dwarf rating of L indicates a low level of infection).

#	Genotype	Days-to-heading	Days-to-maturity	Plant height (cm)	Tillers (m^2)	Lodging (%)	Grain yield (kg/ha)	Stripe rust	Leaf rust	Barley yellow dwarf	Loose smut
1	Australia-78	111	155	106	587	0	6,222	0	5R	L	1
2	Australia-43	116	155	108	693	0	5,777	0	0	L	0
3	Australia-10	110	156	105	600	20	5,777	10R	0	L	0
4	Australia-77	115	154	111	667	0	5,777	5R	0	L	0
5	Australia-40	114	156	112	733	10	5,777	0	0	0	0
6	Australia-39	114	156	106	613	10	5,333	0	0	L	0
7	Australia-56	112	156	111	600	0	5,333	5R	0	0	0
8	Australia-60	115	153	112	600	5	5,333	0	0	L	0
9	Australia-69	114	156	104	693	5	5,333	0	0	L	0
10	Australia-64	107	150	103	560	0	5,333	20R	0	0	0
11	Australia-76	109	154	114	500	0	5,199	10MR	0	L	2
12	Australia-29	115	156	102	720	40	5,199	0	0	0	0
13	Australia-28	115	156	104	667	0	5,155	5R	0	L	0
14	Australia-52	114	156	111	667	0	5,066	10R	0	L	0
15	Australia-71	108	153	108	600	45	5,066	20R	0	L	0
16	Australia-44	110	155	100	793	0	4,888	0	0	0	2
17	Australia-55	112	156	105	547	0	4,888	5R	0	L	0
18	Australia-66	114	155	100	467	0	4,888	10R	0	0	0
19	Shafaq x AS	113	154	103	587	0	4,888	5R	5M	L	0
20	Australia-26	110	155	95	600	40	4,888	10R	0	L	0
21	Australia-42	111	152	110	667	5	4,844	5R	0	L	0
22	Australia-36	118	156	102	533	0	4,800	0	0	L	0
23	Australia-75	109	153	102	693	0	4,755	5R	0	L	0
24	Australia-41	112	153	111	760	10	4,711	0	0	0	0
25	Australia-50	112	156	108	787	30	4,711	0	0	L	0
26	Australia-58	117	155	100	667	20	4,711	20R	0	L	0
27	Australia-80	113	152	107	667	5	4,711	0	0	0	1
CHECKS											
28	Fakhre Sarhad	117	155	101	655	0	4,622	5R	0	L	0
29	Bathoor-08	113	154	102	600	11	5,342	5R	5R	L	1
30	Pirsabak-13	113	154	96	665	2	4,657	5R	0	L	0
31	Morocco	112	155	107	405	18	2,071	100S	60S	L	0

PAKISTAN AGRICULTURAL RESEARCH COUNCIL (PARC)
Food Quality & Safety Research Institute, Karachi University Campus, Karachi, Pakistan.

Correlations between dough properties of control and pentosan-added flours.

Salman Khurshid, Shahid Yousaf, Saqib Arif, and Qurrat ul Ain Afzal.

The relationship between dough development time (DDT) and other dough parameters. The relationships between DDT and other dough parameters were determined. We found that DDT was significantly ($P < 0.01$) positively related with dough stability (Fig. 1), but negatively correlated ($r = –0.430$) with mixing tolerance index. This shows that the longer time taken by flour to develop dough has higher stability and lower mixing tolerance index. Borghi et al. (1996) indicated that DDT is positively related with dough stability and inversely related with dough softening. Anjum and Walker (2000) suggested that development time and stability of dough was negatively related with softening of dough.

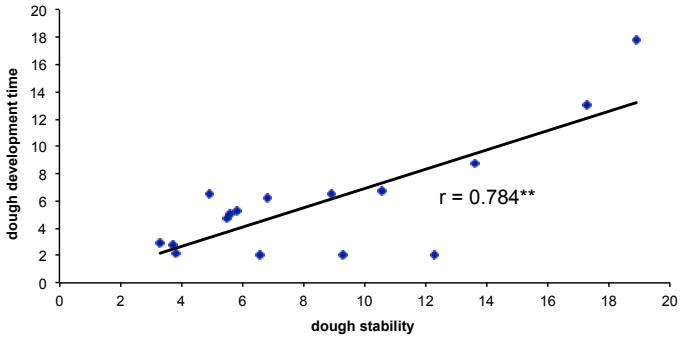

Fig. 1. Relationship between dough development time and dough stability.

The relationship between dough stability (DST) and the mixing tolerance index (MTI). The relationship between dough stability and mixing tolerance index was determined (Fig. 2). We found that DST was significantly ($P < 0.01$) negatively correlated with the MTI. Preston et al. (1992) also recorded the significant negative correlation ($r = –0.83$, $P < 0.001$) between DST and the MTI, which indicates that flour with a good tolerance to mixing had a high stability value but a low MTI value. The flour mixing strength for dough is generally correlated with DST (Hamada et al. 1982; Bietz 1986).

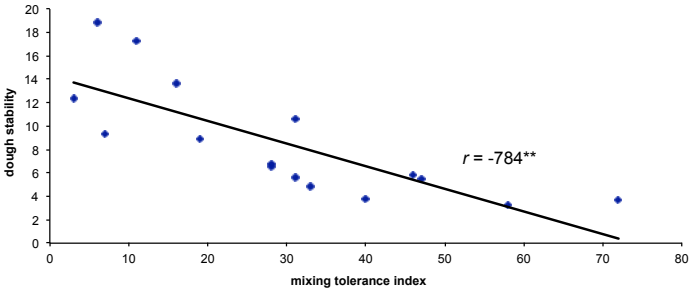

Fig. 2. Relationship between dough stability and the mixing tolerance index.

The influence of pentosans on dough properties were assessed by determining correlation coefficients among dough parameters of pentosans added to wheat flours (Table 1).

Table 1. The relationships among water absorption (WA), dough development time (DDT), dough stability (DS), and the mixing tolerance index (MTI) in the presence of pentosans (water-extractable and water-unextractable).

	Correlation coefficients (r)					
	In the presence of water-extractable pentosans			In the presence of water-unextractable pentosans		
	DDT	DST	MTI	DDT	DST	MTI
WA	0.212	0.184	–0.180	0.089	0.048	–0.010
DDT		0.868**	–0.707**		0.418*	–0.333
DST			–0.827**			–0.746**

The relationship between water absorption (WA) and dough parameters in the presence of pentosans. The relationship between WA and dough parameters in presence of water-extractable pentosans (WEP) was determined. Similar to the control flours, WA did not relate with dough parameters of WEP-added flours. The correlation coefficients (r) of WA with DDT, DST, and MTI were found to be 0.212, 0.184, and –0.180, respectively.

The relationships between WA and various dough parameters in presence of WUP were obtained and found to be similar to the results of the control flours. The WA did not relate with dough parameters. The correlation coefficients (*r*) between WA and DDT, DST, and MTI of the WUP-supplemented flours were 0.089, 0.048, and –0.010, respectively.

The relationship between DT and other dough parameters in the presence of pentosans. The relationship between DDT and other dough parameters were found to be similar in the presence or absence of WEP. However, the strength of the relationships was stronger in the presence of WEP. The correlation coefficients (*r*) of DDT with DST and MTI in presence of WEP were 0.868** and –0.707**, respectively.

The relationships between DDT and other dough parameters were simmilar in the presence or absence of WUP. However, the strength of relationships was weaker in the presence of WUP. The correlation coefficients (*r*) of DDT with DST and MTI were 0.418* and –0.333, respectively.

The relationship between DST and MTI of dough in the presence of pentosans. The relationship between DST and the MTI of wheat flour in presence of WEP was similar to that in the absence of WEP. However, the significantly negative correlation ($r = –0.827$, $P < 0.01$) between DST and MTI was slightly greater in magnitude in presence of WEP.

The relationship between DST and MTI was similar in presence or absence of WUP. The correlation coefficient (*r*) between DST and MTI in presence of WUP was significantly negative ($r = –0.746$; $P < 0.01$).

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The influence of pentosans on the stability and tolerance index of wheat dough.

Shahid Yousaf, Salman Khurshid, Qurrat ul Ain Akbar, and Saqib Arif.

Influence of water-extractable pentosans (WEP) on dough stability. The influence of WEP on the DST of dough increased the stability in all cultivars tested (Fig. 3). Maeda and Morita (2006) indicated that the addition of water-soluble pentosan significantly improved the dough properties for breadmaking. They further suggested that this could be due to the characteristics of water-soluble pentosan fraction, i.e., a higher ratio of xylose to arabinose, a greater amount of ferulic acid, and a better foaming stability. Subba Rao et al. (2004) found a lesser influence of native cold water-soluble polysaccharides compared to malted cold water-soluble polysaccharides obtained from ragi on dough stability. They recorded that malted cold water-soluble polysaccharides significantly decreases DST. We also observed that the increase was signifi-

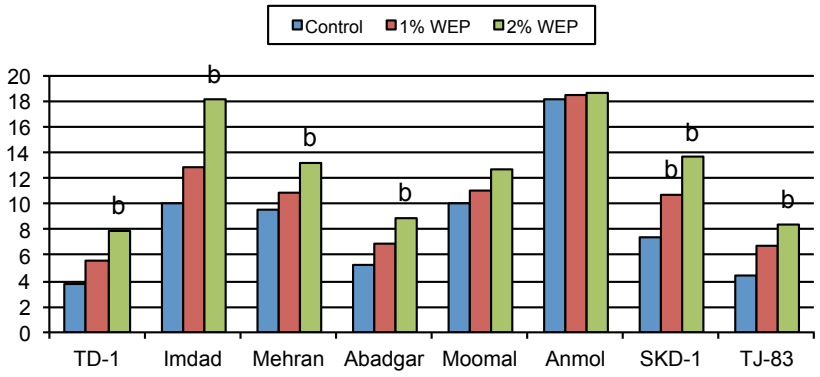

Fig. 3. Effect of water-extractable pentosans (WEP) on the dough stability of different hard white spring wheat flours. Bars labeled with a 'b' indicate that they are significantly different from the control at $P<0.05$.

cant (P<0.05) at 2% addition level in all cultivars except Moomal and Anmol, whereas the increase was insignificant (P > 0.05) at 1% level in all cultivar doughs.

The percent increase in DST of different cultivars is shown (Fig. 4). At 1% addition level, the increase in DST ranged between 2.2 and 52.3%. Further increase is seen at 2% addition level to range between 27 and 108%. The highest increase was exhibited in varieties TD-1, TJ-83 and SKD-1 with a percent increase of 108, 91 and 84% respectively.

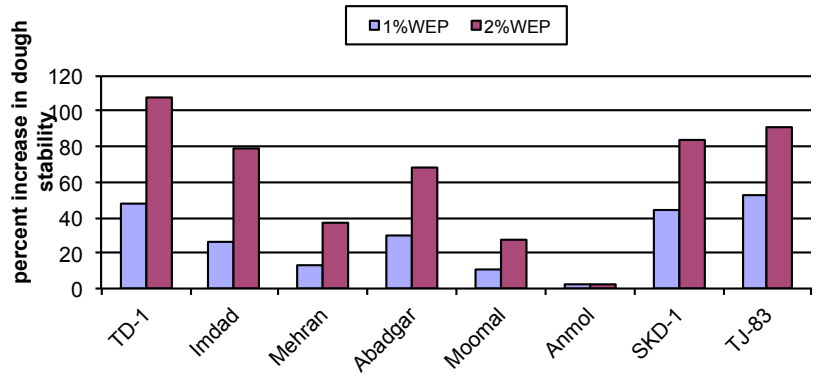

Fig. 4. The magnitude of the effect of water-extractable pentosans (WEP) (percent increase) on dough stability of hard white spring wheat flour.

Influence of water-unextractable pentosans (WUP) on dough stability. The effect of WUP on the DST of each cultivar is shown (Fig. 5). The addition of WUP caused an increase in DST of nearly all the cultivars except Anmol and Mehran. In a converse manner to other cultivars, the DST of the cultivar Anmol exhibited a significant (P < 0.05) decrease in DST with increasing levels of WUP. Compared to this, the cultivar Mehran showed an irregular pattern with insignificant (P > 0.05) changes in DST. Previous reports also found that the addition of WUP increases the resistance of dough to extension (Jelaca and Hlynka 1972; Courtin et al. 1999).

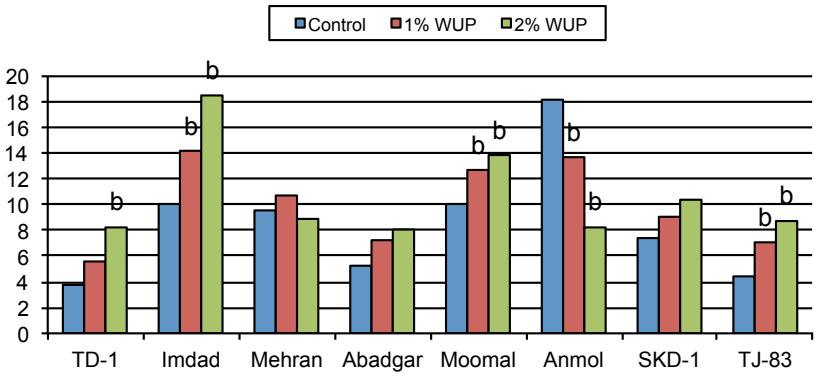

Fig. 5. Effect of water-unextractable pentosans (WUP) on dough stability of different hard white spring wheat flours. Bars labeled with a 'b' indicate that they are significantly different from the control at P<0.05.

The percent increase or decrease in DST on the addition of WUP to different cultivar flours is shown (Fig. 6). The amount of WUP largely influenced the extent of the increase in DST. With the exception of cultivars Anmol and Mehran, the DST of all the cultivars increased with an increase in WUP. The percent increase in DST was higher on addition of 2% WUP to wheat flours (38–118%), compared to that at the 1% level (23–59%). The highest increase in DST was observed in cultivars TD-1, TJ-83, and Imdad, with increases of 118%, 98%, and 82%, respectively.

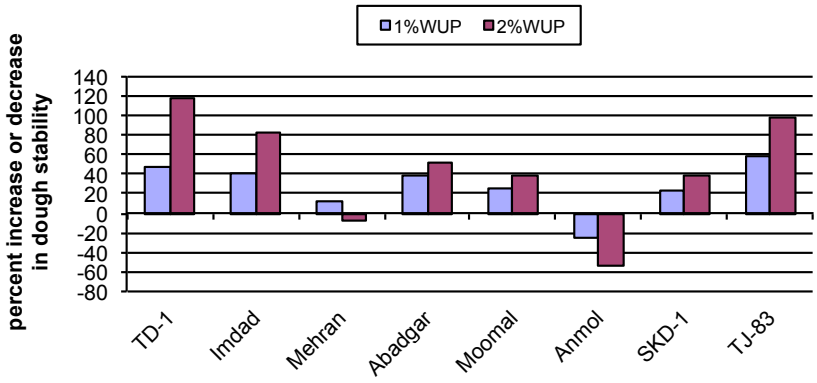

Fig. 6. The magnitude of the effect of water-unextractable pentosans (WUP) (percent increase or decrease) on the dough stability of hard white spring wheat flour.

Influence of water-extractable pentosans on mixing tolerance index (MTI). The WEP influence the MTI of cultivars (Fig. 7, p. 56). The addition of WEP decreased the MTI values of the flours of all cultivars. The addition of WEP improved the MTI and lowered the dough breakdown rates of all flours. Better mixing tolerance reflects good dough-

handling properties and is generally desirable for bread baking (Bergman et al. 1998). Stojceska and Ainsworth (2008) indicated that dietary fiber significantly, ($P < 0.001$) inversely influenced the degree of softening.

The MTI decreases in upon the addition of WEP to the flour of different cultivars (Fig. 8). Apparently, MTI decreases with increasing amounts of WEP. At a 1% level, the decrease in MTI ranged between 15.6% and 44.4%. Further decreases (34.4–77.3%) were observed upon a 2% addition of WEP. The maximum decrease in MTI values were seen in the dough of cultivars Imdad, followed by those of SKD-1 and Anmol.

Influence of water-unextractable pentosans on the mixing tolerance index. The level of WUP incluences the MTI of cultivar dough (Fig. 9). We observed that WUP decreased the MTI values of all cultivar doughs except that of Anmol. However, the decrease was statistically significant ($P < 0.05$) only in the MTI of cultivars Imdad and TJ-83 when 2% WUP was added. The reason for the improved MTI could be due to the water absorbing character of WUP.

The magnitude of the WUP influence in terms of percent increase or decrease in MTI of different cultivar doughs are shown (Fig. 10, p. 57). With the exception of the cultivar Anmol, the MTI values of all cultivars decreased after the addition of WUP to wheat flour. At a 1% WUP addition, the decrease in MTI varied between 12 to 47% and further decreases (6–68%) were observed as WUP was increased to 2%. The highest decrease in percentage was found in cultivars Imdad and Moomal.

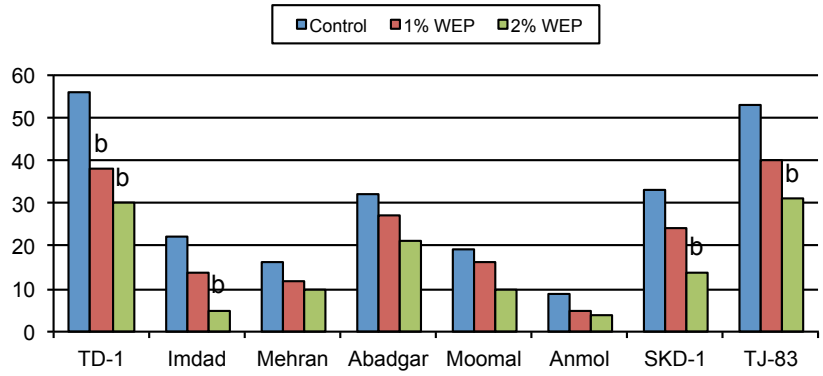

Fig. 7. Effect of water-extractable pentosans (WEP) on the mixing tolerance index of different hard white spring wheat flours. Bars labeled with a 'b' indicated that they are significantly different from the control at $P<0.05$.

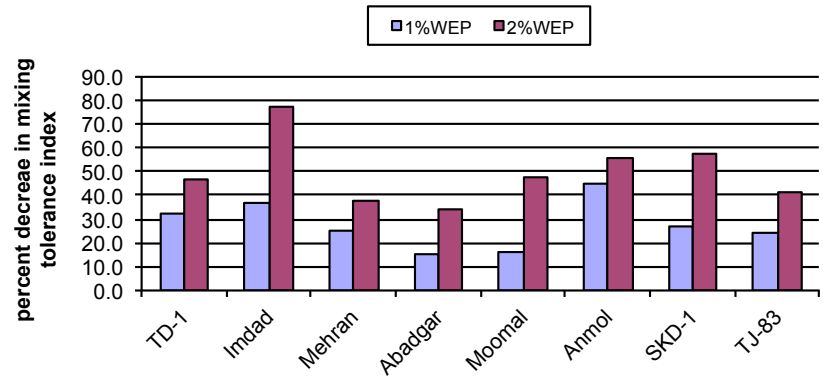

Fig. 8. The magnitude of the effect of water-extractable pentosans (WEP) (percent increase) on the mixing tolerance index of hard white spring wheat flour.

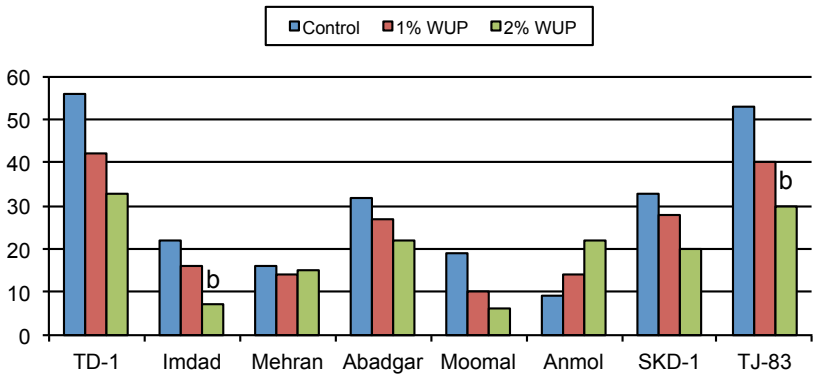

Fig. 9. Effect of water-unextractable pentosans (WUP) on the mixing tolerance index in the dough of different hard white spring wheat cultivars. Bars labeled with a 'b' indicate that they are significantly different from the control at $P<0.05$.

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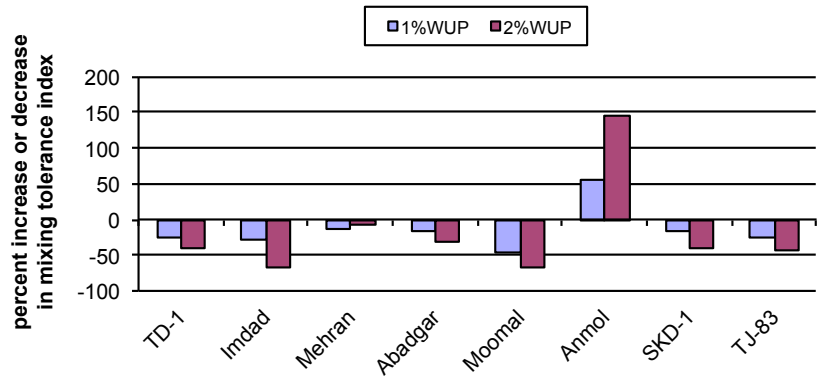

Fig. 10. The magnitude of the effect of water-unextractable pentosans (WUP) (percent increase or decrease) on the mixing tolerance index of hard white spring wheat flour.

The influence of whater-extractable and unextractable pentosans on dough-development time of wheat flour.

Qurrat ul Ain Afzal, Salman Khurshid, Shahid Yousaf, and Saqib Arif.

Influence of water-extractable pentosan on dough-development time (DDT). The addition of WEP influenced the DDT of the flour of each cultivar (Fig. 11). WEP increased the DDT of the flour of all cultivars. A longer mixing time is required when WEP was added to flour. Micniewicz et al. (1991) reported that the addition of water-soluble pentosan increased the DDT of wheat. The WEP, being soluble in water, are able to absorb more water and its addition to flour altered the moisture distribution among flour constituents, which delayed the time required for the development of dough (Brennan and Cleary 2007; Rao et al. 2007; Autio 2006; Wang et al. 2002). However, the increase in DDT with the addition of WEP was only found to be significant ($P < 0.05$) in the Imdad and Mehran cultivars at the 2% level.

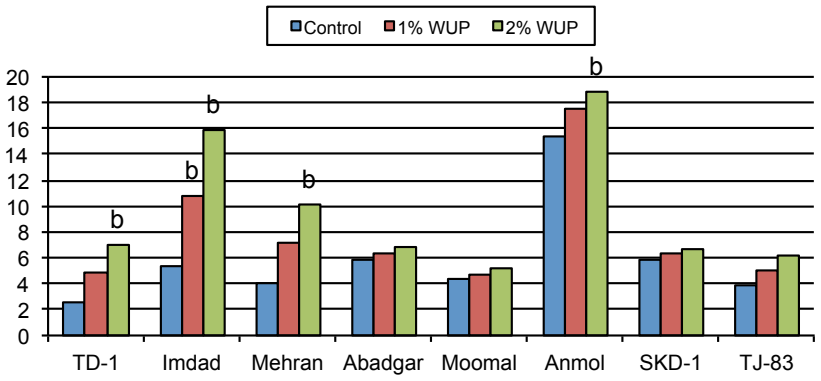

Fig. 11. Effect of WEP on dough development time of different HWSW flours. Bars labeled with a 'b' indicate that they are significantly different from the control at $P<0.05$.

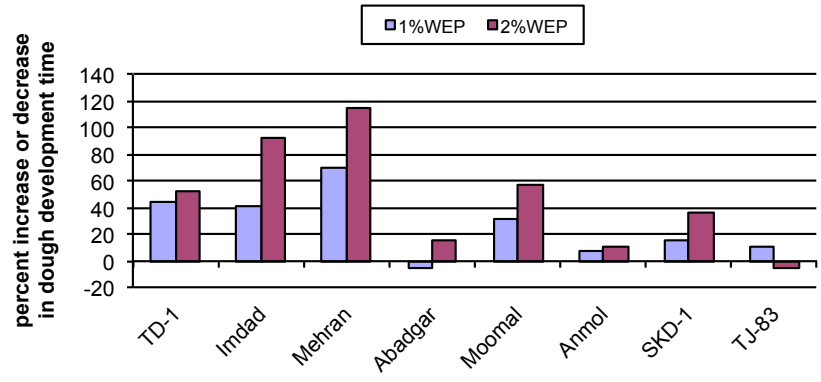

Fig. 12. The magnitude of the effect of water-extractable pentosans (WEP) (percent increase or decrease) on dough development time of the flour of hard white spring wheats.

The increase in DDT was different depending on the cultivar (Fig. 12, p. 57). At 1%, the highest increase in DDT was in the cultivar Mehran, followed by those for cultivars TD-1 and Imdad, over the control, was 71%, 44%, and 41%, respectively. Further increases in the DDT also were observed at the 2% level, in the cultivars Mehran (115%), Imdad (93%), and TD-1 (52%).

Influence of water-unextractable pentosan on dough-development time. Water-unextractabele pentosan was found to be one of the significant sources of variation in DDT and the influence of WUP was greater than that of WEP. We found that the addition of WUP up to 2% delayed the development of dough of all cultivar flours (Fig. 13). Courtin et al. (1999) and Biliaderis et al. (1995) also found that the supplementation of flour with WUP slows the development of dough. Micniewicz et al. (1991) reported that addition of water-insoluble pentosan increased the DDT of wheat. A significant ($P < 0.05$) increase was found in cultivars TD-1, Imdad, Mehran, and Anmol.

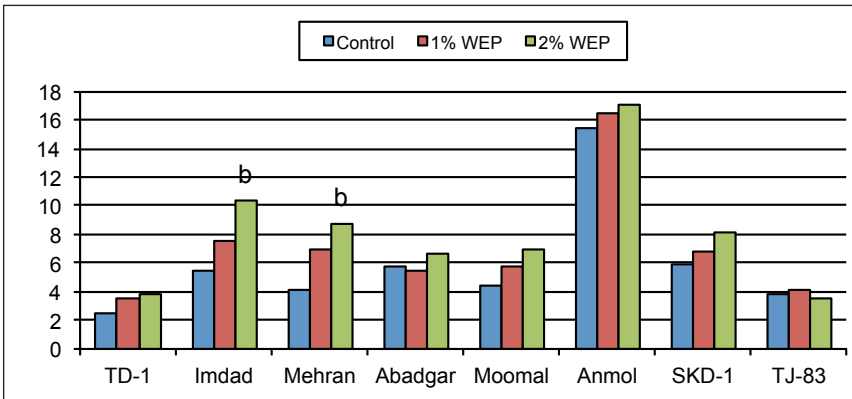

Fig. 13. The magnitude of the effect of water-unextractable pentosan (WUP) (percent increase) on dough-development time of hard white spring wheat flour.

The magnitude of the effect of WUP, in terms of percent increase from the respective control values, varies between cultivars (Fig. 14). At 1%, the percent increase in DDT ranged between 7% and 100%, with the smallest increase in flour of the cultivar Moomal and the greatest increase in the cultivar Imdad. At 2%, the increase ranged between 12% and 194%. The highest increases were observed in the cultivars Imdad, TD-1, and Mehran.

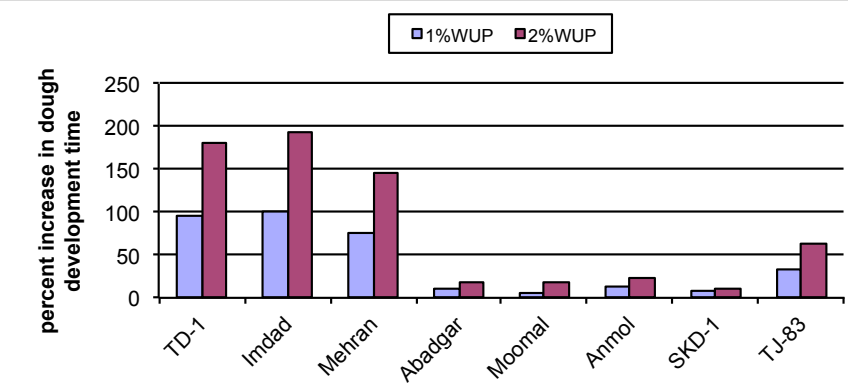

Fig. 14. Effect of water-unextractable pentosan (WUP) on the dough-development time of different hard white spring wheat flour. Bars labeled with a 'b' are significantly different from the control at $P<0.05$.

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Wang M, Hamer RJ, van Vliet T, and Oudgenoeg G. 2002. Interaction of water extractable pentosans with gluten protein: effect on dough properties and gluten quality. J Cereal Sci **36**:25-37.

Dough properties of water-extractable pentosan supplemented flour in different cultivars.

Saqib Arif, Qurrat ul Ain Akbar, Shahid Yousaf, and Salman Khurshid.

Water absorption (WA) of wheat flours. The WA of 1% and 2% WEP-supplemented flours are shown (Fig. 15). The WA of all 1% WEP-added flours varied between 63.9 (TD-1) and 71.0%(SKD-1). The remaining cultivars had WA capacities between 64.7–66.9%. The WA capacities of 2% WEP-substituted flours for optimum dough development varied between 67.0% and 71.0%. The WA of cultivar SKD-1 was the highest and significantly (P<0.05) different from that of other cultivars among 1% and 2% WEP-added flours. The higher WA capacity of flour would be beneficial for making good quality bread.

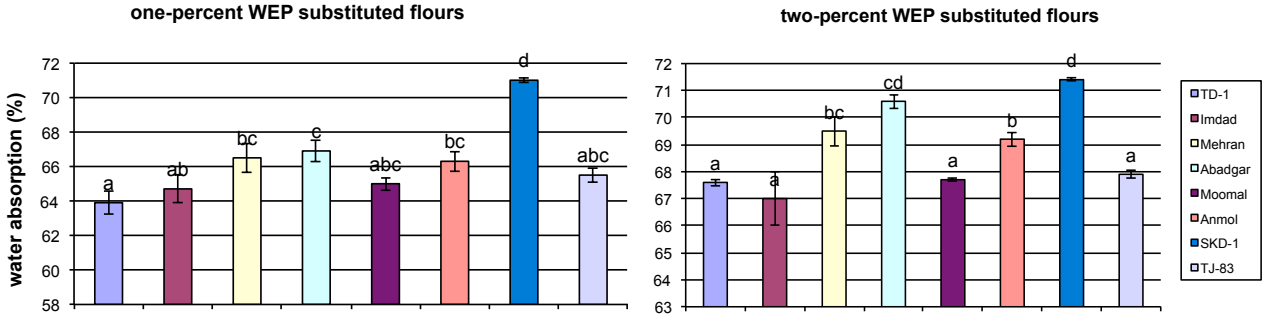

Fig. 15. Water absorption of water-extractable pentosan (WEP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at P<0.05.

Water absorption of 1% and 2% WUP-supplemented flours are shown (Fig. 16). The WA varied between 62.3% and 69.7% with the addition of 1% WUP to the flour. Flour of cultivars TD-1 had the lowest and SKD-1 the highest values. The WA capacities of flours of hard white soft wheat cultivars with 2% added WUP ranged from 62.9% to 70.5% with TD-1 the lowest and SKD-1 having the highest capacities. The WA capacity of SKD-1 was the highest and significantly (P < 0.05) different from WUP-supplemented flours.

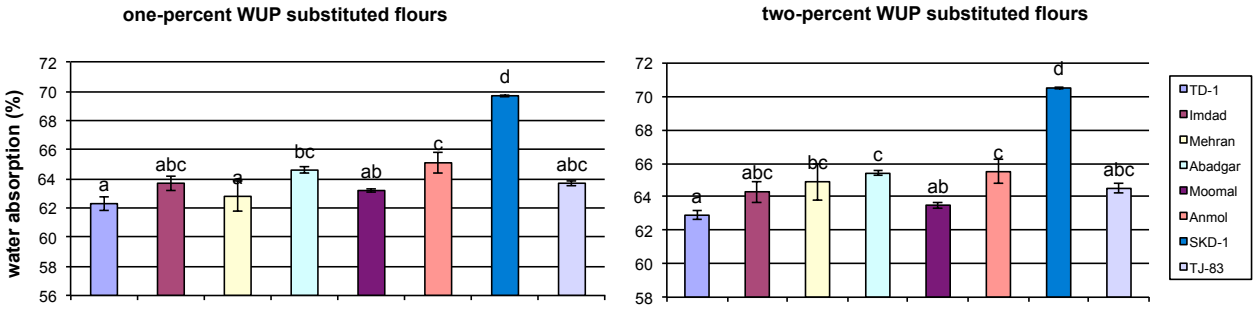

Fig. 16. Water absorption of water-unextractable pentosan (WUP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at P<0.05.

Dough-development time (DDT). The cultivar differences in DDT of 1% and 2% WEP-supplemented flours are shown (Fig. 17, p. 60). One-percent WEP supplemented doughs of all cultivars (except the cultivar Anmol) ranged between 3.6 and 7.6 min. The dough of Anmol tooka much longer time (16.5 min) to develop. At 2% WEP added, the flour of cultivar Anmol took longest (17.1 min) DDT. The DDT of the flour of all other cultivars ranged between 3.6 and 10.4 min. The DDT of Anmol was significantly (P < 0.05) different from that of the other cultivars.

The time required for the DDT of WUP-supplemented flours are given (Fig. 18, p. 60). Dough-development times of 1% WUP-added flour varied between 4.7 and 10.8 min, however, that of cultivar Anmol was exceptionally higher (17.8 min). Cultivar Moomal flour had the lowest DDT, but it was only 0.2 min higher than that of cultivar TD-1. Among the 2% WUP-substituted dough, all cultivars were withing a ranged of 5.2–10.1 min for optimum development.

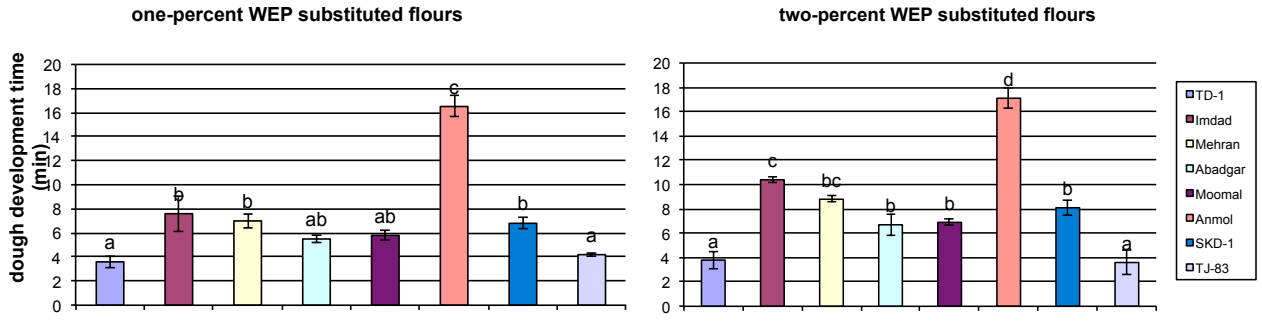

Fig. 17. Dough-development time of water-extractable pentosan (WEP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at $P<0.05$.

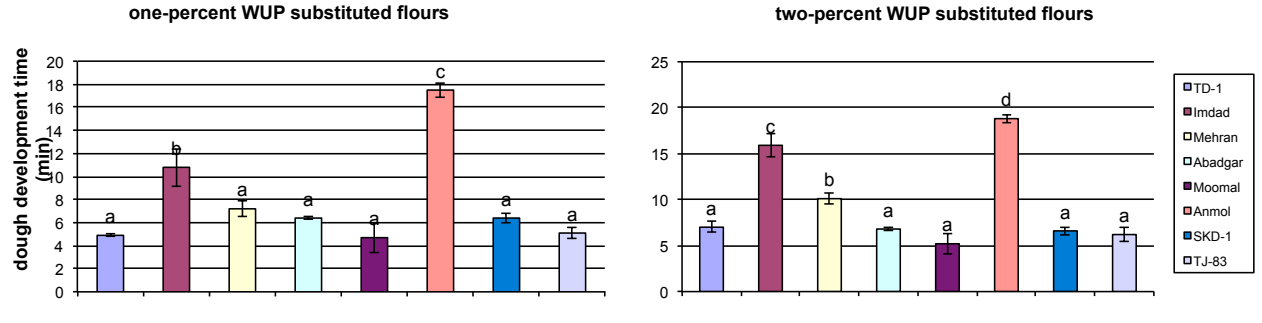

Fig. 18. Dough development time of water-unextractable pentosan (WUP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at $P<0.05$.

However, doughs of two cultivars, Anmol and Imdad, had longer times at 18.8 and 15.9 min, respectively. The shortest DDT was recorded for flour of cultivar Moomal. The DDT of Anmol was significantly ($P < 0.05$) different from that of the other cultivars.

Dough stability (DST). The dough stabilities of WEP-supplemented flours of different cultivars are shown (Fig. 19). The stability of dough of 1% WEP added to the flour of all the cultivars ranged between 5.6 and 18.5 min. The dough of the cultivar Anmol was the most stable; the lowest stability was in the dough of TD-1. With the exception of the cultivars Anmol and Imdad, 2% WEP added to the dough of all cultivars ranged from 7.9 to 13.6 min, with the highest DST in flour of cultivars Imdad and Anmol.

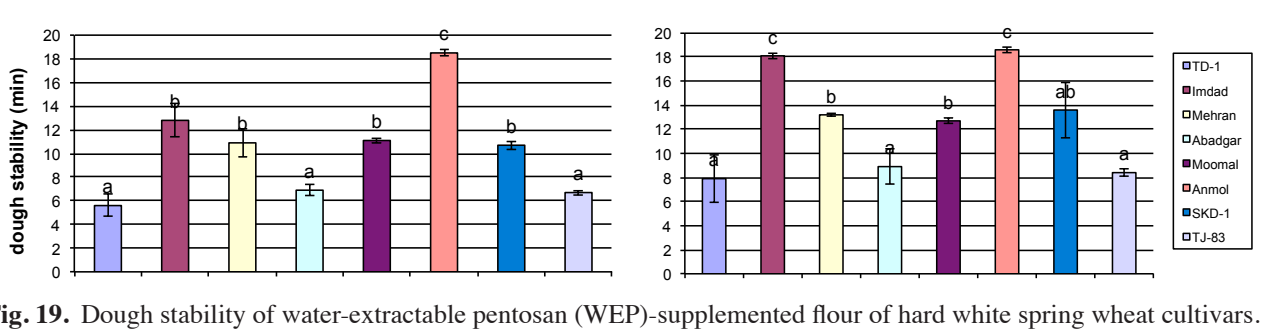

Fig. 19. Dough stability of water-extractable pentosan (WEP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at $P<0.05$.

The DST of 1% WUP-added flour from the different cultivars ranged between 5.6 and 14.1 min (Fig. 20, p.61). The lowest and highest DST values were in flour from the cultivars TD-1 and Imdad, respectively. Among flours with 2% WUP added, the most stable dough was in the cultivar Imdad. The dough of Moomal also exhibited stabilities higher than other cultivars. Dough stabilities of all other cultivars were similar, with an insignificant ($P > 0.05$) difference.

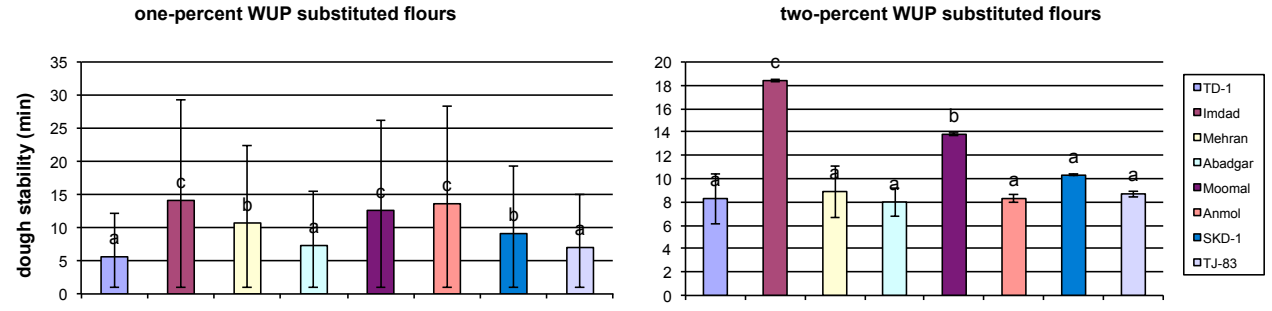

Fig. 20. Dough stability of water-unextractable pentosan (WUP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at $P<0.05$.

Mixing tolerance index (MTI). Among the flours with 1% WEP added, the maximum MTI among the different cultivars was in the dough of Anmol, whereas TD-1 and TJ-83 exhibited lower tolerance during mixing than that of the other cultivars (Fig. 21). Among the flours with 1% WEP added, the MTIvaried between 12 and 24 BU, except for the cultivars Anmol, TD-1 and TJ-83. WIth 2% WEP-supplemented doughs, cultivars Imdad and Anmol had the maximum tolerance during mixing as assessed from their low MTI values. Doughs that showed least tolerance during mixing were from the cultivars TD-1 and TJ-83. Doughs of remaining four cutivars, Mehran, Abadgar, Moomal, and SKD-1, had an MTI ranging from 10–21 BU.

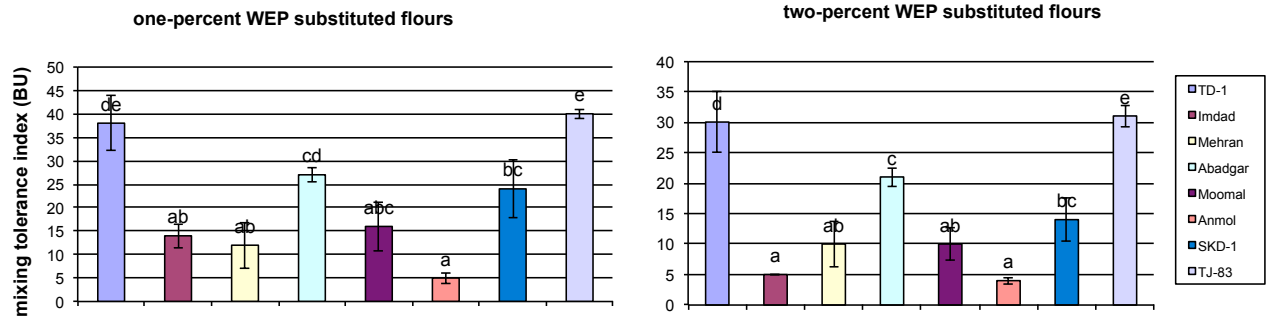

Fig. 21. Mixing tolerance index of water-extractable pentosan (WEP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at $P<0.05$.

The MTI of the 1% WUP-added flours of the different cultivars varied between 10 and 42 BU (Fig. 22). Dough of the cultivar Moomal had the lowest MTI and was not significantly ($P>0.05$) different from that of cultivars Anmol, Mehran, and Imdad, whereas the dough of TD-1 exhibited the highest MTI of all the cultivars and was significantly ($P > 0.05$) indifferent to TJ-83. At 2% WUP, higher tolerance to mixing was exhibited by the doughs of varieties Moomal and Imdad. Whereas, the doughs of TD-1 and TJ-83 found to be the least resistant to mixing. Doughs of all other varieties, Mehran, Abadgar, Anmol and SKD-1, showed MTI ranged between 15 and 22BU and were significantly ($P > 0.05$) indifferent to each other.

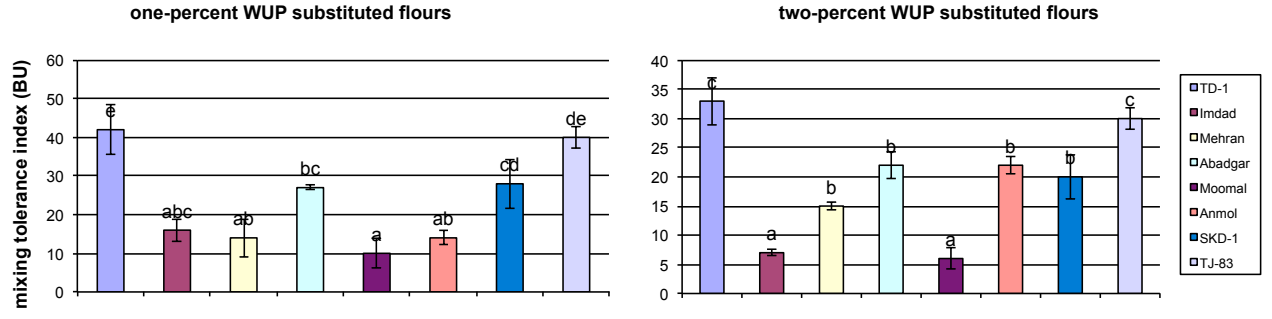

Fig. 22. Mixing tolerance index of water-unextractable pentosan (WUP)-supplemented flour of hard white spring wheat cultivars. Bars labeled with the same letters are not significantly different at P<0.05.

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.

Some results of the program: enlarging the bread wheat gene pool by introgressing desirable genes from alien species at ARISER.

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

Under severe epidemics, e.g., of leaf and stem rust and tan spot disease of wheat, we found that a collection of *T. turgidum* subsp. *dicoccum* (k10456, k12133, k13659, k19352, k19357, and k40030) were resistant to the Saratov population of *Pyrenophora tritici-repentis*. Four lines, k10456, k12133, k13659, and k19352, had a 1 type reaction to the pathogen and two samples, k19357 and k40030, had a 1–2 type reaction. Among a set of introgression lines were lines resistant to stem rust. Sources of resistance to the *P. graminis* were found in unknown samples of *T. turgidum* subsps. *persicum* and *kiharae*, subsp. *dicoccum* line k7507, translocation and substitution chromosomes from *Thinopyrum elongatum* ((2n = 70) T?Ag^{e}–7DL ?Ag^{e} (3B)), and the durum wheat cultivars Saratovskaya 57, Saratovskaya Golden, NICK, Golden Wave, Svetlana, and YAZI 10. Furthermore, lines with resistance to leaf and stem rust (reaction types of 0; and 1) and tan spot (reaction type 1–3) were identified. Some bread wheat lines contain the combinations of genetic material from *Thinopyrum intermedium* and *elongatum*, *T. turgidum* subsps. *dicoccum* and *kiharae*, and durum wheat. In a set of introgression lines from crosses of cultivars Saratovskaya 68, L503, and Dobrynya and *Ae. columnaris* (k1193), lines carrying the combination substituted chromosomes 5D (5Ae^{2}) + 3D (3Ae^{2}) and 6D (6Ae^{2}) + 3D (3Ae^{2}), and a line with 3D (3Ae^{1}) are resistant to leaf rust. This inherited resistance is dominant.

The reaction of introgression lines of spring bread wheat to leaf rust, stem rust and tan spot in 2016.

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

In the 2016 growing season under severe eppidemics of leaf rust, stem rust, and tan spot, a set of introgression lines with genetic material from various relatives of bread wheat and lines derived from crosses of CIMMYT synthetics with Saratov-bred cultivars were evaluated for grain productivity and resistance to disease. Table 1 (p. 63) shows selected lines with resistance to all three diseases. Basically, these lines contains the following combinations of alien genetic material: translocations T7DS–7DL·7Ae#1L (*Th. elongatum*) and T1BL·1R#1S (*S. cereale*) in lines L449, L510, and L521; substitutions 3B (3Ag^{e}) + 3D (3Ag^{e}) (*Th. elongatum* line k-1587) L155; substitution 6D (6Ag^{i}) (*Th. intermedium*) and genetic material from CIMMYT synthetics L14, L236, L443, and L518; T7DS-7DL·7Ae#1L (*Th. elongatum*) + 6D (6Ag^{i}) (*Th. intermedium*) + T1BL·1R#1S (*S. cereale*) line L508. The highest grain productivity among the resistant introgressions was in line L14, with a combination of T7DS–7DL·7Ae#1L *(Th. elongatum*) and 2AL–2AS·2MV#1 (*Ae. ventricosa*) at 2,955 kg/ha. For grain productivity, line L160, with combination of genes from the durum wheat cultivars Saratovskaya 57, Saratovskaya Golden, Lyudmila, and *T. turgidum* subsp. *dicoccum* (2,558 kg/ha); line L82. with the combination T7DS–7DL·7Ae#1L (*Th. elongatum*) + T1BL·1R#1S (*S. cereale*) (2,725кг/ha); and line L443, obtained from crosses of CIMMYT synthetics and Saratov-bred cultivars of spring bread wheat (2,551 kg/ha), were notable.

Table 1. Grain producitivty and leaf rust, stripe rust, and tan spot infection types in a set of spring bread wheat introgression lines.

Line	Pedigree	Grain yield (kg/ha)	Infection type to		
			Leaf rust	Dtem rust	Tan spot
Favorit (check)		2,133	0	0–3	3
Saratovskaya 68 (check)		2,448	3	0–3	3
14	Dobrynya*5//Milan/Prinia	2,955	0	0	3
82	Dobrynya*4//ThatcherLr25	2,725	0	2	1–2
155	S55/Agr.el*4//S29/3/L1015 3Age(3B) 3Age(3D)	2,322	0	1–2	1
160	Ludmila/S55*2/T. dic-s//Saratovskaya Zolotistaya/3/L164//S55	2,558	0	2	1–2
236	Bel/3/Croc/Ae.squar(205)//Weaver/4/Belyanka	1,201	0	0	1–2
383	Dobrynya//6R/Agis181	1,589	0	0	3
439	S55*3/T.dic-s//L2032	2,413	0	0	2–3
443	Belyanka/3/Altar84/Ae.squar(224)//Pgo/4/S68	2,551	0	2	3
449	L505*2/Prohorovka//Belyanka	2,600	0	1	1–2
508	L505/S42/4/L505*3//Proh//L505/3/S70/4/Dobrynya Lr24	2,456	0	0	3
510	U-V2/L505//L503Lr26/3/L505/4/S68	2,294	0	1–2	2
518	Croc/Ae.squar(205)//Weaver/3/L505/4/DobrLr25	2,418	0	2	3
521	Dobr*5/ThatcherL9//L505//L503*3/TRAP≠BOW//Proh/S55	1,606	0	0	2
580	Tulaikovskay10//Agis181/S29+Agis181/S58	1,728	0	0	2
585	Dobrynya Lr25/ Belyanka //L505	2,489	0	2	1–2

ALL-RUSSIAN SCIENTIFIC RESEARCH INSTITUTE FOR AGRICULTURAL CHEMISTRY NAMED AFTER D.N. PRYANISHNIKOV

Pryanishnikova st. 31A, Moscow, 127550, Russian Federation.

Enhancement of adaptive capacity of spring wheat and barley under the action of seed treatment stresses with selenium and silicon.

L.V. Osipova, E.D. Kurnosov, and I.A. Bykovskaya.

Experiments were conducted to study of adaptive capacity of crop–mineral nutrition optimizing micronutrients. This research continues and deepens a previously study on the action of selenium and silicon under abiotic stress.

In the laboratory, we evaluated the impact of the preseeding processing of seeds (PPS) with selenium and silicon in separately and together on the germination of barley seed under exposure to different stresses. The influence of osmotic and salt stress and the effect of silicon and the herbicide Dikvat was assessed by the degree of growth inhibition, changes in the tension stress factors on accumulation of malondialdehyde (MDA), and as a pigment complex.

A nonspecific adaptation, different types of abiotic stress are expressed during the development of oxidative stress, which leads to disruption and damage to the lipid membranes and their degradation product, the accumulation-MDA. Malondialdehyde is considered the criterion of the intensity of the flow of membranous lipid peroxidation (POL) and damage to the membrane.

In optimal conditions, the POL level is constant, thanks to multilevel antioxidant protection. The balance is offset as a response to stress. Germination and growth, during the transition from dark to light, is accompanied by an increase in free-radical oxidation and high values of MDA. Selenium and Silicon, as an integral part of the system of antioxidant protection, reduce the level of stress and lead to a decrease in MDA content (Table 1, p. 64). The basis of action lies in selenium as a protector of some protein in the active center, which contains selenium amino acids. We assume

Table1. The influence of the preseeding processing of seeds (PPS) on the maintenance of photosynthetic pigments and malondialdehyde (MDA; mkM/g of crude weight) in the leaves of plants. Σ pigments = Σ of chlorophylls a, b, and carotinoids (mkg/100 g of crude weight).

PPS	Optimum H_2O		Sucrose (3 atm)		NaCl (150 мМ)		$Cd(NO_3)_2$ (500 мкМ)		Dikvat (0.2 мМ)	
	Σ pigments	MDA	Σ pigments	MDA	Σ pigments	MDA	Σ pigments	MDA	Σ pigments	MDA
H_2O	5.8	22.30	3.65	20.4	10.4	22.9	6.1	23.5	3.5	23.70
Se	17.9	4.40	10.2	8.4	15.2	9.6	11.6	4.3	8.6	5.50
Si	13.8	2.20	13.1	12.0	6.6	11.8	9.3	3.3	14.1	4.70
Se + Si	14.9	0.75	15.3	3.4	17.2	5.2	23.0	2.2	16.8	0.97

the participation of selenium in the regulation of adaptive enzymes and hormones in the synthesis of protective proteins. Silicon is another link to antioxidant protection, presumably associated with changes of structure of compounds.

The stress suppressed the growth processes connected with the need to use proteins for the formation of antioxidants that provide protection against adverse effects. Different types of stress influence the efficiency of the effect of selenium and silicon. When applied separately, the effect of selenium is higher for osmotic and salt stresses; silicon is effected in cadmium and dikvat levels. The PPS with selenium, together with silicon, reduces the oxidizing status of sprouts in the case of all negative impacts.

The optimum conditions for germination in all PPS options also leads to a decrease in MDA content. Chlorophyll, generally due to optimization of function, increases in content in the photosystem followed by an increase in content.

The functioning of photosynthesis is estimated by the content of pigments in the green barley sprouts after incubation in light. A change in content of chlorophyll and carotenoids was observed in the case of all stress factors, which is a part of the adaptive process in plant. A change in pigment structure for optimization of productional process and protection against free radicals. The increased synthesis chlorophylls a and b and carotenoids was noted in stress conditions that provided protection against an increased content of the active forms of oxygen (AFO), which are formed during the development of an oxidizing stress.

The type of a stress determined our strategy to change of content of the separate pigments. In case of osmotic and salt stresses, the content of chlorophyll a increased more than that of chlorophyll b. The effect of cadmium and a dikvat increased the share of carotenoids and the total pigment amount. Any type of preseeding handling of seed increased the general content of photosynthetic pigments, due to an increase in chlorophyll a, providing maintenance for transforming the accumulated light energy of chemical bonds, chlorophyll b, and carotenoids, which protect against photo-oxidation. The combined use of selenium and silicon was the most effective.

A presowing seed treatment reduced the negative impact of abiotic stresses, preventing the destruction of membrane lipids and activating the formation of pigments in the course of a de-etiolyation. The protective effect of selenium and silicon was shown during all vegetative periods and promoted an increase in the adaptive potential of grain crops.

ITEMS FROM UKRAINE

PLANT PRODUCTION INSTITUTE ND. A. V.YA. YURIEV
National Academy of Agrarian Sciences of Ukraine, Moskovsky prospect, 142, 61060, Kharkiv, Ukraine.

Chemical protection of winter bread wheat against root rots and Septoria infection.

N.V. Kuzmenko, A.Ye. Litvinov, and Ye.S. Oleynikov.

Winter wheat is one of the staple cereal crops in Ukraine, and a general level of production is ensured. To date, root rots and *Septoria* infection commonly occur and are the most limiting factors. Root rots damage primary and secondary roots and the base of the stalk. As a result, plants may die during sprouting, although producing shoots, tubers, and flowers, and during grain production. *Septoria* infection damages the leaves, stalks, and spikes. Diseased leaves are pale, gradually losing their green color and withering completely; stalks turn brown, wrinkle, and bend. Diseased plots appear multicolored and sometimes brown. Grains in the spikes are often skinny. Severe *Septoria* infections can cause sterility (Anon 2012). Some plants may die and, as a result, losses in grain yield range from 10–15 % to 30–40 %. *Septoria* infection develops after winter wheat is damaged by root rots. Our investigation studied the phytosanitary role of chemical seed treatment of winter wheat with systemic and contact fungicides for reducing disease loss to root rots and increasing grain yield (Tribel 2001; Anon 2012).

Materials and Methods. All studies were conducted in a stationary, nine-corse rotation field at the laboratory for Plant Production and Cultivar Investigations of the Plant Production Institute nd. a. V. Ya. Yuriev (Eastern Forest-Steppe of Ukraine) during 2012–15. The soil was a typical, medium-humus, black earth soil on loess with up to 5.4%. humus in the plowing layer. Black fallow was used as forecrop for winter bread wheat. Winter wheat was sown at an optimal time (12–19 September). The sowing rate of winter wheat was 4.0 x 10^6 viable seeds/ha. Nutrition was humus, 6.7 t/ha of the crop rotation area, and $N_{(30-60)}P_{(30-60)}K_{(30-60)}$. Additional N_{30} was applied by root feeding during the spring tillering stage and by root feeding at flowering. Agrotechniques were in general use. Wheat seed was pretreated prior to sowing with systemic and contact fungicides. The intensity of disease development was studied using conventional methods (Omelyuty 1986).

The experiment included the following treatments:

- Control (without protection and fertilizers, crop rotation based on natural soil fertility
- Vitavaks 200 FF @ 3.0 L/t (standard, active agents: karboksin (200 g/l) + tyram (200 g/L))
- Sertikor 050 FS @ 1.0 L/t (active agents: metalaksil (M (20 g/L)) + tebukonazol (30 g/L))
- Maxim Forte 050 FS @ 2.0 L/t (active agents: azoksystrobin (10 g/L), tebukonazol (15 g/L), + fludioksonil (25 g/L))
- Kinto Duo @ 2.5 L/t (active agents: trytikonazol (20 g/L) + prochloraz (60 g/L))
- Inshur Perform FS @ 0.5 L/t (active agents: trytikonazol (80 g/L) + pyraclostrobin (40 g/L))
- Lamardor Pro 180 FS @ 0.5 L/t (active agents: protiokonazol (100 g/L), tebukonazol (60 g/L), + fluopyram (20 g/L))
- Lamardor Pro 180 FS @ 0.5 L/t + Gaucho 70 WS (insecticide, active agent: imidaclopryd (700 g/kg)) @ 0.5 kg/t
- Celest Top 312.5 FS @ 1.25 L/t, (active agents: dyfenokonazol (25 g/L) + fludioksonil (25 g/L), and insecticide active agent tiametoksum (262.5 g/L)
- Unta Quadro 373.4 FS @ 1.6 L/t (active agents: protiokonazol (33.3 g/L) + tebukonazol (6.7 g/L) and insecticide active agents imidaklopryd (166.7 g/L) + klotianidyn (166.7 g/L))

Results. Averaged over the years (2013–15) under laboratory conditions, the germination rate in the control (without protection) was 96% (Table 1, p. 66). Pretreatment considerably reduced this index: Celest Top (88%), Maxim Forte (89%), Vitavaks (91%), Inshur Perform (91%), and Lamardor Pro (92%). Chemical treatment with Kinto Duo (94%), Lamardor Pro + Gaucho (94%), and Unta Quadro (94%) were nearly equal to that of the control treatment. The labora-

Table 1. Laboratory and field germination capacity of seeds, tillering ability, and stem density of winter bread wheat depending on a presowing seed treatment. Data averaged over the years 2013–15. The control treatment is without protection and fertilizer.

Treatment	Laboratory studies		Field studies			
	Germination energy (%)	Germination capacity (%)	Growing plants/ 400 seeds		Total tillering	Tillers/m²
			Number	%		
Control	96	97	340	86.0	3.6	1,160
Vitavaks 200 FF (standard)	91	99	280	70.5	4.7	1,300
Maxim Forte 050 FS	89	98	265	66.5	4.6	1,210
Kinto Duo	94	99	290	73.0	4.2	1,075
Inshur Perform FS	91	98	300	76.0	4.4	1,350
Lamardor Pro 180 FS	92	98	280	70.0	4.3	1,140
Lamardor Pro 180 FS + Gaucho 70 WS	94	98	270	68.0	4.4	1,190
Celest Top 312.5 FS	88	98	310	77.0	4.6	1,400
Unta Quadro 373.4 FS	94	98	290	72.0	4.6	1,260
LSD_{05}	4.0	3.0	—	5.0	0.6	260

tory germination rate of seed was 97% (in the control). With a chemical pretreatment, the index ranged between 98–99%. Under field conditions in the control the plants, germination was 86%. Pretreatments reduced field germination from 8.3% (Celest Top) to 20.8% (Maxim Forte).

During the autumn, stem density in the control (without protection and fertilizer) was 1,160 tillers/m². In variants with a chemical pretreatment, the number of tillers ranged between 1,075–1,400 tillers/m², nearly equal to that of the control treatment. Averaged over 2013–15, during spring tillering stage, total tillering in the control was 4.5 tillers/plant; productive tillering at wax-ripeness stage was 2.0 spike-bearing stems/plant (Table 2). In variants with a chemical pretreatment, total tillering ability was 21.1% (Inshur Perform) and 34.8% (Vitavaks) greater than that of the control. Productive tillering in the Lamardor Pro treatment was 35.5% greater than that of the control. In the other treatments; this index ranged between 2.5 spike-bearing stems/plant (Unta Quadro) and 2.8 spike-bearing stems/plant (Vitavaks and Maxim Forte). The number of spike-bearing stems/m² in the control was 570 stems; with a presowing seed treatment, between 630 and 720 spike-bearing stems/m² were observed.

Table 2. Tillering ability and stem density of winter bread wheat during the spring–summer vegetation period depending on presowing seed treatment. Data averaged over the years 2013–15. The control treatment is without protection and fertilizer.

Treatment	Tillering ability at		Number of tillers/m² at		
	Spring tillering (total)	Waxy-ripeness (productive tillering)	Spring tillering	Waxy-ripeness	
				Stems (total)	Productive, spike-bearing stems
Control	4.5	2.0	1,350	1,000	570
Vitavaks 200 FF (standard)	6.9	2.8	1,560	1,150	720
Maxim Forte 050 FS	5.9	2.8	1,450	1,030	650
Kinto Duo	6.4	2.7	1,480	970.0	630
Inshur Perform FS	5.7	2.7	1,540	1,020	630
Lamardor Pro 180 FS	6.3	3.1	1,420	1,110	720
Lamardor Pro 180 FS + Gaucho 70 WS	5.8	2.7	1,580	990.0	630
Celest Top 312.5 FS	6.0	2.6	1,780	1,070	660
Unta Quadro 373.4 FS	6.3	2.5	1,690	1,050	660
LSD_{05}	1.0	0.8	290	230	160

Between 2012–14 at autumn tillering stage, the intensity of *Helminthosporium* (*Bipolaris sorokiniana* Shoemaker) and *Fusarium* (*Fusarium Link*.) root rot development was 3.6% in the control, which did not exceed the economic threshold of harmfulness (economic threshold of harmfulness = 10–15%) (Table 3, p. 67). Averaged over 2013–15, disease development at the end of spring tillering stage was 12.4% (control). The degree of root rot develop-

Table 3. Spread and development of root rots in winter bread wheat depending on a presowing seed treatment. Averaged over the years 2012–15. The control treatment is without fungicide protection or fertilizer.

Treatment	Total tillering					At wax ripeness	
	Autumn		Spring				
	Spread (%)	Development (%)	Spread (%)	Development (%)	Effectiveness (%)	Spread (%)	Development (%)
Control	11.3	3.6	28.7	12.4	—	40.3	13.9
Vitavaks 200 FF (standard)	6.1	1.8	14.7	5.6	54.8	40.8	14.1
Maxim Forte 050 FS	1.0	0.2	5.9	1.9	84.7	43.7	15.3
Kinto Duo	1.9	0.5	4.5	1.4	88.7	41.8	14.8
Inshur Perform FS	3.3	1.0	12.7	4.9	60.5	37.7	12.9
Lamardor Pro 180 FS	0.8	0.2	1.7	0.7	94.3	44.5	16.5
Lamardor Pro 180 FS + Gaucho 70 WS	0.7	0.2	5.1	1.9	84.7	42.2	15.1
Celest Top 312.5 FS	4.5	1.3	15.8	6.4	48.4	41.0	15.0
Unta Quadro 373.4 FS	0.6	0.2	4.1	1.5	87.9	38.8	13.8
LSD_{05}	5.1	1.7	12.6	4.8	—	9.8	3.7

ment at autumn tillering stage with a chemical pretreatment ranged between 1.8% and 0.2%. At the end of the spring tillering stage, the efficiency of the chemical treatments was Celest Top (48.4%), Vitavaks (54.8%), Inshur Perform (60.5%), Maxim Forte and Lamardor Pro + Gaucho (84.7%), Unta Quadro (87.9%), Kinto Duo (88.7%), and Lamardor Pro (94.3%). Chemical treatment at the wax ripeness stage was not effective. The intensity of root rot development in the chemical treatments ranged between 12.9% and 16.5%, whereas the control was 13.9%.

Averaged over 2014–15, the degree of *Septoria* infection on the lower leaves of winter wheat during the autumn tillering stage in the control was 4.3%. With a chemical treatments, this index ranged between 3.5% and 6.4% (Table 4). At the end of the spring tillering stage, the intensity of disease development increased in the control was 13.4%. Chemical treatment provided a moderate effect, from 28.4% (Maxim Forte) to 46.7% (Celest Top). The degree of *Septoria* infection at the milk ripeness stage in the control was 26.4%. This index in variants with a presowing seed treatment ranged 25.2–30.6%. The degree of *Septoria* infection development at wax ripeness stage with a chemical treatment ranged 56.0–59.8%, whereas the control was 54.4%.

Table 4. The development of *Septoria* infection on leaves of winter bread wheat depending on the presowing seed treatment. Averaged over the years 2014–15. The control treatment is without fungicide protection or fertilizer.

Treatment	The development of Septoria infection on leaves, %				
	Lower layer at			Upper layer at	
	Autumn tillering	Spring tillering	Technical effectiveness (%)	Milky ripeness	Waxy ripeness
Control	4.3	13.4	—	26.4	54.4
Vitavaks 200 FF (standard)	4.7	9.4	34.0	29.2	56.7
Maxim Forte 050 FS	5.8	8.3	40.7	30.6	58.2
Kinto Duo	3.5	10.1	28.4	27.6	57.1
Inshur Perform FS	4.7	9.2	33.8	26.8	56.0
Lamardor Pro 180 FS	3.6	9.1	37.2	27.1	56.3
Lamardor Pro 180 FS + Gaucho 70 WS	5.1	8.9	39.4	25.2	57.2
Celest Top 312,5 FS	6.4	7.5	46.7	26.8	56.4
Unta Quadro 373.4 FS	4.7	8.9	39.7	27.7	59.8
LSD_{05}	—	0.8	—	—	—

Under meteorological conditions and phytosanitary state, averaged over 2013–15, grain yield was 5.92 t/ha in the control (Table 5, p. 68). The saved grain yield with an $N_{(30-60)}P_{(30-60)}K_{(30-60)}$ treatment with a chemical pretreatment was from 0.05 t/ha (Vitavaks) to 0.46 t/ha (Lamardor Pro + Gaucho). The 1,000-kernel weight increased from 0.36 g (Unta Quadro) to 1.52 g (Celest Top), compared with that of the control (44.51 g). Averaged over 2014–15, saved grain yield

Table 5. Grain yield of winter bread wheat depending on a presowing seed treatment. Averaged over the years 2013–15. The control treatment is without chemical protection or fertilizer.

Treatment	Grain yield (t/ha)	Saved grain yield, t/ha, with $N_{(30-60)}P_{(30-60)}K_{(30-60)}$	1,000-kernel weight (g)
Control	5.92	—	44.51
Vitavaks 200 FF (standard)	5.97	0.05	44.14
Maxim Forte 050 FS	6.29	0.37	45.58
Kinto Duo	6.23	0.31	45.44
Inshur Perform FS	6.15	0.23	45.66
Lamardor Pro 180 FS	6.31	0.39	45.92
Lamardor Pro 180 FS + Gaucho 70 WS	6.38	0.46	46.00
Celest Top 312,5 FS	6.16	0.24	46.03
Unta Quadro 373.4 FS	6.25	0.33	44.87
LSD_{05}	—	0.60	0.98

treated with the fungicide Inshur Perform was 0.30 t/ha vs. 6.07 t/ha in the control. A conditional net profit of 332.5 hrn./ha and a profitability of 105% were obtained.

Averaged over the years 2014–15 the use of organic-mineral fertilizers contributed to a considerable increase of grain quality of winter bread wheat. The protein content in grain was 13.2 %; the crude gluten in the flour was 26.0 %; the gluten quality was 72 units of IDG; the flour strength was 212 alveograph units; the bread volume/100-g flour was 700 ml and the total bread-making estimate was 8.3. The protect with an organic-mineral fertilizer application contributed to a considerable increase of protein content in grain by 1.4–1.8 %, the crude gluten in the flour by 3.2–7.2 %. The total bread-making estimate increased up to 8.8 (the level of tendency) in variants with applying tank mixture of Lamardor Pro + Gaucho and also insecticide-fungicide Celest Top and Unta Quadro treatments.

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ITEMS FROM THE UNITED STATES OF AMERICA

COLORADO

COLORADO STATE UNIVERSITY
Wheat Breeding and Genetics Prograom, Department of Soil and Crop Sciences, Ft. Collins, CO 80523, USA.

S.D. Haley, J. Stromberger, E. Hudson-Arns, S. Seifert, T. Anderson, M. Santra, H. Wang, C. Beil, and Z. Afshar.

Wheat breeding and genetics.

The primary goals of the CSU Wheat Breeding and Genetics Program are to 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 conduct research to improve understanding of genetic and environmental factors that affect wheat yield and end-use quality.

Production conditions and cultivar distribution. Total Colorado winter wheat production in 2016 was estimated at 105.12 x 10^6 bushels, a 30% increase from the 2015 crop and 39% higher than the 10-year average. Average grain yield at 48.0 bushels/acre was the highest yield on record, 7% higher than the previous record from 2010 and 38% higher than the 10-year average. The area harvested for grain was estimated at 2.19 x 10^6 acres, equal to the harvested acres in 2015.

Planted acreage estimates of the top 10 cultivars for the 2016 crop were as follows: Byrd – 33.2%, Hatcher – 13.5%, Brawl CL Plus – 9.0%, Snowmass – 6.1%, TAM 111 – 4.0%, Denali – 3.9%, Winterhawk – 3.6%, TAM 112 – 2.1%, SY Wolf – 1.3%, and Antero – 1.2%.

Development of new HRW and HWW cultivars. Field trials in 2016 were successfully harvested at most of our 21 trial locations spread out across Colorado and other states. Trials at the following locations were not harvested due to one reason or another (i.e., hail, field variability, etc): Akron, CO; Genoa, CO; Healy, KS; and Farmington, NM. Overall, trial data were sound and good progress was made for grain yield, stripe rust resistance, and straw strength.

The experimental line CO11D446 was approved for release and will be marketed under the name **Langin**. Langin has shown slightly higher yield than that of Byrd, good drought tolerance, good quality and test weight, and good stripe rust resistance.

Experimental lines CO12D2011, CO14A058, and CO14A065 were advanced toward foundation seed production in autumn 2016 to potentially enable release in autumn 2017. CO12D2011 is a high-yielding HWW with very high test weight, good straw strength and stripe rust resistance, lower polyphenol oxidase (PPO) activity than most other HWW cultivars, and good quality characteristics. CO14A058 and CO14A065 are HRW lines that carry the A- and D-genome quizalofop herbicide tolerance traits.

Nine HWW and seven HRW experimental lines were advanced toward breeder seed production in autumn 2016 to enable advance toward foundation seed production in autumn 2017. All of the lines have shown good yield, stripe rust resistance, and improved straw strength. Each of the HWW lines has shown quality characteristics similar to those of Sunshine or Snowmass; three of these also are being increased in Yuma, AZ. One of the HRW lines is a two-gene Clearfield wheat in a Byrd background.

Sixty-eight experimental lines were advanced toward pre-breeder seed production in autumn 2016 to enable advancement toward breeder seed production in autumn 2017. Eighteen of these are two-gene Clearfield lines, eight are new quizalofop herbicide-tolerant lines, 10 are solid or semi-solid stem lines for wheat stem sawfly resistance, 14 are

HWW lines with quality similar to that of Sunshine or Snowmass, and 13 are conventional HRW lines. The majority of these lines are doubled haploid lines produced by Heartland Plant Innovations (Manhattan, KS) or in our DH lab at CSU. All of the quizalofop herbicide-tolerant lines also are being increased in Yuma, AZ, with both bulk and headrow purification increases.

Application of DNA marker-assisted selection in breeding. DNA marker-assisted selection (MAS) efforts in our program involve two distinct, yet complementary, activities: trait-specific MAS for key traits and next-generation DNA sequencing using genotyping-by-sequencing (GBS). Trait-specific MAS is used to facilitate the transfer of new genes from unadapted germplasm and characterize experimental lines developed in the breeding program. Genotyping-by-sequencing is being used for genomic selection (GS) and genome-wide association analysis (GWAS) to identify important genes.

Trait-specific MAS for transferring new genes currently involves new sources for stem (Ug99) and stripe rust resistance, two new sources for wheat stem sawfly resistance, a new source for zero PPO, and a new source for high amylose wheat (obtained from Arcadia). In autumn 2015 and spring 2016, nearly 800 individual plants were tested with one or more DNA markers. Once the traits are transferred to an elite line or cultivar, we then use these materials in forward-crossing with other lines in the breeding program.

Screening of experimental lines via MAS currently involves screening of all of the lines in our preliminary yield nursery (~1,500 lines/year) and all of the doubled haploid lines generated by our program (~2,000-3,000 lines/year). KASP markers are available, or we have developed our own, for most of the traits we are targeting, including herbicide tolerance (Clearfield and quizalofop), gluten strength, high grain protein content, preharvest sprouting (PHS) tolerance, and multiple disease and insect resistance traits. These activities help us to fully characterize lines that are under testing in field trials.

Since 2011, we have done GBS on 14,734 samples (breeding lines and cultivars); 4,155 of these are currently in the process. In 2016–17, we are going to utilize a new sequencing facility that will double the numbers of marker data-points we receive, which will allow us to double the numbers of lines we are doing for just slightly higher cost. Using these data and data collected in the breeding program, we have successfully implemented GS for a variety of traits, most notably PHS tolerance, stripe rust resistance, and important quality traits. Genomic selection prediction models for more genetically complex traits, such as yield and test weight, show promise and are now being used for rough screening purposes and to help plan new crosses earlier in the breeding cycle.

In 2015–16, we purchased three new equipment items to help increase our DNA marker capacity, a 384-well real-time PCR head for KASP detection, a 384-well liquid handling system, and a 96-well plate freeze-dryer for DNA extraction. We also recently partnered with Stephen Pearce (33% share) on the purchase of a new high-end computer server for improved bioinformatic processing of GBS data and data storage.

Wheat quality improvement. Comprehensive milling and baking quality tests were done on 210 samples from the 2015 state cultivar testing program (UVPT and IVPT). A summary report of these data was included in the *Field Days Edition* of *Making Better Decisions*. Quality ratings of cultivars in the Variety Characteristics Table (in the same report) were updated based on these quality data.

In addition to the cultivar trial samples, comprehensive milling and baking quality tests were done on three locations of the CSU Elite Trial (102 samples) and two locations of the Advanced Yield Nursery (276 samples). Small-scale quality testing (i.e., mixographs, PPO tests, and SRC) was done on 493 samples from the PYN.

Solvent retention capacity (SRC), using water as a solvent, was implemented over the last year to provide a more rapid and accurate assessment of water absorption in our quality lab. Tests conducted in the lab have shown a near-perfect correlation between water–SRC and farinograph water absorption. We are using these data to characterize both HWW and HRW lines in the breeding program. Genomic selection models for water SRC show promise for use in rough, early screening in the breeding program. As we obtain more SRC data on breeding lines, we will conduct GWAS to hopefully identify the genes involved in expression of higher water absorption.

We conducted water SRC testing on 156 samples of a DH population from a cross between Snowmass and Antero. The population also was characterized for presence and absence of the glutenin trait in Snowmass. We demonstrated that the higher water absorption property of Snowmass is not related to the gluten strength trait.

We have implemented a laboratory protocol for whole-grain bake testing. We plan to use this over the coming year with Elite HWW breeding lines to hopefully identify a HWW line more closely resembling Snowmass. We are collaborating with Adam Heuberger to assess flavor and aroma properties of some of these materials.

Russian wheat aphid and wheat stem sawfly resistance. Our work on insect resistance has recently been focused mostly on wheat stem sawfly (WSS) resistance and less on Russian wheat aphid (RWA) resistance. We continue to make crosses and develop lines with resistance to RWA (*Dn7* gene). None of these lines have been advanced beyond the CSU Elite Trial.

Over the last three years, our efforts with WSS resistance have been focused on establishing field trials in the WSS-affected area and transferring the solid-stem trait to Colorado-adapted germplasm as fast as we can. Our efforts with incorporation of the solid-stem trait are being aided by DNA marker-assisted selection and excellent support with solid-stem assessments by Frank Peairs' team.

Three years of field trials at New Raymer have yielded very good results. In 2014 and 2015 we identified one line, CO11D1397, that seemed to show some form of nonsolid-stem resistance, however, this line did very poorly in 2016 and did not show much less stem breakage in response to WSS in our trials and the farmer's surrounding field at New Raymer. This line has thus been discarded from further release consideration.

In 2016, we tested a group of 107 solid or semi-solid stem lines at both New Raymer and Orchard. These lines were all DH lines derived by single backcrosses with Byrd (80 lines) or Antero (27 lines). Severe WSS infestation occurred at New Raymer and somewhat less (though significant) at Orchard. Good data on cutting and yield under sawfly pressure were obtained both locations and 12 lines were advanced for further testing in 2017. Ten of these lines are under preliminary seed increase and testing in the 2017 CSU Elite Trial (two lines lacked sufficient seed for testing in the Elite Trial).

An additional 79 experimental lines were selected from headrows and advanced for testing at both New Raymer and Orchard in 2017. These lines included a separate set of Byrd- and Antero-derived DH (23) lines and the remainder (56) derived from crosses with Judee and Bearpaw. All of these lines showed good stem solidness in headrows in the field and many of the Judee-derived lines showed excellent stripe rust resistance.

Personnel updates. In January 2017, Zaki Afshar joined our program to work on an M.S. degree focusing on disease resistance research in winter wheat.

KANSAS

KANSAS STATE UNIVERSITY
Environmental Physics Group, Department of Agronomy, 2004 Throckmorton Plant Sciences Center, Manhattan, KS 66506-5501, USA.
http://www.agronomy.k-state.edu/people/faculty/kirkham-mb/index.html

Soil chemical properties and growth of cover crops in a dry year.

Oliver W. Freeman II and M.B. Kirkham.

Cover crops are now recommended in rotation cycles to increase soil carbon sequestration (Lal 2014). In the 2016 *Annual Wheat Newsletter* (Vol. 62), we reported the soil chemical changes between the autumn of 2010 and the autumn of 2011 after growing six cover crops at two locations in Kansas; Hutchinson, in the south-central part of the state, and Manhattan, in the northeast. We reported that carbon increased in the soil at Manhattan, but not at Hutchinson, after the growth of the cover crops. However, that period received average amounts of rainfall at both locations. We planted the

cover crops again in the autumn of 2011, but by that time, the soil was dry due to a drought, especially at Hutchinson. Here we report the effects of the drought at Hutchinson on growth of the cover crops in 2011–12. We also report the soil chemical properties pre-planting and post-harvest, which included measurements of pH, organic matter, total nitrogen, and total carbon.

Six cover crops were studied, which were three legumes or alfalfa (*Medicago sativa* L.), Austrian winter pea (*Pisum sativum var. arvense Poir.*), and red clover (*Trifolium pratense* L.), and three non-legumes, which were triticale (X *Triticosecale*; *Triticum* x *Secale*), winter oats (A*vena sativa* L.), and winter wheat (*Triticum aestivum* L.). Areas that had been in fertilizer-intensive no-till cropping systems in the past were selected for the plots, so no fertilizer was added during the experiment.

The cover crops were planted in the autumn of 2011 at two different times, 14 October, 2011, and 20 November, 2011, and the cover crops at the two different planting times were chemically terminated in the spring on 23 April, 2012, and 18 May, 2012, respectively. The soil was a Funmar-Tarver loam (fine-loamy, mixed, superactive, mesic Pachic Argiustolls), and sampled at the 0–30 cm depth on 1 November, 2011, and 6 June, 2012. After the cover crops were killed, the residue was left on the surface of the ground. 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, Kansas.

Starting in January, 2011, drought conditions developed in Hutchinson. Between 1 January, 2011, and 31 December, 2011, rainfall was 31.8 cm below normal. Between 1 January, 2012, and 30 June, 2012, Hutchinson received 10 cm less rain than normal. The seeds of the cover crops were planted into a dry seed bed.

Plots were arranged in a randomized complete block design with four blocks. Cover crops were planted in 6 m x 12 m plots within each block (replication) (six plots in each replication for the six cover crops). Two soil samples from each plot were taken, which gave eight values for each soil measurement (four replications x two soil samples). Freeman (2014) gives the methods for the statistical analyses of the crops.

None of the leguminous cover crops (alfalfa, red clover, or Austrian winter pea) emerged. Only stands of winter oats, triticale, and winter wheat were obtained, and Table 1 shows the dry matter for these cover crops. The lack of emergence of the leguminous cover crops allows comparison of soil with and without cover crops.

Table 1. Cover crop dry matter (kg/ha) of three cover crops that grew at Hutchinson, Kansas, 2011–12. Three leguminous cover crops (alfalfa, red clover, Austrian winter pea) did not emerge due to the dry soil. (Data from Freeman 2014) (Values followed by the same letter are not significantly different ($\alpha = 0.05$)).

Planting date and harvest date	Oats	Triticale	Wheat	Row means
14 October, 2011–23 April, 2012	1,475	1,491	829	1,265 b
20 November, 2011–18 May, 2012	2,470	2,313	1,271	2,018 a
Cover crop means	1,973 a	1,902 a	1,050 b	

We do not know why winter oats, triticale, and winter wheat were able to germinate in dry soil, whereas the leguminous crops could not. These results suggest that the seeds of the non-leguminous crops were better able to germinate and emerge at low soil water potentials than those of the leguminous crops.

Table 2 (p. 73) shows the pH, organic matter, nitrogen, and carbon in the soil sampled in the autumn of 2011 and again in the spring of 2012 after the non-leguminous cover crops were harvested. The pH increased between the autumn of 2011 and the spring of 2012, and the increase occurred both in plots without cover crops and in plots with cover crops. In general, the organic matter, total nitrogen, and total carbon did not change between the autumn of 2011 and the spring of 2012, and this was true both for plots with cover crops and plots without cover crops. The one exception was total nitrogen in the plots with winter wheat. The wheat apparently took up the nitrogen and reduced the nitrogen in the soil to levels below detection (< 0.05% N). These results suggest that nitrogen should have been added to the plots before winter wheat was planted, and if it had been, its dry matter might have increased. Wheat had the lowest dry matter of the three non-leguminous cover crops (Table 1). The one year's growth of the cover crops during the dry year did not increase the soil organic matter or the carbon. These results showed that cover crops did not increase soil carbon in a dry year.

Table 2. The pH, organic matter (OM), nitrogen, and carbon in the 0 to 0.3 m depth of a Funmar-Tarver loam soil at Hutchinson, KS, in the autumn of 2011 before planting of three leguminous and three non-leguminous winter cover crops. Soil again was sampled in the spring of 2012 after the cover crops were harvested. None of the legumes emerged. Only the non-leguminous cover crops produced dry matter. See text for details. The values for soil properties are the averages and standard deviations of eight replications (eight soil samples) († No leguminous cover crop emerged; the soil was bare. ND = not detectable (<0.05% N))

	Leguminous cover crop planted†			Non-leguminous cover crop planted		
Soil property	**Alfalfa**	**Clover**	**Pea**	**Oats**	**Triticale**	**Wheat**
Hutchison, KS, Autumn, 2011						
pH	5.7±0.1	5.8±0.1	5.7±0.1	5.7±0.0	5.6±0.1	5.6±0.1
OM (%)	1.4±0.1	1.3±0.2	1.3±0.1	1.3±0.0	1.3±0.1	1.3±0.1
N (%)	0.07±0.01	0.07±0.00	0.08±0.00	0.07±0.01	0.07±0.01	0.08±0.01
C (%)	0.77±0.01	0.68±0.02	0.75±0.04	0.72±0.06	0.73±0.01	0.71+0.04
Hutchinson, KS, Spring, 2012						
pH	6.2±0.1	6.1±0.1	6.0±0.1	6.0±0.1	6.1±0.1	6.0±0.2
OM (%)	1.5±0.04	1.3±0.1	1.5±0.1	1.4±0.1	1.5±0.0	1.3±0.1
N (%)	0.07±0.00	0.07±0.01	0.10±0.01	0.07±0.01	0.07±0.01	ND
C (%)	0.75±0.04	0.71±0.04	0.77±0.01	0.70±0.02	0.78±0.04	0.67±0.03

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KANSAS STATE UNIVERSITY
The Wheat Genetics Resource Center, Departments of Plant Pathology and the USDA–ARS Hard Red Winter Wheat Genetic Research Unit, Throckmorton Plant Sciences Center, Manhattan, KS 66506-5501, USA.
www.ksu.edu/wgrc

The karyotype of Agropyron cristatum *and its comparison with that of bread wheat using FISH with single-gene probes.*

Mahmoud Said, Eva Hřibová, Jan Vrána, and Jaroslav Doležel (Institute of Experimental Botany, Olomouc, Czech Republic); and Tatiana V. Danilova, Bernd Friebe, and Bikram S. Gill.

Agropyron cristatum L. (2n=2x=14, PP), commonly known as crested wheatgrass, is a wild relative of wheat and an attractive source of novel genes for its improvement. Because alien gene transfer by interspecific hybridization is affected by chromosome colinearity, establishing syntenic relationships between the chromosomes of the donor alien species and wheat is important. To date, identification of all chromosomes of *A. cristatum* is not possible, and its molecular karyotype has not been developed. With the aim of identifying chromosomes of *A. cristatum* by FISH, its genomic DNA was sequenced and several tandem repeats were discovered. Their location on mitotic chromosomes by FISH revealed a specific distribution pattern for six of them. The use of one tandem repeat, together with 45S rDNA as probes for FISH, enabled us to identify all seven chromosomes of *A. cristatum*. In order to analyze the structure and homoeology of *A. cristatum* chromosomes, 42 FLcDNA from the seven chromosome groups of wheat were localized by FISH on chromosomes of crested wheatgrass cv. Parkway. Important structural rearrangements were observed for chromosomes 2P, 4P, 6P, and 7P, whereas no major rearrangements were detected for the remaining three chromosomes. The results of this work provide new insights into the genome evolution within the tribe Triticeae and will facilitate the use of crested wheatgrass in alien introgression breeding of bread wheat. [P0297]

Towards the map-based cloning of the C locus in hexaploid wheat.

Vijay K. Tiwari and Nidhi Rawat (Department of Plant Science and Landscape Architecture, University of Maryland, College Park, MD 20742, USA); Nathan Meier, Anupama Joshi, Bikram S. Gill, and Jesse Poland; Jeffrey M. Leonard (Department of Crop and Soils Scineces, Oregon State University, Corvallis, OR 97331, USA); Raju Datla, Daoquan Xiang, Teagen Quilichini, and Prakash Venglat (National Research Council Canada, Saskatoon, SK, Canada); and Shichen Wang (Genomics and Bioinformatics Services, Texas A&M University, College Station, TX).

The *C* locus, an important gene mapped on chromosome 2D of wheat, is responsible for compact spike and reduced plant height in hexaploid wheat. The *C* locus also is known as the compactum locus, and it has a pleiotropic effect on many traits because it affects spike morphology and grain size, shape, and number, directly or indirectly affecting the agronomic performance of wheat. Genetic analysis and molecular characterization of the *C* locus is needed to understand the underlying mechanism. A limited number of mapping studies were conducted on this trait, and the exact chromosomal location was ambiguous. Using radiation hybrid (RH) and genetic mapping, we placed the *C* locus in the centromeric part of wheat chromosome 2DS. High-resolution RH and genetic mapping refined the C locus to a 230-Kb region, whose annotation indicated seven putative candidate genes. We performed RNAseq of a control and a compactum line at three

different stages of spike development and, based on differential gene expression data, we retained four genes for further studies. These four genes are being tested for candidacy of the *C* locus. [P0870]

Homoeologous recombination-based transfer of the wheat streak mosaic and Triticum mosaic virus resistance gene Wsm3 from Thinopyrum intermedium to wheat.

Tatiana V. Danilova, Bernd Friebe, and Bikram S. Gill; and Guorong Zhang (Kansas Agricultural Experiment Station, Hays, KS).

Wheat streak mosaic, caused by a virus (WSMV), is an important disease of bread wheat worldwide. To date, only three genes conferring resistance to WSMV have been named and two, *Wsm1* and *Wsm3*, were derived from the distantly related wild relative *Th. intermedium*. *Wsm3* is only available in the form of the compensating wheat–*Th. intermedium* whole-arm Robertsonian translocation T7BS·7S#3L. Whole-arm alien transfers usually suffer from linkage drag, which prevents their use in cultivar improvement. We used *ph1b*-induced homoeologous recombination to shorten the *Th. intermedium* segment and recover a recombinant chromosome consisting of the short arm of wheat chromosome 7B, part of the long arm of 7B, and the distal 43% of the long arm derived from the *Th. intermedium* chromosome arm 7S#3L. The recombinant chromosome T7BS·7BL-7S#3L confers resistance to WSMV at 18ºC and 24ºC and also confers resistance to *Triticum* mosaic virus, but only at 18ºC. *Wsm3* is the only gene conferring resistance to WSMV at a high temperature of 24ºC. We also developed a user-friendly molecular marker that will allow to monitor the transfer of *Wsm3* in breeding programs. *Wsm3* is presently being transferred to adapted hard red winter wheat cultivars and can be used directly in wheat improvement. [P0897]

Recurrent activation of a latent centromere in the pericentromeric region of maize chromosome 3.

Hainan Zhao, Zixian Zeng, and Jiming Jiang (University of Wisconsin-Madison, Madison, WI); Dal-Hoe Koo and Bikram S. Gill; Fangpu Han (Chinese Academy of Sciences, Beijing, China); and James A. Birchler (University of Missouri, Columbia, MO).

In most eukaryotes, centromere identity is determined by the presence of nucleosomes containing CENH3, a centromere-specific histone H3 variant. New centromeres can form de novo at noncentromeric regions, which are known as neocentromeres. Some chromosomal regions are prone to neocentromere formation, suggesting that neocentromere activation is nonrandom process. However, the determinants of neocentromere formation have remained elusive. We discovered that a pericentromeric region of maize chromosome 3, 2 Mb from the centromere (Cen3) underwent at least three independent neocentromere activation events. We analyzed the genomic and epigenomic features associated with Cen3, the neocentromeres, and an inactivated centromere of an ancestral chromosome 3. We find that the neocentromeric region lacks genes and is associated with low levels of transcription and relatively high levels of DNA methylation. These genomic and epigenomic features may provide a favorable chromatin environment for recurrent neocentromere activation. [W397]

Major, structural, genomic alterations are associated with hybrid speciation in Aegilops markgrafii (Triticeae).

Tatiana V. Danilova, Alina Akhunova, Eduard Akhunov, Bikram S. Gill, and Bernd Friebe.

Most grasses of the Triticeae tribe have syntenic chromosomes, except for a few species with rearranged genomes. *Aegilops markgrafii* (2n=14), a diploid wild relative of wheat, has highly asymmetrical chromosomes indicative of many chromosomal rearrangements that reshaped its genome. Molecular cytogenetics and next-generation sequencing were used to explore genome organization and speciation. We applied fluorescence in situ hybridization (FISH) with a set of 101 physically mapped wheat cDNA markers to establish the *Ae. markgrafii* chromosome macrostructure and homoeologous relationships. Two chromosomes were colinear and maintained cross-genome synteny, whereas the rest were highly rearranged as a result of inter- and intrachromosomal translocations and inversions. Location of near-centromeric cDNAs and centromeric repeats showed that the centromeres were not involved in rearrangements. To investigate the relationship between chromosomal alterations and the patterns of molecular evolution in the rearranged fractions of the *Ae.*

markgrafii chromosomes, we characterized the genome using shallow, whole-genome, shotgun sequencing and whole-exome capture. The composition of transposable elements was established and their distribution along the chromosomes was studied by FISH. The pattern of some dispersed repeats reflected the chromosomal rearrangements and differentiated chromosomal blocks with diverse phylogenetic affinity. Comparative analysis of *Ae. markgrafii*, barley, and hexaploid wheat orthologous gene sequences revealed rearranged chromosomal blocks with different levels of sequence divergence suggesting their origin from different parental genomes associated with hybrid speciation. [W976]

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

Marsha Boswell.

Kansas Hard Red Winter Wheat Tour 2017.

Day 1: Too early to know full extent of damage. *It's too early to tell* was the theme of day 1 of the 2017 Wheat Quality Council's Hard Winter Wheat Tour across Kansas. About 70 scouts left Manhattan early Tuesday morning, 2 May, and made their way east to west across the state, ending up in Colby by evening. The average yield for the day between 18 cars and 222 stops was 43 bushels/acre, down from 47.1 bushels/acre over the same area last year.

The wheat looked good early in the day, with adequate moisture and very little disease pressure or damage. But as the cars made their way into central Kansas, participants started seeing some of the effects of the 22–23 April and 27 April freezes that affected a big portion of the middle of the state. These freeze events were overshadowed in the news by a blizzard that affected the western third of the state over the weekend of 29 April through 1 May.

However, the freezes may cause significant damage in many areas because the crop was in boot and early heading stages at the time. The extent of that damage will not fully show until a week to 10 days following the event. Scouts reported that more than half of the wheat they saw on day 1 was in the boot stage and 39% was headed. According to the National Agricultural Statistics Service, as of 30 April, 44% of the wheat was headed statewide.

Wheat tour scouts also noted some disease pressure in central parts of the state, including stripe rust, which is a devastating fungal disease.

Kansas Wheat CEO Justin Gilpin recommends that farmers invest in fungicides to control the rust issues. Some wheat across the state, especially later maturity and wheat after soybeans, has good yield potential. Farmers were encouraged to work with their crop consultants and consider applying a fungicide.

Throughout the state, tour participants noted a lot of mud, but as the groups headed farther west, they ran into fields with snow cover, beginning around Norton and Graham counties. They noted additional disease pressure, most significantly wheat streak mosaic virus, barley yellow dwarf virus, and leaf rust and stripe rust, and also noticed some nitrogen deficiency and some aphids, as evidenced by beneficial ladybugs.

The weight of the weekend's heavy snow laid the wheat over on its side, which is something the wheat can likely recover from if the stems aren't broken. With snow still covering many of the fields, it's too early to estimate what percentage of the plants have irreparable damage.

This loss of a portion of the crop comes at a tough time for wheat farmers. The ag economy is not faring well, and bushels are a necessity to offset low prices. A weather-related crop disaster forces these Kansas food producers to rely on the strong farm safety net that is provided by crop insurance in the farm bill.

Farmers should note that if your wheat crop was affected by any of the freeze or snow events, it's critical to notify your crop insurance agent as soon as possible, even if you aren't able to fully evaluate its true damage or recovery potential.

According to Walter V.M. Filho of Serra Morena Corretora, an import/export company in São Paulo, Brazil, the world has a deluge of wheat, but America has the best baking wheat, which is something that people need to realize.

The wheat tour is not only about evaluating the wheat throughout the state, but also about developing relationships with other participants. Mr. VM Filho has been on the tour many times and continues to come back, not only to learn about the quality of the current crop but also to strengthen business relationships with friends and colleagues.

Day two of the 2017 Wheat Quality Council's Hard Winter Wheat Tour across Kansas started off slowly, as scouts were not able to evaluate many of the fields in the western third of the state.

About 70 scouts left Colby early Wednesday morning, 3 May, and made their way south and east across the state, ending up in Wichita by evening. The average yield for the day between 18 cars and 205 stops was 46.9 bushels/acre; which is down from 49.3 bushels/acre over the same area last year.

Even before winter storm Ursa crippled the western third of the state over this past weekend, the wheat was struggling. Wheat streak mosaic virus (WSMV) had already moved into the area, spread by the wheat curl mite, which uses volunteer wheat as a green bridge to move into newly emerging wheat. Because of the economy, there was not as much money for controlling volunteer wheat last autumn.

According to K-State agronomy specialist Jeanne Falk-Jones, there were plenty of green bridges because there was not a lot of money in wheat budgets last year, so when it comes to paying to control volunteer wheat, there was not as much.

Weather conditions started off with adequate moisture at the start of the season but went downhill after the beginning of October, so there were poor stands in many fields.

WSMV was really bad in the western two tiers of counties according to Kansas Wheat's Aaron Harries, VP of Research and Operations, whcih was a big problem for the 2017 crop and will probably have a lot more impact on yield than the snow damage even would, a serious concern. At this point in the year, there is nothing producers can do for WSMV. Producers are at the mercy of the disease, and will have to wait and see how much it cuts back yield. In some cases, some fields were destroyed because the insurance had already zeroed out those fields. It is all about controlling volunteer wheat in the autumn. From a research standpoint, the Kansas Wheat Commission is putting some big funding into projects with Kansas State University to develop genetic resistance, and there is some good, new genetic resistance, but it will take a couple more years to get that crossed into the cultivars that exist in the marketplace.

The tour provides a formula to use and a component of that formula is the row space and height of the wheat plant and being able to count the number of stalks or heads in 1 foot. In the area where snow had flattened the wheat, that can not be done, so no estimate yields were made on those fields. Rather, they were observed and notes taken with no way to accurately determine a yield, which would only be a guess. Those fields were not included in the average for western Kansas. Thus, the estimates may be skewed a little bit toward central Kansas, but most of the participants will take that into consideration when they submit their estimates.

Tthe snow disappeared in Hodgeman County to the east and Meade County to the south, and scouts were able to start making yield assessments. The wheat in south-central Kansas looks really good, there is obviously plenty of moisture. Most of the fields were pretty clean. Yields might not be quite as high just because some of the stands are a little thinner. Some fields are projected to be above 70 bushels/acre. Freeze damage is hard to determine, and it is still a little bit early to see the impact of the freeze about a week ago. The biggest disease issue in south-central Kansas was barley yellow dwarf and some reports of rust. However, if the weather dries out and warms up rust may become more common.

The 2017 Wheat Quality Council's Hard Winter Wheat Tour across Kansas wrapped up on 4 May, as scouts traveled from Wichita to Manhattan. The 3-day average over the fields that were calculated was 46.1 bushels/acre. Whereas an estimated 7.4×10^6 acres of wheat were planted in the autumn, tour participants saw many areas where disease, damage from snow, and freeze damage may eliminate those fields, which was accounted for in the final estimates.

The official tour projection for total production numbers of hard red winter wheat to be harvested in Kansas is 281,707,913 bushels. If realized, this would be 185×10^6 bushels less than the 2016 crop. This number is calculated based on the average of estimated predictions from tour participants who gathered information from 469 fields across the state. The number of stops was down significantly from 655 fields during the 2016 tour, primarily due to snow cover in the western third of the state, where tour scouts were not able to take calculations.

The tour provides a formula and a component of that formula is row space, the height of the wheat plant, and being able to count the number of stalks or heads in one foot. In the area where snow had flattened the wheat, that is not possible. So the decision was made not to try to estimate yields on those fields. Rather, they were looked at and notes taken, because there is no way to accurately determine a yield. Because it would only be a guess, those fields were not included in the average for western Kansas. Some fields where those parameters could be determined were used as part of the average.

The Hard Winter Wheat tour is sponsored by the Wheat Quality Council. This year's tour hosted 70 participants from five countries and 24 states in 18 vehicles traveling across the state on six routes. When winter storm Ursa crippled the western third of the state over one weekend, there was no way to delay the tour. Instead, tour participants made observations as a snapshot in time, but the industry will continue to watch what happens in central parts of the state with potential freeze damage and how the wheat responds once the snow in western Kansas melts.

MINNESOTA

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

J.A. Kolmer, Y. Jin, and M.E. Hughes.

Wheat Rusts in the United States in 2016.

Wheat stem rust (caused by *Puccinia graminis* f. sp. *tritci*). Wheat stem rust was neither widespread nor severe in the U.S. in 2016 with the exception of Louisiana where stem rust was widespread near the end of the season. Wheat stem rust was only reported in Texas, Louisiana, Mississippi, Georgia, Illinois, Indiana, New York, and Washington. Wheat stem rust was first reported in sentinel plots in extreme southern Texas the first week of March. Race QFCSC is the only race identified from collections processed to date. Race QFCSC was the most commonly identified wheat stem rust race in the U.S. the last decade.

Wheat leaf rust (caused by *Puccinia triticina*). Wheat leaf rust was widespread from the east coast, to the Great Lakes States, and in the Great Plains from Texas to North Dakota in 2016. Although wheat leaf rust was generally found at low to moderate levels, it did develop to significant levels in areas of the Great Plains and mid-Atlantic states. In Oklahoma, a 5% loss due to leaf rust was estimated, followed by losses of 3% in Virginia, 2% in Texas, 2% in Wisconsin, and 1% or less in all other states.

Wheat stripe rust (caused by *Puccina striiformis* f. sp. *tritici*). Wheat stripe rust was very widespread across the U.S. in 2016, with reports from 31 states and four Canadian provinces, which was the widest distribution in the U.S. since 2010. In many areas, the application of fungicides and use of resistant cultivars mitigated the heavy stripe rust disease pressure.

A complete summary of wheat rusts in the U.S. for the 2016 crop season can be found at:
https://www.ars.usda.gov/ARSUserFiles/50620500/Cerealrustbulletins/16CRBFIN.pdf

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2016 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1, Lr2a, Lr2c, Lr3, Lr9, Lr16, Lr24, Lr26, Lr3ka, Lr11, Lr17, Lr30, LrB, Lr10, Lr14a, Lr18, Lr21, Lr28, Lr39,* and *Lr42*.

Race	Virulence combination (ineffective Lr genes)	Southeast		Northeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
MBBJG	1,3,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
MBDSB	1,3,17,B,10,14a	1	1.0	0	0.0	0	0.0	2	2.1	0	0.0	1	0.8	0	0.0	4	0.8
MBDSD	1,3,17,B,10,14a,39	1	1.0	0	0.0	1	1.7	14	14.6	27	28.1	25	20.8	0	0.0	68	13.7
MBPSB	1,3,3ka,17,30,B,10, 14a	2	2.0	0	0.0	0	0.0	9	9.4	0	0.0	0	0.0	0	0.0	11	2.2
MBTNB	1,3,3ka,11,17,30,B, 14a	34	34.3	4	18.2	43	72.9	0	0.0	4	4.2	3	2.5	0	0.0	88	17.7
MBTSB	1,3,3ka,11,17,30,B, 10,14a	3	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	0.6
MCDSB	1,3,26,17,B,10,14a	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
MCDSD	1,3,26,17,B,10,14a,39	0	0.0	1	4.5	0	0.0	1	1.0	0	0.0	1	0.8	0	0.0	3	0.6
MCGJG	1,3,26,11,10,14a,28	0	0.0	1	4.5	0	0.0	0	0.0	0	0.0	2	1.7	0	0.0	3	0.6
MCPSB	1,3,26,3ka,17,30,B,10, 14a	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2016 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, *Lr39*, and *Lr42*.

Race	Virulence combination (ineffective Lr genes)	Southeast		Northeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
MCPSD	1,3,26,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0.0	0	0.0	3	3.1	2	1.7	0	0.0	5	1.0
MCTNB	1,3,26,3ka,11,17,30,B,14a	14	14.1	0	0.0	5	8.5	1	1.0	2	2.1	0	0.0	0	0.0	22	4.4
MCTQB	1,3,26,3ka,11,17,30,B,10	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MCTSB	1,3,26,3ka,11,17,30,B,10,14a	2	2.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
MDBJG	1,3,24,10,14a,28	0	0.0	8	36.4	0	0.0	0	0.0	0	0.0	4	3.3	0	0.0	12	2.4
MDDSB	1,3,24,17,B,10,14a	0	0.0	1	4.5	0	0.0	0	0.0	0	0.0	2	1.7	0	0.0	3	0.6
MDJSB	1,3,24,11,17,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
MDMJG	1,3,24,3ka,30,10,14a,28	0	0.0	2	9.1	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	3	0.6
MDNSN	1,3,24,3ka,17,B,10,14a,21,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	1.7	0	0.0	2	0.4
MDTSB	1,3,24,3ka,11,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
MFGJG	1,3,24,26,11,10,14a,28	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MFPSB	1,3,24,26,3ka,17,30,B,10,14a	0	0.0	1	4.5	0	0.0	0	0.0	1	1.0	4	3.3	0	0.0	6	1.2
MGPSB	1,3,16,3ka,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	2	2.1	0	0.0	0	0.0	0	0.0	2	0.4
MGPSD	1,3,16,3ka,17,30,B,10,14a,39	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MJBJG	1,3,16,24,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	10	8.3	0	0.0	10	2.0
MJDSB	1,3,16,24,17,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
MJMGJ	1,3,16,24,3ka,30,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
MLDSB	1,3,9,17,B,10,14a	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MLDSD	1,3,9,17,B,10,14a,39	1	1.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	2	0.4
MLJSD	1,3,9,11,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
MLPSD	1,3,9,3ka,17,30,B,10,14a,39	2	2.0	0	0.0	0	0.0	9	9.4	11	11.5	2	1.7	0	0.0	24	4.8
MMDSD	1,3,9,26,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
MMNSD	1,3,9,26,3ka,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
MMPSD	1,3,9,26,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0.0	8	8.3	4	4.2	0	0.0	0	0.0	12	2.4
MNDSD	1,3,9,24,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	1	1.0	1	1.0	0	0.0	0	0.0	2	0.4
MNKSB	1,3,9,24,11,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
MNMPS	1,3,9,24,3ka,30,B,14a,18,21,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
MNPSD	1,3,9,24,3ka,17,30,B,10,14a,39	3	3.0	0	0.0	0	0.0	8	8.3	15	15.6	7	5.8	0	0.0	33	6.7
MPPSD	1,3,9,24,26,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0.0	4	4.2	4	4.2	2	1.7	0	0.0	10	2.0
MPTSD	1,3,9,24,26,3ka,11,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
PBDGG	1,2c,3,17,10,28	0	0.0	4	18.2	1	1.7	0	0.0	0	0.0	0	0.0	3	75.0	8	1.6
PBDGJ	1,2c,3,17,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2016 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, *Lr39*, and *Lr42*.

Race	Virulence combination (ineffective Lr genes)	Southeast		Northeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
PBDJJ	1,2c,3,17,10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	2	2.1	0	0.0	0	0.0	2	0.4
PBDQG	1,2c,3,17,B,10,28	0	0.0	0	0.0	2	3.4	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
PBDQJ	1,2c,3,17,B,10,28,39	0	0.0	0	0.0	0	0.0	1	1.0	7	7.3	0	0.0	1	25.0	9	1.8
PBJQJ	1,2c,3,11,17,B,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	1	0.2
PCJQG	1,2c,3,26,11,17,B,10,28	0	0.0	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	1	0.2
TBBGJ	1,2a,2c,3,10,28,39	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
TBBGS	1,2a,2c,3,10,21,28,39	0	0.0	0	0.0	0	0.0	2	2.1	0	0.0	9	7.5	0	0.0	11	2.2
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	2	1.7	0	0.0	3	0.6
TBRKJ	1,2a,2c,3,3ka,11,30,10,14a,18,28,39	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TBTNB	1,2a,2c,3,3ka,11,17,30,B,14a	4	4.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	4	0.8
TCGKG	1,2a,2c,3,26,11,10,14a,18,28	0	0.0	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	1	0.2
TCRFG	1,2a,2c,3,26,3ka,11,30,14a,18,28	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	12	12.1	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	13	2.6
TCTKG	1,2a,2c,3,26,3ka,11,17,30,10,14a,18,28	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TCTNB	1,2a,2c,3,26,3ka,11,17,30,B,14a	3	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	0.6
TCTSB	1,2a,2c,3,26,3ka,11,17,30,B,10,14a	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TDBJQ	1,2a,2c,3,24,10,14a,21,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	5	4.2	0	0.0	5	1.0
TDRJG	1,2a,2c,3,24,3ka,11,30,10,14a,28	1	1.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TDTSB	1,2a,2c,3,24,3ka,11,17,30,B,10,14a	2	2.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TFBJJ	1,2a,2c,3,24,26,10,14a,28,39	0	0.0	0	0.0	0	0.0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
TFBJQ	1,2a,2c,3,24,26,10,14a,21,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	4	3.3	0	0.0	4	0.8
TFPSB	1,2a,2c,3,24,26,3ka,17,30,B,10,14a	0	0.0	0	0.0	3	5.1	0	0.0	0	0.0	0	0.0	0	0.0	3	0.6
TFTSB	1,2a,2c,3,24,26,3ka,11,17,30,B,10,14a	0	0.0	0	0.0	3	5.1	0	0.0	0	0.0	0	0.0	0	0.0	3	0.6
TLPSD	1,2a,2c,3,9,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
TNBGJ	1,2a,2c,3,9,24,10,28,39	5	5.1	0	0.0	0	0	8	8.3	5	5.2	4	3.3	0	0.0	22	4.4
TNBJJ	1,2a,2c,3,9,24,10,14a,28,39	1	1.0	0	0.0	0	0	14	14.6	2	2.1	18	15.0	0	0.0	35	7.1
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,14a,28,39	0	0.0	0	0.0	0	0	1	1.0	0	0.0	0	0.0	0	0.0	1	0.2
TPBGJ	1,2a,2c,3,9,24,26,10,28,39	0	0.0	0	0.0	0	0	0	0.0	4	4.2	2	1.7	0	0.0	6	1.2
TPDGJ	1,2a,2c,3,9,24,26,17,10,28,39	0	0.0	0	0.0	0	0	0	0.0	0	0.0	1	0.8	0	0.0	1	0.2
Total		99		22		59		96		96		120		4		496	

Table 2. Number and frequency (%) of isolates of *Puccinia triticina* in the United States in 2016 virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance gene	Southeast		Northeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		WA		Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	99	100.0	22	100.0	59	100.0	96	100.0	96	100.0	120	100.0	4	100.0	496	100.0
Lr2a	33	33.3	0	0.0	6	10.2	28	29.2	13	13.5	45	37.5	0	0.0	125	25.2
Lr2c	33	33.3	4	18.2	9	15.3	29	30.2	24	25.0	46	38.3	4	100.0	149	30.0
Lr3	99	100.0	22	100.0	59	100.0	96	100.0	96	100.0	120	100.0	4	100.0	496	100.0
Lr9	13	13.1	0	0.0	0	0.0	59	61.5	46	47.9	38	31.7	0	0.0	156	31.5
Lr16	1	1.0	0	0.0	0	0.0	2	2.1	0	0.0	12	10.0	0	0.0	15	3.0
Lr24	13	13.1	12	54.5	6	10.2	39	40.6	32	33.3	71	59.2	0	0.0	173	34.9
Lr26	35	35.4	3	13.6	12	20.3	20	20.8	21	21.9	18	15.0	0	0.0	109	22.0
Lr3ka	88	88.9	7	31.8	55	93.2	47	49.0	45	46.9	27	22.5	0	0.0	269	54.2
Lr11	81	81.8	5	22.7	52	88.1	5	5.2	10	10.4	9	7.5	0	0.0	162	32.7
Lr17	76	76.8	11	50.0	59	100.0	69	71.9	83	86.5	56	46.7	4	100.0	358	72.2
Lr30	88	88.9	7	31.8	55	93.2	46	47.9	45	46.9	26	21.7	0	0.0	267	53.8
LrB	75	75.8	7	31.8	58	98.3	69	71.9	81	84.4	55	45.8	1	25.0	346	69.8
Lr10	43	43.4	18	81.8	11	18.6	95	99.0	90	93.8	116	96.7	4	100.0	377	76.0
Lr14a	94	94.9	18	81.8	55	93.2	84	87.5	78	81.3	102	85.0	0	0.0	431	86.9
Lr18	16	16.2	0	0.0	0	0.0	0	0.0	2	2.1	3	2.5	0	0.0	21	4.2
Lr21	0	0.0	0	0.0	0	0.0	2	2.1	0	0.0	21	17.5	0	0.0	23	4.6
Lr28	24	24.2	15	68.2	3	5.1	28	29.2	24	25.0	66	55.0	4	100.0	164	33.1
Lr39	15	15.2	1	4.7	1	1.7	79	82.3	86	89.6	78	65.0	1	25.0	261	52.6
Lr42	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Total	99		22		59		96		96		120		4		496	

Table 3. Estimated small grain losses due to rust in 2016 (T = trace (less than 1% loss statewide); — no state estimates available; Kansas losses are preliminary 2016 wheat disease loss estimates. USA Total does not include states for which loss or production data is not available).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
Alabama	170	70.0	11,900	—	—	—	—	—	—
Arizona	7	95.0	665	—	—	—	—	—	—
Arkansas	115	54.0	6,210	0	0	T	T	1	63
California	170	78.0	13,260	—	—	—	—	—	—
Colorado	2,190	48.0	105,120	0	0	0	0	5	5,533
Delaware	65	67.0	4,355	0	0	T	T	1	44
Florida	17	30.0	510	—	—	—	—	—	—
Georgia	110	46.0	5,060	0	0	1	38	0	0
Idaho	710	94.0	66,740	0	0	0	0	6	4,260
Illinois	470	74.0	34,780	—	—	—	—	—	—
Indiana	280	81.0	22,680	0	0	1	229	3	701
Iowa	17	63.0	1,071	—	—	—	—	—	—
Kansas	8,200	57.0	467,400	0	0	1	6,156	9	46,791
Kentucky	400	80.0	32,000	0	0	T	T	5	1,684
Louisiana	20	45.0	900	T	T	1	9	T	T
Maryland	260	64.0	16,640	—	—	—	—	—	—
Michigan	570	89.0	50,730	0	0	T	T	3	1,301
Minnesota	8	61.0	488	0	0	1	5	3	15
Mississippi	50	48.0	2,400	0	0	T	T	T	T
Missouri	570	70.0	39,900	0	0	T	T	—	—
Montana	2,150	49.0	105,350	0	0	0	0	3	3,258
Nebraska	1,310	54.0	70,740	0	0	T	T	7	5,325
Nevada	6	75.0	450	—	—	—	—	—	—
New Jersey	21	64.0	1,344	—	—	—	—	—	—
New Mexico	205	22.0	4,510	—	—	—	—	—	—

Table 3. Estimated small grain losses due to rust in 2016 (T = trace (less than 1% loss statewide); — no state estimates available; Kansas losses are preliminary 2016 wheat disease loss estimates. USA Total does not include states for which loss or production data is not available).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
New York	115	74.0	8,510	—	—	—	—	—	—
North Carolina	355	41.0	14,555	0	0	1	147	1	147
North Dakota	120	48.0	5,760	0	0	0	0	1	58
Ohio	560	80.0	44,800	—	—	—	—	—	—
Oklahoma	3,500	39.0	136,500	0	0	5	7,184	18	29,963
Oregon	710	50.0	35,500	0	0	0	0	T	T
Pennsylvania	150	68.0	10,200	—	—	—	—	—	—
South Carolina	50	43.0	2,150	0	0	0	0	0	0
South Dakota	1,100	58.0	63,800	T	T	T	T	7	4,802
Tennessee	335	73.0	24,455	0	0	T	T	T	T
Texas	2,800	32.0	89,600	0	0	2	1,829	12	12,218
Utah	112	60.0	6,720	—	—	—	—	—	—
Virginia	175	53.0	9,275	0	0	3	238	T	T
Washington	1,670	78.0	130,260	0	0	0	0	2	1,984
West Virginia	4	61.0	244	—	—	—	—	—	—
Wisconsin	250	79.0	19,750	T	T	2	403	8	1,601
Wyoming	125	34.0	4,250	—	—	—	—	—	—
USA % Loss				T		1.0		7.2	
USA Total	30,222	55.3	1,671,532.0		T		16,238		119,749

Table 4. Estimated losses in spring and durum wheat due to rust in 2016 (T = trace (less than 1% loss statewide), — = no state estimate available, USA Total does not include states for which loss or production data is not available).

SPRING WHEAT

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
Colorado	10	88.0	880	0	0	0	0	T	T
Idaho	395	87.0	34,365	0	0	0	0	4	1,432
Minnesota	1,260	59.0	74,340	0	0	1	743	2	1,517
Montana	2,110	36.0	75,960	0	0	0	0	1	767
Nevada	3	67.0	201	—	—	—	—	—	—
North Dakota	5,850	46	269,100	0	0	T	T	1	2,718
Oregon	87	51.0	4,437	0	0	0	0	0	0
South Dakota	1,050	45.0	47,250	T	T	T	T	5	2,487
Utah	8	58.0	464	—	—	—	—	—	—
Washington	530	51.0	27,030	0	0	0	0	2	552
USA % Loss				T		0.1		1.8	
USA Total	11,303	47.2	534,027		T		743		9,473

DURUM WHEAT

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
Arizona	96	98.0	9,408	—	—	—	—	—	—
California	47	86.0	4,042	—	—	—	—	—	—
Idaho	10	75.0	750	0	0	0	0	0	0
Montana	765	41.0	31,365	0	0	0	0	1	317
North Dakota	1,440	40.5	58,320	0	0	0	0	0	0
South Dakota	7	33.0	231	—	—	—	—	—	—
USA % Loss				0		0		0.3	
USA Total	2,365	44.0	104,116		0		0		317

Table 5. Estimated losses in barley, rye, and oat due to rust in 2016 (T = trace (less than 1% loss statewide), — = no state estimate available, NA = data not available, USA Total does not include states for which loss or production data is not available).

BARLEY

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
Arizona	15	128.0	1,920	—	—	—	—	—	—
California	55	75.0	4,125	—	—	—	—	—	—
Colorado	74	129.0	9,546	0	0	0	0	T	T
Delaware	25	76.0	1,900	—	—	—	—	—	—
Idaho	580	107.0	62,060	0	0	0	0	T	T
Kentucky	NA	NA	NA	0	0	T	T	0	0
Maryland	34	72.0	2,448	—	—	—	—	—	—
Michigan	NA	NA	NA	0	0	0	0	0	0
Minnesota	79	66.0	5,214	0	0	0	0	0	0
Montana	780	60.0	46,800	0	0	0	0	T	T
North Dakota	640	67.0	42,880	0	0	0	0	0	0
Oregon	32	67.0	2,144	0	0	T	T	T	T
Pennsylvania	38	75.0	2,850	—	—	—	—	—	—
South Dakota	NA	NA	NA	0	0	0	0	0	0
Utah	19	82.0	1,558	—	—	—	—	—	—
Virginia	12	67.0	804	0	0	5	38	0	0
Washington	93	77.0	7,161	0	0	T	T	0	0
Wisconsin	NA	NA	NA	T	T	1	NA	T	T
Wyoming	82	96.0	7,872	—	—	—	—	—	—
USA % Loss				T		0.019		T	
USA Total	2,558	77.9	199,282		T		38		T

RYE

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
Georgia	30	21.0	630	—	—	—	—		
Illinois	NA	NA	NA	—	—	—	—		
Kansas	NA	NA	NA	—	—	—	—		
Kentucky	NA	NA	NA	0	0	0	0		
Maine	NA	NA	NA	—	—	—	—		
Maryland	NA	NA	NA	—	—	—	—		
Michigan	NA	NA	NA	0	0	0	0		
Minnesota	NA	NA	NA	—	—	—	—		
Nebraska	NA	NA	NA	—	—	—	—		
New Jersey	NA	NA	NA	—	—	—	—		
New York	NA	NA	NA	—	—	—	—		
North Carolina	NA	NA	NA	0	0	0	0		
North Dakota	NA	NA	NA	0	0	T	T		
Oklahoma	75	25.0	1,875	—	—	—	—		
Pennsylvania	NA	NA	NA	—	—	—	—		
South Carolina	NA	NA	NA	0	0	0	0		
South Dakota	NA	NA	NA	—	—	—	—		
Texas	NA	NA	NA	—	—	—	—		
Virginia	NA	NA	NA	—	—	—	—		
Wisconsin	NA	NA	NA	T	T	T	T		
Other states	309	35.4	10,946	—	—	—	—		
USA % Loss				T		T			

Table 5. Estimated losses in barley, rye, and oat due to rust in 2016 (T = trace (less than 1% loss statewide), — = no state estimate available, NA = data not available, USA Total does not include states for which loss or production data is not available).

OAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
Alabama	20	55.0	1,100	—	—	—	—		
Arkansas	8	73.0	584	—	—	—	—		
California	11	65.0	715	—	—	—	—		
Colorado	10	80.0	800	—	—	—	—		
Georgia	15	58.0	870	0	0	9	86		
Idaho	15	83.0	1,245	0	0	0	0		
Illinois	20	81.0	1,620	—	—	—	—		
Indiana	NA	NA	NA	0	0	0	0		
Iowa	43	76.0	3,268	—	—	—	—		
Kansas	30	57.0	1,710	—	—	—	—		
Kentucky	NA	NA	NA	0	0	T	T		
Louisiana	NA	NA	NA	0	0	5	NA		
Maine	24	71.0	1,704	—	—	—	—		
Michigan	30	58.0	1,740	0	0	0	0		
Minnesota	120	68.0	8,160	T	T	3	252		
Mississippi	NA	NA	NA	0	0	T	T		
Missouri	19	60	1,140	—	—	—	—		
Montana	28	47.0	1,316	—	—	—	—		
Nebraska	25	60.0	1,500	—	—	—	—		
New York	60	55.0	3,300	—	—	—	—		
North Carolina	9	60.0	540	0	0	T	T		
North Dakota	110	66.0	7,260	1	73	3	225		
Ohio	25	74.0	1,850	—	—	—	—		
Oklahoma	8	43.0	344	—	—	—	—		
Oregon	10	90.0	900	—	—	—	—		
Pennsylvania	50	67.0	3,350	—	—	—	—		
South Carolina	7	46.0	322	0	0	2	7		
South Dakota	110	82.0	9,020	0	0	15	1,592		
Texas	60	50.0	3,000	0	0	T	T		
Utah	NA	NA	NA	—	—	—	—		
Virginia	NA	NA	NA	—	—	—	—		
Washington	7	61.0	427	—	—	—	—		
Wisconsin	100	66.0	6,600	T	T	1	67		
Wyoming	7	55.0	385	—	—	—	—		
USA % Loss				0.11		3.4			
USA Total	981	66.0	64,770		73		2,228		

ITEMS FROM MONTANA

MONTANA STATE UNIVERSITY
Department of Plant Sciences and Plant Pathology, Bozeman, MT 59771, USA.

2016 Spring Wheat Program.

Luther Talbert, Nancy Blake, Hwa-Young Heo, Andrea Varella, Jason Cook, and Brittney Brewer.

Approximately 2.3 x 10^6 acres of hard red spring wheat were seeded in 2016. The season was characterized by early season moisture, which led to more disease than is typical. Stripe rust, tan spot, and wheat streak mosaic virus occurred sporadically throughout the state. Leading cultivars in Montana were Vida, Reeder, Corbin, and Mott. The cultivar Egan, with resistance to the orange wheat blossom midge, was grown commercially in impacted areas in western Montana. Egan has the high grain protein gene introduced from the cultivar GluPro. A new cultivar, **Lanning** (PI# 676978, PVP Certificate# 201600298) was recommended for release. Lanning has performed well in dryland areas of Montana, and has stronger gluten than the most widely grown cultivars. 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 high loaf volume.

Host plant quantitative trait loci affect specific behavioral sequences in oviposition by a stem-mining insect. 2016.

Andrea C. Varella, David K. Weaver, Robert K.D. Peterson, Jamie D. Sherman, Megan L. Hofland, Nancy K. Blake, John M. Martin, and Luther E. Talbert.

Host–plant selection for oviposition is important for progeny performance and survival for phytophagous insects. Specific cues from the plant influence insect oviposition behavior. Three QTL in wheat have been identified as influencing resistance to the wheat stem sawfly (WSS). Near-isogenic lines for each of the three QTL were used to test whether female WSS were able to discriminate variation in plant cues resulting from allelic changes. A QTL on chromosome 3B, previously associated with stem solidness, was shown to affect WSS oviposition behavior, host preference, and field infestation. Decreased preference for oviposition was also related to an allele at a QTL on chromosome 2D. A QTL on chromosome 4A affected host–plant attractiveness to females but did not change oviposition preference after females landed on the stem. Thus, oviposition decisions require that phytophagous WSS have the capability to discriminate plant cues associated with allelic variation and combinations of alleles across host plant quantitative loci. The multidisciplinary approach used here may lead to the identification of plant genes to complement the use of antibiosis due to solid stems to control the wheat stem sawfly.

Impact of a quantitative trait locus for productive tiller number on plasticity of agronomic traits in spring wheat.

A.M. Nasseer, J.M. Martin, H-Y. Heo, N.K. Blake, J.D. Sherman, M. Pumphrey, K.D. Kephart, S.P. Lanning, and L.E. Talbert.

Plasticity in development may allow a single wheat genotype to perform well in different environments. One trait that shows plasticity in wheat is productive tiller number (PTN), or tillers that produce heads with seed. This research tested the impact of a previously identified allele at the QTL *QTn.mst-6B* on yield and its components in a set of near isogenic

lines grown under conditions that differed in terms of resource availability. Results were that an allele at *QTn.mst-6B* enhanced early tiller number (ETN). Under favorable conditions, the large number of early tillers also resulted in high PTN. Seed number per head and seed weight was affected negatively by *QTn.mst-6B* high tiller allele. Results showed that ETN more often developed into PTN in less competitive environments and did not in high competition and low water settings. The high plasticity of PTN based on environment was associated with high plasticity in grain yield.

2016 Winter Wheat Program.

Phil Bruckner, Jim Berg, and Ron Ramsfield.

Montana harvested winter wheat acreage for 2016 was 2.15 x 10^6 acres averaging ~49 bu/acre (total production ~105 x 10^6 bushels). Leading cultivars were Yellowstone (18.8%), Judee (18.1%), Warhorse (10.0%), Brawl CLP (7.3%), Decade (5.0%), Bearpaw (4.4%), and CDC Falcon (4.4%). 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 noodle color and textural characteristics.

Loma (PI# 680576, PVP Certificate# 201700021) was released to Montana producers in autumn 2016. Loma is a semisolid-stemmed (similar to Genou), medium-late maturing, medium short statured wheat, with white chaff. Loma has above average yield and average test weight and protein. Loma is resistant to both stripe and stem rust. Loma is a medium low polyphenol oxidase line with above average mill and bake.

Results from the 2016 Montana Winter Wheat Variety Test can viewed at http://plantsciences.montana.edu/crops/index.html.

Quantitative genetics, plant breeding, and small grain quality.

Jack Martin (quantitative genetics and plant breeding), Mike Giroux (small grain quality), Alanna Schlosser, Andy Hogg, Darby Kammeraad, Rachel Johnston, Emma Jobson, and Justin Vetch.

We published two studies on genes impacting wheat product quality. Hystad et al. (2016) reported that null polyphenol oxidase (PPO) alleles are useful in improving white salted noodle color stability. Null PPO alleles would be useful to incorporate in any wheat cultivars destined to be used in fresh market noodles or refrigerated dough products to decrease development of off colors. Kammeraad et al. (2016) reported the impact of a series of puroindoline alleles created and selected to impart discrete grain hardness levels. Hardness was highly correlated with flour yield and particle size but did not significantly impact dough mixing or bread baking properties. The various puroindoline and null PPO alleles are available for use in wheat breeding programs.

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ITEMS FROM NORTH DAKOTA

NORTH DAKOTA STATE UNIVERSITY
Department of Plant Sciences, Loftsgard Hall, 78 Bolley Dr., Fargo, ND 58108, USA.

Meiotic homoeologous recombination-based alien gene introgression in wheat.

Xiwen Cai.

Wheat production has constantly encountered various biological (diseases and insects) and environmental (drought and salt) threats. There is an urgent need to genetically empower wheat to overcome these threats for sustaining wheat production. However, wheat has a narrow genetic basis due to the nature of its origin and evolution, and this has become a critical bottleneck for the genetic improvement of wheat. Fortunately, wheat has a huge number of wild relatives, many of which contain favorable genes wheat does not, and they represent an invaluable gene pool for wheat improvement. Recent advances in genomics offer new opportunities to unleash genetic diversity in the wild grasses for wheat improvement. It is time to unlock this gene pool for boosting the genetic potential of modern wheat.

Biological barriers limit the entrance of wild grass genes into wheat. Special genetic manipulation, i.e., chromosome engineering, is required to harness genetic diversity in the wild grasses for wheat improvement, bridging the gene flow from wild grasses into wheat and broadening the genetic basis of wheat. An effective meiotic homoeologous recombination-based genetic system (*ph1b* mutant) has been developed to shuffle the genes of wheat and wild grasses for the creation of desired genetic makeups. Recently, this genetic system has been further optimized using modern genomics techniques by the wheat research teams at North Dakota State University and USDA–ARS. A number of wild grass-derived genes for resistance to major wheat diseases and tolerance to various environmental stresses have been incorporated into the wheat genome through the *ph1b*-induced homoeologous recombination in our recent studies. Some have been utilized in wheat breeding for cultivar development. Obviously, these wild grass-derived germplasm lines enrich the gene pool for wheat improvement and ultimately sustain wheat production under various stresses. In addition, we have been transferring the *ph1b* deletion mutant into the major classes of US wheats. This will allow for direct access of US wheats to the wild grass gene pool and enhance gene transfer from wild grasses to U.S. wheats.

In summary, we have been bridging the gene flow from wild grasses into wheat to broaden the genetic basis of wheat and to empower wheat for genetic improvement. This research strengthens the defense of wheat against biotic and abiotic threats and sustains wheat production under various biological and environmental stresses. This will potentially increase the economic profitability of wheat production by improving grain yield potential and reducing the inputs of wheat farming. In addition, this work has opened new opportunities to improve the end-use quality and nutritional value of wheat grain by exploring the genetic diversity of wild grasses.

USDA–ARS CEREAL CROPS RESEARCH UNIT
1307 18th Street N, Fargo, ND 58102-2765, USA.

Genomic analysis and tools for the Septoria nodorum blotch susceptibility gene Snn2 in wheat.

Sudeshi Seneviratne (Department of Plant Sciences, North Dakota State University, Fargo, ND 58102, USA) and Timothy L. Friesen and Justin D. Faris.

Septoria nodorum blotch of wheat is caused by *Parastagonospora nodorum* and leads to significant yield losses as well as reductions in grain quality and grain weight. The wheat *Snn2* gene confers sensitivity to the necrotrophic effector SnTox2 of *P. nodorum*. A compatible *Snn2*-SnTox2 interaction is important in conferring both seedling and adult-plant susceptibility. This study developed the tools and resources necessary to clone and characterize the *Snn2* gene. A saturated genetic linkage map was developed using a segregating population of 164 $F_{7:8}$ recombinant inbred lines derived from a cross between the SnTox2-insensitive wheat line BR34 and the SnTox2-sensitive line Grandin. Markers were identified by SNP genotyping using the 90K iSelect wheat SNP chip and previously mapped simple sequence repeat markers. New markers were developed based on whole-genome sequence scaffolds and wheat survey sequences identified using SNP contextual sequences. These efforts allowed us to delineate *Snn2* to a genetic interval of 1.5 cM and a physical segment of 1.7 Mb. A high-resolution mapping population consisting of at least 3,000 F_2 plants will be screened to refine the *Snn2* region. In addition, we have developed an ethyl methanesulfonate-induced mutant population to identify *Snn2*-disrupted mutants for purposes of functional analyses and for conducting RenSeq. Results of this study will increase our knowledge of wheat-*P. nodorum* interactions, which will help to develop better host resistance through genetic manipulation.

Quantification of disease expression conferred by three host gene-necrotrophic effector interactions in the wheat-Parastagonospora nodorum pathosystem.

Amanda R. Peters (Department of Plant Sciences, North Dakota State University, Fargo, ND 58102, USA) and Timothy L. Friesen and Justin D. Faris.

Septoria nodorum blotch (SNB) induces cell death in wheat through the production of necrotrophic effectors (NEs). Our objective is to determine the relative importance of three host gene-NE interactions in causing disease. A recombinant inbred population that segregates for the NE sensitivity genes *Tsn1*, *Snn1*, and *Snn3-B1*, which interact with the NEs SnToxA, SnTox1, and SnTox3, respectively, was developed for genetic analysis. Results from infiltrations using *Pichia pastoris* cultures expressing each NE individually were used to map the three genes onto a whole-genome linkage map, which was assembled using SSR markers and the wheat 9K iSelect SNP array. Phenotypic data was collected by conducting spore inoculations using various isolates that produced one or more of the three NEs, and subsequent QTL analysis was conducted to determine the effects of the compatible host gene-NE interactions in causing disease. The amount of disease variation explained by the different interactions varied among isolates and, in some cases, the evaluation of NE gene-knockout isolates compared to corresponding wild types indicated strong epistasis for some host gene-NE interactions. Experiments to determine if NE expression is associated with disease significance are currently being conducted. Results from this research will contribute to the understanding this pathosystem and provide researchers with knowledge for reducing losses to SNB.

Unraveling the genetics of wheat-necrotrophic pathogen interactions.

Justin D. Faris, Timothy L. Friesen, and Steven S. Xu; and Zhaohui Liu (Department of Plant Pathology, North Dakota State University, Fargo, ND 58105, USA).

Interactions between wheat and the necrotrophic pathogens *Parastagonospora nodorum* (Pn) and *Pyrenophora tritici-repentis* (Ptr), which cause the foliar diseases Septoria nodorum blotch (SNB) and tan spot, respectively, involve host genes that recognize pathogen-produced necrotrophic effectors (NEs) in an inverse gene-for-gene manner to cause disease. Over the past decade, we have identified and characterized numerous host gene-NE interaction pairs, and we have cloned two wheat NE sensitivity genes, namely *Tsn1* and *Snn1*. *Tsn1*, which confers sensitivity to ToxA produced by both

Ptr and Pn, is a member of the NB-LRR class of disease resistance-like genes. *Snn1* recognizes the Pn NE SnTox1 and is a wall-associated kinase, which are known to serve as pathogen recognition receptors associated with disease resistance. These results suggest necrotrophic specialists such as Ptr and Pn use NEs to exploit pathways often associated with resistance to biotrophs. So far, it appears that genetic variation in the wheat-Pn system mostly involves host gene-NE interactions (nine have been identified), but the situation in the wheat-Ptr system is more complex. Whereas the *Tsn1*-ToxA interaction is consistently associated with disease in the wheat-Pn system, it is background-dependent in the wheat-Ptr system. We have also identified a major dominant race-nonspecific tan spot resistance gene on wheat chromosome arm 3BL. Therefore, both resistance and susceptibility genes are likely involved in the wheat-Ptr system. This work has shed light on the mechanisms associated with necrotrophic effector triggered susceptibility, but has also revealed that breeders may face a conundrum in that introgression of biotroph resistance genes may concomitantly introduce necrotroph susceptibility genes.

SOUTH CAROLINA

CLEMSON UNIVERSITY
Department of Plant and Environmental Sciences, Pee Dee Research and Education Center, Florence, SC 29506, USA.

'Celiac-safe' wheat genotypes: A target not beyond reach.

S. Rustgi and N. Gandhi; and D. von Wettstein, N. Ankrah, R. Gemini, and P. Reisenauer (Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164, USA).

Prolamins, dubbed as gluten, represent the major seed storage proteins in wheat grains and cherish the glory of being one of the most consumed dietary proteins in the world. In addition, gluten also was found responsible for a variety of dietary disorders in susceptible individuals (Sapone et al. 2012). According to an estimate, about 7.5% of the U.S. population is affected by the 'gluten syndrome'. The only effective therapy known so far is lifelong adherence to a diet of abstinence, which is difficult to practice, if not impossible. In recent years, wheat sales have suffered a setback due to increasing public awareness about gluten-induced disorders and their reliance on misconceptions or rumors (https://wholesale.wf.com/food_for_thought/gluten-sensitivitys-impact-on-the-milling-industry/). On the other hand, the market for gluten-free commodities is constantly strengthening and projected to touch \$7.59 x 10^9 by 2020 (http://www.marketsandmarkets.com/PressReleases/gluten-free-products.asp). Based on our findings and parallel research conducted elsewhere, we hypothesize that it is possible to develop a general dietary therapy for gluten syndrome by eliminating or detoxifying the cause of these disorders (Osorio et al. 2012). We tested our hypothesis first by tissue-specific suppression of the wheat genes encoding a DNA glycosylase, *DEMETER*, and a Fe–S cluster biogenesis enzyme. These genes collectively control transcriptional activation of about 100 different prolamins, except high-molecular-weight glutenins, which also are indispensible for baking (Rustgi et al. 2016). Second, ectopic expression of a glutamine-specific endoprotease from barley and a post-proline cleaving endopeptidase from *Flavobacterium* in wheat grain. The combination of 'glutenases' was earlier tested by others and us to completely detoxify gluten proteins to nonimmunogenic peptides (Osorio et al. 2012; Rustgi et al. 2014, 2015). Endosperm-specific silencing of the wheat genes encoding the DEMETER enzyme and a Fe–S cluster biogenesis enzyme will be respectively achieved by a TALE (transcription activator-like effector) repressor and an RNA-guided Cas9 (CRISPR associated protein 9) nuclease. The gene-editing reagents mentioned above are being used in a combination to pyramid the effects of silencing genes encoding DEMETER and the Fe–S cluster biogenesis enzyme in a single genotype. So far, wheat genotypes exhibiting up to 76% reduction in immunogenic prolamins were identified and efforts to obtain genotypes with >90% suppression in the gluten content are underway (Rustgi et al. 2016). Similarly, wheat genotypes expressing two glutenases in their endosperms were obtained (Rustgi et al. 2014, 2015) and their detailed biochemical characterization is in process. We briefly summarize the progress made on the former approach below.

Development of gene-silencing constructs. In order to achieve co-suppression of the master regulators of prolamin accumulation in wheat grain, the following two constructs were developed *i*) a DEMETER-specific, TALE-repressor-based donor construct and *ii*) an Fe–S cluster biogenesis, gene-specific CRISPR/Cas9 construct. The donor construct carries a TALE repressor that targets a 17-nucleotide sequence, in the promoter region of the wheat *DEMETER* homoeologues, and the CRISPR/Cas9 construct targets a 22-bp site in the gene encoding an Fe–S cluster biogenesis enzyme. In the donor construct, the *DEMETER* TALE repressor is cloned under the control of a maize endosperm-specific promoter and a nopaline synthase (*nos*) terminator, whereas in the nuclease construct, the single guide RNA was cloned under the control of the Rice snoRNA U3 promoter and the gene encoding Cas9 nuclease was cloned under the control of the P1 promoter. However, insertion of the DEMETER TALE repressor at the target genomic site can be achieved without co-transformation with the nuclease construct, but at a negligible frequency. Thus, to increase the recombination frequency and consequently the possibilities of integration at the target site the two constructs, donor and nuclease will be co-transformed to the plants (for further details, see Rustgi et al. 2016).

Biolistic transformation of wheat microspore embryoids. To develop microspore embryoids for genetic transformation, 80 spikes from 20 plants of the wheat cultivar WestBred 926, grown at the Washington State University Plant Growth Facility, were collected and pretreated with a 2 mM $CuSO_4$ solution prepared in 0.4 M mannitol (Brew-Appiah et al. 2013; Rustgi et al. 2017). After pretreatment, the spikes were sterilized with a common bleach solution and embryogenic microspores were isolated in a 0.4 M mannitol solution. Subsequently, ~15,000 microspores were transferred to induction media (number estimated via hemocytometer) and about 450 of these resulted in microspore embryoids. Three hundred, seven- to eight-week-old microspore embryoids were transferred to regeneration media in Petri dishes and bombarded with gold particles coated with a mixture of the CRISPR Cas9 construct, the donor construct, and the *Bar* gene construct, pDPG165, used in a 2:2:1 proportion (Fig. 1a). About 200 microspore embryoids survived the ballistic trauma and were transferred to the regeneration medium (Fig. 1b). Of these 200 pollen embryoids, 120 regenerated into green plantlets and were transferred to the rooting medium (Fig. 1c and d; consult Table 1 for the sequence of events with dates from

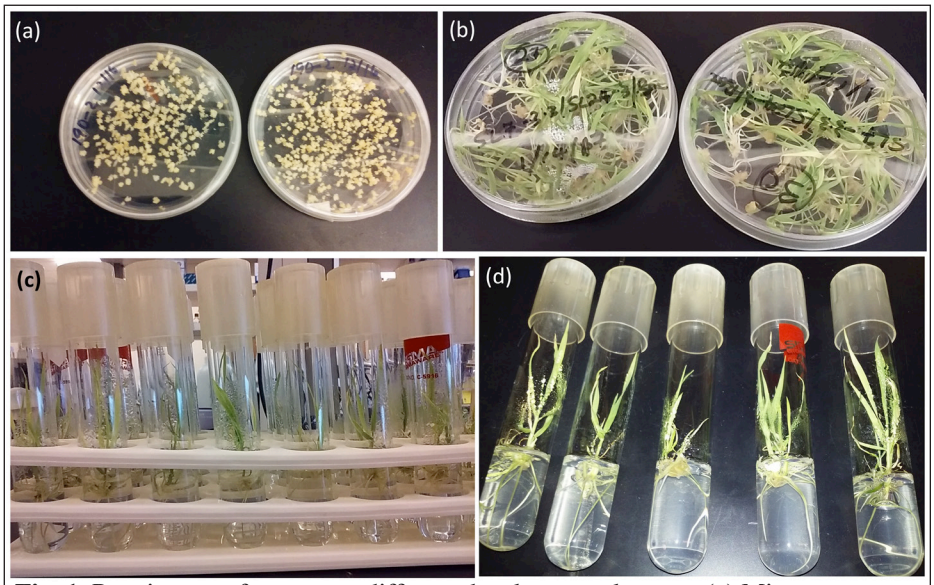

Fig. 1. Putative transformants at different developmental stages. (a) Microspore-derived calli of WestBred926 on induction medium, 190-2. Notice calli are ready for use in biolistic transformation. (b) Calli regenerating into green plants after microprojectile bombardment. (c and d) Plantlets transferred to culture tubes on regeneration or rooting medium.

Table 1. Sequence of events from collection of spikes to the production of putative transformants.

Date	# of explants	Spikes collected	Microspores transferred to induction medium	Embryoids obtained	Embryoids bombarded	Embryoids transferred to regeneration medium	Green regenerants	Fertile plants
11/10/16	20	80						
11/20–24/16			~15,000					
12/18/16				~450				
12/24/16					~300			
12/30/16						200		
2/10–20/17							120	

the collection of spikes to the production of putative transformants). Fifty of the 120 regenerants survived the colchicine treatment applied prior to transferring plants to the greenhouse. Leaves from 37 of these 50 plants were collected for DNA extraction and to test the integration of the DEMETER TALE repressor at the target site.

Collectively, the major outcomes of this research will be the development of wheat genotypes with near complete elimination/detoxification of immunogenic prolamins, high lysine content, and enhanced bioavailability of prolamins to the consumers. Moreover, these wheat genotypes will serve as the first prophylactic dietary therapy available to the gluten intolerant, sensitive, and allergenic individuals.

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SOUTH DAKOTA

SOUTH DAKOTA STATE UNIVERSITY
Departments of Biology and Microbiology and Plant Science, Brookings, SD 57007, USA.

De novo assembly of wheat root transcriptomes and transcriptional signature of its longitudinal differentiation.

Ghana Shyam Challa (Department of Plant Science) and Wanlong Li (Department of Biology and Microbiology).

Hidden underground, root systems constitute an important part of the plant for its development, nourishment, and sensing the soil environment around it, but we know very little about its genetic regulation in crop plants such as wheat. In this study, we attempted to understand the gene repertoire of wheat root systems using 454 titanium FLX and HiSeq sequencing technologies. Although the 454 titanium FLX platform was used to sequence transcriptome of root tips, the HiSeq technology was used for sequencing the mRNA transcripts from the root tips (meristem zone) and the rest of the root tissue (maturation zone). Cleaned reads were *de novo* assembled to construct the reference transcriptomes for root in reference cultivar Chinese Spring. The 454 reads were assembled into 24,986 transcripts with a completeness of 54.84 %, and the HiSeq reads were assembled into 91,543 protein-coding transcripts and 16,074 noncoding transcripts with a completeness of 90.32% for full-length conserved eukaryotic genes. Approximate 6.8% of the coding transcripts and ~2.2% noncoding transcripts are not present in the current wheat genome assembly. Function annotation of both assemblies indicated a similar gene ontology pattern and showed that ~5% of the transcripts are root-specific. Transcription quantification identified 1,728 differentially expressed transcripts, 1,083 were up-regulated and 645 down-regulated in root tips, accounting for 1.89% of the protein-coding RNA transcriptome. Their expression patterns match their function in root development. Expression of genes encoding transcription factors functioning in cell proliferation and genes coding for starch metabolism enzymes are enriched in root tips, but expression of genes for lateral root development, vascular development and lignin biosynthesis was enriched in the maturation zone. This study provided the first view of wheat root transcriptome under different developmental zones and laid a foundation for functional analysis for wheat root development and growth using a reverse genetic approach.

VIRGINIA

VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY
Department of Crop and Soil Environmental Sciences, Blacksburg, VA 24061, USA.

EASTERN VIRGINIA AGRICULTURAL RESEARCH AND EXTENSION CENTER
Warsaw, VA 22572, USA.

TIDEWATER AGRICULTURAL RESEARCH AND EXTENSION CENTER
Suffolk, VA 23437, USA.

C. Griffey, W. Thomason, J. Seago, K. Brasier, N. Meier, N. Carpenter, B. Ward, L. Liu, and E. Rucker (Crop and Soil Environmental Sciences, Virginia Tech); R. Pitman and J. Fitzgerald (Eastern Virginia Agricultural Research and Extension Center); S. Malla (Texas A&M AgriLife Research & Extension Center, Texas A&M, Uvalde, TX 78801); D. Schmale III and N. McMaster (Plant Pathology, Physiology and Weed Science, Virginia Tech); and M. Balota, J. Oakes, and H. Mehl (Tidewater Agricultural Research and Extension Center).

2016 Wheat Production in the Commonwealth of Virginia.

Growing conditions. Statewide temperatures and rainfall in autumn 2015 were generally near the 30-year means and mostly conducive for wheat seeding, although some areas were delayed due to excess moisture. Areas of wet weather slowed wheat planting in some areas but, by mid-November, winter wheat planting was estimated to be 71% complete, compared with 77% by this date over the last 5-yr. Both November and December were warmer than the long-term average and were favorable for small grain growth, especially benefitting late plantings. On 1 December, 82% of the wheat crop was estimated to be good or excellent. Temperatures in January and February were near normal, whereas March was again much warmer than the 30-yr average. These warmer temperatures encouraged small grain growth, to excess in some fields and areas. By the end of March, the crop was progressing several weeks ahead of normal. Freezing temperatures in the second week of April severely damaged small grain fields in parts of the state, but damage was confined to the areas that were the coldest and those fields that were most advanced. Still, by 29 April, 64% of the wheat crops were rated good or excellent. April was dry in most areas of Virginia, whereas May brought rain showers almost daily through the first three weeks of the month. By 22 May, 91% of the wheat crop was estimated to have reached heading, compared with 92% for this date for the previous five years. On this date, 65% of the wheat crop was rated good or excellent, whereas 29% was estimated to be in fair condition. By 12 June, 9% of wheat harvest was complete, compared to 10% complete in 2015.

Production. The Virginia Department of Agriculture and Consumer Services estimated that Virginia farmers would harvest 10.3 x 10^6 bushels (276,000 Mg) of winter wheat in 2016, which is a 26% decrease from 2015. Average wheat yield was estimated to be 59 bushels/acre (3965 kg/ha), down seven bushels (470 kg) from 2015 and down four bushels (270 kg) from earlier estimates.

Disease incidence and severity. Many wheat diseases were prevalent and widespread throughout the Commonwealth in 2016, and stripe rust (*Puccinia striiformis*) was more widespread and severe than previously noted in the past 27 years. Entries in Virginia's 2016 state wheat variety trials were rated for disease severity (0 = no infection to 9 = severe infection) at five diverse locations. The 133 entries in the 2016 trial had mean powdery mildew (*Blumeria graminis*) ratings that varied from 0 to 6 at four test sites and mean ratings of 1.9 on the Eastern Shore (Accomack County), 2.2 in the northeastern region (Richmond County), 2.3 in the Tidewater region (City of Suffolk), and 2.4 in the southern Piedmont region (Nottoway County). *Barley/Cereal Yellow Dwarf Virus* infection was moderate at the southwestern test site (0–4) near Blacksburg, VA. Leaf rust (*Puccinia triticina*) was prevalent in several regions with ratings ranging from 0 to 9 at three sites and from 1 to 8 at another site. Mean leaf rust ratings varied from 1.9 on the Eastern Shore, 2.9 in the Tidewater, 3.0 in the northeastern, and 3.3 in the southwestern regions of the state. Race surveys conducted by Dr. James

Kolmer at the USDA–ARS Cereal Disease Lab on 16 *P. triticina* collections from Blacksburg, Blackstone, Holland, Mt. Holly, and Warsaw, VA, identified three different races of leaf rust with races MBTNB and MCTNB being most common. The other race identified at Warsaw, VA, was MNPSD. Stripe rust (*Puccinia striiformis*) ratings ranged from 0 to 8 among entries evaluated at three locations, and mean test ratings varied from 1.6 in the Tidewater, 1.9 on the Eastern Shore, and 2.2 in northeastern regions. Stripe rust samples from Blacksburg, Holland, Painter, and Warsaw, VA, were sent to Dr. Xianming Chen at USDA–ARS in Pullman, WA. Three races were identified, including PSTv-37 (virulence for *Yr6*, *7*, *8*, *9*, *17*, *27*, *43*, *44*, *YrExp2, and YrTr1*) from Blacksburg, Holland, and Painter; PSTv-52 (*Yr6*, *7*, *8*, *9*, *17*, *27*, *43*, *44*, and *YrExp2*) from Blacksburg, Holland, and Warsaw; and PSTv-198 (*Yr6*, *7*, *8*, *9*, *27*, *43*, *44*, and *YrExp2*) from Painter and Warsaw. Leaf blotch ratings among entries varied from 1 to 5 at Painter, VA, with a test average of 1.8.

State cultivar tests. Wheat trials were planted no-till at Holland and Shenandoah Valley sites at 48 seeds/f^2. The tests at Blackstone, Blacksburg, Orange, Painter, and Warsaw were planted conventional-till at 44 seeds/f^2. Past seasons across Virginia have provided the opportunity to evaluate day length sensitivity, spring freeze damage, and resistance of lines to many diseases as noted above. In 2016, spring freeze severely damaged many of entries that were either early heading and/or day length insensitive. Entries that were susceptible to one or more of the major diseases noted above also were severely damaged. Mean yields over six sites varied from 32 bu/acre (2,152 kg/ha) in the southern Piedmont to 79 bu/acre (5,313 kg/ha) in the southwestern region. Cultivar Hilliard had the highest overall mean yield at 66.4 bu/acre (4,465 kg/ha). Cultivars that yielded significantly higher than the over locations mean of 55.8 bu/acre (3,753 kg/ha) in 2016 included Hilliard, MAS 61, MAS 65, Pioneer Brand 26R59, L11550, MAS 67, Pioneer Brand 26R20, AgriMAXX 474, L11541, CROPLAN 8550, MAS 35, MAS 6, MAS 7, SY 547, and USG 3197. Three of these cultivars, including Hilliard, L11550, and L11541, also had test weights that were significantly higher than the mean of all lines tested.

Newly released cultivars. The hard red winter wheat cultivar **Vision 50** (VA09HRW-64) and three soft red winter wheat cultivars, including **VA10W-96** (16162660), **VA10W-119** (SH7200), and **VA11W-106** (L11550), were released by the Virginia Agricultural Experiment Station in May 2016.

Virginia Wheat Yield Contest results. The 2016 contest was conducted statewide and the results can be found in the table below. Congratulations to our winners!

Soft wheat					
Place	**Grower**	**Farm**	**County**	**Yield bu/acre**	**Cultivar**
1	Alan & Justin Welch	Welch Farms, Inc	Northumberland	96.9	Pioneer 26R10
2	William L. Andrews	W. L. Andrews Farms	Essex	88.3	AgriMaxx 444
3	Boogie Davis	Davis Produce	New Kent	87.6	USG 3404
4	Evan Perry	Corbin Hall Farm	Middlesex	79.1	Pioneer 26R20
Hard Wheat					
1	Chuck and Joe King		Montgomery	86.0	Vision 45
2	Dan Brann	Brann Farms	Montgomery	80.3	Vision 45
3	Paul Davis	Davis Produce	New Kent	71.8	Vision 45
4	Craig Brann		Northumberland	56.8	5210 HR

Evaluating nitrogen use efficiency in wheat by ground and aerial remote sensing.

Maria Balota and Joseph Oakes.

In the second year of collecting ground and aerial remote sensing measurements in wheat, nitrogen use efficiency (NUE) tests are being conducted at the Tidewater AREC in Suffolk and Eastern Virginia AREC in Warsaw, VA, by Kyle Brasier, graduate student of Dr. C.A. Griffey. They are interested in the development of faster yet more precise ways to non-destructively evaluate NUE in wheat in the field. For this project, 14 wheat cultivars are being evaluated under two nitrogen fertility treatments: a low fertility treatment with a total of 60 pounds of N/acre and a normal fertility treatment with a total of 120 pounds of N/acre. During the vegetative stages, Kyle is collecting several measurements using standard handheld equipment including normalized difference vegetative index (NDVI) and canopy temperature (CT). Maria

and Joseph are collecting aerial images from an AscTec Falcon 8 UAV platform to be compared with the ground-based data and other much more time consuming measurements that Kyle is collecting. If we can develop and use UAV-based vegetation indices instead of ground-taken NDVI and CT, then many hours of field work could be eliminated. But the most important advantage of using methods that require short vs. long time of measurement is weather changes through the day, i.e., temperature, sun angle, wind velocity, and cloud cover, that influence canopy properties and, therefore, NDVI and CT, making data difficult to interpret.

The unmanned aerial vehicle (UAV) measurements were taken with three different sensors, a red-green-blue (RGB) digital camera, a multispectral camera, and a thermal camera. After image processing with several software programs including AscTec Navigator, Pix4D, ArcGIS, and Image J, we computed several color space characteristics such as hue angle, intensity, saturation, along with vegetation indices derived from them, i.e., green area (GA) and greener area (GGA), and UAV-based NDVI and CT. During the 2015–16 growing season, aerial and ground RGB indices outperformed NDVI when assessing yield differences. We also found that RGB indices are well correlated with NDVI, with the best correlation being at GS75. We also have learned that aerial NDVI has a very high correlation with ground collected NDVI (R^2=0.89) and is a better indicator of yield than ground collected NDVI (Fig. 1). Using an infrared camera attached to the UAV, we are able to see which cultivars show stress and have a higher canopy temperature when the N rate is cut in half (Fig 2). Measurements such as NDVI and canopy temperature that would have taken hours to measure by hand can now be done in a matter of minutes with the assistance of the UAV. We have seen that the data from the UAV is comparable, if not better than the ground-collected data.

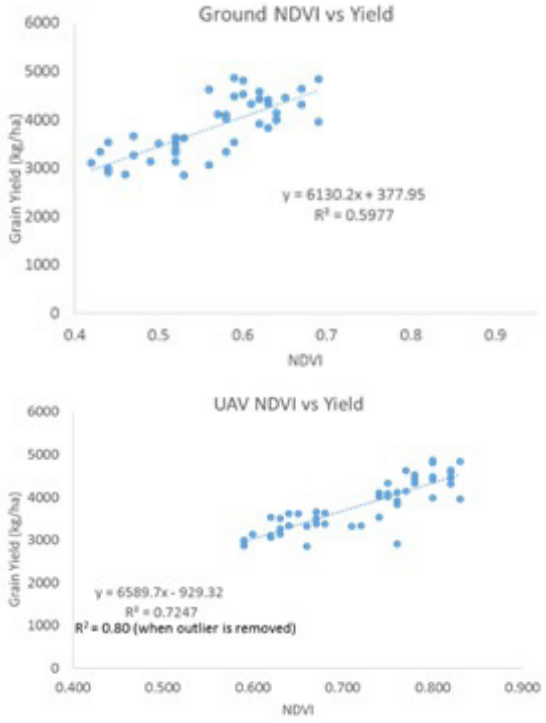

Fig. 1. Comparison of relationships between ground normalized difference vegetative index (NDVI) and yield (top) and aerial NDVI and yield (bottom) at growth stage 75 in Warsaw, VA.

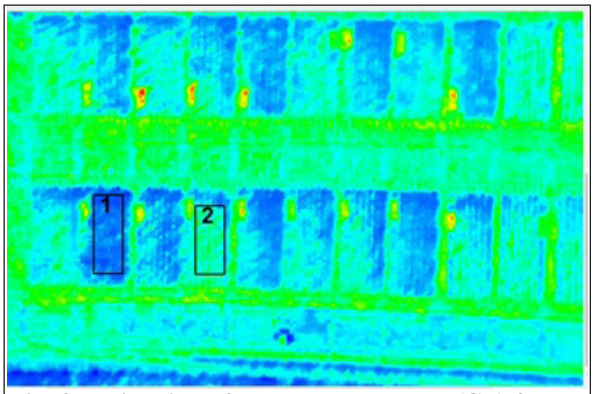

Fig. 2. Estimation of canopy temperature (CT) from thermal images taken by an unmanned aerial vehicle platform. Plot 1 received 120 pounds of N and is cooler and healthier (18°C) than plot 2 that received only 60 pounds of N, for which CT is 24°C.

Using UAV remote sensing for nitrogen management in wheat.

Joseph Oakes, Maria Balota, and Wade Thomason.

In the first year of a study examining the potential use of UAVs for N management in wheat, the decision of whether or not to apply N at Zadoks growth stage (GS) 25 (Zadoks et al. 1974) is based on the number of tillers present at that time (Alley et al. 2009). If tiller number is less than 1,000 tillers/m^2, an N application is necessary for the crop to develop any reasonable yield potential. When tiller number is in excess of 1,000 tillers/m^2, no N application is needed until GS 30. Tissue testing is recommended as the best tool to determine wheat N need at GS 30 (Alley et al. 2009). While years of research have shown that tiller counts and tissue testing are reliable methods of determining optimum N rate, both of these methods require several labor-intensive measurements to be made in each wheat field (Phillips et al. 2004). Also, a significant time lag is involved between sampling and the return of laboratory results (Thomason et al. 2010). In addition, multiple samples per field may be needed to represent those fields with large variations, so the process may be prohibitive due to both labor and cost. Wheat growers in the Virginia could easily benefit from a system that streamlines and automates this process.

With the advent of the UAV and new remote sensing technologies, we now have the opportunity to use these technologies to determine crop N need by flying over the field with one of several sensors. These sensors have the ability to instantly determine the crop's nutrition status and its need for fertilizer,.eliminating the labor required to collect tiller counts and the time lag involved in tissue testing, will enable growers to quickly make N fertilizer decisions. If successful, N rates can be calculated from the aerial NDVI and color space indices, and this information can be used to build N prescription maps for wheat fields. These maps will be developed in such a way that the prescription information can be put directly into the sprayer software to read and apply N based and the actual plant needs and field variability. The variable rate N application maps will assist growers in making more timely N applications based on crop growth, need, and soil variability. This process has the potential to increase yields by applying N as required by crops, reduce production costs by growers spending less on N fertilizers when and where they are not needed, and maintain a safe environment by N being taken up by the crops rather than leached in soils and watersheds.

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Breeding for improved nitrogen use efficiency.

Kyle Brasier (Ph.D. candidate of Dr. Carl Griffey).

Wheat yield improvement during the second half of the 20th century is largely attributed to a combination of increased rates of nitrogen (N) fertilization and the introduction of dwarf cultivars exhibiting a positive response to added nitrogen. However, yield gains derived exclusively from higher rates of N fertilization reduce grower profit potential and may contribute to environmental degradation due to its mobility within the soil profile. In this study, the effects of N rate and timing on dry grain yield (0% moisture) and plant N content were evaluated in a panel of 12 soft red winter wheat lines. On average, grain yield was reduced by 4.3 and 10.3 bu/acre under moderate (90 lb N/acre) and low (60 lb N/acre) N rates respectively compared to the standard (120 lb N/acre), while application timing effects did not significantly differ across the panel of wheat lines. However, application timing effects were detected for individual wheat lines (e.g., KY06C-1003-139-8-3; Fig. 3). Additionally, applications split 25% at the five tiller stage and 75% (30 + 90 lbs N/acre) at stem elongation under standard N rates significantly increased grain N

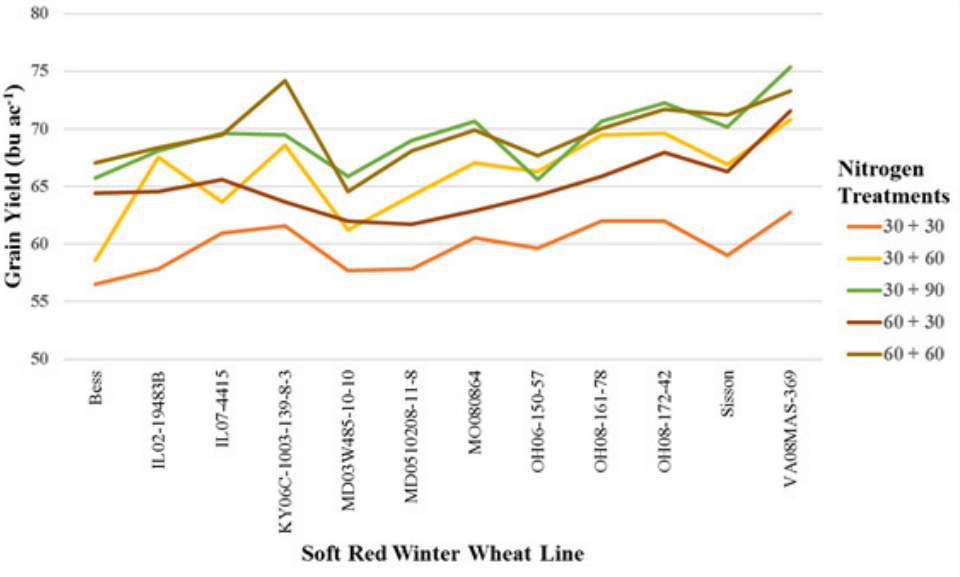

Fig 3. Average grain yield for wheat line across seven Virginia environments under five nitrogen treatments ranging from 60 (orange) to 120 (green and brown) pounds total spring nitrogen/acre.

content but reduced above-ground biomass relative to evenly split N applications (60 + 60 lbs N/acre) at the same growth stages. Results indicate strong breeding potential for plant response to applied nitrogen and that future improvements in grain production efficiencies will likely stem from a combination of more precise on-farm management and the utilization of well-adapted wheat cultivars.

Improving grain yield in soft winter wheat in Virginia using genomic data.

Brian Ward (Ph.D. graduate of Dr. Carl Griffey).

In multiple species, genome-wide association (GWA) studies have become an increasingly prevalent method of identifying the quantitative trait loci (QTL) that underlie complex traits. Despite this, relatively few GWA analyses using high-density genomic markers have been carried out on highly quantitative traits in wheat. My research utilized high-density DNA marker data to perform GWA on multiple yield-related traits using a panel of 329 soft red winter wheat genotypes grown in four environments in Virginia. In addition, the marker data was used to examine linkage disequilibrium and population structure within the testing panel. The results indicated that a 2G:2B translocation from the species *Triticum timopheevii* was responsible for the majority of observed population structure. In addition, a total of 50 significant marker-trait associations were identified for various traits.

However, a subsequent study cast some doubt upon the reproducibility and reliability of plant QTL identified via GWA analyses. We used two highly-related panels of different genotypes grown in different sets of environments across the Eastern United States to attempt to identify highly stable QTL. However, no QTL were shared across panels for any trait, suggesting that 'QTL x environment' and 'QTL x genetic background' interaction effects are significant, even when testing across many environments.

In light of the challenges involved in QTL mapping, prediction of phenotypes using whole-genome marker data is an attractive alternative. However, many evaluations of genomic prediction in crop species have utilized models adapted from animal breeding. These models cannot directly account for 'genotype x environment' interaction, and hence are often not suitable for use with lower-heritability traits assessed in multiple environments. We sought to test genomic prediction models capable of more *ad-hoc* analyses, utilizing highly unbalanced experimental designs consisting of individuals with varying degrees of relatedness. The results suggest that these designs can successfully be used to generate reasonably accurate phenotypic predictions. In addition, multivariate models can dramatically increase predictive accuracy for some traits, though this depends upon the quantity and characteristics of 'genotype x environment' interaction.

Identification and genetic mapping of leaf and stripe rust resistance.

Neal Carpenter (Ph.D. candidate of Dr. Carl Griffey).

The genetic mapping of leaf and stripe rust resistance the soft red winter wheat cultivar Jamestown was finished recently. Phenotypic data was collected at diverse locations for resistance to leaf rust (NC, TX, and VA) and stripe rust (AR, NC, GA, TX, and VA). The Jamestown population was genotyped with a public 90K iSelect SNP array. Analysis of the population identified two QTL for leaf rust resistance on chromosome 5B and two QTL for stripe rust resistance on chromosomes 3B and 6A. These QTL were associated with both infection type and disease severity. Phenotypic variation as high as 22.1% was explained by the putative leaf rust resistance QTL of Jamestown on 5B. Variation explained by the putative stripe rust resistance QTL of Jamestown on 3B and 6A was as high as 11.1% and 14.3%, respectively. Introgression and pyramiding of these QTL with other genes conferring resistance to leaf and stripe rusts via marker-assisted selection will facilitate development of soft red winter wheat cultivars having more durable resistance.

Jamestown was postulated to contain the leaf rust resistance gene *Lr18*. A seedling, leaf rust screening study was conducted with a population of 186 lines from the cross of 'Pioneer 25R47/Jamestown' screened with *P. triticina* pathotype TNRJ. An additional 1,600 individuals from eight additional populations of 200 individuals per population were created and screened with TNRJ to validate that cultivar Jamestown did possess *Lr18*. Analysis of the 'Pioneer 25R47/Jamestown' population identified markers that were tightly linked with *Lr18*, which were validated in two other

populations. The results of the linkage analysis identified one marker tightly linked within 5 cM of *Lr18* in all three populations.

Soft red winter wheat cultivar 2013412 (SS8412) is a broadly adapted, high-yielding, full-season, short height semi-dwarf with exceptional adult plant resistance to *Puccinia triticina*. A doubled-haploid population was evaluated for leaf rust resistance at Blacksburg and Warsaw, VA. Genotyping was completed using genotyping-by-sequencing. The results of the first year were conclusive in that a few markers on chromosome 1B accounted for a majority of variance (49%) associate with leaf rust resistance in SS8412. These results will be validated in a second year study including four additional doubled-haploid populations in VA, NC, IL, and TX.

Identification of molecular markers for improved milling and baking quality in soft red winter wheat.

Nick Meier (Ph.D. candidate of Dr. Carl Griffey).

Due to evolving consumer preferences, millers and bakers are placing added value on improved or unique quality and nutrition in their flour. Currently, there is very little information available on QTL and minor genes (needed to improve quantitative traits) influencing milling and baking traits in SRW Wheat. In order to address this issue, molecular markers associated with improved quality must be identified for use in marker-assisted breeding. Mapping populations derived from the crosses 'Pioneer 26R46/Tribute' (127 double haploids) and 'Pioneer 25R47/Jamestown' (186 recombinant inbred lines) were grown in Blacksburg and Warsaw, VA, during 2015–16 under optimum conditions. The test is being repeated at the same locations in 2016–17. Milling yield, flour protein, solvent retention capacity, cookie diameter, top grade, kernel hardness, softness equivalence, and several other traits differ significantly between the four parents. Phenotypic data was collected at the USDA–ARS Soft Wheat Quality Lab in Wooster, OH, under the guidance of Dr. Byung-Kee Baik. Genotypic data was generated with the Illumina 90k SNP chip. Potentially significant markers associated with improved quality were identified on all 21 chromosomes and influence 12 different traits. The most significant QTL are on chromosomes 3A, 6A, 7A, 1B, and 2D. Conclusive and detailed results will be available during the winter of 2017–18.

Integrated management of Fusarium head blight and deoxynivalenol contamination in soft red winter wheat in Virginia.

Hillary Mehl.

New cultivars with moderate resistance to *Fusarium* head blight (FHB) and deoxynivalenol (DON) contamination have been developed for Virginia and the surrounding region, but DON contamination in wheat continues to be a perennial problem for growers in the state. Judicious use of fungicides based on FHB-risk models provides some control of FHB and DON, but integrated management approaches that incorporate cultivar selection, appropriate fungicide chemistries, and optimal timing of fungicide applications are needed to minimize the impacts of FHB and DON in a cost-effective manner. The overall goal of this project is to identify the most effective and economical approaches to FHB and DON management in soft red winter wheat (SRWW). The specific objectives are to 1) evaluate the integrated effects of fungicide and genetic resistance on FHB and DON and 2) contribute to a multi-state dataset that will be used to conduct an economic analysis of integrated management of FHB/DON. In 2016, the effectiveness of one and two application fungicide programs for FHB and DON management was evaluated on four wheat cultivars (Shirley, Jamestown, Hilliard, and Agrimaxx 426). Shirley is a popular, late-heading cultivar that is susceptible to FHB. Jamestown is an early-heading cultivar with moderate resistance to FHB. Hilliard and Agrimaxx 426 are two new releases from the Virginia Tech small grains breeding program with mid-season flowering and moderate resistance to FHB/DON. An untreated check was compared to one or two fungicide applications starting at anthesis (Table 1, p. 100). Plots were inoculated 24 hours after anthesis with a spore suspension of *F. graminearum*. FHB incidence and severity, *Fusarium* damaged kernels (FDK), yield, and DON content of the harvested grain were determined from each plot (Table 1, p. 100). As expected, Shirley had the highest severity of FHB and DON contamination. Hilliard and Agrimaxx 426 had the lowest levels of FHB among the four cultivars. Yields of Shirley and Hilliard were comparably high, and Agrimaxx 426 had the lowest yield. All fungicide treatments lowered disease severity in Shirley and Jamestown, but there was less of an effect for the

moderately resistant cultivars Hilliard and Agrimaxx 426. Fungicides increased yield and decreased DON contamination, but there was not a consistent benefit to two versus a single fungicide application. Results demonstrate the importance of cultivar selection and a single, well-timed fungicide application for management of FHB and DON.

Table 1. Impact of cultivar and fungicides on Fusarium head blight (FHB), yield, and DON contamination of wheat in Virginia, 2016. F10.5.1 = Feekes stage 10.5.1 (anthesis, 50% flowering). All plots were inoculated with a spore suspension of *F. graminearum* 24 h after the first fungicide application with the exception of the untreated, noninoculated control. % FHB = percent spikelets with signs and symptoms of FHB. %FDK = percent Fusarium damaged kernels. Means in a column followed by the same letter(s) are not significantly different according to Tukey HSD (*P*=0.05).

Cultivar	Fungicide treatment and timing	% FHB		% FDK		Yield (bu/acre)		DON (ppm)	
Shirley	Untreated	30	ab	41	ab	56	c–h	2.87	a
	Prosaro SC 6.5 fl oz (F10.5.1)	19	c–e	11	c	75	a–c	0.70	c
	Prosaro SC 6.5 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	15	c–f	13	bc	78	a	0.20	c–e
	Caramba EC 14 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	14	c–f	11	c	75	a–c	0.20	c–e
	Proline SC 5.7 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	17	c–f	10	c	77	ab	0.29	c–e
	Untreated, noninoculated	35	a	48	a	60	a–g	1.76	b
Jamestown	Untreated	22	b–d	18	bc	32	ij	0.42	c–e
	Prosaro SC 6.5 fl oz (F10.5.1)	13	c–f	5	c	49	d–i	0.12	de
	Prosaro SC 6.5 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	10	ef	3	c	61	a–f	0.00	e
	Caramba EC 14 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	11	ef	4	c	55	c–h	0.13	de
	Proline SC 5.7 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	11	d–f	3	c	54	d–h	0.09	de
	Untreated, noninoculated	22	bc	16	bc	36	h–j	0.05	e
Hilliard	Untreated	15	c–f	28	a–c	52	d–i	0.51	c–e
	Prosaro SC 6.5 fl oz (F10.5.1)	13	c–f	15	bc	58	b–g	0.54	c–e
	Prosaro SC 6.5 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	11	ef	13	bc	67	a–d	0.17	c–e
	Caramba EC 14 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	13	c–f	10	c	68	a–d	0.13	de
	Proline SC 5.7 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	10	ef	13	bc	63	a–e	0.12	de
	Untreated, noninoculated	15	c–f	21	a–c	52	d–i	0.62	cd
Agrimaxx 426	Untreated	18	c–f	16	bc	33	ij	0.29	c–e
	Prosaro SC 6.5 fl oz (F10.5.1)	14	c–f	7	c	40	g–j	0.16	c–e
	Prosaro SC 6.5 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	10	ef	3	c	27	j	0.06	e
	Caramba EC 14 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	8	f	4	c	41	f–j	0.07	de
	Proline SC 5.7 fl oz (F10.5.1) + Folicur SC 4 fl oz (4 days later)	10	ef	5	c	44	e–j	0.12	de
	Untreated, noninoculated	12	c–f	17	bc	37	h–j	0.22	c–e

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WASHINGTON

USDA–ARS WESTERN WHEAT QUALITY LABORATORY
E-202 Food Quality Building, Washington State University, Pullman, WA 99164, USA.
www.wsu.edu/~wwql/php/index.php

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

The mission of the lab is two-fold: conduct milling, baking, and end-use quality evaluations on wheat breeding lines, and conduct research on wheat grain quality and utilization. Our web site: http://www.wsu.edu/~wwql/php/index.php provides great access to our research and methodology. Our research publications are available on our web site.

Morris and Engle lead the Pacific Northwest Wheat Quality Council, a consortium of collaborators who evaluate the quality of new cultivars and advanced breeding lines. Our current activities and projects include grain hardness and puroindolines, waxy wheat, polyphenol oxidase (PPO), arabinoxylans, SDS sedimentation test, soft durum wheat, grain flavor, and Falling Number.

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www.ars-grin.gov/npgs

National Small Grains Collection activities.

H.E. Bockelman, Agronomist and Curator.

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

Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN): http://www.ars-grin.gov/npgs. Certain accessions may not be available from the National Small Grains Collection due to intellectual property rights (PVPO) or insufficient inventories. Accessions registered in the *Journal of Plant Registrations* (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* and *Secale* in the past year.

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

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
677227 JPR	*Triticum aestivum* subsp. *spelta*	Wirtas	Poland	Olsztyn
677329 PVP	*Triticum aestivum* subsp. *aestivum*	26R59	United States	Iowa
677361	*Triticum aestivum* subsp. *aestivum*	07OR1023	United States	Nebraska
677362	*Triticum aestivum* subsp. *aestivum*	07OR1062	United States	Nebraska
677363	*Triticum aestivum* subsp. *aestivum*	07OR1066	United States	Nebraska
677364	*Triticum aestivum* subsp. *aestivum*	07OR1071	United States	Nebraska
677365	*Triticum aestivum* subsp. *aestivum*	07OR1074	United States	Nebraska
677366 JPR	*Triticum aestivum* subsp. *aestivum*	GA 03564-12E6	United States	Georgia
677863	*Triticum aestivum* subsp. *aestivum*	NX11MD2337	United States	Nebraska
677864	*Triticum aestivum* subsp. *aestivum*	NX12Y8174	United States	Nebraska
677865	*Triticum aestivum* subsp. *aestivum*	NX12Y8175	United States	Nebraska
677866	*Triticum aestivum* subsp. *aestivum*	NX12Y8176	United States	Nebraska
677867	*Triticum aestivum* subsp. *aestivum*	NX12Y8178	United States	Nebraska
677868	*Triticum aestivum* subsp. *aestivum*	NX12Y8186	United States	Nebraska
677869	*Triticum aestivum* subsp. *aestivum*	NX12Y8187	United States	Nebraska
677870	*Triticum aestivum* subsp. *aestivum*	NX12Y8188	United States	Nebraska
677871	*Triticum aestivum* subsp. *aestivum*	NX12Y8189	United States	Nebraska
677872	*Triticum aestivum* subsp. *aestivum*	NX12Y8190	United States	Nebraska
677873	*Triticum aestivum* subsp. *aestivum*	NX12Y8205	United States	Nebraska
677874	*Triticum aestivum* subsp. *aestivum*	NX12Y8209	United States	Nebraska
677875	*Triticum aestivum* subsp. *aestivum*	NX12Y8210	United States	Nebraska
677876	*Triticum aestivum* subsp. *aestivum*	NX12Y8212	United States	Nebraska
677877	*Triticum aestivum* subsp. *aestivum*	NX12Y8213	United States	Nebraska
677878	*Triticum aestivum* subsp. *aestivum*	NX12Y8214	United States	Nebraska
677879	*Triticum aestivum* subsp. *aestivum*	NX12Y8215	United States	Nebraska
677880	*Triticum aestivum* subsp. *aestivum*	NX12Y8221	United States	Nebraska
677881	*Triticum aestivum* subsp. *aestivum*	NX12Y8222	United States	Nebraska

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

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
677882	*Triticum aestivum* subsp. *aestivum*	NX12Y8223	United States	Nebraska
678374 JPR	*Triticum aestivum* subsp. *aestivum*	H192	China	Beijing
678375 JPR	*Triticum aestivum* subsp. *aestivum*	H782	China	Beijing
678430 PVP	*Triticum aestivum* subsp. *aestivum*	Bolles	United States	Minnesota
678431 PVP	*Triticum aestivum* subsp. *aestivum*	A040064G1	United States	Iowa
678432 PVP	*Triticum aestivum* subsp. *aestivum*	A050068B1	United States	Iowa
678433 PVP	*Triticum aestivum* subsp. *aestivum*	A050264A1	United States	Iowa
678434 PVP	*Triticum aestivum* subsp. *aestivum*	W040376U1	United States	Iowa
678435 PVP	*Triticum aestivum* subsp. *aestivum*	W040592H1	United States	Iowa
678436 PVP	*Triticum aestivum* subsp. *aestivum*	W050021Y1	United States	Iowa
678437 PVP	*Triticum aestivum* subsp. *aestivum*	W050037I1	United States	Iowa
678438 PVP	*Triticum aestivum* subsp. *aestivum*	W050115K1	United States	Iowa
678439 PVP	*Triticum aestivum* subsp. *aestivum*	W050200H1	United States	Iowa
678440 PVP	*Triticum aestivum* subsp. *aestivum*	W050216N2	United States	Iowa
678441 PVP	*Triticum aestivum* subsp. *aestivum*	W050369F1	United States	Iowa
678442 PVP	*Triticum aestivum* subsp. *aestivum*	Jasper	United States	Washington
678443 PVP	*Triticum aestivum* subsp. *aestivum*	WB9208	United States	Minnesota
678621 PVP	*Triticum aestivum* subsp. *aestivum*	SY Assure	United States	Iowa
678623 PVP	*Triticum aestivum* subsp. *aestivum*	SY Touchstone	United States	Iowa
678624 JPR	*Triticum aestivum* subsp. *aestivum*	ShunMai Triplet	China	
678626 PVP	*Triticum aestivum* subsp. *aestivum*	SY 944	United States	Idaho
678627 PVP	*Triticum aestivum* subsp. *aestivum*	SY Grit	United States	Idaho
678628 PVP	*Triticum aestivum* subsp. *aestivum*	SY Rustler	United States	Idaho
678629 PVP	*Triticum aestivum* subsp. *aestivum*	UI Magic	United States	Idaho
678630 PVP	*Triticum aestivum* subsp. *aestivum*	UI Palouse	United States	Idaho
678681 PVP	*Triticum aestivum* subsp. *aestivum*	Boost	United States	South Dakota
678682 PVP	*Triticum aestivum* subsp. *aestivum*	Surpass	United States	South Dakota
678683 PVP	*Triticum aestivum* subsp. *aestivum*	Patwin-515HP	United States	California
678853 PVP	*Triticum aestivum* subsp. *aestivum*	UI-WSU- Huffman	United States	Idaho
678854 PVP	*Triticum aestivum* subsp. *aestivum*	WB4303	United States	Missouri
678855 PVP	*Triticum aestivum* subsp. *aestivum*	WB4462	United States	Missouri
678856 PVP	*Triticum aestivum* subsp. *aestivum*	WB4483	United States	Missouri
678857 PVP	*Triticum aestivum* subsp. *aestivum*	WB4515	United States	Missouri
678858 PVP	*Triticum aestivum* subsp. *aestivum*	WB4721	United States	Missouri
678859 PVP	*Triticum aestivum* subsp. *aestivum*	WB7566	United States	Missouri
678860 PVP	*Triticum aestivum* subsp. *aestivum*	WB9200	United States	Missouri
678861 PVP	*Triticum aestivum* subsp. *aestivum*	WB9312	United States	Missouri
678862 PVP	*Triticum aestivum* subsp. *aestivum*	WB9483	United States	Missouri
678936 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Jet	United States	Colorado
678944 PVP	*Triticum aestivum* subsp. *aestivum*	Pritchett	United States	Washington
678945 PVP	*Triticum aestivum* subsp. *aestivum*	Langin	United States	Colorado
678964 PVP	*Triticum aestivum* subsp. *aestivum*	AGS 2027	United States	Georgia
678965 PVP	*Triticum aestivum* subsp. *aestivum*	L11544	United States	Georgia
678966 PVP	*Triticum aestivum* subsp. *aestivum*	Sequoia	United States	Washington
678967 PVP	*Triticum aestivum* subsp. *aestivum*	122001W	United States	Iowa
678968 PVP	*Triticum aestivum* subsp. *aestivum*	SY Rockford	United States	Iowa
678969 PVP	*Triticum aestivum* subsp. *aestivum*	SY Saltese	United States	Iowa
678970 PVP	*Triticum aestivum* subsp. *aestivum*	AGS 2055	United States	Arkansas
679596 PVP	*X Triticosecale spp.*	946802617	United States	Idaho
679598	*Triticum aestivum* subsp. *aestivum*	Line 128-10	United States	Washington

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

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
679599	*Triticum aestivum* subsp. *aestivum*	Line 17-2	United States	Washington
679600	*Triticum aestivum* subsp. *aestivum*	Line 171	United States	Washington
679601	*Triticum aestivum* subsp. *aestivum*	Line 83	United States	Washington
679602	*Triticum aestivum* subsp. *aestivum*	Line 153	United States	Washington
679603	*Triticum aestivum* subsp. *aestivum*	Line 37-4	United States	Washington
679604	*Triticum aestivum* subsp. *aestivum*	Line 701B11	United States	Washington
679605	*Triticum aestivum* subsp. *aestivum*	Line 17-3	United States	Washington
679606	*Triticum aestivum* subsp. *aestivum*	Line 5-1	United States	Washington
679607	*Triticum aestivum* subsp. *aestivum*	Line 7-1	United States	Washington
679608	*Triticum aestivum* subsp. *aestivum*	Line 313	United States	Washington
679609	*Triticum aestivum* subsp. *aestivum*	Line 195	United States	Washington
679610	*Triticum aestivum* subsp. *aestivum*	Line 71	United States	Washington
679611	*Triticum aestivum* subsp. *aestivum*	Line 178	United States	Washington
679612	*Triticum aestivum* subsp. *aestivum*	Line 291	United States	Washington
679613	*Triticum aestivum* subsp. *aestivum*	Line 174	United States	Washington
679614	*Triticum aestivum* subsp. *aestivum*	Line 186	United States	Washington
679615	*Triticum aestivum* subsp. *aestivum*	Line 51	United States	Washington
679616	*Triticum aestivum* subsp. *aestivum*	Line 131	United States	Washington
679617	*Triticum aestivum* subsp. *aestivum*	Line 67	United States	Washington
679618	*Triticum aestivum* subsp. *aestivum*	Line 10	United States	Washington
679619	*Triticum aestivum* subsp. *aestivum*	Line 47	United States	Washington
679620	*Triticum aestivum* subsp. *aestivum*	Line 224	United States	Washington
679621	*Triticum aestivum* subsp. *aestivum*	Select Line 47	United States	Washington
679622	*Triticum aestivum* subsp. *aestivum*	Line 75	United States	Washington
679623	*Triticum aestivum* subsp. *aestivum*	Line 7-10	United States	Washington
679624	*Triticum aestivum* subsp. *aestivum*	Select Line 16-13	United States	Washington
679625	*Triticum aestivum* subsp. *aestivum*	Line 9	United States	Washington
679626	*Triticum aestivum* subsp. *aestivum*	Line 131-1	United States	Washington
679951 PVP	*X Triticosecale spp.*	FL01143	United States	Florida
679952 PVP	*Triticum aestivum* subsp. *aestivum*	NF101	United States	Oklahoma
679953 PVP	*Triticum aestivum* subsp. *aestivum*	Vision 50	United States	Virginia
679954 PVP	*Triticum aestivum* subsp. *aestivum*	L11550	United States	Virginia
679955 PVP	*Triticum aestivum* subsp. *aestivum*	SH7200	United States	Virginia
679956 PVP	*Triticum aestivum* subsp. *aestivum*	16162660	United States	Virginia
679964 PVP	*Triticum aestivum* subsp. *aestivum*	NS Presser CLP	United States	Montana
679968 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Evina	United States	Colorado
679969	*Triticum aestivum* subsp. *aestivum*	NW05MD6011-10-2	United States	Nebraska
679970	*Triticum aestivum* subsp. *aestivum*	NW05MD6011-4-3	United States	Nebraska
679971	*Triticum aestivum* subsp. *aestivum*	NW05MD6011-5-3	United States	Nebraska
679972	*Triticum aestivum* subsp. *aestivum*	NW05MD6011-23-4	United States	Nebraska
679973	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-3-2	United States	Nebraska
679974	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-7-1	United States	Nebraska
679975	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-9-1	United States	Nebraska
679976	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-11-4	United States	Nebraska
679977	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-13-4	United States	Nebraska
679978	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-17-2	United States	Nebraska
679979	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-18-2	United States	Nebraska
679980	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-18-4	United States	Nebraska
679981	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-23-3	United States	Nebraska
679982	*Triticum aestivum* subsp. *aestivum*	NW05MD6012-24-1	United States	Nebraska

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

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
679983	*Triticum aestivum* subsp. *aestivum*	NW05MD6014-15-4	United States	Nebraska
679984	*Triticum aestivum* subsp. *aestivum*	NW05MD6014-17-1	United States	Nebraska
679985	*Triticum aestivum* subsp. *aestivum*	NW05MD6014-24-3	United States	Nebraska
679986	*Triticum aestivum* subsp. *aestivum*	NM05MD6015-13-4	United States	Nebraska
679987	*Triticum aestivum* subsp. *aestivum*	NW05MD6016-4-3	United States	Nebraska
679988	*Triticum aestivum* subsp. *aestivum*	NW05MD6018-12-2	United States	Nebraska
679989	*Triticum aestivum* subsp. *aestivum*	NW04Y2210	United States	Nebraska
679990	*Triticum aestivum* subsp. *aestivum*	NW06Y2471	United States	Nebraska
679991	*Triticum aestivum* subsp. *aestivum*	NW06452	United States	Nebraska
679992	*Triticum aestivum* subsp. *aestivum*	NW08611	United States	Nebraska
679993	*Triticum aestivum* subsp. *aestivum*	NW10408	United States	Nebraska
679994	*Triticum aestivum* subsp. *aestivum*	NW10409	United States	Nebraska
679995	*Triticum aestivum* subsp. *aestivum*	NW10410	United States	Nebraska
679996	*Triticum aestivum* subsp. *aestivum*	NW10483	United States	Nebraska
679997	*Triticum aestivum* subsp. *aestivum*	NW10496	United States	Nebraska
679998	*Triticum aestivum* subsp. *aestivum*	NW10503	United States	Nebraska
679999	*Triticum aestivum* subsp. *aestivum*	NW10630	United States	Nebraska
680574 PVP	*Triticum aestivum* subsp. *aestivum*	AG Robust	United States	Colorado
680575 PVP	*Triticum aestivum* subsp. *aestivum*	AG Gallant	United States	Colorado
680576 PVP	*Triticum aestivum* subsp. *aestivum*	Loma	United States	Montana
680589 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Drive	United States	Colorado
680612 PVP	*Triticum aestivum* subsp. *aestivum*	UI Sparrow	United States	Idaho
680616 PVP	*Triticum aestivum* subsp. *aestivum*	Stardust	United States	Oklahoma
680626 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Chrome	United States	Colorado
680627 PVP	*Triticum aestivum* subsp. *aestivum*	Long Branch	United States	Colorado
680639 JPR	*Triticum aestivum* subsp. *aestivum*	Earl	United States	Washington
681595 PVP	*Triticum aestivum* subsp. *aestivum*	Tatanka	United States	Kansas
681613 PVP	*Triticum aestivum* subsp. *aestivum*	122003W	United States	Iowa
681614 PVP	*Triticum aestivum* subsp. *aestivum*	122004W	United States	Iowa
681615 PVP	*Triticum aestivum* subsp. *aestivum*	122005W	United States	Iowa
681616 PVP	*Triticum aestivum* subsp. *aestivum*	122006W	United States	Iowa
681617 PVP	*Triticum aestivum* subsp. *aestivum*	122008W	United States	Iowa
681618 PVP	*Triticum aestivum* subsp. *aestivum*	Shelly	United States	Minnesota
681619 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Anchor	United States	Colorado
681649 PVP	*Triticum aestivum* subsp. *aestivum*	Norwest Tandem	United States	Oregon
681650 PVP	*Triticum aestivum* subsp. *aestivum*	Norwest Duet	United States	Oregon
681653 PVP	*Triticum aestivum* subsp. *aestivum*	Tekoa	United States	Washington
681654 PVP	*X Triticosecale spp*.	Circuit	Canada	Ontario
681713	*Triticum aestivum* subsp. *aestivum*	SXD43	United States	Montana
681723 PVP	*Triticum aestivum* subsp. *aestivum*	W06-703w28	United States	Illinois
681724 PVP	*Triticum aestivum* subsp. *aestivum*	112374W	United States	Illinois
681725 PVP	*Triticum aestivum* subsp. *aestivum*	Starburst	United States	Illinois

IV. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2017 SUPPLEMENT

R.A. McIntosh[1], J. Dubcovsky[2], W.J. Rogers[3], C.F. Morris[4], and X.C. Xia[5].

[1]The University of Sydney, Plant Breeding Institute Cobbitty, PMB 4011, Narellen, NSW 2570, Australia. robert.mcintosh@sydney.edu.au.
[2]Department of Plant Sciences, University of California, Davis, CA 95616, USA. jdubcovsky@ucdavis.edu.
[3]Catedra de Genetica y Fitotecnia, DCBA y B, Facultad de Agronomia, CIISAS, CIC–BIOLAB AZUL, Universidad Nacional del Centro de la Provincia de Buenos Aires, Argentina; Av. Rep. Italia 780, CC47 73 Azul, Provincia de Buenos Aires, Argentina. CONICET–INBA–CEBB–MdP. rogers@faa.unicen.edu.ar.
[4]USDA–ARS Western Wheat Laboratory, Pullman, WA 99164-6394, USA. morris@wsu.edu
[5]Institute of Crop Science, National Wheat Improvement Centre, Chinese Academy of Agricultural Sciences, 12 Zhongguancun South St, Beijing 100081, China. xiaxianchun@caas.cn.

The most recent version of the Catalogue, compiled for the 12Th International Wheat Genetics Symposium held in Yokohama, Japan, is available on the Komugi (http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp) and GrainGenes (http://wheat.pw.usda.gov/GG2/*Triticum*/wgc/2008/) websites. Supplements 2013–14 and 2015–16 also are available at those sites.

Laboratory Designators

ui Hole D
University of Idaho
1693 S 2700 W
Aberdeen, ID 83210
USA

Morphological and Physiological Traits

1. Gross Morphology:Spike characteristics
1.1. Squarehead/spelt
Add at the end of section:
A nucleotide change in the microRNA172 binding site of the *Q* locus played a critical role in wheat domestication and the origin of free-threshing modern wheats {11192}.

5. Anthocyanin Pigmentation
5.3. Red/purple coleoptiles

***Rc-D1*.**
***RcD1a*.** **v:** Add: Gaoyuan 115 {11160}.
c: *TaMYB-D1* isolated from Gaoyuan 115 was proposed as the candidate gene {11160}.

5.5. Purple grain/pericarp
At the end of section add:
A set of Saratovskaya 29 NILs is described in {11136}.

18. Dormancy (Seed)
18.1. Germination index
***TaSdr-A1*.** {11199} 2A {11119}.
ma: *Xgwm95-2A* – 1.4 cM – *TaSdr-A1* – 1.5 cM – *Xgwm372-2A* {11199}.
TaSdr-A1a {11119}. **v:** Yangxiaomai {11119}.
Associated with low germination index.
TaSdr-A1b {11119}. **v:** Zhongyou 9507 {11119}.
Associated with high germination index.

Change present entry ***TaSdr*** to ***TaSdr-B1***

20. Earliness per se

Eps-1A^m. **ma:** Add: The circadian clock gene *Elf3* was identified as a candidate gene for *Eps-A^{m}1* {11120}.

Following the *Eps-A1b* add:

Eps-D1 {111903}. 1DL {M11193}.

v: Earliness allele: Cadenza and Spark {11193}. Lateness allele: Avalon and Rialto{11193}.

ma: The earliness allele was associated with a subtelomeric deletion containing three candidate genes, one of which was *TaELF-D1* {11193}. A QTL for heading date co-segregated with *TaELF3-1DL* in an RIL population derived from 'Gaocheng 8901 / Zhoumai 16' {11194}; a deletion of the *Eps-1D* region was associated with earlier flowering.

29. Glaucousness (Waxiness/Glossiness)

29.2 Epistatic inhibitors of glaucousness

QTL

Leaf glaucousness

RAC875 (glaucous) / Kukri (nonglaucous). Several QTL affected leaf glaucousness, the strongest of which was *QW.aww-3A*; QTL of lesser effect, *QW.aww-3B* and *QW.aww-3D,* were detected at homoeologous regions on chromosomes 3B and 3D, respectively {11131}.

24. Flour Color

Add to the present information:

Lutein is one of the carotenoids contributing to flour color. Esterification of lutein contributes to its stability during storage. A locus controlling esterification was located in chromosome 7D.

Lutein esterification

Lute {11189}. 7DS {11189}. **bin:** 7DS4-0.61-1.00.

ma: *Xwmc438-7D* – 15.1 cM – *Lute*/*XwPt-1163*/*XwPt-3727* – 17.7 cM – *Xbarc154-7* {11189}. Assigned to BAC TaBAC470M18 {11189}.

Alleles:

Lute High lutein ester.

v: Indis {11189}; Sunco*2/Indus Der. DM5685*B12 {11189}. Most bread wheat accessions.

lute Low lutein ester.

v: Haruhikari {11189}.

Sunco is low lutein but high ester, whereas Haruhikari is low lutein and zero ester. Lutein esters were not detected in durum {11189}.

33. Grain Traits

Variation in grain traits based on gene homology with other species

Insert above *TaSAP-A1*.

Tabas1-B1 {M11198}. 2BL {M11198}.

ma: *Xbarc167-2B* – 10.38 cM – *Tabas1* – 5.23 cM – *Xcfa2278-2B* {11198}.

c: BAS1is a type of 2-Cys peroxiredoxin in a large peroxidase family.

Tabas1-B1a {11198}. **v:** Jing 411 {M11198}.

Associated with higher TKW.

Tabas1-B1b {11198}. **v:** Hongmanchun 21 {11198}.

Associated with lower TKW.

TaGW-A2 {11121,11122}. Orthologous to the rice RING-type E3 ubiquitin ligase OsGW2 that functions as a negative regulator of grain weight.

6A {11121}.

ma: TaGW2 was mapped on the 'Spark / Rialto' DH population to chromosome 6A and linked to markers BS000072146, BS000105973 and CA643341 at 46.8 cM {11121}.

c: GenBank KP749901.1 {11122}.

A loss-of-function mutation in *TaGW2-A1* was associated with a 6.6% increase in grain weight in tetraploid and hexaploid wheat {11122}.

Insert after *TaSAP-A1*.

TaTGW6-A1 {11196}. 3AL {11196}.

ma: *Gene-3665_61* – 2 cM – *TaTGW-A1* – 18 cM – *BobWhite_c47304_56* {M11196}.

c: TGW6 in rice encodes an indole-3-acetic acid -glucose hydrolase {11196}.

TaTGW-A1a {11196}.

v: Doumai {11196}; Zhou 8425B {11196}.

Associated with higher TKW.

TaTGW-A1b {11196}.

v: Chinese Spring {11196}.

Associated with lower TKW.

TaTGW-B1 {11196}. 3BL {11196}.

TaTGW-D1 {11196}. 3DL {11196}.

TaTGW-7A {11197}. 7AS {11197}. **Bin:** C–7AS8–0–0.45.

ma: *SLAF49035* – 3.02 cM – *TaTGW7A/TG* – 9.19 cM – *Xbarc-7A* {M11197}.

c: Traes–7AS_378A12AA9.1. *GW2* in rice encodes an E3 ubiquitin ligase {11197}.

TaTGW-7Aa {11197}. **v:** Jing 411 {M11197}.

Associated with higher TKW.

TaTGW-7Ab {11197}. **v:** Hongmanchun 21 {11197}.

Associated with lower grain weight.

44. Height

44.2. Reduced Height: GA-sensitive

Rht24. {11185}. *QTL_height_6A_1* {11183}; *QPH.caas-6A* {11184}. 6AL {11185}.

v: Aikang 58 {11185}.

ma: *Xwmc256-6A* – 2.71 cM – *TaGa3* – 7.05 cM – *TaAP2* – 0.24 cM – *Rht24* – 1.61 cM – *TaFAR* – 13.87 cM – *Xbarc103-6A* {11185}.

Rht24 was identified in many Chinese cultivars and a low number of European wheats based on flanking markers designed from *TaAP2* and *TaFAR* {11185}.

46. Hybrid Weakness

46.5. Hybrid weakness type III

Nec1 {11158}. 7DS {11158}.

v: (*Triticum turgidum* subsp. *durum* cv. Langdon / *Aegilops tauschii* KU-2828) amphiploid {11158}.

al: *Aegilops tauschii* KU-2828 {11158}.

ma: *Xbarc352-7D* – 5.3 cM – *Lr34* – *Xgwm295-7D* – 4.0 cM – *Xbarc154-7D* – 1.7 cM – *Nec1* – 13.2 cm – *Xcfd-7D* {11158}.

Although this form of hybrid necrosis is caused by complementary genes mapping of *Nec1* was based on a cross of necrotic and non-necrotic 'Langdon / *Aegilops tauschii*' amphiploids. Consequently only *Nec1* was mapped {11158}.

53. Male Sterility

53.3 Photoperiod and/or temperature-sensitive male sterility (PTGMS)

List as the first entry:

tmsBS20T {11157}. 2BL {11157}. v: BS20-T {11157}.
ma: *Xgwm403-2B* – 2.2 cM – *tmsBS20T* – 4.5 cM – *Xgwm374-2B* {11157}.

***wptms1*.** Add note:
Chromosome 5B was also implicated in spontaneous mutant line Xinong 291S; a second gene was not located {11143}.

70. Response to Vernalization

Immediately above the ***Vrn-1*** heading continue the existing paragraph with: 'The *Vrn-D4* locus in TDF includes a duplication of ~290-kb region from chromosome arm 5AL inserted into the proximal region of chromosome arm 5DS. This translocated segment includes a functional copy of *VRN-A1* that carries distinctive mutations in its coding and regulatory regions {11123}.

***Vrn-2*.** Continue the current introductory paragraph with: 'A triple *Vrn2* mutant (PI 676269, synthetic *vrn2-null*) is available in hexaploid wheat combining the non-functional *vrn-A2* allele present in most polyploid wheats with a *Vrn-B2* deletion from tetraploid wheat, and a nonfunctional *vrn-D2* allele from *Aegilops tauschii* {11124}.'

***Vrn-B2*.** 4BL {11163}.
A study of winter wheats 2174 and Jagger showed that 2174 has a tandem repeat of *Vrn-B2,* whereas Jagger has a deletion of this gene {11163}. Identical apparently functional sequences of *Vrn-B2* were found in contig sequences of Chinese Spring obtained from chromosomes 4BS, 2BS, and 5DL {11163}.

***Vrn-D2*.** 4DL {11163}.

71. Restorers for Cytoplasmic Male Sterility

71.4 Restorers for temperature-sensitive *Aegilops kotschyi* cytoplasm

Two recessive genes for temperature-sensitive sterility as follows.

***rfv*$_1^{sp}$** {11151}. 1BS {11151}. **v:** MS line KTP116A *rfv*$_2$ {11151}.
ma: *Xgwm413-1B* – 8.9 cM – *rfv*$_1^{sp}$ – 12 cM – *Xgwm11-1B* {11151}.

***rfv*$_2$** {11151}. 2A {11151}. **v:** MS line KTP116A *rfv*$_1^{sp}$ {11151}.
ma: *Xwmc474-2A* – 23.9 cM – *rfv*$_2$ – 13.7 cM – *Xwmc644-2A* {11151}.

86. Proteins

86.2. Enzymes

86.2.30. Starch branching enzyme II

***SbeII*.**
Continue the present text with: 'Combined loss-of-function mutations in *SbeIIa-A*, *SbeIIa-B*, *SbeIIb-A*, and *SbeIIb-B* (PI 670160) increased amylose content by 66% and resistant starch by 753% relative to the control in tetraploid wheat cv. Kronos {11125}. A combination of these four mutations with mutations of *SbeIIa-D* in hexaploid wheat (PI 670160) increased amylose content by 63% and resistant starch by 1,057% in field experiments relative to the control {11126}.

86.3. Endosperm storage proteins

86.3.1.3. *Glu-3*
Add after the *GLU3* description and immediately before listing *Glu-A3*:
'Characterization of near isogenic lines for the different *Glu3* alleles provides a useful quantification of their contribution to bread-making quality {11129}.'

Pathogenic Disease/Pest Reaction

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

Pm2

Add note at end of section:

Several alleles of *Pm2* with wheat and alien origins have been reported in Chinese genotypes – see temporary designations.

Pm56 {11155}. Derived from *S. cereale*. 6AS (T6RS.6AL) {11155}.
v: LM47-6 {11155}. **al:** *S. cereale* cv. Qinling {11155}.
Study of misdivision products from a double monosomic 6A, 6R located *Pm5*6 to the subterminal region of 6RS {17026}.

Pm57 {11159}. Derived from *Ae. searsii*. 2BL (T2BS·2BL-2S^{S}#1L) {11159}.
v: Line 89-346, TA5108 {11159}; Line 89(5)69 TA5109 {11159}.
Line 89-346 has a 28% distal *Ae. searsii* segment and line 89(5)69 has a 33% distal *Ae. searsii* segment {11159}.

Pm58 {11171}. *PmTA1662* {11171}. Derived from *Ae. tauschii*. 2DS {11171}.
v: Reference line to be chosen and accessioned {11171}.
dv: *Ae. tauschii* TA1662 {11171}.
m**a:** Co-segregation with KASP™ markers *K-TP331370, K-TP338253, K-Tp15990*, and *K-Tp313873* {11171}.

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

PmHo {11176}. 2AL {11176}. **v:** Mv Hombar {11176}.
ma: *XwPt-665330* – 0.3 cM – *PmHo* – 0.1 cM – *XwPt-3114 {11176}*.

PmLX66 {11162}. 5DS {11162}. **v:** Liangxing 66 {11162}.
PmLX66 was allelic with *Pm2* {11162}.

PmTb7A.1 {11130}. 7AL {11130}. **bin:** 7AL18-0.90-1.00.
dv: *Triticum monococcum* subsp. *aegilopoides* PAU5088 *PmTb7A.2* {11130}.
ma: Mapped to a 4.3 region flanked by wPt4553 and Xcfa2019-7A {11130}. Estimated to be 46 cM proximal to *Pm1* {11130}.

PmTb7A.2 {11130}. 7AL {11130}.
dv: *Triticum monococcum* subsp. *aegilopoides* PAU5088 *PmTb7A.1* {11130}.
ma: Mapped to a 0.8 cM region flanked by *MAG1759* and *MAG2185b* {11130} in the region of *Pm1* {11130}.

PmW14 {11162}. 5DS {11162}. **v:** Wennong 14 {11162}.
PmWE14 was allelic with *Pm2* {11162}.

PmWE99 {11166}. Derived from *Thinopyrum intermedium*. 2BS {11166}.
bin: 2BS-0.84-1.00. **v:** WE99 {M18037}.
ma: *Pmw99* – 10.4 cM – *Xgwm148-2B* – 3.1 cM – *Xbarc55-2B* {11166}.
GISH failed to detect alien chromatin.

Mlm2033. Please correct the earlier entry listed as *Mlm3033*.
ma: *Xwgrc353*/*Xwggc4659* – 0.84 cM – *Mlm2033*/*Xmag8626*/*Xmag9060*/*Xmag2185*/*Xmag5240* – 0.06 cM – *Xmag8415*/*Xmag8220* {11190}.

Mlm80. **ma:** *Xwggc4655* – 0.29 cM – *Mlm80* – 0.57 cM – *Xwgrc253*/*Xwgrc271* {11190}.

90.4. QTL for resistance to *Blumeria graminis*

QPm-tut-4A {11154}. 4AL {11154}.
v: DT4AL-TM Line 8.1 {11154}.
tv: *Triticum aestivum* subsp. militinae (AAGG) {11154}.
The 7G segment carrying this resistance likely replaces most of the 7BS segment known to be part of chromosome 4A {11154}.

96. Reaction to *Fusarium* spp.
96.1. Disease: Fusarium head scab, scab
Fhb1. Add comment at end of section:
Lines combining *Fhb1*and *Sr2* are reported in {11170}; *Fhb1* is located about 2 cM proximal to *Sr2*.

'SYN1 / Ocoroni' DH population: three QTL from SYN1 were identified, *QFhs.cim-2D* (PVE 25%), *QFhs.cim-7A* (PVE 4.7%) and *Qfhs.cim-7A* (PVE 4.2%) {11165}.

98. 1 Reaction to *Magnaporthe grisea* (Herbert) Barr Add: **Syn. *Pyricularia oryzae***

Current *Mg* list.

98.2 Reaction to *Magnaporthe oryzae*.

Wheat cultivars carrying the 2NS translocation from *Aegilops ventricosa* had 50.4 to 72.3% less head blast than those without 2NS when inoculated with an older isolate (MoT) of *Magnaporthe oryzae* (*Triticum* pathotype) under growth chamber conditions. When inoculated with recently collected isolates from wheat, cultivars with 2NS had 64.0 to 80.5% less head blast {11127}.

101. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter, *Zymoseptoria tritici*
Add the synonym species name as above.

Stb3. [*Slb3*{1586}]. 6DS, according to {10556} this location is not correct{10105}. 7AS{10556, 11191}.
v: Israel 493{1586}.
ma: Please delete present material and replace with: *Xcfa2028-7A* — 12.4 cM — *Stb3*/*Xwmc83-7A* — 2/1 cM — *Xbarc222-7A* {11191}

102. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano); *Parastagonospora nodorum*
102.2 Sensitivity to SNB toxins (necrotrphic effectors)

Tsn1. The ma: line listed above this heading should be inserted in the *Tsn1* entry section.

Snn1. *KASP marker Bs00093078_51* was developed at Wang map position 8.361 in the UK MAGIC population {11133}.

QTL: Add:
QSnn.niab-5A.1 {11133} **v:** Identified in the UK MAGIC population {11133}.

105. Reaction to *Puccinia graminis* Pers.
Sr2. Add comment at end of section:
Lines combining *Sr2* and *Fhb1* are reported in {11170}; *Sr2* is located about 2 cM distal to *Fhb1*.

Sr9.
Sr9h. Add note at end of section:
Although {11149} concluded that *Sr28* was present in VL404 and Janz, it is more likely that the gene described is the linked gene *Sr9h*. *Sr9h* was frequently present in landraces with field resistance to early isolates of the *Pgt* race Ug99 group {11147}.

Sr11. **v2:** Add: Charter Sr9h {11177}; Trident Sr38 {11177}.
ma: *KASP_6BL_IWB46893* – 0.3 cM – *Sr11*/*KASP_6BL_IWB10724* – 0.3 cM – *KASP_6BL_IWB72471* {11177}.

Sr13. Add at end of section:
Markers *Xgwm427-6A* and *AFSr13S* (proximal) and *Xdupw-6A* (distal) showed variable but close (<10 cM) linkage with *Sr13* in six durum crosses – these markers were variously applicable across durum backgrounds, but only *Xgwm427-6A* was variable in a range of hexaploid derivatives with *Sr13* likely originating from a single source {11146}.

Sr26. Add note:
Secondary recombinants with shortened 6AL#1L segments involving chromosomes 6A and 6D are reported in {11141}; five 6A recombinants were accessioned in the Australian Winter Cereals Collection.

Sr28. **v:** Add: SD 1691, CI 12499 {11148}.
ma: *Xwmc332* – 1.4 cM – *r28* – 6.0 cM – *wPt-7007* {11148}; *Sr28* – 1.6 cM – *wPt-7004* {11148}; *Sr28* – 0.6 cM – *wPt-7004* {11148}.
Although {11149} concluded that *Sr28* was present in VL404 and Janz it is more likely that the gene described is the linked gene *Sr9h*.

Sr35. To the chromosome location add: ‚3A^{m}L {11140}.
ma: Add: *AK331487* – 0.02 cM – *Sr35* – 0.98 cM – *AK332451* {11140}.
c: *Sr35* is has a coiled-coil-NBS-LRR structure {11140}.

Sr42. Add note at end:
A genetic analysis of six lines, Blouk, Coni, Niini, Pfuneye, Ripper, and Tinkio, is reported in {11132}. All had single genes with linkage to *Xcfd49-6D* ranging from 3.9–12.5 cM, and the genes were not distinguished clearly from *Sr42* or *SrTmp* {11132}.

Sr45. **su:** CS1D5406 {11134}.
ma: *Xgwm106-1D*/*BE44426* – 1.82 cM – *Sr45* – 0.39 cM – *csssu45*/*Af45* {11134}.
To present note add:
One race distinguishing *Sr45* and *Sr21* is reported in {11134}.

Sr56. **bin:** Correct to: 5BL16-0.79-1.00.
ma: Replace present information with: *Xsun209* (SSR) – 2.6 cm – *Sr56* – 1.2 cM – *Xsun320* (STS from wPt-7665) {10851}.

Sr59. **ma:** Three rye-based KASP markers identified lines with *Sr59* {11066}.

SrPI410966 {11180}. 2BS {11180}. **v:** PI 410966 {11180}.
The marker profile for this gene was very similar to that of a line with *Sr36* {11180,10825}. Specificity tests were not reported.

SrTmp. **v:** Add: Digalu {11132}; Ember {11152}; Guard-1 {11152}; Kenya Robin {11152}; Morvarid {11132}; Overland {11152}; Ripper {11132}; Shield {11152}.

Sr10187. *SrTA10187* {11181}.
ma: Add: *6DS0027* – 0.2 cM – *Sr10187* – 0.2 cM – *6DS00273* {11181}; *Sr10187* – 0.2 cM – *6DS0039* {11181}.

At the end of the gene list:
Genotype lists: {Add: 17006}.

106. Reaction to *Puccinia striiformis* Westend.

106.1. Designated genes for resistance to stripe rust

Yr5. **i:** Add: Lemhi+Yr5 {11153}.
ma: *Xwmc175-2B* – 4.6 CM – *Yr5*/ *TaAffrx.65234.1.S2-at*/*Ta.28038* – 0.7 cM – *S23M41-310*/ *STS:S23M41-275* {11153}.

Yr6. **v2:** Add: Cadenza Yr7 {11187}.
ma: *Xgwm577-7B* – *Yr6* <0.4 cM {11187}. Narrowed to an ~60-kb region including *Xgwm577* {11188}. Given the location of *Xgwm577*, the gene location should be 7BL.

Yr7. **v2:** Cadenza *Yr6* {11187}.
ma: *Xwmc175A-2B* – *Yr7* <0.4 cM {11187}.

Yr10. **v:** Add: AC Radiant {11167}; Jacmar {11145}.
c: Yr10 has a CC-NBS-LRR structure {11145}. GenBank AF149112 {11145}.

Yr15. **ma:** Add: *Xbarc8-1B* – 3.9 cm – *Yr15* – 2.5 cM – *Xgwm413-1BS* {11173}.

Yr18. **v:** Add: Libellula {11139}; Strampelli {11139}.
Libellula had an additional four QTL and Strampelli had an additional 3 QTL {11139}.

Yr32. **v:** Toisondor {11144}.

Yr36. **c:** Add: *Sr36* was shown to reduce the ability of the thylakoid-associated ascorbate peroxidase to detoxify reactive oxygen species {11128}.

Yr47. **bin:** 5BS6-0.81-1.00.
ma: Change present entry to: *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xcfb309-5B* – *Xsun480*/*Xmag705*/*Xfcp552-5B* – 0.4 cM – *Yr47* – 4.3 cM – *icg16c008*/*Xgwm234-5B* {11200}; *Xsun180* – 0.4 cM – *Lr52* – 0.2 cM – *Yr47* – 1.4 cM – *Xgwm234-5B* {11200}.

Yr51. *YrAW1* {10850}. **v2:** Correct to: *AUS27859 Yr57 {10850}.*
ma: Replace the present entry with: *Xowm45F3R304A* – 1.2 cM – *Yr51* – 2.5 cM – *Xsun104-4A* – 1.8 cM – *Xgwm160-4A* {10850}.

Yr57. *YrAW2* {10963}.

Yr60. Modify the current entry to the following:
Yr60 {10968}. 4AL {10968}. **v1:** Almop, Avocet*3//Lalbmono1B*4/Pavon GID 5934039 {10968}.
v2: LB (Pavon1B) *Yr29* {10968}.
ma: *Xwmc313*/*Xwmc219-4A* – 0.51 cM – *Yr60*/*Xwmc776-4A* {10968}.
Yr60 was estimated to be about 10 cM distal to *Yr51*.

Yr69. Add: Derived from *Thinopyrum ponticum*.

Yr77 {11174}. Adult-plant resistance. *QYr.ucw-6D* {11174} 6DS {11174}.
v: PI 322118 {11174}; PI 164377 {11174}; PI 388095 {11174}; PI 520350 {11174}; PI 623378 {11174}.
ma: *Yr77* was strongly associated with *IWA167* in the region *Xbarc54-6D* (6DS) – 15.2 cM – *IWA167* (6DS) – 3.9 cM – *Xcfd188-6D* (6DL) {11174}.
Among the listed accessions two were from India, one from Pakistan, one from Iran, and one from the USA.

Yr78 {11174}. Adult-plant resistance. *QYr.ucw-6B* {11174}.
6BS {11174}. **v:** PI 519805 {11174}; Nine others {11174}.
ma: The *Yr78* peak fell within a 4.3-cM interval, IWA7257 – *Xwmc737-6B* {11174}.

106.2. Temporarily designated genes for resistance to stripe rust

YrF {11156}. 2BS {11156}. **v:** Francolin#1 *Yr46* {11156}.
Francolin#1 also is released under the names Ufam and BARI Gom 27 {11156}.

YrJ22 {11195}. 2AL { 11195.}. **v**: Jimai 22 {11195}.
ma: *Xgwm382-2AL* – 1.0 cM – *YrJ22* – 7.3 cM – *IWA1348* {11195}.

Yrwh2 {11150}. Recessive. 3BS {11150}. **v:** Wuhan 2 {11150}.
ma: *Xwmc540-3B* – 5.9 cM – *Yrwh2* – 10 cM – *Xgwm566-3B* {11150}.

106.3. Stripe rust QTL

'Camp Remy / Recital': Add:Differential reactions of RILs possessing different QTL occurred between old and new *P. striiformis* races {11144}.

'Coker 9835 (S) / VA96W-270' RIL population: Adult-plant resistance was conferred by *QYr.ar-3BS* (nearest markers *Xbarc147, ger9-3p,* and *IWA6092*) and *QYr.ar-4BL* (nearest markers *Xbarc163, Xcfd39*, and several *IWA* markers {11175}. Cultivar Pat had the same haplotype {11175}.

'USG 3555 / Neuse': Add:Three QTL on chromosomes 1AS, 4BL, and 7D (not *Yr18*) were derived from USG 3555 and one QTL on chromosome 3A was from Neuse {11142}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

Lr19. **v:** Pallada {11161}.

Lr48. **ma:** Add: *Xsun563*/*Xsun497* – 0.6 cM – 5 SNP markers/*Lr48* – 0.3 cM – *IWB70147* – 2.0 cM – *Xbarc0-7-2B* – 9.4 cM – *Lr13* {11172}.
Add comment: The suggestion that this gene is present in 13 Australian cultivars carrying *Lr48* markers and, hence, *Lr48* {11172} needs verification.

Lr52. **bin:** 5BS6-0.81-1.00.
ma: Change present entry to: *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xcfb309-5B* – *Xsun480*/*Xmag705*/*Xfcp552-5B* – 0.4 cM – *Yr47* – 4.3 cM – *icg16c008*/*Xgwm234-5B* {11200}; *Xsun180* – 0.4 cM – *Lr52* – 0.2 cM – *Yr47* – 1.4 cM – *Xgwm234-5B* {11200}.

Lr70 {10904}. 5DS {10904}. **v2:** KU3198 Lrk1 {10904}.
ma: *Lr70* – 5.6 cM – *Xbarc130-5D* – 1.7 cM – *Xwmc233-5D* {10904}.

Lr75. Remove the 'P' from the synonym. **bin:** 1BS10-0.5-1.00.
v2: Update to: Forno *Lr14a Lr34* {11053}.
bin: Update to: *Xgwm604-1B* – 1.6 cM – *Lr75* – 2.70 cM – *swm271* – 0.14 cM – *Xgwm11-1B*/*Xgwm18-1B*/*swm294*/*swm278*/*swm275* {11053}.

Lr77 {11164}. Adult-plant resistance 3BL {11164}.
v: Tc*3 / Santa Fe 8-1C.9 {11164}.
v2: Duster *Lr3a Lr11 Lr34* PI 639233{11164}; Santa Fe *Lr3a Lr17a Lr37* PI 641772{11164}.
ma: *IWB32653* – 1.15 cM – *KASP23680* – 1.15 cM – *Lr77*/*KASP10344*/*Kasp73555* – 0.62 cM – *KASP12260* – 2.46 cM – *IWB79797* {11164}.

LrK1 {10904}. 5BS {10904}. **v2:** Ku3198 *Lr70* {10904}.
ma: *LrK1* – 0.6 cM – *Xcfd20*/*Xgwm234-5B* {10904}.
LrK1 could be *Lr52* or an allele {10904}.

At the end of the gene lists:
Genotype lists: Insert 'Croatian cultivars {11135}'. 'Kazakhstan cultivars {11161}'.
At the end of section add:
See {11178} for review and analysis of leaf rust resistance genes in six durum wheats.

111. Reaction to *Sitodiplosis mosellana* (Gehin)

Sm1. **v:** Add: Augusta {11137}; Robigus {11137}; Skalmeje {11137}.
ma: Add: A combination of 2BS-5344126_kwm707 and 2BS-6229175_kwm693 appeared to be predictive of *Sm1*, but there was variation between sources {11137}.

113. Reaction to Soil-Borne Cereal Mosaic Virus (SBCMC)

Sbm1. **v:** Add: Claire {11138}; Moulin {11138}; Tremie {11138}.
ma: Add: *E37M49* – 9.0 cM – *Sbm1* – 1.0 cM – *Xgwm469-5D* – 2.0 cM – *Xwmc765-5D* {11138}. Resistant cultivars carried 152- or 154-bp alleles at *Xgwm469-5D*; all susceptible genotypes had a null allele {11138}.

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

Ut4 Add reference {,11168}. *QUt.spa-7B* {11168}. 7B {11168}.
v: TD1{11168}; Glenlea {11168}; 9340-CP {11168}.
The current information listed for *Ut-X* can be transferred to *Ut5* using *Ut-X* as a synonym.

Ut5 {11168}. *Ut-X* {1164}.

Ut6 {11169}. *QUt.spa-5B* {11168}. 5BL {11169}.
v: AC Foremost {11169}; AC Karma {10040}; AC Vista {11168}; Chinese Spring {11169}; Glenlea {11169}; HY320 {11169}; Oasis {11169}.
ma: *Xgpw5029-5B* – 2.8 cM – *Ut6* – 2.8 cM – *Xbarc232-5B* {11169}.

Ut7 {11168}. *QUt.spa.7A* {11168}. 7A {11168}.
v: SC8021V2 {11168}.

Ut8 {11168}. *QUt.spa-3A* {11168}. 3A {11168}.
v: 9340-SP{11168}; Glenlea {11168}.

Ut9 {11168}. *QUt.spa-6B* {11168}. 6B {11168}.
v: SC8021V2 {11168}.

Ut10 {11168}. *QUt.sps-6D* {11168}. 6D {11168}.
v: SC80-21V2 {11168}.

QTL
Existing entry: Correct spelling of: Blizard.
'Idaho 444 (R) / Rio Blanco S': RIL population: Three QTL for dwarf bunt resistance: *QDB.ui-7DS* (R^2 = 0.3–0.6), *QDB.ui-1A* (r^2 = 0.11–0.15) and *QDB.ui-2B* (R^2 = 0.06). Two PCR-based markers were developed for the wPt-2565 sequence on chromosome 7DS {11182}.

119. Reaction to Wheat Streak Mosaic Virus

***Wsm1*.** 4D = T4DL·4J^{S}S. **v:** Mace PI 651043 {11179}.
Add note: *Wsm1* confers resistance at temperatures below 19C {11179}.

122. Reaction to Wheat Yellow Mosaic Virus

Following the entry *YmYF* and above the QTL: add:
QYr.nau-2D {11186}. 2DL {11186}. **bin:** 2DL9-0.76-1.00.
v: Yining Xiaomai {11186}.
ma: *Xwmc41-2D* – 3.7 cM – *2SNP86.2* – 0.4 cM – *QYm.nau-2D* – 1.0 cM – *2EST784* {11186}.

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Updates.

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

Scientific journals and publications:

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

Units of measurement:

bp = base pairs
bu = bushels
cM = centimorgan
ha = hectares
kDa = kiloDaltons
m^2 = square meters
m^3 = cubic meters
μ = micron
masl = meters above sea level
me = milli-equivalents
mL = milliliters
mmt = million metric tons
mt = metric tons
Q = quintals
T = tons

MISCELLANEOUS TERMS:

Al = aluminum
AFLP = amplified fragment length polymorphism
ANOVA = analysis of variance
A-PAGE = acid polyacrylamide gel electrophoresis
APR = adult-plant resistance
AUDPC = area under the disease progress curve
BC = back cross
BW = bread wheat
CHA = chemical hybridizing agent
CMS = cytoplasmic male sterile
CPS = Canadian Prairie spring wheat
DH = doubled haploid
DON = deoxynivalenol
ELISA = enzyme-linked immunosorbent assay
EMS = ethyl methanesulfonate
EST = expressed sequence tag
FAWWON = Facultative and Winter Wheat Observation Nursery
GA = gibberellic acid
GIS = geographic-information system
GM = genetically modified
GRIN = Germplasm Resources Information Network
HPLC = high pressure liquid chromatography
HMW = high-molecular weight (glutenins)
HRSW = hard red spring wheat
HRRW = hard red winter wheat
HWSW = hard white spring wheat
HWWW = hard white winter wheat
ISSR = inter-simple sequence repeat
IT = infection type
kD = kilodalton
LMW = low molecular weight (glutenins)
MAS = marker-assisted selection
NSF = National Science Foundation
NILs = near-isogenic lines
NIR = near infrared
NSW = New South Wales, region of Australia
PAGE = polyacrylamide gel electrophoresis
PCR = polymerase chain reaction
PFGE = pulsed-field gel electrophoresis
PMCs = pollen mother cells
PNW = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada)
PPO = polyphenol oxidase
QTL = quantative trait loci
RAPD = random amplified polymorphic DNA
RCB = randomized-complete block
RFLP = restriction fragment length polymorphism
RILs = recombinant inbred lines
RT-PCR = real-time polymerase-chain reaction
SAMPL = selective amplification of microsatellite polymorphic loci
SAUDPC = standardized area under the disease progress curve
SCAR = sequence-characterized amplified region
SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis
SE-HPLE = size-exclusion high-performance liquid chromatography
SH = synthetic hexaploid

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

VI. ADDRESSES OF CONTRIBUTORS.

The e-mail addresses of contributors denoted with a '*' are included in section VII.

ARGENTINA

CATEDRA DE GENETICA Y FITOTECNIA DCBA y B, Facultad de Agronomia, CIISAS, CIC-BIOLAB AZUL, Universidad Nacional del Centro de la Provincia de Buenos Aires, Argentina. Av. Rep. Italia 780, CC47 73 Azul, Provincia de Buenos Aires, Argentina. CONICET-INBA-CEBB-MdP. W.J. Rogers*.

AZERBAIJAN

GENETIC RESOURCES INSTITUTE Azerbaijan National Academy of Science, Baku, Azerbaijan. Mehraj Abbasov*, Zeynal Akparov, Khanbala Rustamov, Sevda Babayeva, Vusala Izzatullayeva, Fatma Sheykzamanova, Sveta Rzayeva, Elchin Hajiyev.

AUSTRALIA

THE UNIVERSITY OF SYDNEY Plant Breeding Institute Cobbitty, PMB 4011, Narellen, NSW 2570, Australia. Robert McIntosh*.

BRAZIL

BRAZILIAN AGRICULTURAL RESEARCH CORPORATION — EMBRAPA TRIGO Centro Nacional de Pesquisa de Trigo, Rodovia BR 285, Km 174, Caixa Postal 451, 99001-970, Passo Fundo, Rio Grande do Sul, Brazil. 54 3316.5817 or 54 99915.9163 (TEL); 54 3316.5801 (FAX). Eduardo Caierão*, Ricardo Lima de Castro, Márcio Só e Silva, Pedro Luiz Scheeren, Aldemir Pasinato.

FEPAGRO NORDESTE C.P. 20, 95.000-000 Vacaria, Rio Grande do Sul, Brazil. Marcelo de Carli Toigo, Rogério Ferreira Aires.

CANADA

NATIONAL RESEARCH COUNCIL CANADA Saskatoon, SK, Canada. Raju Datla, Daoquan Xiang, Teagen Quilichini, Prakash Venglat.

CZECH REPUBLIC

INSTITUTE OF EXPERIMENTAL BOTANY Centre of the Region Haná for Biotechnological and Agricultural Research, CZ 78371, Olomouc, Czech Republic. Mahmoud Said, Eva Hřibová, Jan Vrána, Jaroslav Doležel.

GERMANY

INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG (IPK) Corrensstraße 3, 06466 Gatersleben, Germany. (049) 39482 5229 (TEL); (049) 39482 280/5139 (FAX). http://www.ipk-gatersleben.de. A. Börner*, M. Agacka-Mołdoch, D.Z. Alomari, M.G. Cardelli, A.M. Castro, Yu.V. Chesnokov, A.K. Chistyakova, M. Dell' Arciprete, J.I. Dietz, K. Eggert, G.S. Gerard, D. Giménez, K. Jończyk, U. Lohwasser, G. Lori, I. Malbrán, E.V. Morozova, Q.H. Muqaddasi, M. Nagel, S.V. Osipova, H.M. Pardi, A.E. Perelló, L. Perello, A.V. Permyakov, M.D. Permyakova, T.A. Pshenichnikova, M.A. Rehman Arif, M.S. Röder, S.V. Rudakov, A.S. Rudakova, E.G. Rudikovskaya, A.V. Rudikovsky, L. Saldúa, M. Schierenbeck, U. Skomra, L.V. Shchukina, S. Shokat, M.R. Simón, A.V. Simonov, R. Tarawneh, J.P. Uranga, M.E. Vicente, N. von Wirén, M. Yanniccari, Chr. D. Zanke.

INDIA

AGRICULTURAL RESEARCH STATION Niphad, Maharashtra, India. D.A. Gadekar

BHABHA ATOMIC RESEARCH CENTRE

Nuclear Agriculture & Biotechnology Division Trombay, Mumbai–400085, India. 91-22-25592640 (TEL); 91-22-25505151/25505326 (FAX). G. Vishwakarma, Vikas, Bikram K. Das*, K. Suryavanshi, A.S. Shitre.

Moleuclar Biology Division Trombay, Mumbai-400085, India. A. Saini.

ICAR–INIDAN INSTITUTE OF WHEAT & BARLEY RESEARCH Karnal, Haryana. Satish Kumar, India. M.S. Saharan, Indu Sharma, C.N. Mishra.

SHER-E-KASHMIR UNIVERSITY OF AGRICULTURAL SCIENCES AND TECHNOLOGY–JAMMU Division of Genetics & Plant Breeding, Faculty of Agriculture (FoA), Chatha–18009, Jammu, India. Bikram Singh.

SHER-E-KASHMIR UNIVERSITY OF AGRICULTURAL SCIENCES AND TECHNOLOGY OF KASHMIR Division of Genetics & Plant Breeding, Faculty of Agriculture, SKUAST–K Wadura Campus, Sopore–193201, Kashmir, India. www.skuastkashmir.ac.in/. R.R. Mir, M.A. Khan, M. Ashraf Bhat, Sandhya Tyagi, Rahul Nelwadker, Tahir Yusuf, Safoora Shafi, Asma Hamid, Parvez Sofi, Kamaludin.

WHEAT RESEARCH UNIT Dr. PDKV, Akola, Maharashtra, India. N.R. Potdukhe, S.R. Bharad.

MEXICO

CIMMYT INT (INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER) Km. 45, Carretera, México-Veracruz, El Batán, Texcoco CP 56237, Edo. de México, Mexico. 52 (55) 5804 2004 or 52 (595) 952 1900 (TEL). http://http://www.cimmyt.org. Ravi P. Singh.

NATIONAL INSTITUTE FOR FORESTRY, AGRICULTURE, AND LIVESTOCK RESEARCH (INIFAP–CIRNO) Campo Experimetal Norman E. Borlaug Apdo. Postal 155, km 12 Norman E. Borlaug, entre 800 y 900, Valle del Yaqui, Cd. Obregón, Sonora, México CP 85000. Guillermo Fuentes-Dávila*, Ivón Alejandra Rosas-Jáuregui, Carlos Antonio Ayón-Ibarra, Pedro Félix-Valencia, José Luis Félix-Fuentes, Miguel Alfonso Camacho-Casas, Gabriela Chávez-Villalba, Rebeca Pinto-González, Víctor Valenzuela-Herrera, Pedro Figueroa-López, Alberto Mendoza-Lugo, Carlos Antonio Ayón-Ibarra.

PAKISTAN

CIMMYT INT (INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER) Pakistan Office, CSI, Building, NARC, Park Road, Islamabad 44000, Pakistan. Monsif Ur Rehman, Muhammad Imtiaz*.

NATIONAL AGRICULTURAL RESEARCH CENTRE (NARC) Crop Diseases Research Institute, Islamabad. Pakistan. Shahzad Asad, Anjum Munir.

NUCLEAR INSTITUTE FOR FOOD AND AGRICULTURE (NIFA) Plant Breeding and Genetics Division, P.O. Box 446, Tarnab, Peshawar, Pakistan. Babar Manzoor Atta*, Abdul Jabbar Khan, Fazle Subhan, Muhammad Irfaq Kahn, Farooq-i-Azam, Akhtar Ali.

PAKISTAN AGRICULTURAL RESEARCH COUNCIL (PARC)

Food Quality & Safety Research Institute Karachi University Campus, Karachi, Pakistan. Saqib Arif*, Salman Khurshid, Shahid Yousaf, Qurrat ul Ain Afzal.

PARC Islamabad Pakistan. Atiq Ur Rehman.

PEOPLES REPUBLIC OF CHINA

NATIONAL WHEAT IMPROVEMENT CENTRE Institute of Crop Science, Chinese Academy of Agricultural Sciences, 12 Zhongguancun South St, Beijing 100081, China. Xian Chun Xia*.

RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE FOR SOUTH-EAST REGIONS – ARISER Department of Genetics, Laboratory of Genetics and Cytology. Toulaikov Str., 7, Saratov, 410020, Russian Federation. 8452-64-76-88 (FAX). S.N. Sibikeev*, A.E. Druzhin*, L.T. Vlasovets, T.D. Golubeva, T.V. Kalintseva, T.L. Vlasovec.

ALL-RUSSIAN SCIENTIFIC RESEARCH INSTITUTE FOR AGRICULTURAL CHEMISTRY NAMED AFTER D.N. PRYANISHNIKOV Pryanishnikova st. 31A, Moscow, 127550, Russian Federation. L.V. Osipova*, E.D. Kurnosov, I.A. Bykovskaya*.

UKRAINE

PLANT PRODUCTION INSTITUTE ND. A. V.YA. YURIEV National Academy of Agrarian Sciences of Ukraine, Moskovsky prospect, 142, 61060, Kharkiv, Ukraine. N.V. Kuzmenko*, A.Ye. Litvinov.

THE UNITED STATES OF AMERICA

CALIFORNIA

UNIVERSITY OF CALIFORNIA Department of Agronomy and Range Science, One Shields Drive, Davis, CA 95616, USA. Jorge Dubcovsky*.

COLORADO

COLORADO STATE UNIVERSITY Wheat Breeding and Genetics Prograom, Department of Soil and Crop Sciences, Ft. Collins, CO 80523, USA. S.D. Haley*, J. Stromberger, E. Hudson-Arns, S. Seifert, T. Anderson, M. Santra, H. Wang, C. Beil, Z. Afshar.

IDAHO

USDA–ARS NATIONAL SMALL GRAINS GERMPLASM RESEARCH FACILITY 1691 S. 2700 W., P.O. Box 307, Aberdeen, ID 83210, USA. 208-397-4162 ext. 112 (TEL); 208-397-4165 (FAX). http://www.ars-grin.gov/npgs. H.E. Bockelman*.

KANSAS

KANSAS STATE UNIVERSITY

Applied Wheat Genomics Group and the Wheat Genetics Resource Center Department of Plant Pathology, Throckmorton Hall, Manhattan, KS 66506-5502, USA. 913-532-6176 (TEL); 913 532-5692 (FAX). http://www.wheatgenetics.org and http://www.k-state.edu/wgrc. W. John Raupp*, Bikram S. Gill*, Dal-Hoe Koo*, Bernd Friebe*, Tatiana Danilova*, Jesse Poland*

Environmental Physics Group Department of Agronomy, Throckmorton Hall, Manhattan, KS 66502, USA. 913-532-5731 (TEL); 913-532-6094 (FAX). http://www.agronomy.k-state.edu/people/faculty/kirkham-mb/index.html. Oliver W. Freeman, M.B. Kirkham*.

Department of Agronomy Throckmorton Hall, Manhattan, KS 66506, USA. Alan K. Fritz*.

USDA–ARS PLANT SCIENCE RESEARCH UNIT Throckmorton Hall, Manhattan, KS 66506-5502. Robert L. Bowden*.

KANSAS WHEAT 1990 Kimball Avenue, Manhattan, KS 66506, USA. Marsha Boswell*.

MARYLAND

UNIVERSITY OF MARYLAND Department of Plant Science and Landscape Architecture, College Park, MD 20742, USA. Nidhi Rawat*, Vijay Tiwari*.

MINNESOTA

USDA–ARS CEREAL DISEASE LABORATORY University of Minnesota, 1551 Lindig St., St. Paul, MN 55108, USA. 612-625-7295 (TEL); 651-649-5054 (FAX). www.ars.usda.gov/mwa/cdl. James A. Kolmer*, Y. Jin, Mark E. Hughes*.

MONTANA

MONTANA STATE UNIVERSITY Department of Plant Sciences and Plant Pathology, Bozeman, MT 59771, USA. James Berg*, Luther Talbert, Nancy K. Blake, Hwa-Young Heo, Andrea Varella, Jason Cook, Brittney Brewer, David K. Weaver, Robert K.D. Peterson, Jamie D. Sherman, Megan L. Hofland, John M. Martin, A.M. Nasseer, M. Pumphrey, K.D. Kephart, S.P. Lanning, Phil Bruckner, Ron Ramsfield, Jack Martin, Mike Giroux, Alanna Schlosser, Andy Hogg, Darby Kammeraad, Rachel Johnston, Emma Jobson, Justin Vetch.

NORTH DAKOTA

NORTH DAKOTA STATE UNIVERSITY Departments of Plant Sciences and Plant Pathology, Loftsgard Hall, 78 Bolley Dr., Fargo, ND 58108, USA. Xiwen Cai*, Sudeshi Seneviratne, Amanda R. Peters, Zhaohui Liu.

USDA–ARS CEREAL CROPS RESEARCH UNIT 1307 18th Street N, Fargo, ND 58102-2765, USA. Justin D. Faris*, Timothy L. Friesen, Steven S. Xu.

OREGON

OREGON STATE UNIVERSITY Department of Crop and Soils Sciences, Corvallis, OR 97331, USA. Jeffrey M. Leonard.

SOUTH CAROLINA

CLEMSON UNIVERSITY Department of Plant and Environmental Sciences, Pee Dee Research and Education Center, Florence, SC 29506, USA. Sachin Rustgi*, N. Gandhi.

SOUTH DAKOTA

SOUTH DAKOTA STATE UNIVERSITY Departments of Biology and Microbiology and Plant Science, Brookings, SD 57007 USA. Wanlong Li*, Ghana Shyam Challa.

TEXAS

TEXAS A&M AGRILIFE RESEARCH Genomics and Bioinformatics Services, 101 Gateway Blvd., Suite A, Room 107, College Station, TX 77845-4636 USA. Shichen Wang.

TEXAS A&M AGRILIFE RESEARCH & EXTENSION CENTER Texas A&M, Uvalde, TX 78801. S. Malla.

VIRGINIA

VIRGINIA POLYTECHNIC AND STATE UNIVERSITY

Department of Crop and Soil Environmental Sciences, Blacksburg, VA 24061, USA. Carl A. Griffey,* Wade E. Thomason, John E. Seago*, Kyle Brasier, Nick Meier, Neal Carpenter, Brian Ward, L. Liu, E. Rucker.

Department of Plant Pathology, Physiology and Weed Science, Blacksburg, VA 24061, USA. D. Schmale III, N. McMaster.

EASTERN VIRGINIA AGRICULTURAL RESEARCH & EXTENSION CENTER Warsaw, VA 22572, USA. R. Pitman, J. Fitzgerald.

TIDEWATER AGRICULTURAL RESEARCH AND EXTENSION CENTER Suffolk, VA 23437, USA. Maria Balota, Joseph Oakes, Hillary Mehl.

WASHINGTON

USDA–ARS WESTERN WHEAT QUALITY LABORATORY E-202 Food Quality Building, Washington State University, Pullman, WA 99164, USA. www.wsu.edu/~wwql/php/index.php. Craig F. Morris*, Douglas A. Engle, Mary L. Baldridge, Gail L. Jacobson, E. Patrick Fuerst, William J. Kelley, Shelle Lenssen, Eric Wegner, Alecia Kiszonas, Shawna Vogl, Janet Luna, Stacey Sykes, Leonardo Pierantoni, Jessica Murray, Maria Itria Ibba, José Orenday-Ortiz, Derick Jiwan, Eden Stout.

WASHINGTON STATE UNIVERSITY Department of Crop and Soil Sciences, School of Molecular Bioscience & Center for Reproductive Biology, Pullman, WA 99164-6420, USA. D. von Wettstein, N. Ankrah, R. Gemini, P. Reisenauer.

VII. E-MAIL DIRECTORY OF SMALL GRAINS WORKERS.

These E-mail addresses are updated each year only for contributors to the current *Newsletter*, therefore, some addresses may be out of date. Names followed by [17] were verified with this issue of the *Newsletter,* other numbers indicate the last year that the E-mail address was verified.

Name (year updated)	E-mail address	Affiliation
Abbasov, Mehraj [17]	mehraj_genetic@yahoo.com	Genetic Resources Inst, Baku, Azerbaijan
Ahamed, Lal M	lal–pdl@yahoo.com	IARI, New Delhi, India
Akhtar, Lal H	lhakhtar@yahoo.com	Reg Agr Res Inst, Bahawalpur, Pakistan
Ahlers, Haley [16]	hahlers@k-state.edu	Kansas State University, Manhattan
Akhunov, Eduard [16]	eakhunov@k-state.edu	Kansas State University, Manhattan
Alaux, Michael [10]	michael.alaux@versailles.inra.fr	INRA, France
Aldana, Fernando	fernando@pronet.net.gt	ICTA, Guatemala
Allan, Robert E	allanre@mail.wsu.edu	USDA–ARS, Pullman, WA
Altenbach, Susan	altnbach@pw.usda.gov	USDA–WRRE, Albany, CA
Altman, David	dwa1@cornell.edu	ISAAA–Cornell University, Ithaca, NY
Alvarez, Juan B	alvarez@unitus.it	Univeristy of Córdoba, Argentina
Anderson, Jim M [09]	ander319@umn.edu	University of Minnesota, St. Paul
Anderson, Joseph M [10]	janderson@purdue.edu	Purdue University, W. Lafayette, IN
Anderson, Olin [09]	Olin.Anderson@ars.usda.gov	USDA–WRRE, Albany, CA
Appels, Rudi [16]	rappels@agric.wa.gov.au	Murdoch University, Perth, Australia
Arif, Saqib [17]	saqiawan@yahoo.com	Pakistan Agric Res Council, Karachi
Armstrong, Ken	armstrongkc@em.agr.ca	AAFC–Ottawa, Ontario, Canada
Arthur, Cally [11]	callyarthur@cornell.edu	Borlaug Global Rust Initiative, Ithaca, NY
Atta, Babar Manzoor [17]	babar_niab@hotmail.com	Nuc Inst Food Agric, Peshawar, Pakistan
Aung, T	taung@mbrswi.agr.ca	AAFC–Winnipeg, Canada
Avksentyeva, Olga A [13]	avksentyeva@rambler.ru	Kharkov Karazin Natl Univ, Ukraine
Babaoglu, Metin	metin_babaoglu@edirne.tagem.gov.tr	Thrace Ag Research Institute, Turkey
Babu, KS	kurrrasbabu@yahoo.com	Direct Wheat Research, Karnal, India
Bacon, Robert	rb27412@uafsysb.uark.edu	University of Arkansas, Fayetteville
Baenziger, P Stephen [16]	pbaenziger1@unl.edu	University of Nebraska, Lincoln
Baker, Cheryl A	cbaker@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Baker, JE	baker@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Balyan, Harindra S [10]	hsbalyan@gmail.com	Ch. Charan Singh Univ, Meerut, India
Bancroft, Ian	ian.bancroft@bbsrc.ac.uk	John Innes Centre, Norwich, UK
Barnard, Anri D	anri@kgs1.agric.za	Small Grain Institute, South Africa
Barreto, D	dbarreto@cnia.inta.gov.ar	INTA, Buenos Aires, Argentina
Barker, Susan	sbarker@waite.adelaide.edu.au	Waite, University Adelaide, Australia
Bariana, Harbans	harbansb@camden.usyd.edu.au	PBI Cobbitty, Australia
Barkworth, Mary	uf7107@cc.usu.edu	USDA–ARS, Logan, UT
Bartos, Pavel	bartos@hb.vruv.cv	RICP, Prague, Czech Republic
Bean, Scott R	scott@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Beazer, Curtis	cbeazer@dcwi.com	AgriPro Seeds, Inc., Lafayette, IN
Bechtel DB	don@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Bedö, Zoltan [12]	bedo.zoltan@agrar.mta.hu	Martonvásár, Hungary
Bentley, Stephen	bentleys@phibred.com	Pioneer Hi-Bred–Frouville, France
Berezovskaya, EV	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Berg, James E [17]	jeberg@montana.edu	Montana State University, Bozeman
Bergstrom, Gary	gcb3@cornell.edu	Cornell University, Ithaca, NY
Berzonsky, William A	berzonsk@badlands.nodak.edu	North Dakota State University, Fargo
Bhagwat, SG [10]	sbhagwat@barc.gov.in	Bhabha Atomic Res Center, India

Name (year updated)	E-mail address	Affiliation
Bhatta, MR	rwp@nwrp.mos.com.np	Natl Wheat Research Program, Nepal
Bykovskaya, Irina [17]	bykovskaya_irina@bk.ru	All-Rus Sci Res Inst Agric Chem, Moscow
Bivilienė, Aušra [15]	agb@agb.lt	Plant Gene Bank, Dotnuva, Lithuania
Blake, Nancy [15]	nblake@montana.edu	Montana State University, Bozeman
Blake, Tom	isstb@montana.edu	Montana State University, Bozeman
Blanco, Antonia	blanco@afr.uniba.it	Institue of Plant Breeding, Bari, Italy
Blum, Abraham	vcablm@volcani.agri.gov.il	Volcani Center, Israel
Bockelman, Harold E [17]	Harold.Bockelman@ARS.USDA.GOV	USDA–ARS, Aberdeen, ID
Bockus, William W [13]	bockus@k-state.edu	KS State University, Manhattan
Boggini, Gaetano	cerealicoltura@iscsal.it	Exp Inst Cereal Research, Italy
Boguslavskiy, Roman L	boguslavr@rambler.ru	Kharkov Inst Plant Protection, Ukraine
Bonman, J. Michael [17]	Mike.Bonman@ARS.USDA.GOV	USDA–ARS, Aberdeen, ID
Börner, Andreas [17]	boerner@ipk-gatersleben.de	IPK, Gatersleben, Germany
Borovskii, Genadii	borovskii@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Boswell, Marsha [17]	mboswell@kswheat.com	Kansas Wheat, Manhattan
Botha-Oberholster, Anna-Marie	ambothao@postino.up.ac.za	University of Pretoria, South Africa
Bowden, Robert L [17]	Robert.Bowden@ARS.USDA.GOV	USDA–ARS, Manhattan, KS
Boyd, Lesley A [10]	lesley.boyd@bbsrc.ac.uk	John Innes Centre, Norwich, UK
Brahma, RN	amaljoe@rediffmail.com	Indian Agric Res Inst, Wellington
Brantestam, Agnese Kolodinska	agnese.kolodinska@nordgen.org	Nordic Gene Bank, Alnarp, Sweden
Brendel, Volker	vbrendel@iastate.edu	Iowa State University, Ames
Brown, John S	john.brown@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Brammer, Sandra P	sandra@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Bradová, Jane	bradova@hb.vurv.cz	RICP, Prague, Czech Republic
Braun, Hans J [08]	H.J.Braun@cgiar.org	CIMMYT, México
Brennan, Paul	paulb@qdpit.sth.dpi.qld.gov.au	Queensland Wheat Res Inst, Australia
Brooks, Steven A [08]	steven.brooks@ars.usda.gov	USDA–ARS, Stuttgart, Arkansas
Brown, Douglas	dbrown@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Brown, James	jbrown@bbsrc.ac.uk	JI Centre, Norwich, UK
Brown-Guedira, Gina [08]	Gina.Brown-Guedira@ars.usda.gov	USDA–ARS, Raliegh, NC
Bruckner, Phil [15]	bruckner@montana.edu	Montana State University, Bozeman
Bruns, Rob	rbruns@frii.com	AgriPro Wheat, Berthoud, CO
Buerstmayr, Hermann	buerst@ifa-tulln.ac.at	IFA, Tulln, Austria
Burd, John D	jdburd@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Burns, John	burnsjw@wsu.edu	Washington State University, Pullman
Busch, Robert	Robert.H.Busch-1@umn.edu	USDA–ARS, St. Paul, MN
Bux, Hadi [12]	hadiqau@gmail.com	University of Sindh, Jamshoro, Pakistan
Byrne, Pat	pbyrne@lamar.colostate.edu	Colorado State University, Ft. Collins
Caccamo, Mario [10]	Mario.Caccamo@bbsrc.ac.jk	John Innes Centre, Norwich, UK
Cai, Xiwen [17]	xiwen.cai@ndsu.edu	North Dakota State University, Fargo
Caierão, Eduardo [17]	eduardo.caierao@embrapa.br	EMBRAPA–Trigo, Passo Fundo, Brazil
Caley, MS	margo@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Cambron, Sue [10]	cambron@purdue.edu	Purdue University, W. Lafayette, IN
Camerini, Massimiliano	massimiliano.camerini@unimol.it	University of Molise, Italy
Campbell, Kimberly G [09]	kim.garland-campbell@ars.usda.gov	USDA–ARS, Pullman, WA
Carillo, Jose M [08]	josem.carrillo@upm.es	Univ Politécnica de Madrid, Spain
Carmona, M	mcarmona@sion.com.ar	University of Buenos Aires, Argentina
Carson, Marty [10]	marty.carson@ars.usda.gov	USDA–ARS, St. Paul, MN
Carver, Brett F [09]	brett.carver@okstate.edu	Oklahoma State University, Stillwater

Name (year updated)	E-mail address	Affiliation
Casada, ME	casada@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Casanova, Nicholás [08]	nicocasanova@hotmail.com	University of Córdoba, Argentina
Cattonaro, Federica [10]	cattonaro@appliedgenomics.org	IGA, Italy
Cerana, María M	macerana@agro.uncor.edu	Córdoba National University, Argentina
Chalhoub, Boulous	chalhoub@evry.inra.fr	INRA, Evry, France
Chapin, Jay	jchapin@clust1.clemson.edu	Clemson University
Chapon, Michel [08]	michel-chapon@wanadoo.fr	Bourges, France
Chao, Shioman [08]	chaos@fargo.ars.usda.gov	USDA–ARS, Fargo, ND
Chen, Peidu [09]	pdchen@njau.edu.cn	Nanjing Agricultural University, PR China
Chen, Xianming	xianming@mail.wsu.edu	USDA–ARS, Pullman, WA
Chhuneja, Parveen	pchhuneja@rediffmail.com	Punjab Agric Univ, Ludhiana, India
Christiansen, Merethe	mjc@sejet.com	Sojet Plantbreeding, Denmark
Christopher, Mandy	Mandy.Christopher@dpi.qld.gov.au	Leslie Res Centre, Toowomba, Australia
Chung, OK	okchung@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Cisar, Gordon L [08]	rsi.gordon@comcast.net	
Clark, Dale R [08]	dclark@westbred.com	Western Plant Breeders, Bozeman, MT
Comeau, André	comeaua@agr.gc.ca	AAFC–Ste-Foy, Quebec, Canada
Condon, Tony	Tony.Condon@csiro.au	CSIRO, Canberra, Australia
Contento, Alessandra	ac153@mail.cfs.le.ac.uk	University of Leicester, UK
Cortés-Jiménez, Juan M [11]	cortes.juanmanuel@inifap.gob.mx	INIFAP, Obregon, Mexico
Costa, Jose M [08]	costaj@umd.edu	University of Maryland, College Park
Couture, Luc	couturel.stfoyres.stfoy@agr.gc.ca	AAFC–Ste-Foy, Quebec, Canada
Cowger, Cristina [08]	christina_cowger@ncsu.edu	North Carolina State University, Raleigh
Czarnecki, E	eczarnecki@mbrswi.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Daggard, Grant	creb@usq.edu.au	Univ of Southern Queensland, Australia
Datta, Dibendu [08]	dd221004@hotmail.com	Directorate of Wheat Research, India
Danilova, Tatiana [17]	tatianad@k-state.edu	Kansas State University, Manhattan
Davydov, VA	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Das, Bikram K [17]	bikram_das2001@yahoo.com	Bhaba Atomic Res Cen, Mumbai, India
Debes, Julia [15]	jdebes@kswheat.com	Kansas Wheat, Manhattan
Del Duca, Fabio	f.dd@ibestvip.com.br	EMBRAPA, Brazil
Del Duca, Leo JA	leodelduca@gmail.com	EMBRAPA, Brazil
Delibes, A	adelibes@bit.etsia.upm.es	Univ Politécnica de Madrid, Spain
del Moral, J.	moral@inia.es	Junta de Extramadura Servicio, Spain
Dempster, RE	rdempster@aibonline.org	Amer Inst Baking, Manhattan, KS
de Sousa, Cantído NA	cantidio@cnpt.embrapa.br	EMBRAPA, Brazil
DePauw, Ron	depauw@em.agr.ca	AAFC–Swift Current
Devos, Katrien	kdevos@uga.edu	University of Georgia, Athens
Dion, Yves	yves.dion@cerom.qc.ca	CEROM, Quebec, Canada
Dill-Macky, Ruth	ruthdm@puccini.crl.umn.edu	University Of Minnesota, St. Paul
Dotlacil, Ladislav	dotlacil@hb.vurv.cz	RICP, Prague, Czech Republic
Dolezel, Jaroslav [10]	dolezel@ueb.cas.cz	Inst Exp Bo, Olomouc, Czech Republic
Dorlencourt, Guy	dorlencourt@phibred.com	Pioneer Hi-bred–Frouville France
Dowell, Floyd E	floyd.dowell@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Drake, David R [10]	drdrake@ag.tamu.edu	TX AgriLife Extension, San Angelo
Dreccer, F	fernanda.dreccer@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Druzhin, Alex E [17]	alex_druzhin@mail.ru	Agric Res Inst SE Reg, Saratov, Russia
du Toit, Andre [08]	andre.dutoit@pannar.co.za	PANNAR Res, South Africa
Dubcovsky, Jorge [17]	jdubcovsky@ucdavis.edu	Univesity of California, Davis
Dubin, Jesse	JDubin@cimmyt.mx	CIMMYT, Mexico

Name (year updated)	E-mail address	Affiliation
Dubois, María E	mdubois@agro.uncor.edu	Córdoba National University, Argentina
Dubuc, Jean-Pierre	jeanpierredubuc45@hotmail.com	Cap-Rouge, Quebec, Canada
Duncan, Robert W [10]	rduncan@tamu.edu	TX AgriLife Extension, College Station
Dundas, Ian	idundas@waite.adelaide.edu.au	University of Adelaide, Australia
Dunphy, Dennis	dennis.j.dunphy@monsanto.com	Monsanto Corp., Lafayette, IN
Dvorak, Jan	jdvorak@ucdavis.edu	Univesity of California, Davis
Eastwood, Russell	russell.eastwood@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Edge, Benjamin [08]	bedge@clemson.edu	Clemson University, SC
Edwards, Dave [10]	dave.edwards@uq.edu.au	University of Queensland, Australia
Edwards, Ian	edstar@iinet.net.au	Edstar Genetics Pty Ltd, Australia
Egorov, Tsezi [10]	ego@ibch.ru	Shemyakin Ovchinnikov Inst, Moscow
Elias, Elias [08]	Elias.Elias@ndsu.nodak.edu	North Dakota State University, Fargo
Elliott, Norman C	nelliott@ag.gov	USDA–ARS, Stillwater, OK
Endo, Takashi R	endo@kais.kyoto-u.ac.jp	Kyoto University, Japan
Eversole, Kellye [10]	eversole@eversoleassociates.com	Eversole Associates, Rockville, MD
Evseeva, Nina V [13]	evseeva@ibppm.sgu.ru	Inst Biochem Physiol Plants, Saratov, Russian Federatioin
Faberova, Iva	faberova@genbank.vurv.cz	RICP, Prague, Czech Republic
Fahima, Tzion	rabi310@haifauvm.bitnet	University of Haifa, Israel
Faris, Justin D [17]	Justin.Faris@ARS.USDA.GOV	UDSA–ARS–CCRU, Fargo, ND
Fazekas, Miklós	forizsne@dateki.hu	Karcag Research Institute, Hungary
Fedak, George	fedakga@em.agr.ca	AAFC, Ottawa, Ontario
Federov, AK	meraserv@mega.ru	Russian Univ People Friend, Moscow
Feldman, Moshe	lpfeld@weizmann.weizmann.ac.il	Weizmann Institute, Rehovot, Israel
Fellers, John P [08]	jpf@pseru.ksu.edu	USDA–ARS, Manhattan, KS
Feuillet, Catherine [10]	catherine.feuillet@clermont.inra.fr	INRA–Clermont-Ferrand, France
Fox, Paul	pfox@alphac.cimmyt.mx	CIMMYT–Mexico
Fogelman Jr, J Barton	jbarton@ipa.net	AgriPro Seeds, Inc., Jonesboro, AK
Frank, Robert W	frankr@idea.ag.uiuc.edu	University of Illinois, Urbana
Fritz, Alan K [16]	akf@k-state.edu	Kansas State University, Manhattan
Friebe, Bernd [17]	friebe@k-state.edu	Kansas State University, Manhattan
Fuentes-Davila, Guillermo [17]	fuentes.davila@gmail.com	INIFAP, Obregon, Mexico
Gaido, Zulema	zulgaido@agro.uncor.edu	University of Córdoba, Argentina
Gailite, Agnese [15]	agnese.gailite@silava.lv	Genetic Res Cent, Rigas, Latvia
Gale, Sam [15]	Sam.Gale@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Garvin, David [08]	Garvi007@umn.edu	USDA–ARS, St. Paul, MN
Giese, Henriette	h.giese@risoe.dk	Risoe National Lab, DK
Gil, S Patricia	patrigil@agro.uncor.edu	University of Córdoba, Argentina
Gilbert, Jeannie	jgilbert.winres.winnipeg2@agr.gc.ca	AAFC, Winnipeg, Canada
Gill, Bikram S [17]	bsgill@k-state.edu	Kansas State University, Manhattan
Giroux, Mike [15]	mgiroux@montana.edu	Montana State University, Bozeman
Gitt, Michael	mgitt@pw.usda.gov	USDA–ARS–WRRC, Albany, CA
Glyanko, AK	ustaft@sifibr.irk.ru	Siberian Inst Pl Physio Biochem, Russia
Gonzalez-de-Leon, Diego	dgdeleon@alphac.cimmyt.mx	CIMMYT–Mexico
Gooding, Rob	rgooding@magnus.acs.ohio-state.edu	Ohio State University, Wooster
Goodwin, Steve [10]	goodwin@purdue.edu	Purdue University, W. Lafayette, IN
Gothandam, KM	gothandam@yahoo.com	Bharathiar University, Coimbatore, India
Grabelnych, Olga I [11]	grolga@sifibr.irk.ru	Siber Inst Plant Physiol, Irkutsk, Russia
Grausgruber, Heinrich	grausgruber@ipp.boku.ac.at	Univ of Agriculture Sciences, Vienna
Graham, W Doyce	dgraham@clust1.clemson.edu	Clemson University, SC

Name (year updated)	E-mail address	Affiliation
Graybosch, Bob [16]	Bob.Graybosch@ARS.USDA.GOV	USDA–ARS, Lincoln, NE
Greenstone, Matthew H	mgreenstone@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Grienenberger, Jean M	grienen@medoc.u-strasbg.fr	University of Strasberg, France
Griffey, Carl [17]	CGriffey@vt.edu	Virginia Tech, Blacksburg
Griffin, Bill	griffinw@lincoln.cri.nz	DSIR, New Zealand
Groeger, Sabine	probstdorfer.saatzucht@netway.at	Probstdorfer Saatzucht, Austria
Guenzi, Arron	acg@mail.pss.okstate.edu	Oklahoma State University, Stillwater
Guidobaldi, Héctor A	guidobaldi@uol.com.ar	Univrsity of Córdoba, Argentina
Guilhot, Nicolas [10]	nicolas.guilhot@clermont.inra.fr	INRA, Clermont-Ferrand, France
Gul-Kazi, Alvina [15]	alvina_gul@yahoo.com	Natl Agric Res Cent, Islamabad, Pakistan
Gupta, Pushpendra K [13]	pkgupta36@gmail.com	Ch. Charan Singh Univ, Meerut, India
Gustafson, Perry [08]	gustafsonp@missouri.edu	USDA–ARS, Columbia, MO
Gutin, Alexander	agutin@myriad.com	Myriad Genetics, Salt Lake City, UT
Guttieri, Mary J [16]	Mary.Guttieri@ARS.USDA.GOV	USDA–ARS, Manhattan, KS
Haber, Steve	shaber.winres.winnipeg2@agr.gc.ca	AAFC, Winnipeg, Manitoba, Canada
Haghparast, Reza	rezahaghparast@yahoo.com	IARI, New Delhi, India
Haley, Scott D [17]	Scott.Haley@colostate.edu	Colorado State University, Ft. Collins
Hancock, June	june.hancock@seeds.Novartis.com	Novartis Seeds Inc., Bay, AR
Harrison, Steve	sharris@lsuvm.sncc.lsu.edu	Louisiana State University, Baton Rouge
Harder, Don	dharder@mbrswi.agr.ca	Winnipeg, Manitoba, Canada
Hart, Gary E	ghart@acs.tamu.edu	Texas A & M Univ, College Station
Hassan, Amjad [08]	amjadhassan@mx1.cc.ksu.edu	COMSATS Inst Inf Tech, Pakistan
Hays, Dirk B	dhays@ag.gov	USDA–ARS, Stillwater, OK
Hayes, Pat	hayesp@css.orst.edu	Oregon State University, Corvallis
He, Zhonghu [08]	z.he@CGIAR.ORG	Chinese Acad Agric Sciences, Beijing
Heo, Hwa-Young [15]	hwayoung@montana.edu	Montana State University, Bozeman
Hearnden, PR	phillippa.hearden@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Hede, Arne R	a.hede@cgiar.org	CIMMYT–Turkey, Ankara
Henzell, Bob	bobh@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland, AU
Hershman, Don	dhershman@ca.uky.edu	University of Kentucky, Lexington
Heslop-Harrison, JS (Pat)	phh4@mail.cfs.le.ac.uk	University of Leicester, UK
Hoffman, David	A03dhoffman@attmail.com	USDA–ARS, Aberdeen, ID
Hohmann, Uwe	uhemail@botanik.biologie.unim-uenchen.de	Botanical Institute, Munich, Germany
Hoisington, David [08]	D.Hoisington@cgiar.org	CIMMYT–Mexico
Hole, David	dhole@mendel.usu.edu	Utah State University, Logan
Holubec, Vojtech [15]	holubec@vurv.cz	Crop Res Inst, Prague, Czech Republic
Howell, Kimberly D [15]	Kim.Howell@ARS.USDA.GOV	USDA–ARS, Raleigh, NC
Howes, Neil	nhowes@mbrswi.agr.ca	Winnipeg, Manitoba, Canada
Hubbard, JD	john@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Huber, Don M	huber@btny.purdue.edu	Purdue University, W. Lafayette, IN
Hucl, Pierre	hucl@sask.usask.ca	University of Saskatchewan, Canada
Huerta, Julio [08]	J.HUERTA@CGIAR.ORG	CIMMYT, México
Hughes, Mark E [16]	Mark.Hughes@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Hulbert, Scot [08]	scot_hulbert@wsu.edu	Washington State University, Pullman
Hunger, Robert [09]	bob.hunger@okstate.edu	Oklahoma State University, Stillwater
Ibrahim, Amir	amir_ibrahim@sdstate.edu	South Dakota State Univ, Brookings
Imtiaz, Muhammad [17]	m.imtiaz@cgiar.org	CIMMYT, Pakistan
Ionova, Helen [10]	ionova-ev@yandex.ru	All-Russian Sci Res Inst, Zernograd
Iori, Angela [11]	angela.iori@entecra.it	CRA–QCE, Roma, Italy

Name (year updated)	E-mail address	Affiliation
Isaac, Peter G	mbnis@seqnet.dl.ac.uk	Nickerson Biocem, UK
Isaía, Juan A [08]	juanandresisaia@hotmail.com	University of Córdoba, Argentina
Ivanušić, Tomislav [10]	tomislav.ivanusic@bc-institut.hr	BC Insitute, Zagreb, Croatia
Jacquemin, Jean	stamel@fsagx.ac.be	Cra-Gembloux, Belgium
Jamali, Karim Dino [13]	karimdino2001@yahoo.com.in	Nuclear Institute Agriculture, Pakistan
Jaiswal, Jai P [10]	jpj.gbpu@gmail.com	GB Pant University, Pantnagar, India
Jayaprakash, P [13]	jpsarit@gmail.com	IARI, Wellington, India
Jelic, Miodrag	miodrag@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Jia, Jizeng	jzjia@mail.caas.net.cn	Chinese Academy of Sciences, Beijing
Jiang, Guo-Liang	dzx@njau.edu.cn	Nanjing Agricultural University, China
Jin, Yue [17]	Yue.Jin@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Johnson, Doug	djohnson@ca.uky.edu	University of Kentucky, Lexington
Johnson, Jerry [09]	jjohnson@griffin.uga.edu	University of Georgia, Griffin
Johnston, Paul	paulj@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland, AU
Jones, Steven S	joness@wsuvm1.csc.wsu.edu	Washington State University, Pullman
Jordan, Mark	mcjordan@agr.gc.ca	AAFC, Winnipeg, Manitoba, Canada
Kalaiselvi, G	kalaipugal@rediffmail.com	Bharathiar Univ, Coimbatore, India
Kalia, Bhanu [15]	bkalia@k-state.edu	Kansas State University, Manhattan
Kalous, Jay [15]	jay.kalous@msu.montana.edu	Montana State University, Bozeman
Karabayev, Muratbek	mkarabayev@astel.kz	CIMMYT, Kazakhstan
Karow, Russell S [08]	russell.s.karow@oregonstate.edu	Oregon State University, Corvallis
Karsai, Ildiko	karsai@buza.mgki.hu	ARI, Martonvasar, Hungary
Kasha, Ken	kkasha@crop.uoguelph.ca	University of Guelph, Canada
Keefer, Peg	peg_keefer@entm.purdue.edu	Purdue University, West Lafayette, IN
Keller, Beat	bkeller@botinst.unizh.ch	University of Zurich, Switzerland
Khusnidinov, ShK	ustaft@sifibr.irk.ru	Irkutsk State Agric Univ, Irkutsk, Russia
Kianian, Sharyiar [08]	s.kianian@ndsu.nodak.edu	North Dakota State University, Fargo
Kidwell, Kim [08]	kidwell@wsu.edu	Washington State University, Pullman
Kindler, S Dean	sdkindler@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Kirkham, MB [17]	mbk@k-state.edu	Kansas State University, Manhattan
Kisha, Theodore	tkisha@dept.agry.purdue.edu	Purdue University, W. Lafayette, IN
Kishii, Masahiro [08]	m.kishii@CGIAR.ORG	CIMMYT, Mexico
Klatt, Art [08]	aklatt@okstate.edu	Oklahoma State University, Stillwater
Kleinhofs, Andy	coleco@bobcat.csc.wsu.edu	Washington State University, Pullman
Knezevic, Desimir	deskok@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Koebner, Robert	mockbeggars@gmail.com	Norwich, UK
Koemel, John Butch	jbk@soilwater.agr.okstate.edu	Oklahoma State University, Stillwater
Koenig, Jean [08]	koenig@clermont.inra.fr	INRA, Clermont-Ferrand, France
Kokhmetova, Alma	kalma@ippgb.academ.alma-ata.su	Kazakh Research Institute of Agriculture
Kolb, Fred [08]	f-kolb@uiuc.edu	University Of Illinois, Urbana
Kolesnichenko, AV	akol@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Kolmer, Jim [17]	Jim.Kolmer@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Koppel, R	Reine.Koppel@jpbi.ee	Jõgeva Plant Breeding Institute, Estonia
Koo, Dal-Hoe [17]	dkoo@k-state.edu	Kansas State Unviersity, Manhattan
Korol, Abraham	rabi309@haifauvm.bitnet	University of Haifa, Israel
Kosina, Romuald [16]	kosina@biol.uni.wroc.pl	University of Wroclaw, Poland
Kovalenko, ED	kovalenko@vniif.rosmail.com	Russian Res Inst Phytopath, Moscow
Krasilovets, Yuri G [09]	ppi@kharkov.ukrtel.net	Inst Plant Production, Karkiv, Ukraine
Krenzer, Gene	egk@agr.okstate.edu	Oklahoma State University, Stillwater
Kronstad, Warren E	kronstaw@css.orst.edu	Oregon State University, Corvallis

Name (year updated)	E-mail address	Affiliation
Krupnov, VA	alex_dr@renet.com.ru	Agric Res Inst SE Reg, Saratov, Russia
Kudirka, Dalia	KUDIRKAD@agr.gc.ca	AAFC, Ottawa, Ontario, Canada
Kudryavtseva, TG	ustaft@sifibr.irk.ru	Irkutsk State Agric Univ, Irkutsk, Russia
Kuhr, Steven L	slkuhr@ccmail.monsanto.com	Hybritech–Mt. Hope, KS
Kumar, Jagdish [16]	moola01@yahoo.com	Indian Agric Res Inst, Wellington
Kumar, Sarvan [11]	sarvandwr@yahoo.co.in	Directorate of Wheat Research, India
Kuraparthy, Vasu [10]	vasu_kuraparthy@ncsu.edu	North Carolina State University, Raleigh
Kurmanbaeva, A.S. [11]	safronat@rambler.ru	Kokshetau State Univ, Kazakhstan
Kuzmina, Natalia	natakuzmina@yandex.ru	Omsk State Pedagogical Univ, Russia
Kuzmenko, Natalia V [17]	ogurtsow@mail.ru	Plant Production Institute, Ukraine
Kyzlasov, VG [11]	norma-tm@rambler.ru	Moscow Agric Res Inst, Russia
Lafferty, Julia	lafferty@edv1.boku.ac.at	Saatzucht Donau, Austria
Lagudah, Evans	e.lagudah@pi.csiro.au	CSIRO, Australia
Lankevich, SV	laser@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Láng, László [13]	lang.laszlo@agrar.mta.hu	Agricultural Inst, Martonvásár, Hungary
Langridge, Peter	plangridge@waite.adelaide.edu.au	University of Adelaide, Australia
Lapitan, Nora LV [08]	nlapitan@lamar.colostate.edu	Colorado State University, Ft. Collins
Lapochkina, Inna F	lapochkina@chat.ru	Research Inst of Agric, Moscow, Russia
Laskar, Bill	laskarb@phibred.com	Pioneer Hi-Bred–Windfall, IN
Leath, Steve	steven_leath@ncsu.edu	USDA–ARS, Raleigh, NC
Leonard, Kurt J	kurtl@puccini.crl.umn.edu	USDA–ARS, St. Paul, MN
Leroy, Philippe	leroy@valmont.clermont.inra.fr	INRA, Clermont
Lekomtseva, Svetlana N [09]	lekom37@mail.ru	Moscow State University, Russia
Lewis, Hal A	halewi@ccmail.monsanto.com	Hybritech–Corvallis OR
Lewis, Silvina	slewis@cirn.inta.gov.ar	CNIA–INTA, Buenos Aires, Argentina
Li, Wanlong [17]	Wanlong.Li@sdstate.edu	South Dakota State University, Brookings
Linc, Gabriella [15]	linc.gabriella@agrar.mta.hu	Agricultural Inst, Martonvásár, Hungary
Line, RF	rline@wsu.edu	USDA–ARS, Pullman, WA
Liu, Dajun	djliu@public1.ptt.js.cn	Nanjing Agricultural University, China
Lively, Kyle	livelyk@phibred.com	Pioneer Hi-Bred–Windfall, IN
Lobachev, Yuri V [11]	lobachyovyuv@sgau.ru	Saratov State Agr Univ, Saratov, Russia
Long, David [10]	david.long@ars.usda.gov	USDA–ARS, St. Paul, MN
Lookhart, George	george@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Luckow, Odean	alvkow@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Lukaszewski, Adam	ajoel@ucrac1.ucr.edu	University of California–Riverside
Luo, Ming Cheng [10]	mcluo@plantsciences.ucdavis.edu	University of CA, Davis
Maas, Fred	fred_maas@entm.purdue.edu	Purdue University, West Lafayette, IN
Mackay, Michael	mackaym@quord.agric.nsw.gov.au	AWEE, Tamworth, NSW, Australia
Maggio, Albino	maggio@trisaia.enea.it	ENEA–Trisaia Research Center, Italy
Maich, Ricardo H [11]	rimaich@agro.unc.edu.ar	University of Córdoba, Argentina
Malik, BS [08]	bsmalik2000@yahoo.com	IARI, New Delhi, India
Manera, Gabriel	gamanera@agro.uncor.edu	University of Córdoba, Argentina
Manifesto, María M	mmanifes@cicv.intgov.ar	INTA Castelar, Argentina
Marais, G Frans [08]	gfm@sun.ac.za	University of Stellenbosch, R.S.A.
Mares, Daryl J [08]	daryl.mares@adelaide.edu.au	University of Adelaide, Australia
Mardi, Mohsen	mardi@abrii.ac.ir	Ag Biotech Res Inst of Iran, Karaj
Marshall, David [08]	David.Marshall@ARS.USDA.GOV	USDA–ARS, Raleigh, NC
Marshall, Gregory C	marshallg@phibred.com	Pioneer Hi-Bred–Windfall, IN
Martin, Erica	erica.martin@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Martín-Sánchez, JA [10]	JuanAntonio.Martin@irta.cat	IRTA, Lleida, Spain

Name (year updated)	E-mail address	Affiliation
Martynov, Sergei [08]	sergej_martynov@mail.ru	Vavilov Inst Plant Prod, St. Petersburg
Mather, Diane	indm@musicb.mcgill.ca	McGill University, Canada
Matthews, Dave [10]	matthews@greengenes.cit.cornell.edu	Cornell University, Ithaca, NY
McCallum, John	mccallumj@lan.lincoln.cri.nz	Crop & Food Res. Ltd, NZ
McGuire, Pat	pemcguire@ucdavis.edu	University of California, Davis
McIntosh, Robert A [17]	robert.mcintosh@sydney.edu.au	PBI Cobbitty, Australia
McKendry, Anne L	mckendrya@missouri.edu	University of Missouri, Columbia
McKenzie, RIH	rmckenzie@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
McVey, Donald	donm@puccini.crl.umn.edu	USDA–ARS, St. Paul, MN
Meena, Raj Pal	adityarajjaipur@gmail.com	Directorate Wheat Research, Karnal, India
Messing, Joachim	messing@waksman.rutgers.edu	Rutgers University, Piscataway, NJ
Mi, Q.L.	qlm@ksu.edu	Kansas State University, Manhattan
Milach, Sandra	mila0001@student.tc.umn.edu	University of Minnesota, St. Paul
Miller, James	millerid@fargo.ars.usda.gov	USDA–ARS, Fargo, ND
Milovanovic, Milivoje	mikim@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Milus, Gene [08]	gmilus@uark.edu	University of Arkansas, Fayetteville
Mishra, Chandra Nath [13]	mishracn1980@gmail.com	Directorate of Wheat Research, Karnal
Miskin, Koy E	miskin@dcwi.com	AgriPro Wheat, Berthoud, CO
Mlinar, Rade	bc-botinec@bc-institut.hr	Bc Institute, Zagreb, Croatia
Mochini, RC	rmoschini@inta.gov.ar	INTA, Castelar, Argentina
Moffat, John	apwheat@frii.com	AgriPro Wheat, Berthoud, CO
Moldovan, Vasile [16]	ameliorareagraului@scdaturda.ro	Agric Research Station, Turda, Romania
Molnár-Láng, Marta	molnarm@fsnew.mgki.hu	Agricultural Inst, Martonvásár, Hungary
Moore, Paul	ejh@uhccvx.uhcc.hawaii.edu	University of Hawaii, Honolulu
Moreira, João C.S.	moreira@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Morgounov, Alexei [08]	a.morgounov@cgiar.org	CIMMYT, Kazakhstan
Morino-Sevilla, Ben	bmoreno-sevilla@westbred.com	Western Plant Breeders, Lafayette, IN
Mornhinweg, Dolores W	dmornhin@ag.gov	USDA–ARS, Stillwater, OK
Morris, Craig F [17]	morris@wsu.edu	USDA–ARS–WWQL, Pullman, WA
Morrison, Laura	alura@peak.org	Oregon State University, Corvallis
Moser, Hal	hsmoser@iastate.edu	Iowa State University, Ames
Mostafa, Ayman	insectarus@yahoo.com	University of Manitoba, Canada
Mujeeb-Kazi, A [15]	kayshtr@gmail.com	Natl Agric Res Cent, Islamabad, Pakistan
Mukai, Yasuhiko	ymukai@cc.osaka-kyoiku.ac.jp	Osaka Kyoiku University, Japan
Murphy, Paul [08]	Paul_Murphy@ncsu.edu	North Carolina State University
Murray, Tim	tim_murray@wsu.edu	Washington State University, Pullman
Muthukrishnan, S [10]	smk@k-state.edu	Kansas State University, Manhattan
Nakamura, Hiro [16]	hiro@affrc.go.jp	National Inst of Crop Science, Tsukuba
Nascimento Jr, Alfredo [11]	alfredo@cnpt.embrapa.br	EMBRAPA–Trigo, Brazil
Nash, Deanna L [15]	deanna@montana.edu	Montana State University, Bozeman
Nass, Hans	nassh@em.agr.ca	AAFC–Prince Edward Island, Canada
Nayeem, KA	kanayeem1@rediffmail.com	IARI Regional Sta, Wellington, India
Niedzielski, Maciej [15]	mniedz@obpan.pl	Botanical Garden, Warsaw, Poland
Nelson, Lloyd R	lr-nelson@tamu.edu	Texas A & M University
Nevo, Eviatar	rabi301@haifauvm.bitnet	University of Haifa, Israel
Nicol, Julie M [08]	j.nicol@cgiar.org	CIMMYT–Turkey, Ankara
Noll, John S	jnoll@em.agr.ca	AAFC–Winnipeg, Canada
Nyachiro, Joseph	jnyachir@gpu.srv.ualberta.ca	University of Alberta
O'Donoughue, Louise	em220cyto@ncccot2.agr.ca	AAFC–Canada
Odintsova, TI	musolyamov@mail.ibch.ru	Vavilov Ins Gen Genet, Moscow, Russia

Name (year updated)	E-mail address	Affiliation
Ogbonnaya, Francis C [08]	F.Ogbonnaya@cgiar.org	ICARDA, Aleppo, Syria
Ogihara, Yasunari	ogihara@kab.seika.kyoto.jp	Kyoto Pref Inst Agric Biotech, Japan
Ohm, Herbert W [10]	hohm@purdue.edu	Purdue Univ, West Lafayette, IN
Ohm, Jay B	jay@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Oman, Jason	jason.oman@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Ortiz-Ávalos, Alma A [11]	ortiz.alma@inifap.gob.mx	INIFAP, Obregon, Mexico
Ortiz Ferrara, Guillermo [08]	oferrara@mos.com.np	CIMMYT, Ramput, Nepal
Osipova, Ludmila V [17]	legos4@yndex.ru	All-Rus Sci Res Inst Agric Chem, Moscow
Osmanzai, Mahmood [08]	m.osmanzai@cgiar.org	CIMMYT, Kabul, Afghanistan
Paelo, Antonio D	adiazpaleo@cnia.inta.gov.ar	CRN INTA Castelar, Argentina
Paling, Joe	jpaling@vt.edu	VA Polytech Inst State Univ, Blacksburg
Papousková, Ludmila [15]	papouskova@vurv.cz	Crop Res Inst, Prague, Czech Republic
Park, SH	seokho@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Pasquini, Mariina [10]	marina.pasquini@entecra.it	CRA–QCE, Roma, Italy
Paux, Etienne [10]	etienne.paux@clermont.inra.fr	INRA, Clermont-Ferrand, France
Payne, Thomas [11]	t.payne@CGIAR.ORG	CIMMYT, México
Penix, Susan	agsusan@mizzou1.missouri.edu	University of Missouri, Columbia
Permyakov, AV	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Perry, Keith	perry@btny.purdue.edu	Purdue University, W. Lafayette, IN
Perry, Sid	sidgsr@southwind.com	Goertzen Seed Research, Haven, KS
Pérez, Beatríz A	baperez@inta.gov.ar	INTA, Castelar, Argentina
Peterson, C James [09]	cjp@oregonstate.edu	Oregon State University, Corvallis
Pickering, Richard	pickeringr@crop.cri.nz	Christchurch, NZ
Piergiovanni, Angela R	angelarosa.piergiovanni@igv.cnr.it	Istituto de Genetica Vegetale, Bari, Italy
Pomazkina, L	agroeco@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Pogna, Norberto	isc.gen@iol.it	Inst Exper Cereal, Rome, Italy
Poland, Jesse [17]	jpoland@k-state.edu	Kansas State University, Manhattan
Poleva, Lina V.	po_linaw@rambler.ru	Agric Res Inst, Moscow, Russian Fed
Porter, David	dporter@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Poulsen, David	davep@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland AU
Poukhalskaya, Nina V [15]	seo@seomax.ru	Agropark, Moscow, Russian Federation
Prabakaran, AJ	amaljoe@rediffmail.com	Regional Station, Wellington, India
Prasad, Manoj	manoj_pds@yahoo.com	Nat Cent Pl Gen Res, New Delhi, India
Premalatha, S	spr_latha@yahoo.co.in	Bharathiar University, Coimbatore, India
Priillin, Oskar	ebi@ebi.ee	Estonian Agricultural University, Harku
Puebla, Andrea F	apuebla@cicv.inta.gov.ar	INTA, Castelar, Argentina
Pukhalsky, VA	pukhalsk@vigg.su	N.I. Vavilov Institute, Moscow
Pumphrey, Michael O [08]	mop3535@ksu.edu	USDA–ARS, Manhattan, KS
Qualset, Cal	coqualset@ucdavis.edu	University of California–Davis
Quaranta, Fabrizio [10]	fabrizio.quaranta@entecra.it	CRA–QCE, Rome, Italy
Quetier, Francis	quetier@genoscope.cns.fr	GENOSCOPE, France
Quick, Jim	jim.quick@colostate.edu	Dakota Grow Pasta Co, Carrington, ND
Rabinovych, Svitlana	bogus@is.kh.ua	Inst Plant Production, Karkiv, Ukraine
Rajaram, Sanjaya	srajaram@cimmyt.mx	CIMMYT, Mexico
Ram, MS	ramms@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Raman, Harsh	harsh.raman@dpi.nsw.gov.au	Wagga Wagga Agric Institute, Australia
Ratcliffe, Roger H	roger_ratcliffe@entm.purdue.edu	USDA–ARS, W. Lafayette IN
Ratti, C	cratte@tin.it	University of Bologna, Italy
Raupp, W John [17]	jraupp@k-state.edu	Kansas State University, Manhattan

Name (year updated)	E-mail address	Affiliation
Rawat, Nidhi [17]	nidhirwt@umd.edu	University of Maryland, College Park
Rayapati, John	nanster@iastate.edu	Iowa State University, Ames
Rebetzke, Greg	Greg.Rebetzke@csiro.au	CSIRO, Canberra, Australia
Reddy, V Rama Koti [08]	drvrkreddy@yahoo.com	Bharathiar University, Coimbatore, India
Rekoslavskaya, NI	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Reisner, Alex	reisner@angis.su.oz.au	Australia
Rekoslavskaya, Natalya I	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Riera-Lizarazu, Oscar	oscar.rierd@orst.edu	Oregon State University, Corvallis
Rife, Trevor [16]	trife@k-state.edu	Kansas State University, Manhattan
Rines, Howard [13]	rines001@umn.edu	University of Minnesota, St. Paul
Rioux, Sylvie	sylvie.rioux@cerom.qc.ca	CEROM, Quebec, Canada
Roberts, John	jrobert@gaes.griffin.peachnet.edu	USDA–ARS, Griffin, GA
Rodríguez, Daniel	daniel.rodriguez@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Rogers, W John [17]	rogers@faa.unicen.edu.ar	Univ Nacional, Buenos Aires, Argentina
Rohrer, Wendy L	wrohrer@vt.edu	Virginia Tech, Blacksburg
Romig, Robert W	bobromig@aol.com	Trigen Seed Services LLC, MN
Romsa, Jay [09]	Jay.Romsa@genmills.com	General Mills
Rosa, André	andre@orsementes.com.br	OR Seed Breeding Co., Brazil
Rosa, OS	ottoni@ginet.com.br	OR Seed Breeding Co., Brazil
Rouse, Matthew [12]	Matthew.Rouse@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Rudd, Jackie [08]	j-rudd@tamu.edu	Texas A&M Agric Res Cen, Amarillo
Rubies-Autonell, C	crubies@agrsci.unibo.it	University of Bologna, Italy
Rustgi, Sachin [17]	rustgi2001@yahoo.com	Clemson University, Florence, SC
Safranski, Greg	greg_safranski@entm.purdue.edu	Purdue University, W. Lafayette, IN
Saini, Ram Gopal	sainirg@rediffmail.com	Punjab Agric Univ, Ludhiana, IndiaSher
Sajjad, Muhammad [14]	msajjadpbg@gmail.com	Arid Agri Univ, Rawalpindi, Pakistan
Salyaev, RK	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Santra, Depak [12]	dsantra2@unl.edu	University of NE, Scottsbluff
Sasaki, Takuji	tsasaki@nias.affrc.go.jp	NAIS, Tsukuba, Japan
Sãulescu, Nicolae	saulescu@valhalla.racai.ro	Fundulea Institute, Romania
Schlegel, Rolf [14]	rolf.schlegel@t-online.de	Retired
Schwarzacher, Trude	ts32@leicester.ac.uk	University of Leicester, UK
Schemerhorn, Brandon J [10]	bschemer@purdue.edu	Purdue University, West Lafayette, IN
Scofield, Steven [10]	scofield@purdue.edu	Purdue University, West Lafayette, IN
Seabourn, BW	brad@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Seago, John E [17]	joseago@vt.edu	Virginia Polytechnic Inst, Blacksburg
Sears, Rollie [09]	Rollin.Sears@syngenta.com	AgriPro Wheat, Junction City, KS
See, Deven [08]	deven_see@wsu.edu	USDA–ARS, Pullman, WA
Sehgal, Sunish K [10]	Sunish.Sehgal@sdstate.edu	South Dakota State University, Brookings
Seitz, LM	larry@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Sessiona, Alan	allen.sessions@syngenta.com	Syngenta, Research Triangle Park, NC
Sethi, Amit P	amit_sethi@hotmail.com	IARI, New Delhi, India
Shafquat, Mustafa N [08]	mshafqat@mx1.cc.ksu.edu	COMSATS Inst Inf Tech, Pakistan
Shah, M Maroof [08]	mmshah@ciit.net.pk	COMSATS Inst Inf Tech, Pakistan
Shaner, Greg	shaner@btny.purdue.edu	Purdue University, W. Lafayette, IN
Sharp, Peter	peters@camden.usyd.edu.au	PBI Cobbitty, Australia
Sheedy, Jason [08]	Jason.Sheedy@dpi.qld.gov.au	Leslie Research Centre, Australia
Sheppard, Ken	ksheppard@waite.adelaide.edu.au	University of Adelaide, Australia
Sherman, Jamie [15]	jsherman@montana.edu	Montana State University, Bozeman
Shields, Phil	shieldsp@phibred.com	Pioneer Hi-Bred, St. Matthews, SC

Name (year updated)	E-mail address	Affiliation
Shindin, Ivan [09]	shelepa@bk.ru	Inst Comp Anal Reg Prob, Khabarovsk, Russia
Shroyer, Jim	jshroyr@ksu.edu	Kansas State University, Manhattan
Shahzad, Armghan	armghan_shehzad@yahoo.com	University of Wales, Bangor, UK
Shufran, Kevin A	kashufran@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Shukle, Richard [10]	shukle@purdue.edu	Purdue University, West Lafayette, IN
Sibikeev, SN [11]	raiser_saratov@mail.ru	ARISER, Saratov, Russian Federation
Siddiqi, Sabir Z	dirrari@mul.paknet.com.pk	Reg Agr Res Inst, Bahawalpur, Pakistan
Singh, Daljit [16]	singhdj2@k-state.edu	Kansas State University, Manhattan
Singh, Gyanendra P [13]	gyanendrapsingh@hotmail.com	Direct Wheat Research, Karnal, India
Singh, JB	jbsingh1@rediffmail.com	IARI, New Delhi, India
Singh, Nagendra	snagarajan@flashmail.com	IARI, New Delhi, India
Singh, Narinder [15]	nss470@k-state.edu	Kansas State University, Manhattan
Singh, Nirupma	nirupmasingh@rediffmail.com	IARI, New Delhi, India
Singh, Rajender [10]	rajenderkhokhar@yahoo.com	Ch Ch Singh Haryana Agric Univ, India
Singh, Ravi P [15]	R.SINGH@CGIAR.ORG	CIMMYT, México
Singh, SS	singhss@rediffmail.ocm	IARI, New Delhi, India
Singh, Sanjay Kumar [12]	sksingh.dwr@gmail.com	Direct Wheat Research, Karnal, India
Sinnot, Quinn	quinn@prime.ars-grin.gov	USDA–ARS, Beltsville, MD
Síp, Vaclav	sip@hb.vurv.cz	RICP, Prague, Czech Republic
Sivasamy, Muruga [13]	iariwheatsiva@rediffmail.com	IARI, Wellington, India
Skinner, Daniel Z	dzs@wsu.edu	USDA–ARS, Pullman, Washington
Skovmand, Bent	bskovmand@cimmyt.mx	CIMMYT–Mexico
Smith, Joe A	jasmith@frii.com	AgriPro Seeds, Inc., Berthoud, CO
Snape, John [10]	john.snape@bbsrc.ac.uk	JI Centre, Norwich, UK
Sommers, Daryl	SomersD@agr.gc.ca	AAFC, Canada
Sorrells, Mark E [09]	mes12@cornell.edu	Cornell University, Ithaca, NY
Sotnikov, Vladimir V	ncpgru@kharkov.ukrtel.net	Inst Plant Production, Kharkov, Ukraine
Souvorova, Katerine Yu	ncpgru@kharkov.ukrtel.net	Yuriev Pl Prod Inst, Kharkov, Ukraine
Souza, Ed [09]	edward.souza@ars.usda.gov	USDA–ARS, Wooster, Ohio
Spetsov, Penko	iws@eos.dobrich.acad.bg	Inst Wheat and Sunflower, Bulgaria
Spivac, VA [13]	spivac_VA@mail.ru	Chernyshevsky Saratov State Univ, Saratov, Russian Federation
Steffenson, Brian	bsteffen@badlands.nodak.edu	North Dakota State University, Fargo
Stehno, I Zdenek [08]	stehno@vurv.cz	RICP, Prague, Czech Republic
Stein, Lincoln	lstein@cshl.org	Cold Spring Harbor Laboratory, NY
Stein, Nils	stein@ipk-gatersleben.de	IPK, Gatersleben, Germany
Stift, G.	stift@ifa-tulln.ac.at	IFA-Tulln, Austria
Stoddard, Fred	stoddard@extro.ucc.edu.oz.ua	University of Sydney, Australia
Stuart, Jeffery J [10]	stuartjj@purdue.edu	Purdue University, West Lafayette, IN
Stupnikova, IV	irina@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Subkova, OV	ariser@mail.saratov.ru	Agric Res Inst SE Reg, Saratov, Russia
Suchy, Jerry	isuchy@em.arg.ca	AAFC–Winnipeg, Manitoba, Canada
Sun, Mei	meisun@hkucc.hku.hk	Hong Kong University
Sutherland, Mark	marksuth@usq.edu.au	Univ of Southern Queensland, Australia
Sykes, Stacy [14]	sykes@wsu.edu	USDA–ARS_WWQL, Pullman, WA
Szabo, Les [12]	Les.Szabo@ARS.USDA.GOV	USDA–ARS, University of Minnesota
Talbert, Luther E [15]	usslt@montana.edu	Montana State University, Bozeman
Tewari, Vinod	vinodtiwari_iari@rediffmail.com	IARI, New Delhi, India
Therrien, Mario C	therrien@mbrsbr.agr.ca	AAFC–Manitoba, Canada

Name (year updated)	E-mail address	Affiliation
Thiessen, Eldon	nass-ks@nass.usda.gov	KS Agric Statistics, Topeka, KS
Thomason, Wade E [10]	wthomaso.vt.edu	VA Polytech & State Univ, Blacksburg
Thompson, John [08]	John.Thompson@dpi.qld.gov.au	Leslie Research Center, Australia
Throne, JE	throne@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Tilley, M	mtilley@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Tinker, Nick	cznt@agradm.lan.mcgill.ca	McGill University, Canada
Vijay Tiwari [17]	vktiwari@umd.edu	University of Maryland, College Park
Tkachenko, OV[14]	oktkachenko@yandex.ru	Vavilov Saratov State Agrarian Univ, Russian Federation
Tohver, Maimu	maimu.tohver@mail.ee	Estonian Agricultural University, Harku
Tomasović, Slobodan [11]	bc-botinec@bc-institut.hr	Bc Institute, Zagreb, Croatia
Townley-Smith, TF	tsmith@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Trottet, Maxime	mtrottet@rennes.inra.fr	INRA, Le Rheu Cedex, France
Torres, Laura	ltorres@agro.uncor.edu	University of Córdoba, Argentina
Torres, Lorena	letorres_k@yahoo.com.ar	University of Córdoba, Argentina
Tranquilli, Gabriela	granqui@cirn.inta.gov.ar	INTA Castelar, Argentina
Tripathy, Subhash Chandra [11]	subhtripathi@gmail.com	Direct Wheat Research, Karnal, India
Tsehaye, Yemane	yemtse@yahoo.com	Inst Biodiversity Conservation, Ethiopia
Tsujimoto, Hisashi	tsujimot@yokohama-cu.ac.jp	Kihara Institute, Japan
Tverdokhleb, O.V. [11]	etverd@meta.ua	Plant Prod Inst VY Yuryev, Ukraine
Tyagi, BS	bst_knl@yahoo.com	Direct Wheat Research, Karnal, India
Ullah, Naimat [11]	naimat681@gmail.com	Quaid-I-Azam University, Pakistan
Urbano, Jose Maria	urbano@phibred.com	Pioneer Hi-Bred, Sevilla, Spain
D'utra Vaz, Fernando B	ferbdvaz@pira.cena.usp.br	University De Sao Paulo, Brazil
Valenzuela-Herrera V [12]	valenzuela.victor@inifap.g0b.mx	INIFAP, Cd. Obregon, México
Vallega, Victor [14]	vicvall@iol.it	Exp Inst Cerealicoltura, Rome, Italy
Varella, Andrea [15]	andrea.varella@msu.montana.edu	Montana State University, Bozeman
Vassiltchouk, NS	ariser@mail.saratov.ru	ARISER, Saratov, Russia
Van Sanford, David [08]	dvs@uky.edu	University of Kentucky, Lexington
Varshney, Rajeev K [08]	R.K.Varshney@CGIAR.ORG	ICRISAT, India
Varughese, George	g.varughese@cgnet.com	CIMMYT, Mexico
Veisz, Ottó	veiszo@penguin.mgki.hu	ARI–HAS, Martonvásár, Hungary
Verhoeven, Mary C	Mary.C.Verhoeven@orst.edu	Oregon State University, Corvallis
Vida, Gyula	h8607vid@ella.hu	ARI–HAS, Martonvásár, Hungary
Vernichenko, IV [16]	i.vernichenko@gmail.com	Russian State Agrarian Univ, Moscow
Vilkas, VK [13]	vk.vilkas@rediffmail.com	IARI, Wellington, India
Voldeng, Harvey	voldenghd.ottresb.ottawaem2@agr.gc.ca	AAFC, Ottawa, Ontario, Canada
Von Allmen, Jean-Marc	bvonal@abru.cg.com	Ciba-Geigy, Basel, Switzerland
von Wettstein, Dietrich H [10]	diter@wsu.edu	Washington State University, Pullman
Voss, Márcio	voss@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Vrdoljak, Gustavo	gvrdoljak@nidera.com.ar	Nidera SA, Buenos Aires, Argentina
Waines, Giles [08]	giles.waines@ucr.edu	University of California, Riverside
Walker-Simmons, MK	ksimmons@wsu.edu	USDA–ARS, Pullman, WA
Wanschura, Lucy A [15]	Lucy.Wanschura@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Wang, Daowen	dwwang@genetics.ac.cn	Chinese Academy of Science, Beijing
Wang, Richard RC	rrcwang@cc.usu.edu	USDA–ARS, Logan, Utah
Ward, Richard	wardri@msu.edu	Michigan State University, East Lansing
Watanabe, Nobuyoshi [08]	watnb@mx.ibaraki.ac.jp	Ibaraki University, Japan
Webster, James A	jwebster@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK

Name (year updated)	E-mail address	Affiliation
Wesley, Annie	awesley@rm.agr.ca	AAFC–Winnipeg, Manitoba
Wicker, thomas [10]	wicker@botinst.unizh.ch	University of Zurich, Switzerland
Wildermuth, Graham	wilderg@prose.dpi.gld.gov.au	Leslie Research Centre, Australia
Williams, Christie [12]	cwilliams@purdue.edu	USDA–ARS, West Lafayette, IN
Wilson, Dean	trio@feist.com	Trio Research, Wichita, KS
Wilson, Duane L [11]	dlwil@k-state.edu	Kansas State University, Manhattan
Wilson, James A	trio@feist.com	Trio Research, Wichita, KS
Wilson, Jeff D	jdw@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Wilson, Paul	wilsonp@phibred.com	Pioneer Hi-bred, Northants, UK
Wilson, Peter	hwaust@mpx.com.au	Hybrid Wheat Australia, Tamworth
Wise, Kiersten A [10]	kawise@purdue.edu	Purdue University, West Lafayette, IN
Worrall, David	agripro@chipshot.net	AgriPro Seeds, Berthoud, CO
Wu, Shuangye [15]	swu4455@k-state.edu	Kansas State University, Manhattan
Xia, Xian Chun [17]	xiaxianchun@caas.cn	Chinese Acad Sci, Beijing, PR China
Yamazaki, Yukiko [14]	yyamazak@lab.nig.ac.jp	Japan
Yau, Sui-Kwong	sy00@aub.edu.lb	American University Beruit, Lebanon
Yen, Yang	yeny@ur.sdstate.edu	South Dakota State Univ, Brookings
Zeller, Frederich	zeller@mm.pbz.agrar.tu-muenchen.de	Technical University Munich, Germany
Zemetra, Robert [08]	rzemetra@uidaho.edu	University of Idaho, Moscow
Zhanabekova, EH	zhanabek@mail.ru	Agric Res Inst SE Reg, Saratov, Russia
Zhang, Peng [08]	peng.zhang@usyd.edu.au	University of Sydney, Australia
Zhu, Yu Cheng	zhuyc@ag.gov	USDA–ARS, Stillwater, OK
Zhmurko, VV	toshinho@rambler.ru	Kharkov National University, Ukraine

VIII. VOLUME 64 MANUSCRIPT GUIDELINES.

The required format for Volume 64 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 44–63 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Use Microsoft Word™ or send an RTF file that can be converted. Please include a separate jpg, gif, or equivalent file of any graphic in the contribution. Submit by E-mail to jraupp@k-state.edu.

DISTRIBUTION:

The only method of distribution of Volume 64 will be electronic PDF either by email or through download from the Kansas State University Research Exchange (K-REx) (https://krex.k-state.edu/dspace/browse?value=Raupp%2C+W.+J.&type=author).

The *Annual Wheat Newsletter* also will continue to be available (Vol. 37–64) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.