ANNUAL WHEAT NEWSLETTER

Volume 62

Contribution no. 17-089-B from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

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Volume 62

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1 September, 2016.

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I. DEDICATION

Lewis E. Browder

Lewis Eugene Browder, 89, of Leonard, Texas, formerly with the USDA–ARS Wheat Research Unit in Manhattan, KS, died Saturday, 28 November, 2015; at the Leonard Manor. Lewis was born 29 January, 1932, in Harmon County, OK, the son of Benjamin Carroll and Fannie Ethel Overall Browder. He was married Zada Lea Thompson.

Dr. Browder was passionate about serving others by helping them grow more wheat. Lewis grew up on a farm in Harmon County, Oklahoma, the epicenter of the Dust Bowl, and had many interesting stories of that life. His parents were proud to send their youngest to college: Cameron University, Oklahoma State University, and then Kansas State University, where he earned his PhD. He travelled to China, Egypt, and Eastern Europe to help researchers there and was among the first to computerize wheat disease research. Dr. Browder was a part of the USDA–ARS at Kansas State University from 1958 to 1988.

Lewis also was passionate about serving others in any other ways he could, from preaching in rural churches, visiting friends in nursing homes, to baking muffins for everyone he knew. He married Zada on 19 December, 1954. Lewis and Zada lived in Manhattan, KS, from 1958 to 2012, when they moved to Leonard, TX. He served as a deacon in the Manhattan, KS, Church of Christ and was currently a member of the Leonard Church of Christ.

Lewis is survived by his wife, Zada; daughter Judy Shaw of Leonard, TX; sons Kelly J. Browder of Albuquerque, NM, and Timothy J. 'TJ' Bowder of Topeka, KS; granddaughters Whitney E. Shaw of Carrollton, TX, and Janie L. Holland of Franklin, TN; grandsons Benjamin E. Shaw of Beijing, China, Andrew F. Browder of Kansas City, MO, and Timothy J. 'TJ' Browder of Topeka, KS; and numerous nieces and nephews.

A memorial service was held 5 December, 2015, in Leonard, TX.

WHEAT WORKER'S CODE OF ETHICS

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

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

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

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

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

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

ITEMS FROM BRAZIL

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

Wheat in Brazil – 2015 crop year.

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

In 2015, the Brazilian wheat production was a little higher than 5 x 10^6 tons (Conab 2016), 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, account for 89.2% 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.

Weather conditions in the south of Brazil were not favorable to wheat in 2015. High temperature associated to high humidity during grain filling increased the incidence of Fusarium head blight.

Table 1. Cultivated area, total production and grain yield of wheat in Brazil in 2015 (* estimated value in March, 2016. Source: CONAB. 2016. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Available at: http://www.conab.gov.br/conabweb/index.php?PAG=131).

Region	Area (ha x 1,000)	Production (t x 1,000)*	Grain yield (kg/ha)*
North	—	—	—
Northeast	—	—	—
West-central	26.2	88.1	3,363.0
Southeast	156.4	507.8	3,247.0
South	2,266.2	4,939.0	2,179.0
Brazil [total]	**2,488.8**	**5,534.9**	**2,260.0**

Reference.

CONAB, 2016. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Disponível em: http://www.conab.gov.br/conabweb/index.php?PAG=131

Performance of wheat cultivars in the state of Rio Grande do Sul, Brazil, in 2014.

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

The Brazilian Commission of Wheat and Triticale Research annually conducts the State Test of Wheat Cultivars in the state of Rio Grande do Sul (STWC–RS) with the aim to support the indications of cultivars. This work has the objective of evaluating wheat cultivar grain yield performance of the STWC–RS in 2014. The yield grain performance of 33 wheat cultivars (Ametista, BRS 327, BRS 331, BRS Guamirim, BRS Marcante, BRS Parrudo, CD 1440, CD 1550, LG Oro, LG Prisma, Estrela Atria, FPS Nitron, Fundacep Bravo, Fundacep Horizonte, IAC 370 Armageddon, IAC 381 Kuara, IAC 385 Mojave, Jadeíte 11, Marfim, Mirante, ORS Vintecinco, Quartzo, TBIO Celebra, TBIO Iguaçu, TBIO Itaipu, TBIO Mestre, TBIO Pioneiro, TBIO Sintonia, TBIO Sinuelo, TEC 10, TEC Frontale, TEC Vigore, and Topazio) was studied in 19 environments (Casca, Caxias do Sul, Coxilha, Cruz Alta – season 1, Cruz Alta – season 2, Cruz Alta – season 3, Júlio de Castilhos, Não-Me-Toque, Passo Fundo – season 1, Passo Fundo – season 2, 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 2014. The experiments were in a randomized block design with three or four replications. Each plot consisted of five rows of 5 m in length with a 0.2 m spacing between rows and a plant density was ~330 plants/m^2. Grain yield data (kg/ha) were subjected to an individual analysis of variance (for each environment) and a grouped analysis of variance (for

all environments). The grouped analysis of variance employed the mixed model (a fixed cultivar effect and randomized environment effect). Grain yield performance of the wheat cultivars was evaluated by analysis of adaptability and stability, employing the method of distance from the ideal cultivar, weighted by the coefficient of residual variation, proposed by Carneiro (1988).

In this analysis, the ideal cultivar was considered as the cultivar with high grain yield, high stability, low sensitivity to adverse conditions of unfavorable environments and the ability to respond positively to improvement of favorable environments. The general average of STWC-RS in 2014 was 3,136 kg/ha. The experiment in São Borja had the highest average for wheat grain yield, 4,925 kg/ha. The maximum wheat grain yield was 5,780 kg/ha, in Coxilha (TBIO Sinuelo cultivar). The Ametista, TEC Vigore, LG Oro, TBIO Celebra, and Topazio cultivars had adaptability and stability in favorable environments (environments with average of wheat grain yield higher than the general average). The cultivars Ametista, Topazio, TBIO Sinuelo, LG Prisma, and LG Oro had adaptability and stability in unfavorable environments (environments with average of wheat grain yield lower than the general average). In general, averaged for all environments, cultivars Ametista (3,671 kg/ha), Topazio (3,522 kg/ha), TBIO Sinuelo (3,557 kg/ha), LG Oro (3,545 kg/ha), and LG Prisma (3,517 kg/ha) were the closest to the ideal cultivar.

Reference.

Carneiro PCS. 1998. New methodologies for analyzing the stability and adaptability of behavior. Ph.D. Thesis in Genetics and Breeding, Federal University of Viçosa. 168 pp.

Wheat crop in the state of Rio Grande do Sul, Brazil, in 2014.

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

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 2014. That year, Rio Grande do Sul harvested 1,180,817 ha of wheat (41.7% of the total area harvested in Brazil), producing 1,670,623 tons of wheat (26.7% of the Brazilian production), with an average of grain yield of 1,415 kg/ha (794 kg/ha above the Brazilian average of 2,209 kg/ha). Among the geographical mesoregions of Rio Grande do Sul (Fig. 1), the RS Northwest mesoregion harvested the largest wheat area, 937,231 ha (79.4% of the cropped area in the state) and had the largest production, 1,141,342 tons of grain (68.3% of state production) (Table 2). However, the average grain yield obtained in this mesoregion was the lowest of the state, 1,218 kg/ha (197 kg/ha below the state average) (Table 2). The RS Northeast mesoregion harvested 53,127 ha of wheat (4.5% of the cropped area in the state), produced 161,595 tons of wheat grain (9.7% of the state production), and had the highest grain yield average in the state, 3,042 kg/ha (1,627 kg/ha above the state average) (Table 2). The 2014 wheat crop in Rio Grande do Sul had unfavorable weather conditions, with average temperature above normal and an excess of rain in the spring. In Passo Fundo, in the Northwest mesoregion, for example, the total rainfall was 586.1 mm in the months of September, October and November. Consequently, the average wheat grain yield, in 2014, was very low in Rio Grande do Sul, especially in the Northwest mesoregion. Comparing the wheat crop data with the results

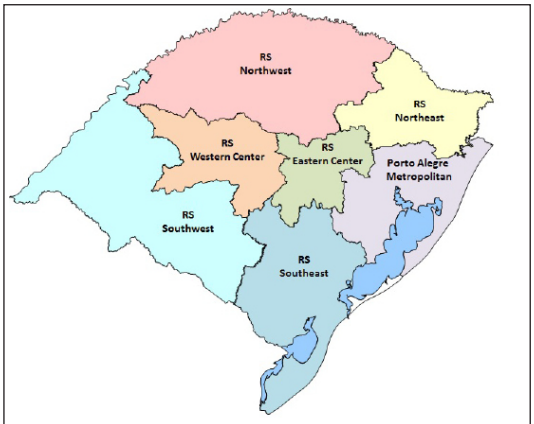

Fig. 1. Mesoregions in the state of Rio Grande do Sul, Brazil.

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 2014 (Source: IBGE. 2016).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	937,231	79.4	1,141,342	68.3	1,218
RS Northeast	53,127	4.5	161,595	9.7	3,042
RS Western Center	97,782	8.3	160,689	9.6	1,643
RS Eastern Center	20,289	1.7	33,038	2.0	1,628
Porto Alegre Metropolitan	3,068	0.3	6,026	0.4	1,964
RS Southwest	55,050	4.6	136,990	8.2	2,488
RS Southeast	14,270	1.2	30,943	1.8	2,168
Rio Grande do Sul state	1,180.817	100.0	1,670,623	100.0	1,415

of the State Test of Wheat Cultivars in Rio Grande do Sul in 2014, we observed that the average grain yield of commercial crops was 1,721 kg/ha below the average of 3,136 kg/ha.

Reference.

IBGE. 2016. Sistema IBGE de Recuperação Automática – SIDRA. Available at: <http://www.sidra.ibge.gov.br/bda/tabela/listabl.asp?z=t&o=11&i=P&c=1612>. Acessed 28 March, 2016. Note: aggregate data studies and research carried out by the IBGE (In Portugese).

ITEMS FROM GERMANY

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

A. Börner, M. Agacka-Mołdoch, G.I. Batalova, D.R. Cárdenas, T. Castellanos, A.M. Castro, Yu.V. Chesnokov, A.M. Dell, J.L. Diaz de Leon, A.V. Doroshkov, G.S. Gerard, D. Gimenez, P. Kouria, J. Ling, U. Lohwasser, G. Lori, Q.H. Muqaddasi, M. Nagel, S.V. Osipova, L. Perello, A.V. Permyakov, M.D. Permyakova, F. Pinto, T.A. Pshenichnikova, C.O. Qualset, M.A. Rehman Arif, M.E. Ricci, M.S. Röder, A. Rojas-Hernandez, E.G. Rudikovskaya, A.V. Rudikovsky, A.A. Shishparenok, M.R. Simón, V.V. Verchoturov, Chr. Zanke, and K. Zaynali Nezhad.

Genome-wide association mapping of anther extrusion in hexaploid spring wheat.

In a number of crop species, hybrids are able to outperform the conventionally bred varieties. The anthers of the autogamous bread wheat plant are normally extruded post anthesis, a trait that is unfavorable for the production of F_1 hybrid grain. Higher anther extrusion (AE) promotes cross fertilization for higher hybrid seed production. Therefore, this study aimes to genetically dissect the AE trait by genome-wide association mapping and determine the main effect QTL. The association mapping approach was used to identify DArT markers potentially linked to AE to unfold the genetic basis of AE in a panel of spring wheat cultivars. Phenotypic data were collected in field trials for three consecutive years (2013–15) and the best, linear, unbiased estimations (BLUEs) were calculated across all years. The extent of the AE correlation between growing years and BLUEs ranged from r = 0.56 (2013 *vs* 2015) to 0.91 (2014 *vs* BLUEs). The level of repeatability was 0.95 for 2013 and 2014 and 0.97 for 2015. The broad sense heritability was 0.84 across all years. Six accessions displayed an AE >80%, and the trait was stable across the years. Genotyping data included 2,575 DArT markers (with minimum of 0.05 minor allele frequency applied) covering the A, B, and D genomes, unevenly, with 409 unmapped markers. Anther extrusion was influenced both by genotype and by the growing environment. In all, 131 significant marker trait associations (MTAs) ($|\log_{10}(P)| \geq$FDR) were established for AE. Anther extrusion behaved as a quantitative trait, with each consistent MTA (across at least two years and BLUEs) contributing a minor to modest proportion (4.29% to 8.61%) of the overall phenotypic variance. The five consistently significant MTAs mapped to chromosomes 5A, 5B, and 6A. The association mapping analysis showed that AE is controlled by many genetic loci, which can affect the trait both positively or negatively. For that reason, gene pyramiding may have potential for breeding for improved AE. The highly significant markers linked to AE could be helpful for marker-assisted selection to transfer AE to high-yielding cultivars, allowing the exploitation of hybrid heterosis in the key crop wheat.

Analysis of main effect QTL and testing of candidate genes for 1,000-kernel weight in European winter wheat by genome-wide association mapping.

Grain weight, an essential yield component, is under strong genetic control and, at the same time, markedly influenced by the environment. Genetic analysis of the 1,000-kernel weight (TKW) by genome-wide association study was performed with a panel of 358 European winter wheat and 14 spring wheat cultivars using phenotypic data of field tests in eight environments. Wide phenotypic variations were indicated for the TKW with BLUEs (best linear unbiased estimations) values ranging from 35.9 g to 58.2 g with a mean value of 45.4 g and a heritability of H^2=0.89. A total of 12 candidate genes for plant height, photoperiodism, and grain weight were genotyped on all cultivars. Only three candidates, the photoperiodism gene *Ppd-D1*, dwarfing gene *Rht-B1,* and the *TaGW-6A* gene, were significant explaining up to 14.4%, 2.3%, and 3.4% of phenotypic variation, respectively. For a comprehensive genome-wide analysis of TKW–QTL genotyping data from 732 microsatellite markers and a set of 7,769 mapped SNP-markers genotyped with the 90k iSELECT array were analyzed. In total, 342 significant ($-\log_{10}$ (P-value) ≥ 3.0) marker trait associations (MTAs) were detected for the SSR-markers and 1,195 MTAs ($-\log_{10}$ (P-value) ≥ 3.0) for SNP-markers in all single environments plus the BLUEs. After Bonferroni correction, 28 MTAs remained significant for SSR-markers ($-\log_{10}$ (P-value) ≥ 4.82) and 58 MTAs for SNP-markers ($-\log_{10}$ (Pvalue) ≥ 5.89). Apart from chromosomes 4B and 6B for the SSR-markers and chromosomes 4D and 5D for the SNP-markers, MTAs were detected on all chromosomes. The highest number of significant SNP-markers was found on chromosomes 3B and 1B, whereas for the SSRs, most markers were significant on chromosomes 6D and 3D. Overall, TKW was determined by many markers with small effects. Only three SNP-markers had R^2 values above 6%.

Quantitative trait loci underlying the adhesion of Azospirillum brasilense cells to the wheat root.

The rhizosphere microflora community influences plant growth and development in numerous ways, in some cases deleteriously and in others beneficially. *Azospirillum brasilense* is among the most well-studied rhizobacteria able to promote plant growth. The capacity for *A. brasilense* cells to adhere on the seedling root is a variable trait in wheat cultivars. The parents of a CIMMYT bread wheat mapping population derived from the cross 'Opata / synthetic hexaploid line WSHD67.2(257)' contrasted for this trait, providing an opportunity to determine its genetic basis. The capacity to adhere effectively was shown by 32% of mapping population individuals. A genetic map was constructed using 157 informative microsatellite loci and 1,356 SNP loci. The resulting QTL analysis identified four chromosomes as harboring loci associated with adhesion. Chromosome 1A was the site of both a major (LOD >3) and a minor (LOD 2–3) QTL, whereas the remaining four minor loci mapped to chromosomes 2D, 5A, and 6B (two loci). *QAdh.uabcs-1A.2* explained 8.6% of the phenotypic variance, and the full set of QTL explained 23.1%. The source of the positive allele of *QAdh.uabcs-1A.2* was the cultivar Opata.

Recognizing that adhesion capacity has a partial genetic basis has implications for the use of biofertilizers, and also suggests that there is potential for using breeding to improve the host's capacity to adhere *A. brasilense* and, by inference, other plant growth-promoting rhizobacteria. The present detection of adhesion capacity QTL provides a number of markers that may have future value in a marker-assisted breeding context.

Studies on osmotic tolerance in bread wheat.

An experiment was conducted to investigate osmotic stress tolerance in a set of 131 bread wheat recombinant inbred lines. The population was developed by crossing a salt-resistant, winter wheat cultivar and a salt-sensitive spring wheat to investigate salt tolerance. Fifteen seeds in three replicates were placed on filter paper and grown in 12% PEG 8000 (polyethylene glycol) for 2 days in dark and 5 days in light. Water was used for the control plates. After 7 days, data was recorded for maximum root (RL) and shoot (SL) length and coleoptile length (CL). A tolerance index (TI) was calculated by dividing corresponding lengths with the respective controls. All the seeds were subjected to 1% H_2O_2 treatment for 24 hours prior to germination. The minimum and maximum CL in control was 1.31 cm and 5.26 cm, respectively, with the mean of 2.8 ± 0.05 cm, whereas these values were reduced to 0.6, 4.03, and 2.32 ± 0.58 cm, respectively, in PEG. The TI ranged from 0.27 to 1.00 with mean of 0.80 ± 0.015. The range for shoot length in control was 2.33 to 18.25 cm with mean of 8.98 ± 0.18 cm. Osmotic stress reduced the shoot length considerably which ranged from 1.31 to 14.81 cm with mean of 5.36 ± 0.19 cm. The mean TI for SL was 0.58 ± 0.017 that ranged from 0.15 to 0.99. RL in control varied from

5.07 to 15.80 cm with mean of 10.04 ± 0.17 cm. Osmotic stress had profound effect on RL as well that was reduced to 7.81 ± 0.18 cm with 2.72 and 12.62 cm being minimum and maximum RL, respectively. The maximum TI for RL was 1.00, the minimum was 0.19 whereas the mean was 0.78 ± 0.015. All the values under osmotic stress were significantly different from their respective controls. This experiment concludes that this population can be a useful asset to study drought tolerance in bread wheat, because it showed considerable variation at seedling stage towards osmotic stress. The data generated here will be used in mapping osmotic tolerance loci in this population.

Genetic dissection of response to water deficit using D-genome introgression lines of bread wheat.

Drought is a most serious abiotic stress affecting crop productivity. One of the species representing a potentially valuable source of genes for stress tolerance is the goat grass *Aegilops tauschii*, known to be the donor of the bread wheat D genome. The D-genome Chinese Spring (Synthetic 6x) introgression lines were exploited in order to determine the genetic basis of variation for the physiological traits gas exchange, chlorophyll fluorescence, leaf pigment content, the activity of various antioxidant enzymes, and shoot biomass under both well-watered and moisture-deficient conditions. A QTL approach was taken to reveal the genetic basis in wheat of traits associated with variation for physiological and biochemical traits. Eleven, D-genome regions harbored QTL associated with traits of relevance to drought tolerance distributed over the four chromosomes, 1D, 2D, 5D, and 7D. The most saturated region was defined by the 24.6-cM interval flanked by *Xgwm539* and *Xgwm1419* microsatellite markers. This region harbored QTL underlying shoot biomass and stomatal control of photosynthesis. Another well-saturated region was detected on on chromosome 7D, lying between *Xgwm1242* and *Xgwm1672*, which housed QTL underlying photosynthetic rate under moisture stress, water use efficiency, and APX activity under both growing conditions. The QTL on chromosomes 1D and 5D mostly were associated with chlorophyll content and chlorophyll fluorescence parameters. Some of them co-localized with the already known loci important for drought tolerance of wheat or other cereals. For the first time in wheat, QTL were found associated with antioxidant enzymes activity playing a significant role in adaptation to drought. We could argue that the major factors regulating networks of functional genes activating during water deficit are localized in at least two regions of the D genome of bread wheat, on chromosomes 2D and 7D.

Genetic architecture of adult-plant resistance to leaf rust in winter wheat.

A GWAS for adult-plant resistance to leaf rust was performed using a core collection of 96 winter wheat accessions sampled from 20 countries across five continents. The panel was evaluated under natural disease epidemics according to the modified Cobb scale in six field trials performed at two locations, Los Hornos and La Plata, Argentina. At each location, three experiments were planted on 21 June, 2012, and 14 June and 31, July 2013. The experimental design was a split - plot with two replications. The main plots were the experiments and the subplots were the 96 genotypes. In addition, the local cultivar Buck SY110, susceptible to prevailing races in the area, was included in all experiments as susceptible control to assess the leaf rust infection levels. The evaluation was initiated when the reference susceptible cultivar showed a clear susceptible reaction in the top three leaves (at early milk development).

The GWAS panel was genotyped with 874 polymorphic DArT markers, assigned to chromosome arms based on an integrated map previously developed. For phenotype–genotype association analysis, the general linear model based on Q-matrix and the mixed linear model using both Q-Matrix and the kinship-Matrix, was used with Tassel 2.1 software. In all cases, only MTAs significant ($P < 0.05$) in at least four of the six environments and with at least two environments with highly-significant differences ($P < 0.01$) in both models were considered to identify leaf rust resistance loci.

A total of 14 significant MTAs assigned to 13 genomic regions on the chromosomes 1BL, 1DS, 2AS, 2BL, 2DS, 3BS, 3BL, 4AL, 6BS (two), 7DS, 5B/7B, and 6AS/6BS were identified. The phenotypic variation explained by significant DArT markers ranged from 4.6% to 14.6%, indicating that the resistance to leaf rust was determined by several genetic factors with small to moderate effects. Furthermore, of the 13 genomic regions identified, those located on 2AS, 2BL, 2DS, 3BS 4AL, and 6BS (one) were mapped on similar chromosome regions to previously reported *Lr* genes. In contrast, the MTAs on 1BL, 1DS, 3BL, 6BS, 7DS, 5B/7B, and 6A/6B were found in regions where, to our knowledge, no previous evidence of *Lr* resistance genes were reported and, therefore, appear to be novel resistance loci to leaf rust. The seven novel resistance loci identified in our study can be used as new sources of resistance to incorporate additional *Lr* resistance loci into adapted wheat cultivars. However, prior validation using biparental populations or near-isogenic lines is required.

Induction of Fusairum head blight tolerance in bread wheat with plant hormones elicitors treatments.

Fusarium head blight (FHB), caused *by Fusarium graminearum* (Schwabe), is one of the most important diseases affecting wheat in all grain-producing regions of the world and causes yield losses, deterioration of the quality and grain contamination with mycotoxins, which constitute a risk to human and animal health, and undertake industrial use.

We studied the possibility of inducing defense mechanisms to the FHB by exogenous application of plant growth regulators in a commercial wheat Klein Zorro and two doubled-haploid lines derived from 'Opata / Synthetic' (OXS) and 'Spark / Rialto' (SXR) crosses. The application of jasmonic acid and gibberellic acid (GA) was carried out at full anthesis and after 48 hours. Treated plants were artificially inoculated with *F. graminearum* using two techniques, spray inoculation with a spore suspension and point inoculation in the central spikelets. Such techniques help to highlight the mechanism of resistance to the penetration of the pathogen (Type-I mechanism) and resistance to spread of the pathogen (Type-II mechanism), respectively.

We studied the disease severity and 1,000-kernel weight in order to determine the behavior of the parameters studied in the different wheats. The cultivar and lines were susceptible to the FHB, however, we noted that some hormonal treatments improved their behavior when inoculated. The application of GA and subsequent inoculation increased the 1,000-kernel weight in OXS and SXR, exceeding the average of 8.73 grams related to their control plants inoculated with *Fusarium*. This positive response possibly is related to the induction of defense mechanisms of the plant that would enable the development of more sustainable control strategies.

Russian wheat Aphid (Diuraphis noxia) antibiotic resistance evaluated in recombinant inbred lines (RILs) of the ITMI population.

The Russian wheat aphid (RWA) is one of the most harmful pests of wheat and barley, causing considerable losses in production. This aphid has evolved numerous biotypes, at least three of them exist in Argentina, showing different characteristics to those from other latitudes. Although, biotype-specific resistance genes have been identified, within the integrated pest management evaluating novel sources of resistance with local populations of pests is critical. For that reason, our aim was to study the antibiotic effect of experimental recombinant inbred lines of wheat on the biological parameters of the RWA. We assessed the immature period (*d*), the reproductive period (RP), fertility in a period of equal extension of *d* (*Md*), total fertility, longevity, and the intrinsic rate of population increase (r_m). The life span and reproduction of RWA biotype 5 were assessed on 113 RILs and both parents (Opata and Synthetic 6x).

Every aphid parameter studied showed significant differences between the genotypes. Three antibiotic lines that lengthened the *d* period were identified, the most antibiotic RIL increased *d* period by 40% compared to the average determined in aphids reared on the RIL population. The RP was significantly lower in the same three RILs, which. in this case. induced a 78% reduction of RP in relation to the average of the population. Total fertility was significantly reduced in aphids reared in the most antibiotic RILs, with 89 % lower levels compared to the population average. Longevity was reduced by 54% in aphids reared in the most antibiotic RILs. The r_m had minimal values in aphids reared on antibiotic RILs, representing a decrease of 67% compared to the population average. Three RILs were identified with significant antibiotic effect that altered RWA life cycle, and these lines can be used as a source of antibiosis genes for breeding resistance in new wheat cultivars.

Evaluation and QTL mapping of the ITMI population grown in the northeastern part of the Russian Federation.

For the first time, a set of 114 recombinant inbred lines of the spring-type. ITMI mapping population were evaluated in environments of north-eastern part of the Russian Federation. Sixteen economically important traits that manifest themselves at different stages of growth were examined each year for 3 years. A total of 55 QTL with LOD scores above 2.0 were identified. We determined that 22 QTL had LOD scores exceeding 3.0. The QTL for traits studied mapped onto 21 chromosomes and manifested themselves under contrasting environmental conditions with varying degrees of reliability. The manifestation of identified QTL may or may not depend on the year of trial, but the evaluated quantitative

traits interact and correlate with each other. The relationships between identified homologous and homeologous QTL with known major genes or QTL responsible for the manifestation of the studied traits in wheat or other Triticeae were investigated. Information about the genes of vegetative growth and flowering is critical to understanding the processes of adaptability of plants to environmental conditions. Therefore, loci should be viewed not as mechanical linkages of genes, but as some organic normalization, as a group of functionally related genes, or as blocks of co-adapted genes. The identified QTL may be of interest for further experiments on genetic control of the corresponding agriculturally valuable traits and for marker-assisted selection in wheat breeding.

Single, marker-trait association analysis in unrelated Iranian bread wheats.

This experiment studied the genetic diversity among some of Iranian bread wheat accessions and perform an SSR marker-trait association analysis. Five microsatellite markers in a QTL location controlling morphological traits on chromosome 4B were applied to evaluate the marker-trait relationship. Chinese Spring was used as the reference genotype to determine SSR allele sizes properly. Fifty-two pure lines, including Chinese Spring wheat, were studied in a field experiment and 14 morphological traits were recorded. Marker-trait association was tested through a completely randomized design, considering alleles as treatments and individual showing the same alleles as replications. Analyzing the 14 traits and five applied SSR markers on the QTL of interest on chromosomes 4B revealed a statistical relationship for three traits. Specific SSR alleles were identified for days-to-flowering, plant height, and number of seed/spike at locus *Xgwm149-4B*. Interestingly, a single allele (153 bp) was identified simultaneously for three desired situations at this locus, such as fewer days to flowering, shorter plant height, and a higher number of seeds/spike. These SSR markers can be applied for marker-assisted selection in bread wheat breeding programs.

Trends in German winter wheat breeding.

The breeding progress of winter wheat in Germany was investigated performing a field trial with 20 cultivars. The set contained 10 entries each, cultivars released between 1891 and 1909 and between 1991 and 2010. A range of agronomic traits, including plant height, flowering time, plot yield, and yield components were considered. Harvest index also was determined.

For flowering time, modern cultivars tend to be earlier, although the old cultivar Rimpaus Früher Bastard (Rimpau's Early Crossbreed) was as early as the earliest modern cultivar. For plant height, a clear reduction in the modern cultivars was observed, ranging from 90 to 120 cm. In contrast, the old cultivars reached 150–180 cm. The reduction in plant height has an evident effect on lodging resistance, with a score of 1 for all modern cultivars. However, three of the tall cultivars, ranging between 140 and 160 cm, also had a score of 1. The reason may be a special elasticity or cell wall stability of the tillers. Reduced plant height also is the reason for reduced straw yield of the modern cultivars. Considering the yield of 20 single spikes, no obvious tendency was found over the years, however, harvest index increased. For the yield components, grain number/spike and 1,000-kernel weight, no clear tendency was observed. Finally, grain yield of the plots did show an increase in the modern cultivars, which may be due to a higher number of spikes/m^2 (not scored).

Genetics of seed longevity.

Seed longevity is determined by genetic factors but also depends on environmental conditions during seed development, harvest, and storage. For time reasons, experiments on seed longevity are mainly performed by exploiting methods of experimental ageing. Whether or not the results obtained after experimental ageing really are equivalent to those found after natural ageing is still obscure.

Recombinant inbred lines of the ITMI mapping population were analysed after artificial ageing and after long-term storage (10^0C / 50% RH) for up to 14 years. The recombinant inbred lines were reproduced either at experimental fields at IPK, Gatersleben, Germany, or the University of California Intermountain Research and Extension Center, Tulelake, California, USA. Four replicates of 50 seeds each were subjected to standard germination tests following the International Seed Testing Association rules and data obtained were used for QTL analysis.

As a result, one locus out of a total of 11, was detected after both experimental and natural ageing of the seeds, however, contributed by different parents. Correlation analysis revealed no relationship between different experimental ageing treatments and long-term storage. In addition to the ageing conditions, the origin of the seed set, i.e., the growing conditions of the mother plants, have a pronounced effect on seed survival.

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ITEMS FROM JAPAN

NATIONAL INSTITUTE OF CROP SCIENCE (NICS)
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Relationship between median flour particle size distribution and flour yield in Japanese hexaploid wheats.

Hiro Nakamura.

Abstract. Flour particle size distribution is a major factor affecting the milling behavior in hexaploid wheats. This research evaluated a new method to assess the milling behavior of Japanese wheat cultivars and determine the relationship between flour yield and median flour particle size distribution. To investigate the higher flour-yielding Japanese wheats, the flour yield of 165 Japanese hexaploid wheat cultivars was investigated in relation to median and mean flour particle size and also the flour particle size distribution patterns as determined by laser diffraction. The results showed that hard and soft wheat cultivars differed in median flour particle size and particle distribution patterns. Eighty percent of the Japanese wheat cultivars had soft or medium-soft particle size distribution patterns. Flour yield also was most strongly associated with the median flour particle size (μm) in the flour samples. These results indicate the potential for developing a flour yield evaluation method in Japanese udon-noodle wheat cultivars using laser diffraction methods, and that median flour particle size analysis could be a useful indicator in flour quality for udon-noodle wheat breeding and evaluation.

Introduction. Developing Japanese udon-noodle wheat cultivars with higher flour yield and enhanced grain quality is important in order to satisfy the demands of Japanese milling companies and improve the international competiveness of Japanese hexaploid wheat. An important factor in Japanese wheat breeding programs is to breed udon-wheat lines with excellent milling quality. Flour hardness is known to be associated with flour strength, but relatively little information has been published about the flour hardness of Japanese wheat cultivars. Furthermore, little research has been conducted on simple and reliable assessments of the flour milling quality needed for Japanese udon-noodle wheats. Flour particle size parameters have been analyzed since the late 1980s by laser-beam diffractometry and detailed flour particle size distributions could be easily determined using a laser light apparatus. Flour particle size distribution is an important indicator of the quality of high-ratio flour, and commercial wheat flour samples are often characterized according to their particle size properties. Thus, determining the relationship between flour yield and flour particle size distribution would be useful. Our objectives were to determine whether the median flour particle size (μm) could be used as an index of flour yield in Japanese udon-noodle wheat breeding programs and develop a suitable method for evaluating the flour yield of Japanese hexaploid wheats.

Results and Discussion. This study showed the correlations between various quality evaluation parameters obtained from the standardized milling of the 165 Japanese wheat samples. The parameters were the flour yield ratio, median and mean flour particle size, and the particle size distribution. The results showed significant correlations between these four parameters. Median flour particle size was significantly correlated with mean flour particle size ($\gamma = 0.97$, $P < 0.01$), flour yield ratio ($\gamma = 0.75$, $P < 0.01$), and flour particle size distribution pattern ($\gamma = 0.87$, $P < 0.01$). Mean flour particle size also was significantly correlated with flour particle size distribution pattern ($\gamma = 0.86$, $P < 0.01$) and flour yield ($\gamma = 0.70$, $P < 0.01$). Furthermore, the particle size distribution pattern was correlated significantly with flour yield ($\gamma = 0.75$, $P < 0.01$). Multiple regression analysis showed that flour yield (Y) was significantly related to median flour particle size (X1) and mean flour particle size (X2) according to the formula $Y = 66.03 + 0.32X1 - 0.16 X2$ ($R = 0.75$). The 165

Japanese wheat cultivars could be categorized into three flour particle size distribution pattern groups, soft, medium-soft, and hard. Representative examples of each pattern are shown; patterns I and II represent the typical bimodal particle size distributions of Japanese soft and medium-soft udon wheats. The flour particle size distribution pattern I was from the soft wheat Norin No. 61, which is associated with a low flour yield. The main peak in particle size occurred at ~20–30 μm in diameter, with a second smaller population ~80–90 μm in diameter. Norin No. 61 was used as a control

to evaluate the udon-noodle making quality of the other wheat cultivar, because it generally is known as one of leading cultivars for udon-noodle products.

Flour particle size distribution pattern II was from the Japanese medium-soft wheat Nabarigoshi. This cultivar also showed a two-peak, bimodal distribution, like pattern I for soft wheat, but the largest proportion of particles was at larger particle sizes, indicating a higher flour yield than for pattern I soft wheats. Flour particle size distribution pattern II also is found in cultivars such as Australian standard white (ASW) and Western white standards (WW) (Nakamura unpublished), indicating a soft wheat milling behavior with a higher flour yield. A major strategy to improve Japanese wheat production is to develop higher flour yielding cultivars similar to ASW and WW.

Flour particle size distribution pattern III was from the Japanese hard wheat Norin No. 75. This hard wheat distribution pattern exhibited only one main peak mode ~80–100 μm in diameter. The main difference between the patterns for hard, soft, and medium-soft wheats is the much lower proportion of smaller particle sizes in the hard wheat. These distribution patterns indicate that the median and mean flour particle sizes of soft wheats typically are lower than those of hard wheats. The greater proportion of smaller particles in soft and medium-soft wheats is due to the fact that, in these two types of wheat, the milling process produces more isolated starch granules than in the hard wheats.

We observed a wide variation in the median particle size of the 165 wheat cultivars, ranging from 26.83 μm for the udon-noodle soft wheat Asakazekomugi to 93.56 μm for the hard wheat Norin No. 13. Therefore, no cultivar had a median flour particle size of more than 100 μm, which is typically associated with a higher flour yield. Hard bread wheats typically have a median flour particle size of more than 100 μm and a large proportion have a hard particle distribution pattern. In the 165 Japanese cultivars examined, 42 were categorized as pattern-I, soft wheat with a median flour particle size of 26.83–37.60 μm, 90 were categorized as pattern-II, medium-soft wheat with a median flour particle size of 35.66–71.32 μm, and only 33 were categorized as pattern-III hard wheat with a median flour particle size of 66.92–93.56 μm. These results indicate that 80% of Japanese wheats are classified as soft, including medium-soft, and only 20% are classified as hard wheat.

Wheat flour yield is the most important technical and economic factor with regard to flour milling, and plays an important part in the buying decisions of many milling companies. Experimental and laboratory milling determines wheat milling quality and, therefore, has received much attention from wheat breeders and flour millers. The soft udon-wheat breeding strategy in Japan is aimed at selecting cultivars with a good udon-noodle making quality and a higher flour yield, which also has a major effect on the quality of noodle products. Overall, however, the most important aspect of wheat quality is a higher flour yield at milling, in order to satisfy market demands in Japan.

Hard and soft wheat cultivars are known to differ in flour yield after milling. The origin of noodles are in China, but udon-noodles, as we know them today, were developed independently in far-east Japan. Soft, medium-soft, and hard wheats could be clearly separated by particle size distribution analysis. Flour particle size distribution depended on flour hardness. Because the flour particle size distributions were either unimodal or bimodal, the standard deviation was irrelevant. Synthetic parameters relating to the flour particle size distributions could be obtained by using multiple regression analysis. The prediction model obtained from the regression analysis indicated that the flour yield of Japanese common wheats could be predicted accurately by inputting X1 and X2 values for median and mean flour particle size, respectively. However, based on the regression equation and the very high correlation between median and mean flour particle size ($\gamma = 0.97$), the most important factor in a milling test for determining flour yield was median flour particle size. The merit of a Brabender Jr. Quadrumat mill is that it is very easy to operate and gives good reproducible results and, therefore, it could be used to evaluate common wheats with respect to differences in flour milling quality. Our results indicate that the median flour particle size could be a useful tool for selecting common wheat lines with a higher flour yield, such as the F_4 early generation. Modern electric and computing technology, i.e., particle dispensing and laser diffraction equipment and analysis software, have made it possible to analyze flour particle size distribution more quickly and with more reproducible results than with other methods such as a sieve analysis. Flour particle size distribution analysis could play an important role in Japanese wheat breeding programs. In general, udon-wheats give a lower flour extraction rates, whereas ASW and/or WW standards will have higher flour extraction rates; an important economic issue for Japanese milling companies. Previously, the flour hardness index was generally determined based on the glassy kernel ratio in wheat flour. However, this method cannot be used to rapidly evaluate the flour yield as part of a wheat-breeding program. Therefore, the objective of the current research was to develop a milling evaluation index in wheat varieties and a method to predict the flour yield using laser diffraction, which is a new technology for Japanese wheat research, instead of using the glassy kernel ratio evaluation. Flour particle size distribution analysis, especially the median flour particle size, could be used in wheat breeding programs to rapidly and reliably evaluate and predict flour yield.

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.

Rust resistance gene identification in four commercial bread wheat cultivars and advanced bread wheat lines for northwestern Mexico during crop season 2013–14.

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Abstract. Commercial bread wheat cultivars Roelfs F2007, Ónavas F2009, Tepahui F2009, and Villa Juárez F2009, released by the wheat program of INIFAP, and 20 advanced lines from the Bread Wheat Improvement and Rust Research Program of CIMMYT, were used to determine the presence of genes *Sr2*, *Sr22*, *Sr24*, *Sr26*, *Sr35*, and *Sr39*. DNA extraction followed the method of Saghai-Maroof et al (1984). Genes identified were *Sr2*, *Sr22*, *Sr24*, *Sr26*, *Sr35*, and *Sr39*. The majority of the genotypes evaluated possess gene *Sr2,* which shows resistance to stem rust. For genes *Sr22*, *Sr24*, *Sr26*, and *Sr35*, the gene of interest was present in at least one genotype evaluated, with the exception of *Sr39*.

Introduction. The Wheat Program of INIFAP in northwest Mexico is one of the most important in the country, because it generates most of the commercial wheat cultivars nationally. Every cropping season at the Norman E. Borlaug Experimental Station, more than 50 outstanding wheat advanced lines from several CIMMYT breeding

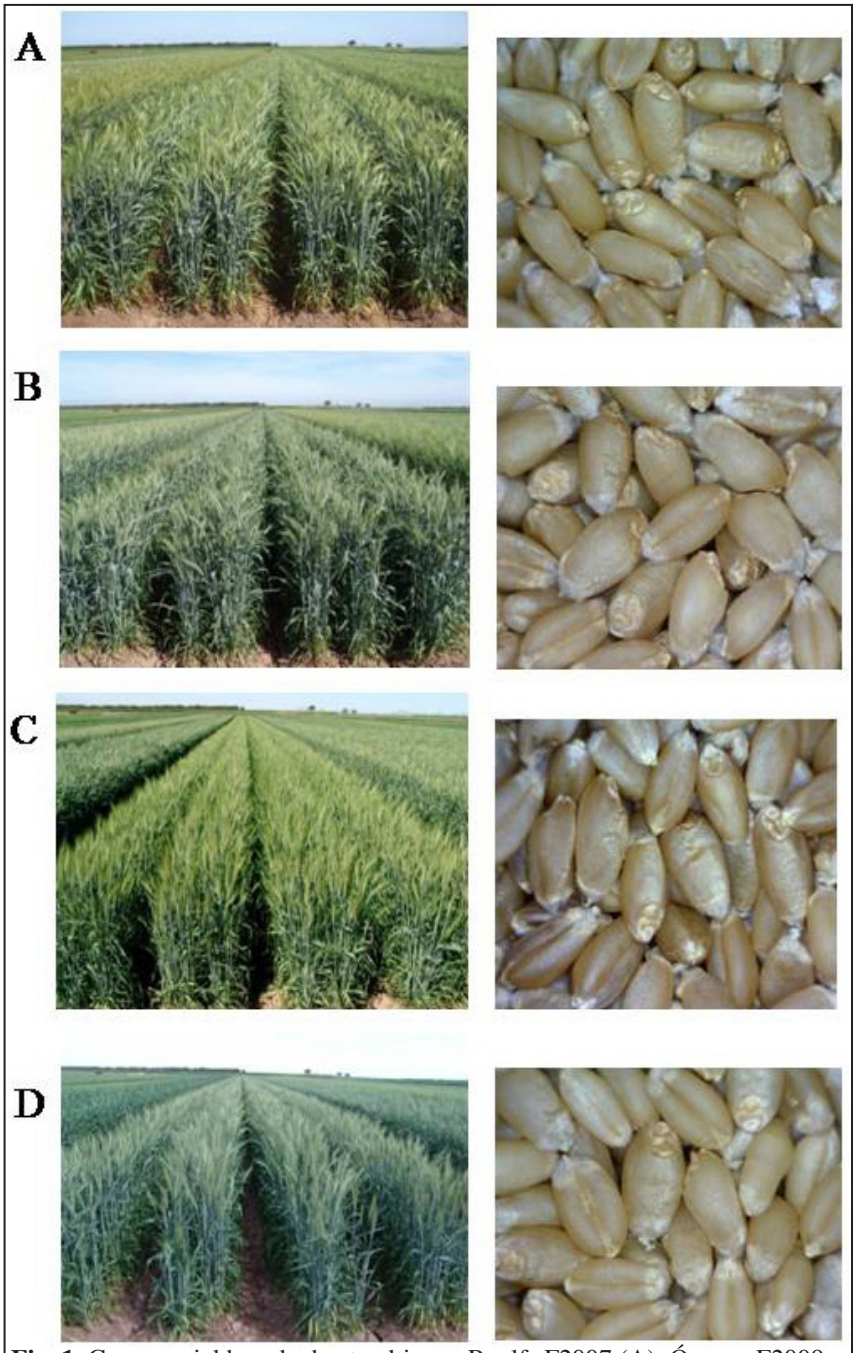

Fig. 1. Commercial bread wheat cultivars, Roelfs F2007 (A), Ónavas F2009 (B), Tepahni F2009 (C), and Villa Juárez F2009 (D), released by the wheat program of INIFAP.

programs are evaluated for specific adaptation to the region, including sowing date, resistance to leaf rust and Karnal bunt, tolerance to water stress, grain yield, and industrial quality. Conventional plant breeding depends on appropriate environmental conditions in which to identify and select desirable plants. Typically, breeders improve crops by crossing plants with desired traits, such as high yield or disease resistance, and selecting the best offspring over multiple generations of testing. A new cultivar could take 8 to 10 years to develop, so it is a slow and expensive process. Breeders are very interested in new technologies that speed up this process or make it more efficient (Byrne and Richardson 2015). Molecular marker technology offers such a possibility. Marker-assisted selection (MAS) involves selecting individuals based on their marker pattern (genotype) rather than their observable traits (phenotype). Since the mid-1990s, the term marker-assisted selection has entered the working vocabulary of plant breeders and geneticists. Marker-assisted selection consists in identifying a DNA sequence that is close, or in the best of the cases, codes, for a gene (or locus) of agronomic interest. This sequence is used as a tool in the selection process, independent of the gene expression or its interaction with the environment (Olmos 2004). Our objective was to evaluate commercial bread wheat cultivars Roelfs F2007, Ónavas F2009, Tepahui F2009, and Villa Juárez F2009 released by the wheat program of INIFAP, and 20 advanced lines from the Bread Wheat Improvement and Rust Research Program of CIMMYT, to determine the presence of genes *Sr2*, *Sr22*, *Sr24*, *Sr26*, *Sr35*, and *Sr39*.

Materials and Methods. This study was carried out in the biotechnology laboratory of the Norman E. Borlaug Experimental Station in the Yaqui Valley, during the crop season 2013–14. Commercial bread wheat cultivars (Fig. 1, p. 14) Roelfs F2007 (Figueroa-López et al. 2011), Ónavas F2009 (Figueroa-López et al. 2013a, b), Tepahui F2009 (Chávez-Villalba et al. 2012), and Villa Juárez F2009 (Valenzuela-Herrera et al. 2012a, b) released by the wheat program of INIFAP, and 20 advanced lines from the Bread Wheat Improvement and Rust Research Program of CIMMYT were used in

Table 1. Bread wheat cultivars and advanced lines used for gene identification for northwest Mexico during the 2013–14 crop season.

Entry	Pedigree and selection history
1	Roelfs F2007
2	Tepahui F2009
3	Ónavas F2009
4	Villa Juárez F2009
5	PBW343//CAR422/ANA/3/Elvira CMSS02M00409S-030M-1Y-0M-040Y-10ZTB-0Y-02B-0Y
6	Sokoll*2/3/Babax/LR42//Babax CMSA05Y01225T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-01Y-0B
7	ROLF07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/Tukuru//FRET2 CMSS06Y00605T-099TOPM-099Y-099ZTM-099Y-099M-11WGY-0B
8	PFAU/Seri.1B//AMAD/3/Waxwing/4/Villa Juárez F2009 CMSS07B00144S-099M-099Y-099M-5WGY-0B
9	CHYAK/Pauraq CMSS07B00275S-099M-099Y-099M-13WGY-0B
10	Tacupeto F2001*2/Kiritati//Villa Juárez F2009 CMSS07B00094S-099M-099NJ-099NJ-16WGY-0B
11	Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto*2/Brambling/5/Pauraq CMSS07B00525T-099TOPY-099M-099NJ-099NJ-1WGY-0B
12	Kachu/BECARD//WBLL1*2/Brambling CMSS07B00580T-099TOPY-099M-099NJ-099NJ-34WGY-0B
13	INIA Churrinche/Kiritati CMSS07Y00433S-0B-099Y-099M-099NJ-099NJ-4WGY-0B
14	CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92/4/MUNAL#1 CMSS07Y00066S-0B-099Y-099M-099Y-38M-0WGY
15	PFAU/Seri.1B//AMAD/3/Waxwing/4/WBLL1*2/Brambling CMSS07Y00196S-0B-099Y-099M-099NJ-099NJ-6WGY-0B
16	WBLL1*2/Kurku/4/PFAU/Seri.1B//AMAD/3/Waxwing CMSS07Y00338S-0B-099Y-099M-099Y-9M-0WGY
17	WBLL4/Kukuna//WBLL1/3/WBLL1*2/Brambling CMSS07Y00348S-0B-099Y-099M-099Y-19M-0WGY
18	ITP40/AKURI CMSS07Y00441S-0B-099Y-099M-099NJ-099NJ-4WGY-0B
19	Milan/S87230//BAV92*2/3/MUU CMSS07Y00983T-099TOPM-099Y-099M-099Y-15M-0WGY
20	Milan/S87230//BAV92*2/3/Tecue#1 CMSS07Y00985T-099TOPM-099Y-099M-099Y-9M-0WGY
21	Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq CMSS07B00525T-099TOPY-099M-099Y-099M-19WGY-0B
22	Kiskadee#1/CHYAK CMSS07B00253S-099M-099Y-099M-14WGY-0B
23	CHYAK1/GRACK CMSS07B00279S-099M-099NJ-099NJ-6WGY-0B
24	Kachu/3/*T. turgidum* subsp. *dicoccum* PI94624/*Ae. tauschii* (409)//BCN/4/2*Kachu CMSS07Y01307T-099Y-7M-0Y-3B-0Y

the study (Table 1, p. 15). DNA extraction was followed the method of Saghai-Maroof et al. (1984). For the PCR, 5 μl of Redtaq ReadyMix (Sigma Chemical, St. Louis, MO, USA) was used, as well as 3 μl of ADN of the materials evaluated and 3 μl of the primer. For electrophoresis, gelred was used for image developing.

Results. The genes identified were *Sr2*, *Sr22*, *Sr24*, *Sr26*, *Sr35*, and *Sr39* (Table 2). We found that the majority of the genotypes evaluated possess gene *Sr2* (Table 3), which shows resistance to stem rust and has been used for ~60 years as a durable and broad-spectrum source of adult-plant resistance (Spielmeyer et al. 2003). For genes *Sr22*, *Sr24*, *Sr26*, and *Sr35*, the gene of interest was present in at least one genotype evaluated, with the exception of *Sr39,* which was not present. *Sr39* confers resistance to the majority of known races of *Puccinia graminis* f. sp. *tritici*, including Ug99 and its variants. With the incorporation of MAS within the traditional breeding system, specific demands and problems of susceptibility to certain pathogens in advanced lines, which would be discarded otherwise, can be solved. Genomic and molecular information published in relation to characters of agronomic interest is increasing. The most simple and efficient way to incorporate this information for developing new wheat cultivars is through MAS breeding.

Table 2. Description of the genes evaluated in bread wheat cultivars and lines for northwest Mexico, during the 2013–14 crop season ([v]Mago et al. 2011, [w]Khan et al. 2005, [x]Mago et al. 2005, [y]Zhang et al. 2010, and [z]Mago et al. 2009).

Gene	Marker	Heritability	Sequence	Fragment	Chromosome
Sr2[v]	Cssr2	co-dominant	F: 5'-CAA GGGTTGCTAGGATTGGAAAAC-3' R: 5'-AGA TAACTCTTATGATCTTACATTTTTCTG-3'	172	3BS
Sr22[w]	CFa2123	co-dominant	F: 5'-CGG TCTTTGTTTGCTCTAAACC-3' R: 5'ACC GGCCATCTATGATGAAG3'	245/260	7A
Sr24[x]	Sr24 #12	dominant	F: 5'CAC CCGTGACATGCTCGTA-3' R: 5'-AAC AGGAAATGAACGACGATGT-3'	600	3DL
Sr26[x]	Sr26 #43	dominant	F: 5'-AAT CGTCCACATTGGCTTCT-3' R: 5'-CGC AACAAAATCATGCACTA-3'	207	6AL
Sr35[y]	CFa219	polymorphic	F: 5'- ACA TGT GAT GTG CGG TCA TT-3' R: 5'- TCC TCA GAA CCC CAT TCT TG-3	243/230	3AL
Sr39[z]	Sr39 #22r	dominant	F: 5'- AGA GAA GAT AAG CAG TAA ACA TG-3' R: 5'- TGC TGT CAT GAG AGG AAC TCT G -3'	487	2B

Table 3. Markers identified for bread wheats for northwest Mexico during the 2013–14 crop season.

Genotype	*Sr2*	*Sr22*	*Sr24*	*Sr26*	*Sr35*	*Sr39*
Roelfs F2007	+	–	–	–	–	–
Tepahui F2009	+	–	–	–	–	–
Ónavas F2009	+	–	–	–	+	–
Villa Juárez F2009	+	–	–	–	–	–
PBW343//CAR422/ANA/3/Elvira	+	–	–	–	–	–
Sokoll*2/3/Babax/LR42//Babax	+	–	–	–	+	–
ROLF07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/Tukuru//FRET2	–	+	+	–	–	–
PFAU/Seri.1B//AMAD/3/Waxwing/4/Villa Juárez F2009	–	+	+	+	–	–
CHYAK/Pauraq	+	–	–	–	–	–
Tacupeto F2001*2/Kiritati//Villa Juárez F2009	+	–	–	+	–	–
Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto*2/Brambling/5/Pauraq	–	–	–	–	–	–
Kachu/BECARD//WBLL1*2/Brambling	+	–	–	–	–	–
INIA Churrinche/Kiritati	+	–	–	–	–	–
CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92/4/MUNAL#1	+	–	–	–	–	–
PFAU/Seri.1B//AMAD/3/Waxwing/4/WBLL1*2/Brambling	+	–	–	–	–	–
WBLL1*2/Kurku/4/PFAU/Seri.1B//AMAD/3/Waxwing	+	–	–	–	–	–
WBLL4/Kukuna//WBLL1/3/WBLL1*2/Brambling	+	–	–	–	–	–
ITP40/AKURI	+	–	–	–	–	–
Milan/S87230//BAV92*2/3/MUU	–	–	–	–	–	–
Milan/S87230//BAV92*2/3/Tecue#1	+	–	–	–	–	–
Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq	+	–	–	–	+	–
Kiskadee#1/CHYAK	+	–	–	–	+	–
CHYAK1/GRACK	–	–	–	+	+	–
Kachu/3/*T. turgidum* subsp. *dicoccum* PI94624/*Ae. tauschii* (409)/. . .	+	–	–	–	+	–

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Salinity and index mixture of surface and aquifer water for agricultural use.

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Introduction. In Sonora, Mexico, irrigation districts in the central and northern regions of the state are operated by water pumps and by dams and gravity in the southern region. Water quality in the first two regions is considered acceptable, although, through time, a gradual increase in salinity has occurred by the overexploitation of aquifers, reaching levels that are not appropriate for crop development. On the other hand, aquifer water provided by gravity has medium to low quality. Water availability in the Mayo Valley captured through the years has not been constant, because rainfall has been limited. This phenomenon became more critical after 1990, and, therefore, has generated the need to use water from aquifers mixed with water from the Adolfo Ruiz Cortinez Dam to suffice the irrigation demand. An increase in the

salt content in the soil through the irrigations applied to crops creates a high-risk situation in terms of soil degradation by salinity. Our objective was to quantify the salinity dynamics of water mixtures in different sections of Canal 3+300, where part of the aquifer water with the highest salt content is pumped into the water stream used in the irrigation district 038, mainly in the lowest area.

Materials and Methods. This study was carried out from November 2002 to March 2003, in three strategic sections of Canal 3+300. Section 1, 0+000 (P_0), was considered as the check, because water flows only by gravity. Section 2, P_1 in the same canal, but in km 14+000; the first water mixture was analyzed in this section, which is in transect from P_0 to P_1 where five wells are located. We expected an increase in salt content after water from the wells is mixed with water from the canal. Some water volume is directed into modules 7, 12, and part of 13. Section 3, P_2 corresponds to km 14+525, after some water is derived to modules 7, 12, and 13; in the transect from P_1 to P_2 where there is a series of wells known as *pozos ruiz*, where the water is conducted through the same ditch to be discharged into Canal 3+300. Water salinity was monitored by taking weekly samples each Thursday between 7 November, 2002, and 27 March, 2003. Electric conductivity (EC dS/m) was determined with a portable conductivity meter (Orion model 125 plus). The water volume used in each monitoring point was obtained from the society of users in District 038. Data was registered and analyzed through dispersion diagrams, and regression analysis among the salinity variables, interpreted by the EC (dS/m) and index mixture (lv) or the relationship between water volume pumped/water volume by gravity.

Mixture index. To establish a reference that would determine water quality produced after *X* volume of aquifer water is added to a *Y* volume flowing in the canal, the following equation was proposed (mixture volume index):

$$Iv = \frac{Vwa}{Vwc}$$

where Iv = quotient of mixed volumes, Vwa = ground water volume (m^3), and Vwc = water volume from the canal (m^3). The index (lv) indicates cubic meters of aquifer water that can be added per cubic meter of water flowing in the canal in order to produce a mixture with a certain electric conductivity (EC), which is an indirect indicator of water salinity. If the

Table 4. Results of water quality in Canal 3+300 during the 2002–03 crop season, in the Mayo Valley, Sonora, Mexico (CV = canal volume; EC (electrical conductivity) = dS/m; GWSW = ground water/ground surface water; and GV = ground volume).

Date	P0 (0+000)		Iv	P1 (14+000)			Iv	P2 (14+525)			Iv
	CV	EC	GWSW	CV	GV	EC	GWSW	CV	GWSW	EC	GWSW
71102	13.80	0.29	0	10.6	0.535	0.33	0.051	4.64	0.700	0.63	0.151
141102	18.50	0.28	0	13.9	0.440	0.43	0.032	7.72	0.800	0.82	0.104
211102	18.90	0.23	0	14.4	0.438	0.43	0.030	7.79	0.900	0.80	0.116
281102	18.05	0.27	0	13.5	0.340	0.45	0.025	7.16	1.000	0.83	0.140
51202	10.50	0.29	0	5.6	0.408	0.39	0.074	2.28	0.800	1.28	0.351
121202	9.90	0.27	0	6.7	0.522	0.57	0.078	3.90	0.800	1.10	0.205
191202	9.81	0.28	0	6.8	0.503	0.56	0.074	4.46	0.800	1.04	0.179
20103	5.42	0.30	0	4.9	0.260	0.64	0.053	3.40	0.900	1.18	0.265
90103	8.10	0.31	0	6.8	0.565	0.58	0.083	4.17	0.900	1.16	0.216
160103	8.82	0.30	0	7.2	0.560	0.64	0.078	3.75	0.800	1.17	0.213
230103	9.04	0.30	0	6.6	0.428	0.61	0.065	3.11	0.900	1.32	0.289
300103	8.05	0.30	0	6.6	0.450	0.62	0.069	3.82	0.900	1.14	0.236
60203	9.39	0.32	0	8.0	0.510	0.61	0.064	4.90	0.900	1.02	0.184
130203	10.92	0.33	0	9.3	0.167	0.56	0.018	4.15	1.100	1.13	0.265
200203	6.37	0.31	0	4.9	0.000	0.40	0.000	1.10	1.000	1.55	0.913
270203	6.22	0.32	0	4.7	0.420	0.57	0.089	2.40	0.900	1.57	0.375
60303	9.55	0.30	0	7.4	0.184	0.43	0.025	4.73	0.750	1.02	0.159
130303	9.38	0.30	0	8.2	0.280	0.47	0.034	4.90	0.950	1.00	0.194
200303	9.40	0.32	0	8.1	0.257	0.47	0.032	3.70	0.700	1.09	0.189
270303	6.30	0.32	0	5.7	0.405	0.47	0.071	2.73	0.800	1.09	0.294

relationship between lv and EC can be explained by simple regression models with good acceptance of its R^2, this would be a useful tool to predict the saline concentration that would be produced after the mixture of both sources of water.

Results and Discussion. Water salinity model from P_0 to P_2 of Canal 3+300. In order to simplify the prediction of salt content in the water in Canal 3+300 by a single model, the three data sets (P_0, P_1, and P_2, Table 4, p. 18) were analyzed as a whole by means of a simple regression model. The results obtained are shown (Fig. 2). The model explains, with a high level of confidence, the relationship between salinity (EC) and the mixture volume index (lv) and indicates an increase in the level of salinity, which will vary based on the different volumes of water mixtures in Canal 3+300 coming from both sources and with different salinity levels. According to the tendency that salinity marks with respect to lv, we observed that the relationship between both variables is valid when the maximum CE value is reached (1.6 to 1.8 dS/m), which caused a volume relationship from 0.7:1 and 0.8:1 (m^3 from the aquifer**:**m^3 from the canal), to obtain the maximum salinity in the irrigation water.

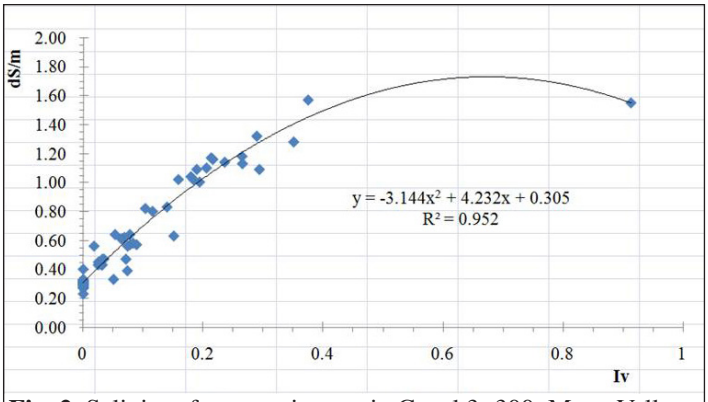

Fig. 2. Salinity of water mixtures in Canal 3+300, Mayo Valley, Sonora, Mexico.

Conclusions. The water moved by gravity and, as long as it is not mixed with aquifer water, maintains a low EC that is classified as a good quality C1. The aquifer water increases the EC once it is mixed. The first approximation of volume index mixtures (lv) indicates that it can be used to predict water quality in the irrigation Canal 3+300.

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Evaluation of commercial bread wheat cultivars and advanced lines in northwest Mexico during the 2009–10 crop season.

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Abstract. Commercial bread wheat cultivars Tacupeto F2001, Kronstad F2004, Navojoa M2007, and Roelfs F2007, and 21 advanced lines were evaluated for their field performance at four sowing dates during the 2009–10 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. The variables that were evaluated were grain yield (t/ha), test weight (kg/hl), protein (%), days-to-flowering, days-to-maturity, and height. The highest grain yield average was 7.7 t/ha in the line 'Thelin/2*WBLL1', which was superior to the commercial check cultivars Kronstad F2004, Roelfs F2007, Navojoa M2007, and Tacupeto F2001 by 811, 401, 246, and 225 kg, respectively. The 30 November sowing date registered the highest yield, with an average of 7.83 t/ha. Line 'PFAU/Milan//Trost/3/PBW65/2*Seri.1B' showed the highest protein average with 13.53%, followed by the check cultivar Kronstad F2004 with 13.35%. Line 'Babax/LR42//Babax/3/ER2000' showed the highest average test weight at 81.67kg/hl. The tallest lines were 'TC870344/GUI//Temporalera M 87/AGR/3/2*WBLL1', 'CAL/NH//H567.71/3/Seri/4/CAL/NH//H567.71/5/2*KAUZ/6/WH576/7/WH 542/8/Waxwing, and 'Thelin/2*WBLL1' with an average of 111 cm. Lines 'Thelin/2*WBLL1' and Chewink had the longest maturity (130 days).

Introduction. About 90% of the wheat produced in Mexico is obtained from sowing during the autumn–winter season under irrigation, primarily in the northwestern and the Bajio Regions. The state of Sonora is outstanding for its area sown with wheat and the volume of grain produced, particularly in the southern part of the state. In this region, durum wheat occupies 90% of the area sown with wheat (OIEDRUS 2015). Bread wheat was the most grown in the state of Sonora until the end of 1980s, but due to its susceptibility to Karnal bunt and the consequent problems of quarantine regulations (SARH 1987) and commercialization, durum wheat cultivars have occupied most of the area grown (Fuentes-Dávila et al. 2014). Bread wheat production in the region has been so limited that the industry has implemented contracts with farmers in order to secure a minimum or reserves. In this way, the risk of depending on the fluctuating values in the international market is diminished. Our objective was to evaluate the field performance of advanced bread wheat lines and commercial check cultivars, during the 2009–10 crop season at the Experimental Station in the Yaqui Valley, Sonora, Mexico.

Materials and Methods. The trial was established during the 2009–10 crop season at the Norman E. Borlaug Experimental Station, located in block 910 of the Yaqui Valley at 27°22'04.64' N and 109°55'28.26' W, 37 masl, with climate warm (BW (h)) and extreme warm and dry (BS (h)), according to Koppen classification modified by Garcia (1964). The experimental plots consisted of four 5-m beds with two rows 0.80 m apart, and a seeding rate of 100 kg/ha. Commercial bread wheat cultivars Tacupeto F2001, Kronstad F2004, Navojoa M2007, and Roelfs F2007, and 21 advanced lines were evaluated in this trial (Table 5) at four sowing dates 15 days apart, starting on 15 November, 2009,

Table 5. Bread wheat cultivars and advanced lines evaluated during the 2009–10 crop season in the Yaqui Valley, Sonora, Mexico.

Entry	Pedigree and selection history
1	Tacupeto F2001
2	Kronstad F2004
3	Navojoa M2007
4	Roelfs F2007
5	TOBA97/Pastor CMSS97M05756S-040M-020Y-030M-015Y-3M-1Y-3M-0Y
6	KAMB1*2/Brambling CGSS01B00069T-099Y-099M-099M-099Y-099M-20Y-0B
7	Betty/3/CHEN/*Ae. tauschii*//2*Opata CMSW00WM00150S-040M-040Y-030M-030ZLM-3ZTY-0M
8	WBLL1*2/Brambling CGSS01B00062T-099Y-099M-099M-099Y-099M-12Y-0B
9	Babax/LR42//Babax*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ CGSS01B00045T-099Y-099M-099M-099Y-099M-26Y-0B
10	Babax/LR42//Babax/3/ER2000 CMSA01Y00176S-040P0Y-040M-030ZTM-040SY-24M-0Y-0SY
11	PFAU/Milan/3/Babax/LR42//Babax CMSS02M00056S-030M-28Y-0M-040Y-25ZTB-0Y-01B-0Y
12	Thelin/2*WBLL1 CGSS02Y00079T-099B-099B-099Y-099M-6Y-0B
13	PBW343//CAR422/ANA/3/Elvira CMSS02M00409S-030M-1Y-0M-040Y-10ZTB-0Y-02B-0Y
14	Babax/LR42//Babax/3/ER2000 CMSA01Y00176S-040P0Y-040M-030ZTM-040SY-30M-0Y-0SY
15	TC870344/GUI//Temporalera M 87/AGR/3/2*WBLL1 CMSA01Y00725T-040M-040P0Y-040M-030ZTM-040SY-10M-0Y-0SY
16	ROLF07/YANAC//Tacupeto F2001/Brambling CGSS05B00121T-099TOPY-099M-099NJ-4WGY-0B
17	Waxwing*2/Kronstad F2004 CGSS04Y00020T-099M-099Y-099ZTM-099Y-099M-3WGY-0B
18	Whear/Kronstad F2004 CGSS04Y00106S-099Y-099M-099Y-099M-9WGY-0B
19	KEA/TAN/4/TSH/3/KAL/BB//TQFN/5/Pavon/6/SW89.3064/7/Sokoll CMSS04Y00153S-099Y-099ZTM-099Y-099M-5WGY-0B
20	CAL/NH//H567.71/3/Seri/4/CAL/NH//H567.71/5/2*KAUZ/6/WH576/7/WH 542/8/Waxwing CMSS04Y00364S-099Y-099ZTM-099Y-099M-2WGY-0B
21	Becard CGSS01B00063T-099Y-099M-099M-099Y-099M-33WGY-0B
22	Whear/Sokoll CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B
23	PFAU/MILAN//Trost/3/PBW65/2*Seri.1B CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B
24	Whear/Kronstad F2004 CGSS04Y00106S-099Y-099M-099Y-099M-3WGY-0B
25	Chewink CGSS03B00074T-099Y-099M-099Y-099M-6WGY-0B-3B

to 31 December. Management of the trial followed the technical recommendations by INIFAP (Figueroa-López et al. 2011a). The variables evaluated were grain yield (t/ha), test weight (kg/hl), protein (%), days-to-flowering, days-to-maturity, and height. Statistical analysis used SAS 9.0 for Windows. The temperature was recorded from the weather station at block 609, because the weather station at the Experimental Station was not operating properly.

Results and Discussion. Significant statistical differences in grain yield were found among the materials evaluated (Fig. 3). The highest average grain yield was 7.7 t/ha in line 'Thelin/2*WBLL1', followed by 'Babax/LR42//Babax*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ' and 'PFAU/Milan/3/Babax/LR42//Babax', both with 7.6 t/ha. Lines 'Whear/Kronstad F2004' and Chewink had differences of 1.04 and 0.886 t/ha less than the highest yielder, respectively. Line 'Thelin/2*WBLL1' was superior to the commercial check cultivars Kronstad F2004, Roelfs F2007, Navojoa M2007, and Tacupeto F2001 by 811, 401, 246, and 225 kg, respectively. Although with the exception of Kronstad F2004, the other cultivars showed good grain yield, between 7.3 and 7.48 t/ha, which were within the expected range (Camacho-Casas et al. 2011; Figueroa-López et al. 2011b; Valenzuela-Herrera et al. 2011). For grain yield by sowing date, the first two dates (15 and 30 November) were statistically similar, although the 30 November date registered the highest yield with an average of 7.83 t/ha (Fig. 4). The difference in yield between the first sowing date and the other three were –136.35 kg, 600.16 kg, and 1,228.25 kg, respectively; the difference between the second date and the other two were 736.51 kg and 1,364.60 kg; and the difference between the third and fourth dates was 628.08 kg. Therefore, if obtaining high yields is the main purpose, we recommend sowing during the last 15 days of November. The line 'PFAU/Milan//Trost/3/PBW65/2*Seri.1B' showed the highest protein average with 13.53%, followed by the check cultivar Kronstad F2004 with 13.35%. Lines Chewink and 'TOBA97/Pastor' showed a protein slightly greater than 13% (Fig. 5, p. 22). The protein range of line 'PFAU/Milan//Trost/3/PBW65/2*Seri.1B' was 13.28–14.08%; the highest value obtained from the fourth sowing date. The average percent protein by sowing date was 12.40%, 12.26%, 12.52%, and 13.17% for the first, second, third, and fourth sowing date (Fig. 6, p. 22). Therefore, if the purpose is to obtain high percentage of protein, we recommend sowing during the last sowing date. Significant statistical differences were detected among lines for test weight; line 'Babax/LR42//Babax/3/ER2000 showed the highest average test weight with 81.67 kg/hl, followed by those of 'Betty/3/CHEN/*Ae. tauschii*//2*Opata' with 81.48 kg/hl, 'PFAU/Milan/3/Babax/LR42//Babax' with 81.39 kg/hl, commercial cultivar Navojoa M2007 with 81.23 kg/hl, and 'Babax/LR42//Babax/3/ER2000' with 81.13 kg/hl. The other commercial cultivars, Roelfs F2007, Tacupeto F2001, and Kronstad F2004, had test weights of 80.44 kg/hl, 80.23 kg/hl, and 80.04 kg/hl, respectively. The first and fourth date registered the highest test weight, which could be product of environmental conditions conducive for better plant development during the crop season (Fig. 7, p. 22). The tallest lines were 'TC870344/GUI//Temporalera M 87/AGR/3/2*WBLL1', 'CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/WH576/7/WH 542/8/Waxwing', and 'Thelin/2*WBLL1' with an average of 111 cm; the shortest line was 'PFAU/MILAN//

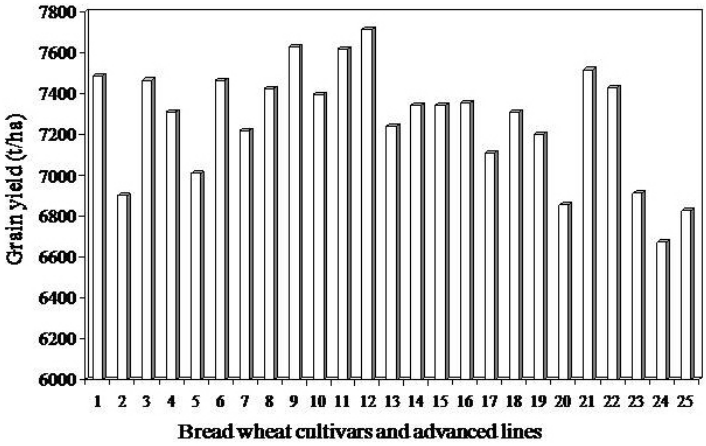

Fig. 3. Grain yield (t/ha) of cultivars and advanced bread wheat lines evaluated during the 2009–10 wheat season in the Yaqui Valley, Sonora, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 5, p. 20 for information on advanced lines 5–25).

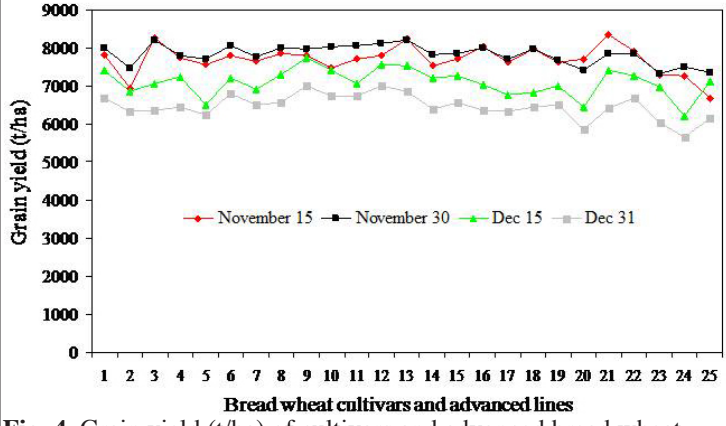

Fig. 4. Grain yield (t/ha) of cultivars and advanced bread wheat lines evaluated by sowing date during the 2009–10 wheat season in the Yaqui Valley, Sonora, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 5, p. 20 for information on advanced lines 5–25).

TROST/3/ PBW65/2*Seri1B' with an average of 98 cm. Lines 'Thelin/2*WBLL1' and Chewink had the longest maturity (130 days) and heading (86 days) after sowing. Line 'Betty/3/CHEN/*Ae. tauschii*//2*Opata' reached physiological maturity in 121 days, whereas 'TOBA97/Pastor' and 'Whear/Spkoll' in 122.

Conclusions.

The experimental bread wheat line 'Thelin/2*WBLL1', with an average grain yield of 7.7 t/ha in the four sowing dates, was superior to commercial cultivars Kronstad F2004, Roelfs F2007, Navojoa M2007, and Tacupeto F2001 by 811, 401, 246, and 225 kg, respectively. The 30 November 30 sowing date registered the highest yield with an average of 7.83 t/ha.

Line 'PFAU/Milan//Trpst/3/PBW65/2*Seri.1B' showed the highest protein average with 13.53%.

Line 'Babax/LR42//Babax/3/ER2000' showed the highest average test weight with 81.67 kg/hl.

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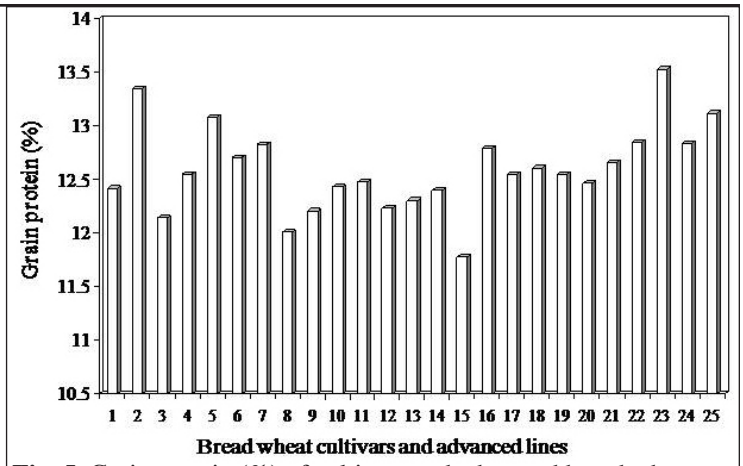

Fig. 5. Grain protein (%) of cultivars and advanced bread wheat lines evaluated during the 2009–10 wheat season in the Yaqui Valley, Sonora, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 5, p. 20 for information on advanced lines 5–25).

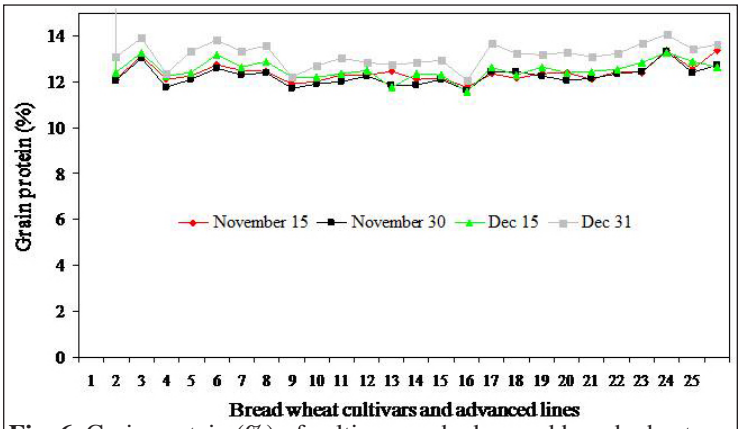

Fig. 6. Grain protein (%) of cultivars and advanced bread wheat lines evaluated by sowing date during the 2009–10 wheat season in the Yaqui Valley, Sonora, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 5, p. 20 for information on advanced lines 5–25).

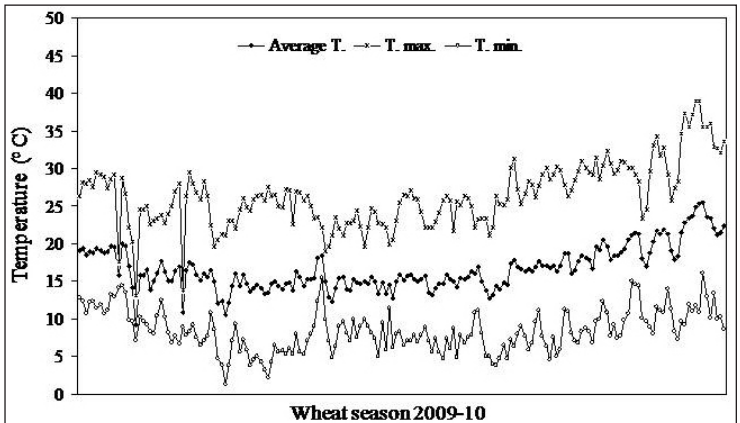

Fig. 7. Maximum, minimum, and average temperature during the 2009–10 autumn–winter wheat season registered in block 609 in the Yaqui Valley, Sonora, Mexico.

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Preliminary evaluation of commercial cultivars and advanced lines of bread wheat under heat stress in the greenhouse.

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Abstract. Commercial bread wheats Roelfs F2007, Ónavas F2009, Tepahui F2009, and Villa Juárez F2009, and 21 advanced lines were sown in pots on 20 January, 2004, in the greenhouse at the Norman E. Borlaug Experiment Station in the Yaqui Valley, Mexico, to evaluate their performance under heat stress. Pots were watered every other day and fertilized at tillering, boot, and flowering. Daily temperatures (°C) during the morning, at noon, and afternoon were recorded for 66 days. The temperature range at 08:00 h was 11.7–30.6°C, avg 20.35°C; 28.3–49.3°C at noon, avg 38.9°C; and 22.6–46.2°C at 15:00 h, avg 38.1°C. Seedling emergence ranged from 83% to 100%. The average relative growth rate of the group was 0.31 cm/day. Line 'Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq' showed the highest relative growth rate at 0.53. The average plant temperature of the group was 22.78°C with a range of 22.3–23.2°C. Lin 'Chyak/Pauraq' was the first to reach heading stage (average 46 days), whereas Villa Juárez F2009 headed in 50 days, Roelfs F2007 and Ónavas F2009 in 52 days, and Tepahui F2009 in 53 days; 22, 29 and 26 days, respectively, before heading under the recommended commercial sowing dates. Physiological maturity of the group was reached in an average of 98 days (range 93–103 days). The number of spikes/plant ranged from 12 to 26, with 'CHYAK1/GRACK' producing the highest number (26.3). The average spike length of the group was 10 cm, with a range of 8.9–11.5. Line 'ROLF07/4/BOW/NKT//CBRD/3/ CBRD/5/FRET2/Tukuru//FRET2' produced the highest number of grains/spike with 59.5. The average grain length was 0.66 cm, and the difference between the longest and shortest grain was quite small (0.09 cm). Biomass dry weight ranged from 11.0 to 24.2 g, with an avg of 17.0. Line 'PBW343//CAR422/ANA/3/Elvira' produced the highest biomass. Culitvar Ónavas F2009 showed the highest grain yield/plant with 26.7 g.

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°C 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. Sowing date is also an important factor for productivity of any crop, because plant development in its various growth stages is influenced positively or negatively by the prevailing weather conditions. In general, wheat yield will be drastically reduced if recommended sowing dates are not followed, 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 a reduction in final grain weight (Félix-Valencia and Fuentes-Dávila 2015). Theferore, subjecting experimental wheat germplasm to conditions of heat stress will generate information and consequently selection of material better adapted to such conditions. Our objective was to determine the performance of several commercial bread wheat cultivars and advanced lines under heat stress conditions in the greenhouse.

Materials and Methods. Commercial bread wheat cultivars Roelfs F2007, Ónavas F2009, Tepahui F2009, and Villa Juárez F2009, and 21 advanced bread wheat lines from CIMMYT (Table 6) were sown on 20 January, 2004, in the greenhouse at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, located in block 910 of the Yaqui Valley at 27°22'04.64"N and 109°55'28.26"W, 37 masl, with warm (BW (h)) and extreme warm and dry (BS (h)) climate, according to the Koppen classification modified by Garcia (1964). Five seeds of each cultivar and line were sown in 5-L plastic pots containing substrate. Three replications (pots) per entry were sown in a completely randomized block experimental design in an 8–9-m area. Pots were watered every other day and fertilized with urea (1.48 g) and 11–52–00 (0.49 g) per pot during tillering, boot, and flowering. Daily temperatures (°C) during the morning, at noon, and during the afternoon were recorded using a digital thermometer (Taylor) for 66 days, starting 21 January and ending 1 May. The variables evaluated were a) percentage of seedling emergence, b) relative growth rate (RGR) (final, calculated as the final height – initial height/days, c) average plant temperature (°C) taken with a laser infrared thermometer (Taylor). Ten readings were taken every three days, beginning during tillering (Feeke's 4 to 7 stage), d) heading, e) anthesis, f) physiological maturity, g) number of spikes/plant, h) average spike length, i) average number of grains/spike, j) grain length (cm), k) biomass dry weight/plant, and l) grain yield (g/plant).

Table 6. Bread wheat commercial cultivars and advanced lines evaluated for tolerance to heat stress in the greenhouse in the Yaqui Valley, Sonora, in 2014.

Entry	Pedigree and selection history
1	Roelfs F2009 | CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B-0Y-0Y
2	Tepahui78 F2009 | CMSW00WM00150S-040M-040Y-030M-030ZTM-3ZTY-0M-0SY-0CEVY-OCEVY
3	Onavas F2009 | CGSS01B00069T-099Y-099M-099M-099Y-099M-20Y-0B-0CEVY-0CEVY
4	Villa Juárez F2009 | CGSS01B00062T- 099Y-099M-099M-099Y-099M-12Y-0B-0CEVY-0CEVY
5	PBW343//CAR422/ANA/3/Elvira | CMSS02M00409S-030M-1Y-0M-040Y-10ZTB-0Y-02B-0Y
6	Sokoll*2/3/Babax/LR42//Babax | CMSA05Y01225T-040M-040ZTP0Y-040ZTM-040SY-12ZTM-01Y-0B
7	ROLF07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/TUKU//FRET2 CMSS06Y00605T-099TOPM-099Y-099ZTM-099Y-099M-11WGY-0B
8	Tacupeto F2001/6/CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/Weaver/5/Pastor/7/ROLF07 CMSS06Y00716T-099TOPM-099Y-099ZTM-099Y-099M-3RGY-0B
9	PFAU/Seri.1B//AMAD/3/Waxwing/4/Villa Juárez F2009 | CMSS07B00144S-099M-099Y-099M-5WGY-0B
10	Chyak/Pauraq | CMSS07B00275S-099M-099Y-099M-13WGY-0B
11	Tacupeto F2001*2/Kiritati//Villa Juárez F2009 | CMSS07B00094S-099M-099NJ-099NJ-16WGY-0B
12	Attila/3*BCN//BAV92/3/Pastor/4/Tacupteo F2001*2/Brambling/5/Pauraq CMSS07B00525T-099TOPY-099M-099NJ-099NJ-1WGY-0B
13	Kachu/Becard//WBLL1*2/Brambling | CMSS07B00580T-099TOPY-099M-099NJ-099NJ-34WGY-0B
14	INIA Churrinche/Kiritati | CMSS07Y00433S-0B-099Y-099M-099NJ-099NJ-4WGY-0B
15	Chibia//PRLII/CM65531/3/SKAUZ/BAV92/4/Munal #1 | CMSS07Y00066S-0B-099Y-099M-099Y-38M-0WGY
16	PFAU/SeriI.1B//AMAD/3/Waxwing/4/WBLL1*2/Brambling CMSS07Y00196S-0B-099Y-099M-099NJ-099NJ-6WGY-0B
17	WBLL1*2/Kuruku/4/PFAU/Seri.1B//AMAD/3/Waxwing | GCMSS07Y00338S-0B-099Y-099M-099Y-9M-0WGY
18	WBLL4/Kukuna//WBLL1/3/WBLL1*2/Brambling | GCMSS07Y00348S-0B-099Y-099M-099Y-19M-0WGY
19	ITP40/Akuri | CMSS07Y00441S-0B-099Y-099M-099NJ-099NJ-4WGY-0B
20	Milan/S87230//BAV92*2/3/MUU | CMSS07Y00983T-099TOPM-099Y-099M-099Y-15M-0WGY
21	Milan/S87230//BAV92*2/3/Tecue #1 | CMSS07Y00985T-099TOPM-099Y-099M-099Y-9M-0WGY
22	Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq CMSS07B00525T-099TOPY-099M-099Y-099M-19WGY-0B
23	Kiskadee #1/Chyak | CMSS07B00253S-099M-099Y-099M-14WGY-0B
24	Chyak1/Grack | CMSS07B00279S-099M-099NJ-099NJ-6WGY-0B
25	Kachu/3/*T. turgidum* subsp. *dicoccum* PI94624/*Ae. tauschii* (409)//BCN/4/2*Kachu CMSS07B00279S-099M-099NJ-099NJ-6WGY-0B

Results and Discussion. The temperatures that prevailed during the evaluation period are shown (Fig 8, p. 25). The range of temperature at 08:00 was 11.7–30.6 °C with an average of 20.35°C, 28.3–49.3°C at noon with an average of 38.9, and 22.6–46.2 °C at 15:00 h with an average of 38.1°C. Seedling emergence ranged from 83 to 100%; lines that did not show 100% emergence were 'Milan/S87230//BAV92*2/3/TECUE#1' and 'Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Payraq' with 83%, and 'PBW343// CAR422/ANA/3/Elvira', 'INIA Churrinche/Kiritati', and 'ITP40/Akuri' with 92%.

The average RGR of the group was 0.31 cm/day (Fig. 9A). Line 'Attila/3*BCN//BAV92/3/Pastor/4/Tacupeto F2001*2/Brambling/5/Pauraq' had the highest RGR with 0.53 cm/day, followed by those of 'Chibia//PRLII/CM65531/3/Skauz/BAV92/4/Munal #1' and 'WBLL1*2/Kuruku/4/PFAU/Seri.1B//AMAD/3/Wazwing' with 0.43 cm/day. Cultivars Ónavas F2009 and Villa Juárez F2009 had an RGR of 0.40 cm/day; Roelfs F2007 and Tepahui F2009 were 0.20 and 0.10 cm/day, respectively. The lowest RGR (0.03 cm) was in line 'PBW343//CAR422/ANA/3/Elvira'.

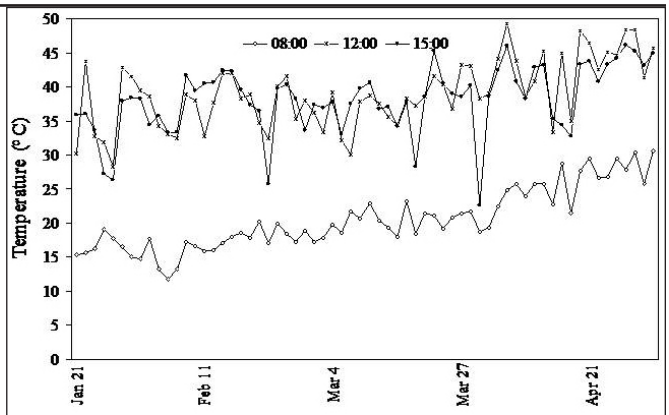

Fig. 8. Daily temperatures recorded at 08:00, 12:00, and 15:00 hours between 21 January and 2 May, 2014 in the greenhouse at the Norman E. Borlaug Experiment Station.

The average plant temperature of the group was 22.78°C with a range of 22.3–23.2, which was rather uniform (Fig. 9B). Lines 'ITP40/Akuri' and 'Chyak 1/Grack' showed the highest temperature and 'Kachu/Becard//WBLL1*2/Brambling' and 'WBLL4/Kukuna//WBLL1/3/WBLL1*2/Brambling' the lowest. The range of plant temperature in the commercial cultivars was 22.5–22.8°C.

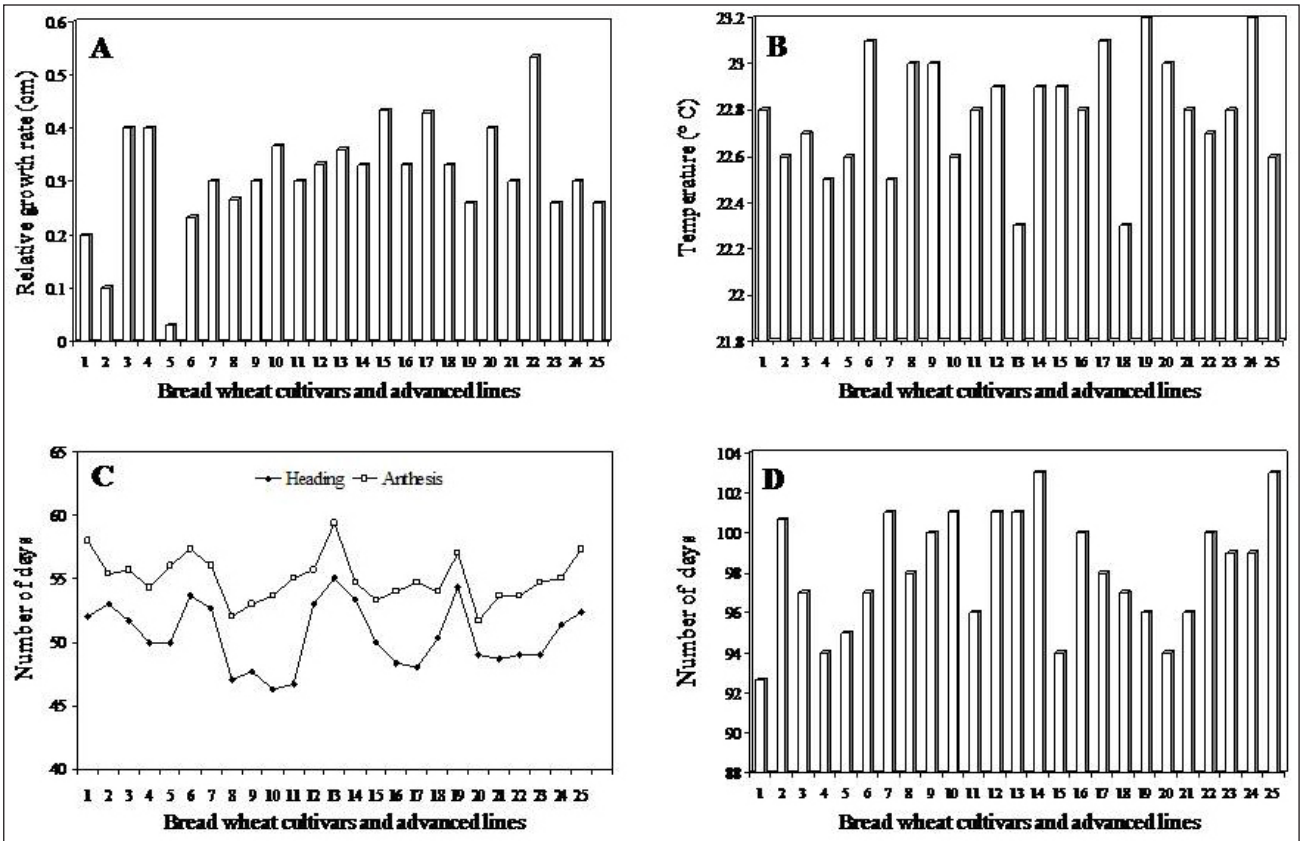

Fig. 9. Relative growth rate (cm) (A), average plant temperature (°C) (B), days-to-heading and days-to-anthesis (C), and days-to-physiological maturity (D) of cultivars and advanced bread wheat lines evaluated under heat stress in the greenhouse in 2014 at the Norman E. Borlaug Experiment Station, Yaqui Valley, Sonor, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 6, p. 24 for information on advanced lines 5–25).

'Chyak/Pauraq' was the first line to reach the heading stage (average 46 days), and 'Kachu/Becard//WBLL1*2/Brambling' headed in 55 days (Fig. 9C). Cultivar Villa Juárez F2009 reached headed in 50 days, Roelfs F2007 and Ónavas F2009 in 52, and Tepahui F2009 in 53 days, these values were 22, 29, and 26 days earlier, respectively, under the recommended sowing dates for commercial cultivation (Figueroa-López et al. 2010, 2013; Chávez-Villalba et al.

2014; Valenzuela-Herrera et al. 2012). Physiological maturity was reached in an average of 98 days, with a range of 93 to 103 (Fig. 9D, p. 25). Roelfs F2007 reached maturity in 93 days and 'INIA Churrinche/Kiritati' and 'Kachu/3/*T. turgidum* subsp. *dicoccum* PI94624/*Ae. tauschii* (409)//BCN/4/2*Kachu' in 103 days. Villa Juárez F2009 matured in 94 days, Ónavas F2009 in 97 days, and Tepahui F2009 in 101 days.

The number of spikes/plant ranged from 12 to 26 (Fig. 10A) with an avg of 16. 'Chyak 1/Grack' produced the highest number of spikes, followed by cultivar Tepahui F2009 (22 spikes); 'Kachu/ Becard//WBLL1*2/Brambling' was the lowest. Roelfs F2007 had a little higher than average with 17 spikes, and Villa Juárez F2009 and Ónavas F2009 with 18 spikes. The average spike length of the group was 10 cm, with a range of 8.9–11.5 (Fig. 10B). 'ROLF07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/Tukuru//FRET2' produced the highest number of grains/spike with 59.5, followed by 'PBW343//CAR422/ANA/3/Elvira' (Fig. 10C). The difference between the highest and the lowest number of grains/spike was quite high at 23. Cultivar Ónavas F2009 produced an average of 54.8 grains/spike; Tepahui F2009 and Roelfs F2007 were a little higher than average with 48.5 and 48.6 grains/spkike, respectively; and Villa Juárez F2009 averaged 47.6 grains/spike. Eight lines produced more grain than Ónavas F2009 Tepahui F2009, and Villa Juárez. Savin et al. (1997) found significant variation in weight reduction and number of grains/spike under heat stress conditions.

The average grain length was 0.66 cm, and the difference between the longest and shortest grain was quite small, 0.09 cm (Fig. 10D). Line 'Tacupeto F2001/6/CNDO/R143//ENTE/MEXI_2/3/*Aegilops tauschii*/4/Weaver/5/Pastor/7/ROLF07' was 0.71 cm, superior to the rest. Blum (1998) reported that stem reserves from pre-anthesis plant assimilation are an important source of carbon for grain filling, when photosynthesis is inhibited by drought, heat, or disease stress during this stage.

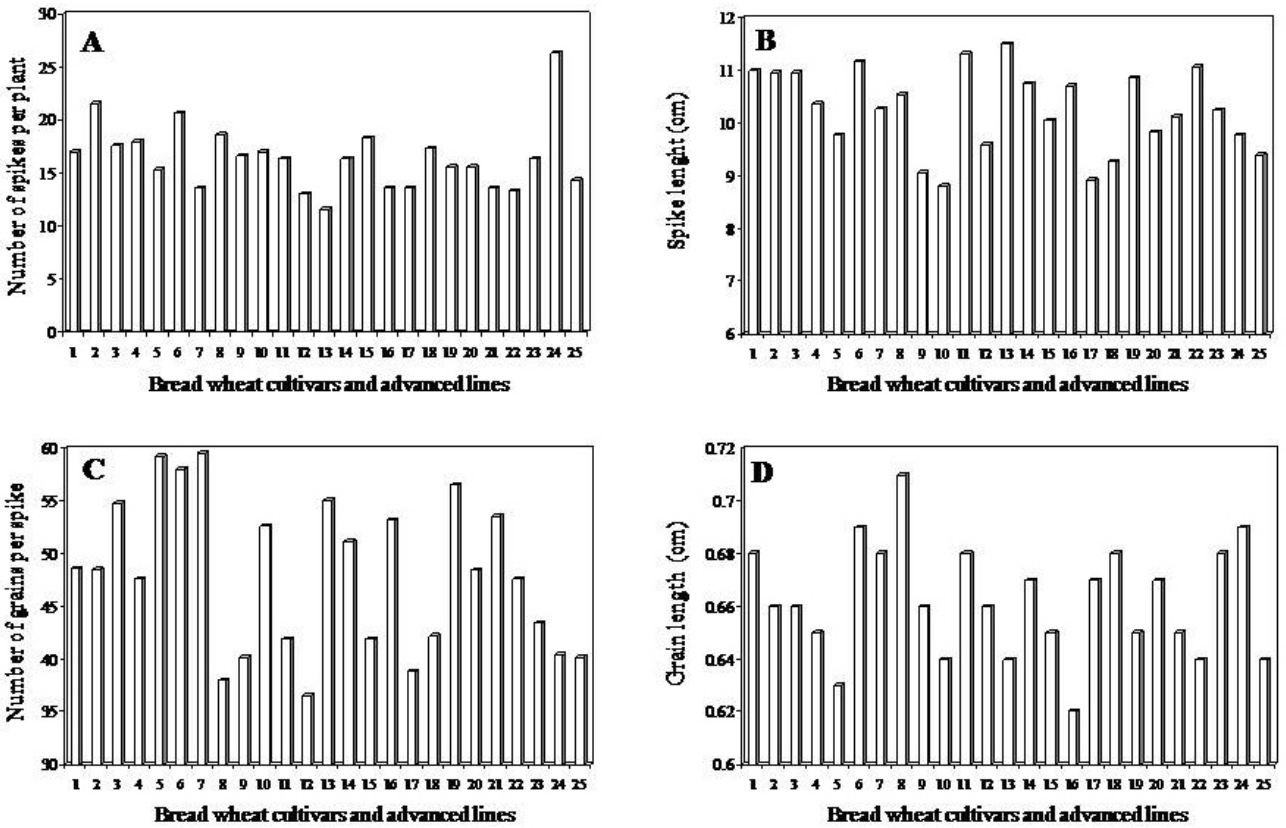

Fig. 10. Number of spikes/plant (A), spike length (cm) (B), number of grains/spike, and grain length (cm) (D) of cultivars and advanced bread wheat lines evaluated under heat stress in the greenhouse in 2014 at the Norman E. Borlaug Experiment Station, Yaqui Valley, Sonor, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 6, p. 24 for information on advanced lines 5–25).

Dry weight biomass was 11.0–24.2 g with an average of 17 g (Fig. 11A, p. 27). 'PBW343//CAR422/ANA/3/Elvira' produced the highest biomass value and 'Chyak/Pauraq' the lowest. Cultivar Villa Juárez F2009 was quite low

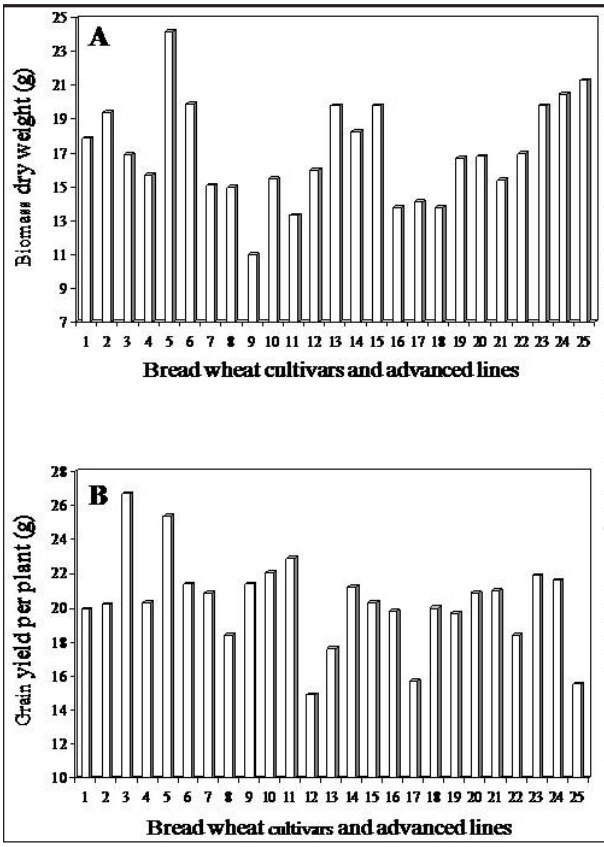

Fig. 11. Biomass dry weight (g) (A) and grain yield/plant (g) (B) of cultivars and advanced bread wheat lines evaluated under heat stress in the greenhouse in 2014 at the Norman E. Borlaug Experiment Station, Yaqui Valley, Sonor, Mexico (1–Tacupeto F2001, 2–Kronstad F2004, 3–Navojoa M2007, and 4–Roelfs F2007) (see Table 6, p. 24 for information on advanced lines 5–25).

at only 15.7 g. Cultivar Ónavas F2009 showed the highest grain yield/plant at 26.7 g, followed by 'PBW343//CAR422/ ANA/3/Elvira' with 25.4 g and 'Tacupeto F2001*2/Kiritati//Villa Juárez F2009' with 22.9 g (Fig. 11B). Cultivars Roelfs F2007, Tepahui F2009, and Villa Juárez F2009 produced 19.9 g, 20.2 g, and 20.3 g, respectively. The lowest grain yield/ plant was in 'Attila/3*BCN//BAV92/3/ Pastor/4/Tacupeto F2001*2/Brambling/5/ Pauraq' with 14.9 g. The reduction in yield is mainly due to a less number of grains produced, which could be a consequence of an increase in high-temperature floral abortion. Stapper and Fischer (1990) indicate that during grain filling and as the temperature rises, plant development accelerates. Even under optimum management conditions, yield may be reduced up to 4% for each 1°C increase. Heat units define the growth stages a thermic constant, because the plant changes the phenological stage once a certain number of heat units are reached, shortening the duration of the wheat cycle (Pascale and Damario 2004).

Conclusions. Promising materials under heat stress conditions of the experiment were the line 'PBW343//CAR422/ANA/3/ Elvira' and commercial bread wheat cultivar Ónavas F2009, because they produced the highest grain yield/plant. The experimental line produced the highest biomass value and was second in number of grains/spike.

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Biological effectiveness of several fungicides for control of Karnal bunt of wheat in the field.

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Abstract. The commercial fungicides Opus, Pointer, Headline, and Varon were evaluated in the field to determine their biological effectiveness to control Karnal bunt of wheat. A completely randomized design was used with four replications. Twenty heads of cultivar Tacupeto F2001 were inoculated during the boot stage with an allantoid sporidial suspension (10,000/mL). Commercial rates indicated on the containers of each product were followed. The first application was carried out 10 days after inoculation (Zadoks 56–58 (Feekes 10.4–10.5)), and the second 10 days later. Inoculated spikes were threshed by hand, and healthy and infected kernels were counted to determine the percentage of infection. The biological effectiveness of the products evaluated were Varon 97.5%, Pointer 97.2%, Opus 96.9%, and Headline 86.87%. The untreated inoculated check had a mean of 28.6% infection. There were no statistical differences for the products evaluated for level of infection after arcsin transformation (Tukey, $p = 0.05$), and no phytotoxic effects of treatments applied to the wheat plant were observed.

Introduction. Karnal bunt of wheat, caused by the fungus *Tilletia indica* (syn. *Neovossia indica* Mitra (Mundkur), is the most important disease of wheat seed and grain in northwest Mexico (Fuentes-Dávila 1997). Losses primarily are due to the negative effect on flour quality and quarantine regulations, both, national and international (SARH 1987; Brennan et al. 1900; SAGARPA 2002). Because there are no immune wheat cultivars to Karnal bunt, chemical control is considered an important measure of an integrated management program of the disease. Due to the biological cycle of *T. indica,* the application of agrochemicals during wheat heading–flowering–anthesis gives greater control of the disease and allows a more profitable economical margin. Over the years, research on chemical control of the disease by foliar applications has been carried out. Singh and Prasad (1980) reported a significant reduction in the level of infection in the field with a single application during the boot stage with benomyl (Benlate), carbendazim (Bavistin), mancozeb (Dithane-M45), or triphenyltin hydrate (Duter). Singh and Singh (1985) reported that of fungicides Bavistin, Baycor, Baytan, Bayleton, Benlate, Blitox, Ceresan, Dinthane M-45, Topsin, and Vitavax, only Baytan and Bayleton were effective on reducing disease severity. Smilanick et al. (1987) reported that in experimental wheat plots artificially inoculated, control of the disease was greater than 80% with two applications of propiconazole or etaconazole and with four applications of mancozeb or copper hydroxide; the best results were obtained when products were applied 72 h after inoculation with the fungus. Figueroa and Valdés (1991) reported the superiority of propiconazole for control of Karnal bunt with foliar applications, when compared with fungicides diniconazole, tebuconazole, flutriafol, fluzilazol, triadimenol, and procloraz. Salazar-Huerta et al. (1997) reported that in experiments during 1986–89, in both experimental plots and commercial fields, propiconazole (Tilt) was the product with the greatest biological effectiveness in controlling the disease, with two applications at the rate of 0.5 L/ha of commercial product; the first application when the crop had 25% heading and the second one 10 days later. Figueroa-López and Alvarez-Zamorano (2000) reported that epoxyconazole (Opus) showed similar levels of efficiency as propiconazole in field trials under artificial inoculation. Fuentes-Dávila et al. (2005) reported that tebuconazole (Folicur) and propiconazole (Tilt) had a biological effectiveness greater than 89% for control of Karnal bunt in artificially inoculated field trials, and Fuentes-Dávila (2007) reported that the biological effectiveness of tebuconazole (Folicur), epoxyconazole (Opus), and propiconazole (Tilt) was 99.8%, 99.6%, and 99.9%, respectively.

In southern Sonora, leaf rust is an endemic and important disease of wheat that has caused epidemics (Dubin and Torres 1981; Figueroa-López et al. 2001), which can only be controlled by proper fungicide applications. Figueroa-López and Cantúa-Ayala (2006) reported that the fungicide Headline (piraclostrobina) and Pointer (flutriafol) were effec-

tive in controlling rust in wheat in field trials (Figueroa-López et al. 2010). Because those products have not been evaluated for Karnal bunt, nor has the newer Tebuconazole, our objective was to evaluate the biological effectiveness of Opus SC (BASF, epoxiconazol 12% a.i. in weight) as the regional check, and Pointer 250SC (Cheminova, flutriafol, 22.70% a.i. in weight), Headline CE (BASF, piraclostrobina, 23.60% a.i. in weight), and Varon 250 CE (Dragon, tebuconazole, not less than 25% a.i. in weight) for control of Karnal bunt in the field under artificial inoculation.

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

Fig. 11. Randomized complete distribution of treatments in the field for control of Karnal bunt by foliar applications during the 2014–15 autumn-winter crop season in the Yaqui Valley, Sonora, Mexico.

Fig. 12. Experimental plots with cultivar Tacupeto F2001 used for evaluation of fungicides for Karnal bunt control during the 2014–15 autumn-winter crop season in the Yaqui Valley, Sonora, Mexico.

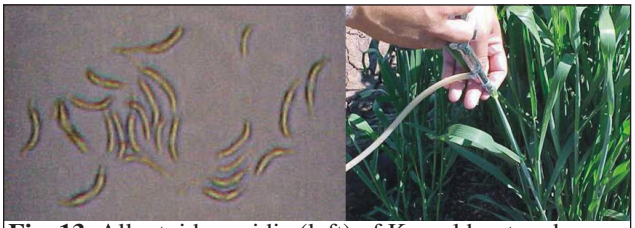

Fig. 13. Allantoid sporidia (left) of Karnal bunt and inoculation by injection into the boot (right).

the volume was based on 250 L of water/ha. To avoid the carry over of the products applied, plastic barriers were used in each plot during the applications (Fig. 14). The first application was carried out ten days after inoculation (Zadoks 56–58 (Feekes 10.4–10.5)) and the second 10 days later. Inoculated spikes were threshed by hand, and the percentage of infection was obtained by counting the number of infected and healthy grains from 20 inoculated spikes from each plot treated with the fungicides and from 20 inocu-

Materials and Methods. The experiment was carried out during the 2014–15 crop season at the Norman E. Borlaug Experimental Station, located in block 910 of the Yaqui Valley at 27°22'04.64" latitude north and 109°55'28.26" longitude west, 37 masl, with climate warm (BW (h)) and extreme warm and dry [BS (h)], according to Koppen classification modified by Garcia (1964). Sowing date was December 18, 2014 with a rate of 80 kg of seed/ha. Treatments were established in a completely randomized experimental design (Fig. 11) with four replications using bread wheat commercial cultivar Tacupeto F2001. The experimental plot consisted of for beds each with two rows 3-m long and 0.80 m between beds (Fig. 12). Inoculations were during the boot stage by injection applying 1 mL per spike with an allantoid sporidial suspension (10,000/mL) in 20 spikes, in the central rows of each plot (Fig. 13). Inoculum was prepared as described by Fuentes-Bueno and Fuentes-Dávila (2007). Commercial rates indicated in the containers of each product were followed: Opus 1 L/ha c.p., Pointer 0.625 L/ha c.p., Headline 0.5 L/ha c.p., and Varon 0.5 L/ha c.p. (Table 7). For application of fungicides, a manual Solo backpack sprayer (15 L) was used with a single nozzle, and

Table 7. Fungicides, formulation, concentration, and rates used to control Karnal bunt by foliar applications during the 2014-15 crop season in the Yaqui Valley, Sonora, Mexico. Formulation is active ingredient in weight and rate is liters of commercial product.

Treatment	Formulation and concentration	Rate CP/ha
Pointer	250 SC 22.7% a.i.	0.625
Headline	CE 23.0% a.i.	0.500
Varon	250 CE ≥ 25% a.i.	0.500
Opus	SC 12% a.i.	1.000
Untreated check		

Fig. 14. Application of fungicides in experimental plots for contrl of Karnal bunt during the 2014–15 autumn-winter crop season in the Yaqui Valley, Sonora, Mexico.

lated spikes from the untreated check. The biological effectiveness was obtained using Abbot's formula: effectiveness of treatments = average percentage of infection of the check – average percentage of infection of the 'treatment / average' percentage of infection of the check x 100. The ANOVA was performed and mean comparison by Tukey's test (p = 0.05) to determine statistical differences among treatments, previous arcsin transformation $\sqrt{X + 0.5}$ (Steel and Torrie 1980). The phytotoxicity was evaluated ten days after each application of the fungicides, according to the EWRS scale (Table 8) (Champion 2000).

Results. The ANOVA of the transformed data of the percent of infected grains with Karnal bunt in 20 spikes in each experimental unit is shown (Table 9). Significant statistical differences were detected between the treatments and the untreated check, with respect to the values of percent infection. The coefficient of variation was 21.09%. Mean comparison by Tukey›s test (Table 10) indicated that all fungicide applications were effective in reducing the percent of infection when compared with the untreated inoculated check, which showed the highest average percent infection (28.6%), with a range between 14.4 and 47.9. The real range of the mean percent of infection obtained in spikes treated with the different products was 0.73–3.78% (Opus average 0.88%, Pointer 0.80%, Headline 3.78%, and Varon 0.73%). The biological effectiveness of the products evaluated were Varon 97.5%, Pointer 97.2%, Opus 96.9%, and Headline 86.87%.

Table 9. Analysis of variance of the percentage of infected grain with karnal bunt, in spikes treated with Opus, Pointer, Headline, and Varon, and in spikes of an untreated check in the Yaqui Valley, Sonora, Mexico, during the 2014–15 autumn-winter crop season.

Source of variation	DF	SS	MS	F value	F tab
Treatments	4	2,198.11	549.53	23.97	3.06
Error	15	343.88	22.93		
Total	19				
C.V. = 21.09					

Table 10. Mean separation by Tukey´s test of the transformed percentages of infected grain with karnal bunt, in spikes treated with Varon, Pointer, Opus, and Headline in the Yaqui Valley, Sonora, Mexico, during the 2014–15 autumn–winter crop season.

Treatment	Infected grain		Mean separation
	Real	Transformed	
Varon	0.73	4.60	A
Pointer	0.80	4.79	A
Opus	0.88	5.08	A
Headline	3.78	10.41	A
Untreated check	28.6	31.86	B

Table 8. Values of the EWRS scale (1–9) to evaluate phytotoxicity in experimental plots, inoculated with Karnal bunt and treated with Varon, Pointer, Opus, and Headline in the Yaqui Valley, Sonora, Mexico, during the 2014–15 autunmwinter crop season.

Value	Effect on plant
1	No effect
2	very light symptoms
3	light symptoms
4	symptoms no reflected in yield
LIMIT OF ACCEPTABILITY	
5	medium damage
6	elevalted damage
7	very elevated damage
8	severe damage
9	complete death

Transformation of the EWRS punctual logarithmic scale to percentage.

Punctual value	Phytotoxicity (%)
1	0.0–1.0
2	1.0–3.5
3	3.5–7.0
4	7.0–12.5
5	12.5–20.0
6	20.0–30.0
7	30.0–50.0
8	50.0–99.0
9	99.0–100

Conclusions. The biological effectiveness of Varon, Pointer, Opus, and Headline for control of Karnal bunt of wheat by foliar applications during heading–flowering–anthesis was 97.5%, 97.2%, 96.9%, and 86.87%, respectively, although they were statistically similar.

According to the EWRS scale, no phytotoxicity was detected on the wheat plants treated with any of the four fungicides.

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Field evaluation of the 3th Wheat Yield Consortium Yield Trial during the 2015–16 crop season.

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Abstract. Commercial bread wheat cultivar Roelfs F2007 and 23 genoypes of advanced bread wheat lines comprising the 3th WYCYT were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora. Plots consisted of one bed, 1-m long with two rows, 0.80 m apart with no replications, and a seed rate of 100 kg/ha. Daily maximum, minimum and average temperature (°C), relative humidity (%), cold hours, and rainfall were recorded during the crop season. The variables evaluated were heading, height, 1,000-kernel weight, and grain yield. Heat waves occurred during 10–21 February; 3–4 March; 2–4, 12–15, and 17–30 April; and 2–10 May, 2016, since maximum temperatures were above 30°C. The period of evaluation of the 3th WYCYT was warm (19.0°C average and 64% RH). The total number of accumulated cold hours was 440. Line 'SUP152//PUB94.15.1.12/WBLL1 (PTSS09GHB00014S-0SHB-099Y-5Y-020Y-0MXI)' showed the highest 1,000-kernel weight (59.2 g), followed by that of 'MEX94.27.1.20/3/Sokoll//Attila/3*BCN/4/PUB94.15.1.12/WBLL1' with 54.5 g. Reedling #1 showed the highest grain yield per plot with 508 g, followed by 'SUP152//PUB94.15.1.12/WBLL1 (PTSS09GHB00014S-0SHB-099Y-15Y-020Y-0MXI)' with 478 g. Roelfs F2007 was 46.8% below the grain yield of Reedling #1, and 49.6% below the average shown in field evaluations in previous seasons. Heading of Roelfs F2007 was reduced by 7.4% and height by 23.2%. Rainfall occurred on 8 January, 2016 (1.7 mm), 8 March (7.5 mm), and 7 April (1.0 mm).

Introduction. The Wheat Yield Consortium (WYC) conducts research on wheat genetics and physiology to improve plant structure, increase the resilience and disease resistance of wheat, and its yield potential in Mexico and abroad (CIMMYT 2016). The Secretariat of Agriculture, Livestock, Rural Development, Fisheries and Food (SAGARPA) is an important financial contributor for the WYC. The main objectives of the WYC are to raise wheat yield potential by 2% globally, with a view to increasing yield potential by 50 percent over 20 years, and raise wheat production by 350,000 tons (10%) in 10 years, 750,000 tons (22%) in 15 years, and 1.7 x 10^6 tons (50%) in 20 years, in the same area currently devoted to wheat production in Mexico. In 2015, main achievements included more than 100 agronomic and physiological traits of 60 elite lines of high-yielding potential from CIMMYT Core Germplasm II set (CIMCOG II), were evaluated with high-throughput phenotyping. Five elite lines were selected after analyzing three years of data collected from consecutive trials of the CIMCOG I set. Some lines were chosen for their resistance to lodging. Aerial phenotyping platforms with remote sensors were used to identify five high-yielding and drought tolerant lines, and seven outstanding heat-tolerant lines from more than 600 elite lines tested in the field. Nine Mexican students undertook doctoral studies in pres-

Table 11. Bread wheat genotypes of the 3th Wheat Yield Consortium Yield Trial, evaluated during the crop season 2015-2016 in a late sowing, in the Yaqui Valley, Sonora. Numbers in bold in parentheses indicate the number of sister lines in the nursery.

Line	Pedigree
1	Pavlovka/V15.89C//NAVJ07/3/ROLF07
2	Sokoll/3/Pastor//HXL7573/2*BAU/4/Parus/Pastor (**3**)
3	Sokoll/3/Pastor//HXL7573/2*BAU/4/Sokoll/WBLL1
4	WBLL4//OAX93.24.35/WBLL1/5/CROC_1/*Ae. tauschii* (205)// BORL95/3/ PRL/SARA//TSI/VEE#5/4/FRET2
5	Seri/BAV92//PUB94.15.1.12/WBLL1 (**2**)
6	Sokoll//PUB94.15.1.12/WBLL1
7	CROC_1/*Ae. tauschii* (224)//Opata/3/PUB94.15.1.12/WBLL1 (**2**)
8	Sokoll//SUP152//PUB94.15.1.12/WBLL1
9	SUP152//PUB94.15.1.12/WBLL1
10	MEX94.27.1.20/3/Sokoll//Attila/3*BCN/4/PUB94.15.1.12/WBLL1 (**2**)
11	Sokoll/WBLL1
12	WBLL1//PUB94.15.1.12/WBLL1 (**2**)
13	WBLL1/6/CMH79A.955/4/AGA/3/4*SN64/CNO67//Inia66/5/NAC
14	Seri/BAV92//PUB94.15.1.12/WBLL1 (**4**)
15	BCN/WBLL1//PUB94.15.1.12/WBLL1
16	Sokoll//PUB94.15.1.12/WBLL1
17	C80.1/3*QT4118//KAUZ/Rayon/3/2*TRCH/4/Berkut/Krichauff (**2**)
18	SUP152//PUB94.15.1.12/WBLL1 (**2**)
19	MEX94.27.1.20/3/Sokoll//Attila/3*BCN/4/PUB94.15.1.12/WBLL1 (**7**)
20	Sokoll
21	Roelfs F2007
22	Kachu #1
23	Baj #1
24	Reedling #1

tigious international universities, with the benefit of acknowledged experts as advisers and using data from the MasAgro Wheat field trials. Three students concluded their doctoral studies, and two more are in line to achieve their degree in the first semester of 2016. Evaluation of the 2nd WYC Yield Trial in five irrigated regions within Mexico, indicated that lines QUAIU, SOKOLL, and line 'C80.1/3*QT4118// KAUZ/Rayon/3/2*TRCH/4/ Berkut/Krichauff' were the best for grain yield in Bajío (states of Guanajuato and Jalisco), and lines 'WBLL1//Yangling Shaanxi/ESDA/3/ROLF07 (PTSS-07GHB00008S-0GHB-0Y-099B-1Y-0Y-0Y-0SMAPY-0B)', 'BCN/WBLL1//PUB94.15.1.12/WBLL1', and 'WBLL1// Yangling Shaanxi/ESDA/3/ROLF07 (PTSS07GHB00008S-0GHB-0Y-099B-1Y-0Y-0Y-0MEDPY-0B)' were outstanding in the northwest (North Baja California, Sonora, and Sinaloa). As a general average, the highest yielding line was 'BCN/WBLL1//PUB94.15.1.12/WBLL1', with 6,417 kg/ha (Solís-Moya et al. 2015). 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 a reduction in final grain weight (Félix-Valencia and Fuentes-Dávila 2015). Given the changing environmental conditions in this region, our objective was to evaluate the performance of the 3th WYCYT Nursery at the Norman E.Borlaug Experimental Station, in a late sowing date during the 2015–16 crop season.

Materials and Methods. Commercial bread wheat cultivar Roelfs F2007 (Figueroa-López et al. 2010) and 23 genoypes of advanced bread wheat lines comprising the 3th WYCYT (Table 11, p. 32) were sown on 29 December, 2015, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, located in block 910 of the Yaqui Valley at 27°22'04.64" N and 109°55'28.26" W, 37 masl, with climate warm (BW (h)) and extreme warm and dry (BS (h)), according to Koppen classification modified by Garcia (1964). Plots consisted of one bed 1-m long with two rows, 0.80 m apart with no replications, and a seed rate of 100 kg/ha. Management of the trial followed the technical recommendations by INIFAP (Figueroa-López et al. 2011). Daily maximum, minimum and average temperature (°C) and relative humidity, as well as rainfall were recorded during the crop season. Cold hours were determined as the temperature ≥0.1 °C to ≤10 °C that occurred during a given hour. The variables evaluated were heading (days), height (cm), 1,000-kernel weight (g), and grain yield (g/plot).

Results and Discussion. Maximum, minimum, and average temperature and relative humidity that prevailed during the period of evaluation are shown (Fig. 15A and B). Average temperature in January was 15.6°C, 18.5°C in February, 18.8°C in March, 21.2°C in April, and 22.3°C in the first ten days of May. However, heat waves occurred 10–21 February; 3–4 March; 2–4, 12–15, and 17-30 April; and 2–10 May, 2016, when maximum temperatures were above 30°C.

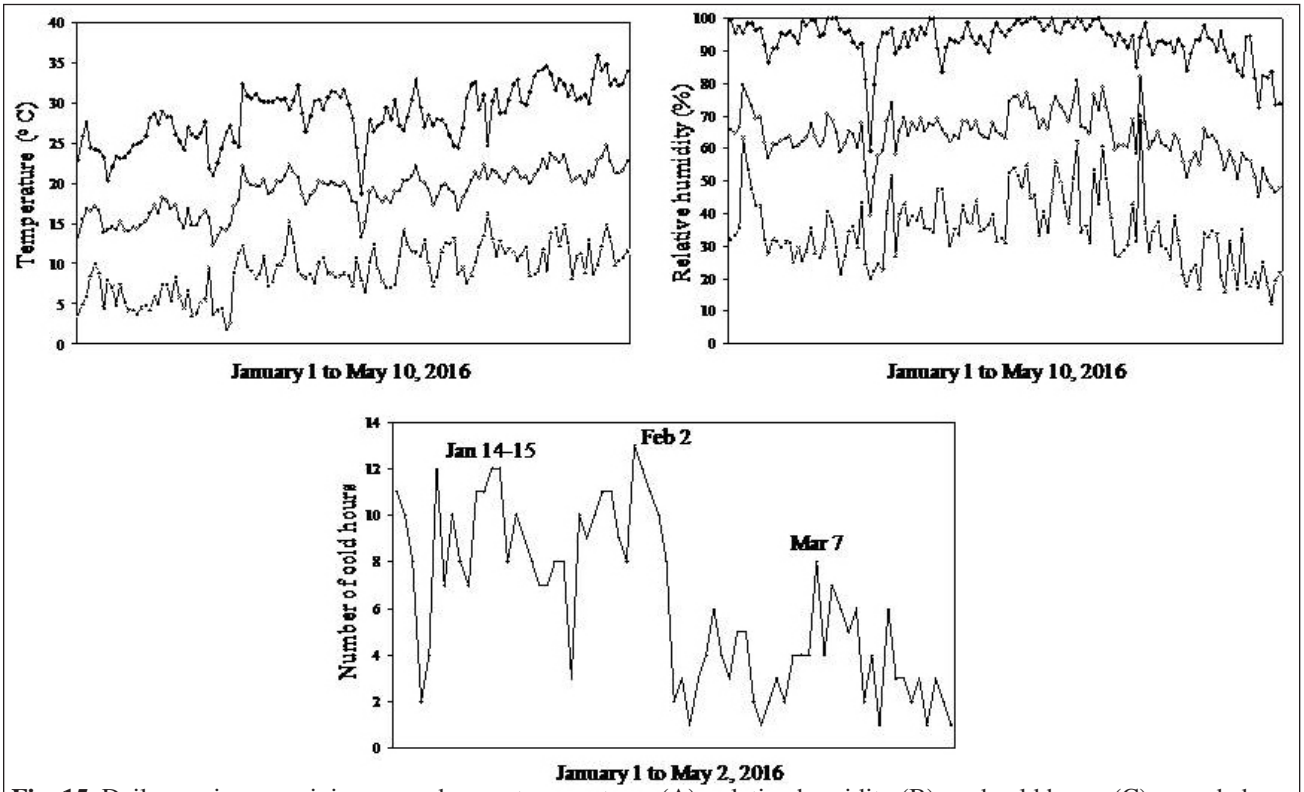

Fig. 15. Daily maximum, minimum, and mean temperatures (A), relative humidity (B), and cold hours (C) recorded from January to May during the autumn–winter 2015–16 wheat season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Average relative humidity in January was 64.9%, 63.9% in February, 70.6% in March, 60.8% in April, and 51.4% in the first ten days of May. In southern Sonora, the interaction of an average 16°C and 68.5% RH during the crop season induces good wheat grain yield (Pedro Félix-Valencia, personal communication). Under these parameters, the period of evaluation of the 3th WYCYT was warm (19.0°C average, and 64% RH), which had a negative effect on grain yield for those farmers that sowed late. Optimum sowing dates in this region based on historical database fall between 15 November and 15 December (Figueroa-López et al. 2011). The greatest number of daily cold hours (CH; Fig. 15C) at 261 was accumulated during January, followed by 92 in February, 62 in March, 24 in April, and 1 in May. The total number of accumulated CH was 440; with 125 during December, 2015 not considered because sowing was on 29 December.

Annual productivity in a given agricultural region may be explained to a great extent by the fluctuation of the temperature. Knowledge of this factor can be capitalized by planning the most appropriate technologies in order to avoid production risks and losses, or to implement alternatives for a good agronomic management (Félix-Valencia et al. 2009). Grain yield is correlated greatly to the number of cold hours accumulated, which allows us to predict the expected yield with an 89% confidence. The relationship shows that a base of 340 CH would expect a grain yield of 4.63 t/ha, and for each increment of 100 CH, yield would increase 330 kg (Félix-Valencia et al. 2009). However, yield at the field level depends upon the farmer's management, because there are fields where grain yield is below 4.63 t/ha and others with yields greater than 7 t/ha. So, if check cultivar Roelfs F2007 (Table 11) showed an average of 6.75 t/ha in field evaluations (Figueroa-López et al. 2010), and if the expected yield is 4.93 t/ha based on 440 CH (Félix-Valencia et al. 2009), then it would be expected that 26.9% of the potential yield was not reached just on the number of CH accumulated from 1 January to 2 May, 2016. The average 1,000-kernel weight was 46.8 g, with a range of 33.9 to 59.2 g (Fig. 16A). Line 'SUP152// PUB94.15.1.12/ WBLL1 (PTSS09GHB00014S-0SHB-099Y-5Y-020Y-0MXI)' showed the highest TKW followed by that of line 'MEX94.27.1.20/3/Sokoll//Attila/3*BCN/4/ PUB94.15.1.12/ WBLL1' with 54.5 g. The average grain yield per plot was 374.9 g, with a range of 256 to 508 g (Fig. 16B). The highest grain yield was shown by the check Reedling #1, followed by line 'SUP152// PUB94.15.1.12/ WBLL1 (PTSS09GHB00014S-0SHB-099Y-15Y-020Y-0M XI)' with 478 g per plot. Roelfs F2007, with a calculated grain yield of 3.4 t/ha, was 46.8% below the grain yield of Reedling #1 and 49.6% below the average shown in field evaluations, which indicates that this cultivar is highly affected by warm weather.

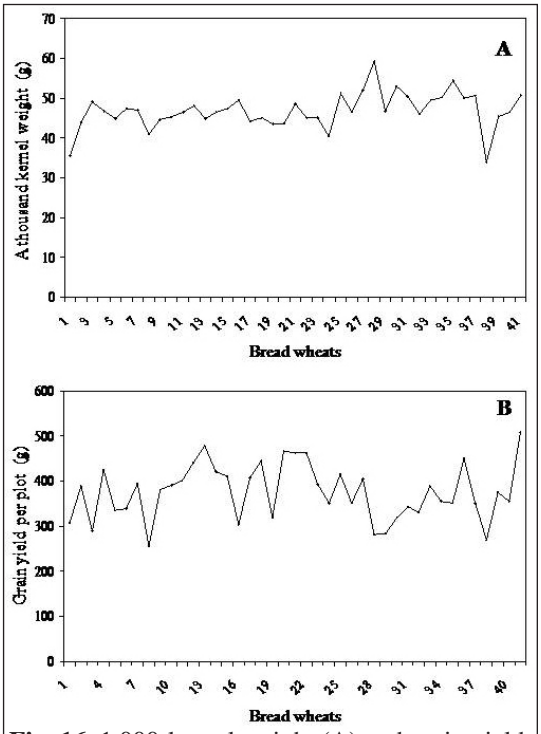

Fig. 16. 1,000-kernel weight (A) and grain yield (B) of 40 advanced bread wheat lines and the cultivar Roelfs F2007 during the 2015–16 wheat season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. Checks are Sokoll (37), Roelfs F2007 (38), Kachu #1 (39), Baj #1 (40), and Reedling #1 (41).

Despite weather conditions during the 2015–16 season, several lines performed well, even without considering the possible effect of the heat waves, especially the one in the middle of February that might have affected tillering, and the one of 3–4 March, which might have affected flowering and seed set. Fokar et al. (1998) indicate that heat stress is the main factor that causes a reduction in wheat productivity due to high temperatures. Savin et al. (1997) found significant variation in weight reduction and in number of grains/spike under heat stress conditions. The reduction in yield is mainly due to less number of grains produced, which could be a consequence by the increase in floral abortion because of the high temperatures. Stapper and Fischer (1990) indicate that during grain filling and as the temperature rises, plant development accelerates; even under optimum management conditions, yield may be reduced up to 4% for each temperature increase of 1°C. Heading of Roelfs F2007 was reduced by 7.4% and height by 23.2% (Fig. 17, p. 35), based on what Figueroa-López et al. (2010) reported for this cultivar. Rainfall occurred on 8 January (1.7 mm), 8 March (7.5 mm), and 7 April (1.0 mm), 2016.

Conclusions. The period of evaluation (1 January to 10 May, 2016) of the 3th WYCYT was warm (19.0°C average, and 64% RH). Heat waves occurred on 10–21 February; 3–4 March; 2–4, 12–15, and 17–30 April; and 2–10 May, 2016, with maximum temperatures were above 30°C. The total number of accumulated cold hours was 440. Check cultivar Roelfs F2007 was 46.8% below the grain yield of Reedling #1 and 49.6% below the average shown in previous field

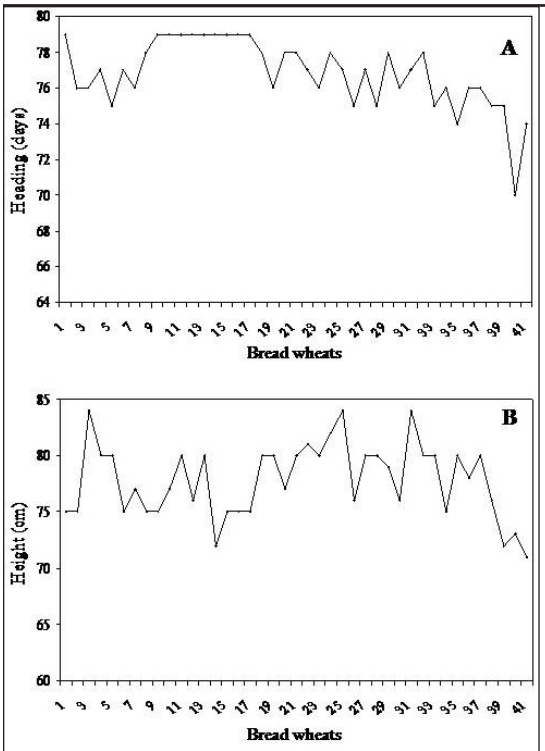

Fig. 17. Heading date (A) and height (B) of 40 advanced bread wheat lines and the cultivar Roelfs F2007 during the 2015–16 wheat season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. Checks are Sokoll (37), Roelfs F2007 (38), Kachu #1 (39), Baj #1 (40), and Reedling #1 (41).

evaluations. Promising materials under heat stress conditions of the evaluation were Reedling #1 (6.35 t/ha), 'SUP152//PUB94.15.1.12/ WBLL1 (PTSS09GHB00014S-0SHB-099Y-15Y-020Y-0MXI)' (5.98 t/ha), 'Seri/BAV92//PUB94.15.1.12/WBLL1 (PTSS09GHB00019S-0SHB-099Y-099B-1Y-0Y-020Y-0MXI)' (5.83 t/ha), and 'Seri/BAV92//PUB94.15.1.12/ WBLL1 (PTSS09GHB00019S-0SHB-099Y-099B-7Y-0Y-020Y-0MXI)' and 'Seri/ BAV92// PUB94.15.1.12/WBLL1 (PTSS09GHB00019S-0SHB-099Y-099B-18Y-0Y-020Y-0MXI)' (5.78 t/ha).

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Re-evaluating resistant and susceptible experimental bread wheat lines for their reaction to Karnal bunt (Tilletia indica Mitra) under artificial field inoculation.

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Abstract. During the 2014–15 autumn–winter crop season in the Yaqui Valley, Sonora, Mexico, we re-evaluated ten resistant and ten susceptible bread wheat lines for their reaction to Karnal bunt under artificial field inoculation. In addition, days-to-flowering, plant height, and 1,000-kernel weight were recorded. The maximum difference in infection (%) between the 2013–14 and 2014–15 cropping seasons within the resistant group was in line 'TAM200/Pastor//TOBA97/3/ Heilo' with 4.52%. The line with the lowest average percentage infection in both seasons was 'SWSR22T.B./5/KAUZ// Altar 84/AOS/3/ KAUZ/4/SW94.15464/6/2*PRL/2*Pastor' with 0.24%, followed by 'BAJ #1/3/Kiritati//Attila*2/Pastor' with 0.48%. With the exception of the KBSUS line, greater differences in percentage of infection were obtained within the susceptible group, which ranged from 5.71% to 28.82%; however, the reaction of all lines fell within the susceptible category. The line with the highest average percentage of infection in both seasons was KBSUS with 99.08%, followed by 'Chewink #1/FRNCLN' with 76.08%. Although the average days-to-flowering were different for the resistant group (87.6 days) and the susceptible group (82.2 days), the susceptible line KBSUS was different than the rest of the lines (70 days). Regarding height, all the lines were categorized as dwarf and semidwarf. The average 1,000-kernel weight was higher in the susceptible group with 37.6 g, whereas the average of the resistant group was 33.9 g. The line in the resistant group with the highest 1,000-kernel weight was 'Saual/4/CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila/5/Saual' with 44.5 g, and 'Chewink #1/FRNCLN' in the susceptible group at 44.4 g.

Introduction. Karnal bunt of wheat caused by the fungus *Tilletia indica* (syn. *Neovossia indica*), affects bread wheat (Mitra 1931), durum wheat, and triticale (X *Triticosecale*; Agarwal et al. 1977). The disease was first identified in India (Mitra 1931), and later in Mexico (Duran 1972), Pakistan (Munjal 1975), Nepal (Singh et al. 1989), Brasil (Da Luz et al. 1993), the United States (APHIS 1996), Iran (Torarbi et al. 1996), and the Republic of South Africa (Crous et al. 2001). The fungus does not infect all the kernels in a spike and not all the spikes in a plant are affected; generally, kernels are partially bunted (Mitra 1935; Bedi et al. 1949; Chona et al. 1961). 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) but is not feasible when quarantines do not allow tolerance levels for seed production. The susceptibility of bread wheat is documented (Fuentes-Dávila et al. 1992, 1993) reaching infection levels above 50% under artificial inoculation. However, Fuentes-Dávila and Rajaram (1994) reported that some bread wheats that consistently show low infection levels. Genetic resistance is the most important tool for disease control and for a better benefit/cost of wheat production, because no fungicide application is needed and/or the number of applications is reduced (Huerta-Espino and Singh 1996). Genetic studies indicate that eight genes confer resistance to *T. indica* (Fuentes-Dávila et al. 1995); however, the resistance mechanisms that might be operating in this interaction are unknown. Since the initiation of the project on Karnal bunt in northwest Mexico in the early 1980s, artificial inoculation in the field have been an essential component (Fuentes-Davila et al. 2001) because disease incidence is quite erratic in the Yaqui Valley (Lira-Ibarra 1992). Artificial inoculation has served to identify both resistant and susceptible germplasm, which have been the bases for comparisons and genetic studies (Fuentes-Dávila and Rajaram 1994; Fuentes-Dávila et al. 1995). Our objective was to re-evaluate ten experimental resistant and ten susceptible bread wheat lines to Karnal bunt under artificial field inoculation at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, because these lines will be used in biochemical and molecular studies in the near future.

Materials and Methods. Evaluation during the 2014–15 crop season was at the Norman E. Borlaug Experimental Station, located in block 910 of the Yaqui Valley at 27°22'04.64" N 109°55'28.26" W, 37 masl, with climate warm (BW (h)) and extreme warm and dry (BS (h)), according to Koppen classification modified by Garcia (1964), in a clay soil with pH 7.8. Sowing dates were 19 and 28 November, 2014, using 8 g of seed for a bed 0.7-m long with two rows. Experimental lines (Table 12, p. 37) were selections from various CIMMYT bread wheat nurseries, where the reaction to artificial inoculation with *T. indica* in a previous crop season was either resistant or susceptible based on several scoring scales (Fuentes-Dávila and Rajaram (1994), Fuentes-Dávila and Ammar (2005), and Fuentes-Dávila and Ireta-Moreno 2006) (Table 13, p. 37).

For inoculation preparation, one-year-old teliospores were scraped off infected grain with a dissecting needle and kept in a water–Tween 20 solution for 24 h. The suspension was filtered through a 60 μm nylon sieve and centrifuged at 3,000 rpm. After discarding the supernatant, 0.5% a.i. sodium hypochlorite was used to disinfect teliospores for 2 min while centrifuging. Teliospores were rinsed twice with sterile distilled water while centrifuging. Teliospores were resuspended in sterile distilled water in a centrifuge tube and 1 mL of the teliospore suspension was spread on Petri plates with 2% water-agar, which were incubated at 18–22°C in the dark. After 6–9 days, teliospore germination was evaluated using a compound microscope at 10X. Pieces of the agar with germinated teliospores were removed and placed upside down on the lid of a Petri plate containing potato-dextrose-agar (PDA). After 10 to 14 days, 2 to 3 mL of sterile distilled water were added to the plates, and the colonies were scraped gently using a sterile spatula. Hyphae and sporidia were inoculated onto other plates with PDA using a sterile syringe, and the plates incubated at 18–22°C in the dark for ~9 days. After incubation, pieces of PDA with the different fungal propagules were transferred and placed upside down on the lids of sterile glass Petri plates in order to induce production of allantoid secondary sporidia (Dhaliwal and Singh 1989; Fuentes-Dávila et al. 1993). Sterile distilled water (3 mL) was added to the bottom of the plates. Water from the plates was collected every 24 h and secondary allantoid sporidia were collected and counted using a heamocytometer. The concentration was adjusted to 10,000 per mL. Five spikes of each experimental line were inoculated by injecting 1 mL of the allantoid sporidial suspension during the boot stage (stage 49, Zadoks et al. 1974) (Fig. 18, p. 38). Stems of the inoculated spikes were identified with a piece of red plastic. An automatic, mist-irrigation system was used during the period of inoculation (January–March) for 20 min, five times each day, and the area was covered with nets to prevent bird damage (Fig. 19, p. 38). Harvest was done manually, and healthy and infected grains were counted by visual inspection to calculate the percentage of infection (infected grains). To determine the

Table 12. Resistant and susceptible bread wheat experimental lines re-evaluated for their reaction to Karnal bunt under artificial field inoculation during the 2014–15 crop season in the Yaqui Valley, Sonora, Mexico.

Entry	Pedigree and selection history
Resistant lines	
1	Kiritati//Attila*2/Pastor/3/Akuri CMSS07Y00143S-0B-099Y-099M-099NJ-099NJ-10WGY-0B
2	BAJ #1/3/Kiritati//Attila*2/Pastor CMSS07Y00288S-0B-099Y-099M-099Y-3M-0WGY
3	Chibia//PRLII/CM65531/3/SKAUZ/BAV92/4/MUNAL #1 CMSS07Y00066S-0B-099Y-099M-099Y-36M-0WGY
4	BAJ #1/3/Kiritati//Attila*2/Pastor CMSS07Y00288S-0B-099Y-099M-099NJ-099NJ-10WGY-0B
5	TAM200/Pastor//TOBA97/3/Heilo CMSS07B00465S-099M-099Y-099M-10RGY-0B
6	Munal #1/Francolin #1 CMSS06B00001S-0Y-099ZTM-099Y-099M-13WGY-0B
7	Saual/Kiritati//Saual CMSS06Y00785T-099TOPM-099Y-099ZTM-099Y-099M-5WGY-0B
8	Saual/4/CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila/5/Saual CMSS06Y01021T-099TOPM-099Y-099ZTM-099Y-099M-13WGY-0B
9	ROLF07/Saual CMSS05B00498S-099Y-099M-099Y-099ZTM-9WGY-0B
10	SWSR22T.B./5/KAUZ//Altar 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*Pastor CMSS08Y01067T-099M-099Y-099M-099Y-5M-0WGY
Susceptible lines	
1	ND643/2*WBLL1//Villa Juarez F2009 CMSS08Y00233S-099Y-099M-099NJ-7WGY-0B
2	Chewink #1/FRNCLN CMSS08Y00486S-099Y-099M-099NJ-18WGY-0B
3	TAM200/Pastor//TOBA97*2/3/Munal CMSS08Y00750T-099TOPM-099Y-099M-099Y-21M-0WGY
4	Danphe #1*2/CHYAK CMSS08Y00869T-099TOPM-099Y-099M-099Y-12M-0WGY
5	Danphe #1*2/CHYAK CMSS08Y00869T-099TOPM-099Y-099M-099NJ-8WGY-0B
6	Mutus*2/Haril #1 CMSS08Y00871T-099TOPM-099Y-099M-099NJ-099NJ-30WGY-0B
7	Tacupeto F2001*2/Brambling//Whear/Sokoll CMSS08B00429S-099M-099NJ-6WGY-0B
8	MEX94.2.19//Sokoll/WBLL1/3/Whear/Sokoll CMSA09M00506S-050ZTM-0NJ-099NJ-3RGY-0B
9	PSN/BOW//SERI/3/Milan/4/Attila/5/KAUZ*2/CHEN//BCN/3/Milan/6/WBLL1*2 /4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/7/IWA 8600211//2*PBW343*2/Kukuna CMSS10Y00731S-099Y-14M-3Y-0B
10	KBSUS

Table 13. Severity scale for Karnal bunt evaluation based on the percentage of infected grains/line.

Score	Reaction
0	no infected grains
0.1–5.0	resistant
5.1–10.0	moderately resistant
10.1–30.0	moderately susceptible
> 30.1	susceptible

resistance of lines inoculated with *T. indica*, days-to-flowering, plant height (cm), and 1,000-kernel weight (g) also were recorded.

Results and Discussion. The maximum difference in infection (%) between 2013–14 and 2014–15 within the group of resistant lines was in 'TAM200/Pastor//TOBA97/3/Heilo' with 4.52%. The difference among the rest of the lines was 0.11–2.57%, which also was considered resistant (Fig. 18). The resistant line most similar during both seasons was 'SWSR22T.B./5/KAUZ//Altar 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*Pastor' at 0.11%.

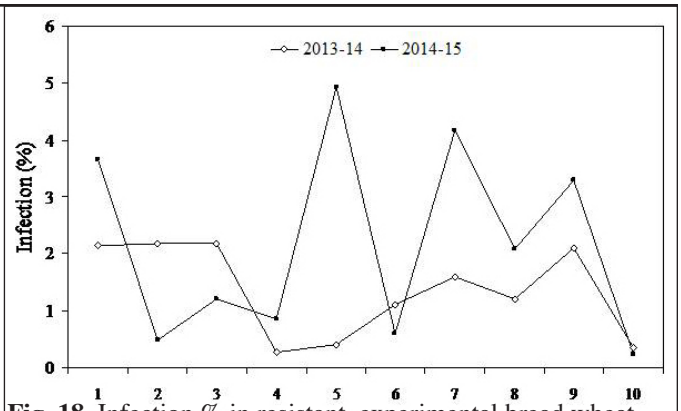

Fig. 18. Infection % in resistant, experimental bread wheat lines artifically inoculated with Karnal bunt for two crop seasons in field at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

With the exception of the KBSUS line, greater differences in infection were obtained within the group of susceptible lines, which ranged from 5.71% to 28.82% (Fig. 19). However, the reaction of all lines fell within the susceptible category (Fuentes-Dávila and Rajaram 1994; Fuentes-Dávila and Ammar 2005; Fuentes-Dávila and Ireta-Moreno 2006). The maximum difference in infection between the 2013–14 and 2014–15 seasons within the susceptible group was in line 'TAM200/Pastor//TOBA97*2/3/Munal' with 28.82%. The most similar degree of susceptibility was observed in line KBSUS, with a difference of 0.02%.

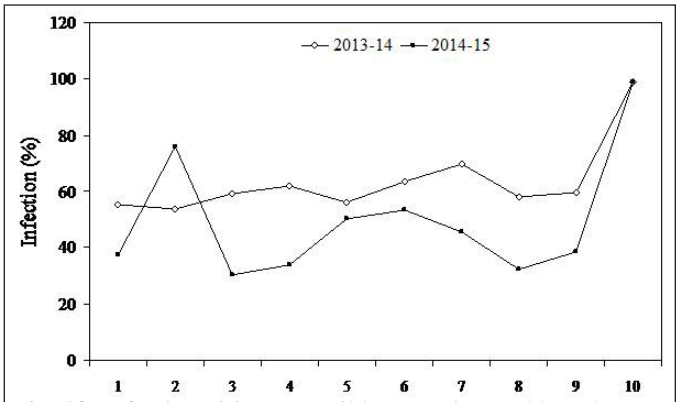

Fig. 19. Infection % in susceptible, experimental bread wheat lines artifically inoculated with Karnal bunt for two crop seasons in field at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

In 2014–15, the range of infection at the first sowing (19 November) for the resistant group was 0.0–6.77% with a mean of 2.28 (Fig. 20). Line 'Saual/4/CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila/5/Saual' did not have any infected grains, whereas 'SWSR22T.B./5/KAUZ//Altar 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*Pastor' had only a 0.48% infection. For the second date (28 November), the range of infection was 0.0–5.26% with a mean of 2.02%. Lines 'BAJ #1/3/Kiritati//Attila*2/Pastor', 'Munal #1/Francolin #1', and 'SWSR22T.B./5/KAUZ//Altar 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*Pastor' did not have any infected grains, and 'BAJ#1/3/Kiritati//Attila*2/Pastor' had only 0.65% infection. The line with the lowest average percentage of infection at both dates was 'SWSR22T.B./5/KAUZ//Altar 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*Pastor' with 0.24%, followed by a 0.48% in 'BAJ #1/3/Kiritati//Attila*2/Pastor'.

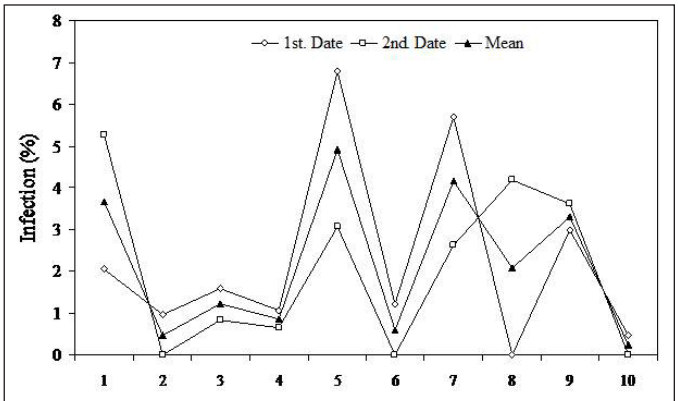

Fig. 20. Infection (%) of experimental bread wheat lines artificially inoculated at 19 (1st date) and 28 (2nd date) November, 2014, which in 2013–14 were resistant under the same conditions at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

The range of infection at the first sowing date for the susceptible group was 22.1–99.2%, with a mean of 45.9 (Fig. 21, p. 39). Line KBSUS showed the highest infection at 99.2%, followed by 'Chewink #1/Frncln' with 55.7%. For the 28 November sowing, the range of infection was 14.2–98.9%, with a mean of 53.6%. Again, KBSUS was the most susceptible at 98.9%, followed by 'Chewink #1/Frncln' with 96.4% infection. KBSUS had the highest average percentage of infection at both dates with 99.08%, followed by 'Chewink #1/Frncln' with 76.08%. The results obtained corroborate the reaction shown by the lines in the 2013–14 season, and that the methodology is effective in determining if the experimental germplasm

is resistant or susceptible, although field evaluation under natural conditions would provide important information in relation to their field resistance.

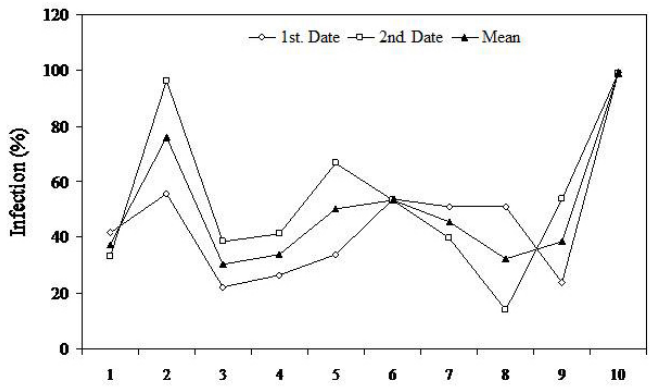

Fig. 21. Infection (%) of experimental bread wheat lines artificially inoculated at 19 (1st date) and 28 (2nd date) November, 2014, which in 2013–14 were susceptible under the same conditions at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Although the average number of days-to-flowering was different between the resistant (87.6 days) and susceptible (82.2) groups, line KBSUS (susceptible) was completely different from the rest of the lines (70 days) (Fig. 22A). For height within the resistant group, the average was 86 cm (Fig. 22B). Lines 'BAJ#1/3/Kiritati//Attila*2/Pastor', 'BAJ#1/3/Kiritati//Attila*2/Pastor', 'TAM200/Pastor//TOBA97/3/Heilo', and 'ROLF07/Saual' were the tallest at 90 cm, and 'Saual/Kiritati//Saual' was the shortest at 75 cm. Within the susceptible group, the average height was 85.5 cm. Line 'Tacupeto F2001*2/Brambling//Whear/Sokoll' was the tallest at 100 cm, and KBSUS the shortest at 60 cm. Despite the height differences, lines from both groups were either dwarf and semidwarf according Paquet's scale (1968), although Huerta Espino and Gonzalez Iñiguez (2000) indicate that plant height in wheat could be triple dwarf (less than 70 cm), double dwarf (70–80 cm), semidwarf (90–95 cm), semidwarf–tall, and tall.

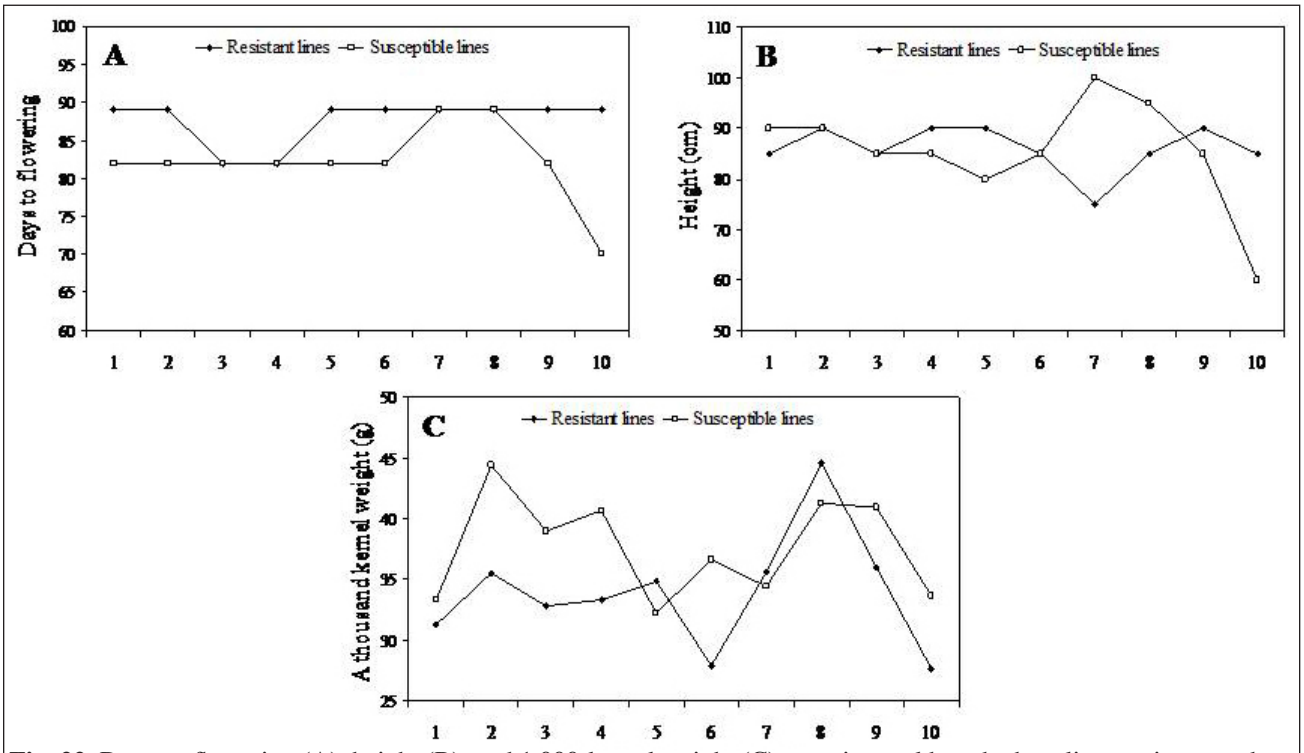

Fig. 22. Days-to-flowering (A), height (B), and 1,000-kernel weight (C) experimental bread wheat lines resistant and susceptible to Karnal bunt re-evaluated during the autumn–winter 2014–15 growing season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

The average 1,000-kernel weight was higher in the susceptible group (37.6 g) than in the resistant group (33.9 g) (Fig. 22C). The resistant line with the highest 1,000-kernel weight was 'Saual/4/CROC_1/*Ae. tauschii* (205)//KAUZ/3/Attila/5/Saual' at 44.5 g, and the lowest as in 'SWSR22T.B./5/KAUZ//Altar 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*Pastor' (27.6 g). The susceptible line with the highest 1,000-kernel weight was 'Chewink #1/Frncln' with 44.4 g, and 'Danphe #1*2/CHYAK' with the lowest (32.2 g). After the line KBSUS, 'Chewink #1/Frncln' had the highest average percentage of infection (76.08), but showed the highest 1,000-kernel weight.

Conclusion. The resistance of ten bread wheat experimental lines and the susceptibility of other ten lines to Karnal bunt was corroborated by artificial field inoculation.

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ITEMS FROM PAKISTAN

NUCLEAR INSTITUTE FOR FOOD AND AGRICULTURE (NIFA)
Wheat group, Plant Breeding and Genetics Division, Peshawar, Pakistan.

Producing quality seed and maintaining released wheat cultivars in Pakistan.

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

Background. Pakistan is the 7th largest producer of wheat in the world, grown by ~80% of all farmers and planted on 40% of the total cultivated area. Wheat contributes 13.1% to the country's agriculture value added and 2.8% to the gross domestic product. Wheat also is a staple food commodity, covering about 58% of the food crop area in Khyber Pakhtunkhwa (KPK). The province is highly deficient in wheat production, of which 92% of its districts fall under an 'extremely deficient' category. The yield of wheat per hectare varies from one place to another, depending on the cultivar planted and the soil fertility. Production can be increased horizontally by increasing the cultivated area and vertically by increasing the yield/acre. The former has very little hope, because the cropping intensity is already very high; however, the later has a large magnitude through continuous release of improved cultivars with different genetic backgrounds.

At NIFA, since 1982, major efforts are underway to enhance the wheat productivity in the country by breeding disease-resistant and high-yielding cultivars. An integrated approach to wheat improvement is used, involving the creation of desirable genetic variability through the use of mutagens, hybridization, and evaluation of local and exotic material. As a result of these efforts, eight high-yielding and disease resistant wheat cultivars have been released for the rainfed and irrigated areas of the KPK.

Overall objectives. Develop new, improved, wheat cultivars coupled with mainting previously released cultivars under the irrigated conditions in KPK.

Specific objective. Produce breeder nucleus seed, prebasic, basic, and certified seed of NIFA wheat cultivars and promote their cultivation in the KPK.

Summary of the work. A total of 3,900 kg of quality seed of NIFA-released, irrigated cultivars was produced and, after processing, certifying, and registering the seed, was distributed to agricultural department and farming communities in the KPK.

Seed production activities at the Institute's Farm. Progeny rows/blocks of NIFA wheat cultivars were planted on available land at the institute. All recommended cultural practices were followed. Progeny rows/blocks, having off-type

plants, were discarded. Breeder nucleus seed was planted for production of pre-basic/basic seed duly inspected by the FSC & RD officials.

Popularization and demonstration plots in farmer's fields. Selected, half-acre, demonstration plots of new released cultivars were planted in farmers' fields (source seed provided free of cost) for quick proliferation of the cultivar.

Expected results and output. The produced breeder nucleus seed, prebasic, and basic seed of the NIFA released cultivars fulfills the mandatory requirement of Agricultural Extension Department. The plantation of selected demonstration plots in the farmer's fields to help quickly popularize NIFA cultivars with subsequent seed proliferation.

Evaluation of wheat genotypes in preliminary and advanced trials under irrigated conditions.

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

New genotypes were evaluated in preliminary yield trials to identify suitable genotypes carrying genes for high yield and disease resistance (*Yr*/*Lr*) under field conditions. One hundred newly selected genotypes were subjected to a field evaluation in two preliminary yield trials under normal, irrigated conditions. Each genotype was planted in four 5-m rows, with two replications in an Alpha Lattice Design. Agronomic and disease resistance data for individual genotype were recorded at specific growth stages.

Preliminary yield trials (PYT) provide an important platform for detailed assessment with regard to yield/yield components of newly selected wheat genotypes isolated from nonreplicated observation nurseries, mutant populations, and recombinants. One hundred genotypes were evaluated in PYT-I and PYT-II including two check cultivars (Bathoor-08 and Pirsabak-2013) in each trial under normal planting conditions at NIFA. Based on yield performance and disease reaction, 15 genotypes were selected in both trials for further evaluation.

In PYT-I, three genotypes produced higher grain yield than the highest yielding check (Bathoor-08; 3,866 kg/ha), whereas 18 genotypes out yielded the low yielding check (Pirsabak-13; 2,900 kg/ha). The highest yielding genotype was CTRN-14085 (4,666 kg/ha), followed by CT 14041 (3,916 kg/ha). In PYT-II, four genotypes out yielded both the check cultivars (Pirsabak-13; 3,733 kg/ha and Bathoor-08; 3,633 kg/ha). CT 14293 (3,966 kg/ha) produced the highest yield, followed by that of CT 14287 (3,933 kg/ha). These new genotypes were isolated for further testing in advanced trials. The morpho-agronomic data of some of the selected lines is presented (Table 1).

Table 1. Morphologic and agronomic traits of selected wheat genotypes from preliminary and advanced yield trials.

Genotype	Days-to-heading	Days-to-maturity	Plant height (cm)	Grain yield (kg/ha)	1,000-kernel weight (g)	Hectoliter weight (g)
Preliminary yeild trial I						
CTRN-140085	128	175	105	4,666	45.5	70.0
CT 14041	127	174	99	3,916	41.9	72.2
CT 14035	132	175	107	3,866	46.5	71.8
Bathoor-08	134	177	103	3,866	41.8	72.2
Pirsabak-13	130	174	105	2,900	45.5	70.7
Preliminary yield trial II						
CT 14293	133	176	104	3,966	40.0	70.0
CT 14287	129	176	110	3,933	43.0	72.0
CT 14328	132	178	106	3,933	41.0	72.7
CT 14294	133	177	100	3,733	35.5	70.0
Bathoor-08	134	176	104	3,633	35.4	72.7
Pirsabak-03	131	174	102	3,733	37.5	73.0
Advanced yield trial I						
WL15-ASYT-2	134	177	102	3,487	37.4	73.6
Bathoor-08	135	176	106	4,087	41.7	73.7
Pirsabak-13	133	176	100	3454	42.1	71.5
Advanced yield trial II						
CT-13186	134	176	101	4276	39.3	72.6
CTRN13121	132	176	113	4010	40.4	72.3
CT-13121	133	176	104	3754	44.7	73.4
Bathoor-08	135	175	112	2788	36.6	70.8
Pirsabak-13	133	175	107	4476	42.1	72.1

Elite wheat genotypes were evaluated in advanced yield trials under irrigated conditions to confirm yield and agronomic traits. Two advanced yield trials (AYTs), comprising of 32 genotypes in each trial including two check cultivars, were planted under normal irrigated conditions. Each trial consist of three replications with four, 5-m rows in a randomized complete block design. All the recommended cultural practices followed by recording of data (agronomic/disease) were carried out for individual experiment.

A total of 36 genotypes were evaluated in two advanced selection yield trials under normal planting conditions at NIFA. In ASYT-1, none of the genotypes out yielded either of the check cultivars (Table 1). However, genotype WL15-ASYT-2 (4,087 kg/ha) out yielded the low yielding check (Pirsabak-13; 3,454 kg/ha). In ASYT-2, nine genotypes out yielded the low yielding check cultivars (Bathoor-08; 2,788 kg/ha). Genotype CT-13186 (4,276 kg/ha) was the second highest yielder, followed by CTRN13121 (4,010 kg/ha) and CT-13121(3,754 kg/ha). These genotypes were selected for evaluation in multi-location yield trials based on high yield and resistance to prevailing diseases of wheat.

Agronomic evaluation of exotic wheat germplasm under irrigated conditions.

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

Field evaluation of exotic wheat germplasm received from the International Maize and Wheat Improvement Center (CIMMYT), Mexico, and the International Center for Agricultural Research in the Dry Areas (ICARDA), Syria, was conducted to identify genotypes adapted to the environmental conditions of the Khyber Pakhtunkhwa (KPK) Province of Pakistan. Global exchange of wheat germplasm from CIMMYT/ICARDA through provision of observation nurseries and trials to cooperating institutions always plays a positive role for selecting the desirable wheat ideotypes.

Nurseries were planted in a nonreplicated fashion based on augmented statistical design. Each entry of the respective nursery was allotted a plot size of 2.5 m^2 with a 30-cm row-to-row spacing. Similarly, the trials consisted of two replications with 4–6 5-m rows in an alpha lattice design. All recommended cultural practices were followed. Data regarding yield and other agronomic traits were recorded for individual entries.

The International Bread Wheat Screening Nursery (47th IBWSN), consisting of 304 genotypes received from CIMMYT, Mexico, was evaluated with local check Bathoor-08. Based on plant type, yield performance, and disease reaction (*Yr* and *Lr*), a total of 58 genotypes were initially selected. The selected genotypes out yielded the check Bathoor-08 by producing grain yield in the range of 5,399 to 8,266 kg/ha (Table 2, p. 44).

The 9th Stem Rust Nursery, consisting of 250 genotypes, was evaluated for yield performance and disease (*Yr*) reaction with the local check Bathoor-08. Out of 250 genotypes, 47 were selected for further evaluation and to confirm their desired traits. The selected genotypes out yielded the check cultivar (5,727 kg/ha) producing grain yield in the range of 5,750 to 6,799 kg/ha.

The Elite Spring Wheat Yield Trial (35th ESWYT), consisting of 50 genotypes, was evaluated for yield performance and disease (*Yr*) reaction with the local check Bathoor-08. Out of 50 genotypes, seven were selected for further evaluation and to confirm their desired traits. The selected genotypes out yielded the check cultivar (2,916 kg/ha) by producing grain yield in the range of 3,114 to 3,749 kg/ha.

The South Asia Bread Wheat Genomic Prediction Yield Trial (SABWGPYT04), consisting of 60 genotypes, was evaluated for yield performance and disease (*Yr*) reaction with the local check Bathoor-08. Out of 60 genotypes, 19 were initially selected for further evaluation and confirmation of their desired traits. The selected genotypes out yielded the check cultivar (Bathoor; 4,290 kg/ha) by producing a grain yield in the range of 4,304 to 5,415 kg/ha (Table 2, p. 44).

The Elite Spring Bread Wheat Yield Trial (CWANA 15th ESBWYT), consisting of 24 genotypes, was evaluated for yield performance and disease (*Yr*) reaction with local check Bathoor-08. Out of 24 genotypes, seven were selected for further evaluation and to confirm their desired traits. The selected genotypes out yielded the check cultivar (4,166 kg/ha) by producing a grain yield of 4,666 kg/ha.

Table 2. Agronomic data of the top five wheat genotypes from several nurseries/yield trials. Agronomic score was on a scale of 1–5, where 5 is the best.

#	Genotype	Days-to-heading	Days-to-maturity	Plant height (cm)	Lodging (%)	Grain yield (kg/ha)	1,000-kernel weight (g)	Agronomic score
47TH INTERNATIONAL BREAD WHEAT SCREENING NURSERY								
1	CT-151199	126	175	105	0	8,266	45.0	3
2	CT-151221	133	174	108	0	7,866	38.4	3
3	CT-151245	126	175	111	0	7,599	41.0	3
4	CT-151089	122	174	102	0	7,199	43.0	3
5	CT-151273	127	174	110	0	7,066	46.0	3
6	Bathoor-08	133	174	105	35	6,490	41.0	2
9TH STEM RUST NURSERY								
1	CTRN-156122	133	173	100	0	6,799	40.0	3
2	CTRN-156039	130	175	96	0	6,533	38.0	3
3	CTRN-156153	132	175	110	0	6,399	44.0	3
4	CTRN-156203	132	174	100	0	6,399	40.0	3
5	CTRN-156093	131	178	106	0	6,333	44.0	3
6	Bathoor-08	134	174	105	40	5,727	40.1	2
SOUTH ASIA BREAD WHEAT GENOMIC PREDICTION YIELD TRIAL 04								
1	CTG-154001	128	176	106	55	5,415	—	2
2	CTG-154033	135	176	102	40	5,332	—	2
3	CTG-154005	135	177	105	15	5,249	—	2
4	CTG-154030	134	175	112	25	4,999	—	3
5	CTG-154058	125	175	104	0	4,707	—	2
6	Bathoor-08	135	175	112	80	4,290	—	1

The Heat Yield Trial/Multiplication nursery, consisting of 335 genotypes, was evaluated for yield performance and disease (*Yr*) reaction with local check Bathoor-08. Out of 335 genotype, 41 genotypes were selected for further evaluation and confirmation of their desired traits. These isolated genotypes will be further tested in preliminary yield trials during next cropping season.

Seeking sources of resistance to Alternaria blight in wheat germplasm.

Kamran Saleem, Sajid Shokat, Hafiz Muhammad Imran Arshad, Mian Abdur Rehman Arif (Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan) and Babar Manzoor Atta.

Climate change, in the current scenario, is manifested in terms of biotic and abiotic stress on field crops. Wheat is widely cultivated crop in Pakistan and, after rice, the second important staple food of the world. Among the biotic stresses that affect wheat, the major bottleneck is rust disease, which drastically changes in severity with environment and host genotype. However, minor diseases also may impact yield loss in wheat. *Alternaria* blight, caused by *Alternaria triticina* (Singh and Srivastava 1997) was observed continuously along with rust and its destruction increases every year. We have a dire need to identify resistance sources in wheat germplasm and make them available for wheat breeding programs.

The use of genetic resistance for disease control in wheat is highly promising. The Wheat Improvement Group of the Nuclear Institute for Agriculture and Biology (NIAB) has developed many advanced lines through crossing elite Pakastani cultivars. These wheat lines were evaluated in different trials for thier resistance to biotic and abiotic stresses. In the current study, the performance of 30 wheat genotypes (16 advanced lines, 13 approved cultivars, and the susceptible check Morocco) were evaluated under natural field conditions for resistance against *Alternaria* blight during the 2014–15 wheat season. The trial was laid out in an alpha-lattice design with two replications keeping a row-to-row distance of 30 cm with with 2.1-m rows. The material was planted on 15 October, 2014, at NIAB, Faisalabad. Standard agronomic practices were applied. The disease first appeared on the Morocco check wheat in February, 2015, and *Alternaria* blight resistance data recorded when Morocco showed more than 20% severity. Disease severity was recorded on 10 random plants at the time of the first observation using the 0–9 scale (Saari and Prescot 1975). The same plants were checked throughout the experiment. Genotypes scored 1–3 were considered resistant, 4 moderately resistant, 5–6

moderately susceptible, and 7–9 as susceptible. For estimating the area under disease progress curve (AUDPC), disease severity was recorded on four different dates with a one-week interval. The range of the severity mean also was determined based on data of 10 leaves/line.

Data of 30 genotypes, for mean disease severity, range, AUDPC, and host response, are presented (Table 3). To determine the source of resistance under natural field conditions, two NIAB advanced lines (NW-1-47-4 and NW-10-32), and two cultivars (NIA-Sunhari and Faisalabad-2008) were immune and had no disease throughout the season. Seven NIAB hybrid lines and five approved cultivars fell into the resistant category. Whereas mean range in the resistant cultivars was 0–5, immune lines exhibited no disease. The maximum range of 5–9 was recorded on Morocco. Variation among the different lines with respect to AUDPC, falling under same category, was observed, and clearly showed the distinct behavior of tested materials as they proceeded to adult stage. This study provides a basis for identifying sources of resistance to *Alternaria* blight in wheat. Immune and resistant germplasm also were evaluated for resistance to leaf and stripe rust after artificial inoculation in separate experiments. Combining these disease and yield data, selected lines will be evaluated in yield trials and a disease screening nursery under artificial inoculation conditions. We will use the identified resistant cultivars and advanced lines in our breeding program depending on their stability in yield and performance.

Table 3. Comparison of resistant and susceptible NIAB hybrids wheat lines and cultivars on the basis of mean severity of disease, mean range, area under the disease progress curve (AUDPC), and host response for *Alternaria* blight (I = immune, R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible).

#	Entry	Origin/Source	Disease severity	Mean range	AUDPC	Host response
1	NW-1-20	NIAB advanced line	2	0–4	22.5	R
2	NW-3-2	NIAB advanced line	5	1–6	64.0	MS
3	NW-10-19	NIAB advanced line	3	1–2	41.5	R
4	NW-31-2	NIAB advanced line	2	0–4	22.2	R
5	NW-1-47-4	NIAB advanced line	0	0	0.0	I
6	NW-1-27-3	NIAB advanced line	1	0–2	11.4	R
7	NW-10-32	NIAB advanced line	0	0	0.0	I
8	NW-1-9-47	NIAB advanced line	5	2–7	33.5	MS
9	NW-10-1111-37	NIAB advanced line	4	2–8	57.0	MR
10	NW-3-3341-7	NIAB advanced line	3	1–4	42.6	R
11	NW-10-1111-5	NIAB advanced line	3	0–5	33.5	R
12	NW-10-1111-3	NIAB advanced line	7	3–9	82.5	S
13	NW-5-1212-1	NIAB advanced line	7	5–8	77.9	S
14	NW-1-8183-8	NIAB advanced line	5	2–6	64.5	MS
15	NW-10-1111-7	NIAB advanced line	4	0–6	70.1	MR
16	NW-5-20-1	NIAB advanced line	3	1–5	14.8	R
17	NIA-Amber	NIA, Tandojam (2010)	4	0–6	22.5	MR
18	NIA-Sunhari	NIA, Tandojam (2010)	0	0	0.0	I
19	NIA-Sundar	NIA, Tandojam (2011)	1	0–3	28.5	R
20	Benazir-12	NIA, Tandojam	4	2–6	44.2	MR
21	Tatara	NIFA, Peshawar	3	1–4	25.5	R
22	Takbeer	NIFA, Peshawar	3	0–4	32.5	R
23	Lalma	NIFA, Peshawar	6	2–8	58.5	MS
24	Galaxy-2013	WRI, AARI, Faisalabad	2	0–5	11.5	R
25	Punjab-2011	WRI, AARI, Faisalabad	4	1–5	40.1	MR
26	Lasani-2008	WRI, AARI, Faisalabad	2	1–4	41.5	R
27	Faisalabad-2008	WRI, AARI, Faisalabad	0	0	0.0	I
28	Sehar-2006	WRI, AARI, Faisalabad	5	4–9	64.2	MS
29	Inqulab-91	WRI, AARI, Faisalabad	6	3–8	78.4	MS
30	Morocco	Control	8	5–9	98.9	S

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Grass endospermal nuclei are selected by means of apoptosis.

R. Kosina.

Studies on early developmental stages of the endosperm in Triticale and its parental species proved that in the coenocyte stage some nuclei are necrotic (Kaltiskes et al. 1975). Surprisingly, the highest frequency of necrotic nuclei (62 %) has been detected not in a hybrid, but in a common wheat cultivar Kharkov. In an addition line with a 3R chromosome from rye, the frequency of the necrotic nuclei reached 39 % (Kaltsikes and Roupakias 1975). Other data shows that pycnotic nuclei amounted to 67% in Triticale (Orlova 1989). Nowadays, these nuclei, previously called necrotic or pycnotic with a highly condensed chromatin, would be described as apoptotic. Evidently, the useless antipodal nuclei undergo apoptosis in Triticale (Wędzony 1995). Wędzony also detected some endosperm regions in Triticale caryopses as defected. In common wheat, degradation of nuclei in synergids and antipodals differ and are described as pycnosis and chromatolysis, respectively (An and You 2004). In the endosperm of an '*Avena barbata*/*A. sativa*' amphiploid, Kosina and Tomaszewska (2011) observed fragmentation of nuclei. Programmed cell death (PCD) occurring in an old starchy endosperm (Young and Gallie 2000) is a different process from that in a free-nuclear stage. The process of apoptosis, or in plants more properly called PCD, in the endosperm of plants of hybrid origin seems to be under a genome-specific control (Kosina and Tomaszewska 2013). When a nucleus approaches PCD, chromatins in genomes of various parental origins are differently condensed. Thus, programmed cell death is an important phenomenon directing the development of endosperm (Becraft 2001). Our data was obtained from the microscopic observations of free-nuclear endosperm in a broad set of grasses, including many species of the Triticeae tribe. The free-nuclear endosperm was isolated from young embryo sacs and mounted in the 1% water solution of acridine orange. This method allows observing the endosperm *in vivo* and differentiates the staining of a native DNA (green) against RNA (red).

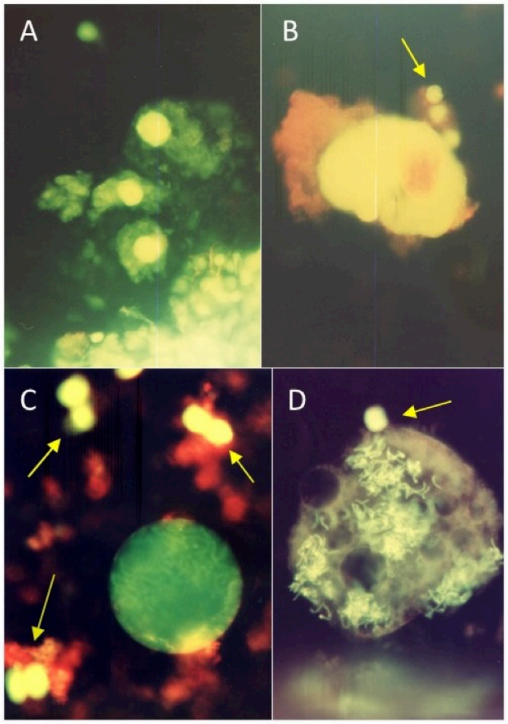

Fig. 1. Apoptotic stadia in a free-nuclear endosperm in some members of the Triticeae tribe. A – apoptotic antipodals in *Elymus hystrix*; B – an apoptotic nucleus in *Elymus glaucus*; three apoptotic nuclei being at the lower level of ploidy are shown by an arrow; C – an antipodal prophase nucleus with green chromosomes in *Lophopyrum elongatum* increases its volume in a hypotonic solution of acridine orange; apoptotic nuclei are marked by arrows; D – the five-polar anaphase in an antipodal cell in an '*Triticum orientale*/*Aegilops tauschii*' amphiploid; a small apoptotic nucleus is adjacent to the antipodal.

In many grasses, highly condensed nuclei were found in antipodals. Antipodals were most often documented as a group of cells at the same stage of the cell cycle. In *Elymus hystrix* L., antipodal nuclei are highly condensed and located in green cytoplasms (Fig. 1A). A similar status of antipodal chromatin is presented for *E. glaucus* Buckley (Fig. 1B); however, a nucleolus is still preserved in a giant nucleus. Three endospermal nuclei with highly condensed chromatin are indicated by an arrow. Cytoplasm also is degraded and fluoresces

red. The nuclei in endosperm can be degraded before condensation of chromatin in antipodal cells.

In *Lophopyrum elongatum* (Host) Á. Löve, such nuclei were observed together with a huge antipodal nucleus with green chromosomes (Fig. 1C, p. 46). In a *Triticum*/*Aegilops* amphiploid, chromosomes of the antipodal nucleus being at the stage of metaphase-anaphase are divided into five, cytogenetically unstable groups (Fig. 1D, p. 46). This example is evidence that unequal (multipolar) mitoses of antipodal or triploid endosperm nuclei provide defected units, subsequently undergoing apoptosis. Near this abnormal antipodal cell, a small apoptotic nucleus is indicated by an arrow.

During the early stages of endosperm development, some regions of embryo sac are degraded (condensed nuclei in a red cytoplasm) and some are mitotically active (Fig. 2). In *Secale sylvestre* Host., an apoptotic part is adjacent to a group of nuclei synchronized in the Rabl prophase (Fig. 2A). Highly condensed nuclei embedded in a red, degraded cytoplasm are close to the interphase nuclei with distinct nucleoli in *Aegilops juvenalis* (Thell.) Eig (Fig. 2B). A group of numerous nuclei in *Elytrigia repens* (L.) Desv. ex Nevski is composed of many nuclei in prophase (red arrows in Fig. 2C) or in interphase, one antipodal polyploid cell in metaphase and some apoptized nuclei marked by green arrows (Fig. 2D).

Our results prove that some regions of grass endosperm are defected, probably due to abnormal (multipolar) mitoses, and nuclei located there are eliminated by PCD. The fate of sister nuclei within the group is the same, PCD or activity in further mitoses, or cell cycles.

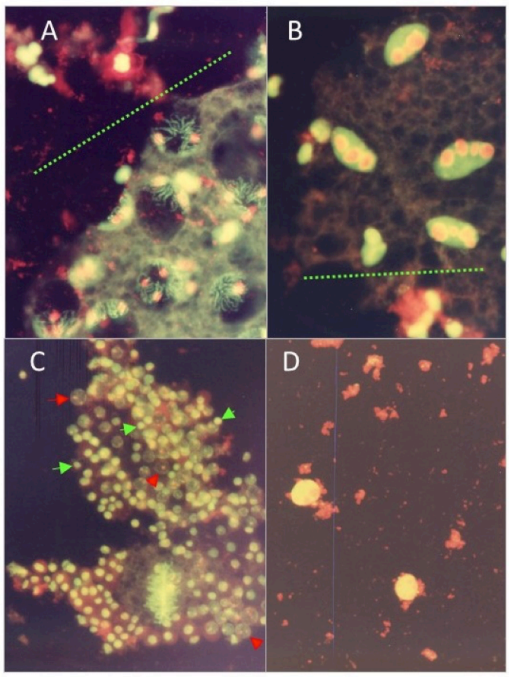

Fig. 2. Apoptotic stadia in a free-nuclear endosperm in some members of the Triticeae tribe. A – two sets of nuclei, apoptotic (above the dotted line)) and in the Rabl prophase in *Secale sylvestre*; B – interphase nuclei and below the dotted line apoptotic ones in *Aegilops juvenalis*; C– prophase (red arrows) and apoptotic nuclei (green arrows) and an antipodal cell in metaphase in *Elytrigia repens*; D – two endospermal apoptotic nuclei in *E. repens*.

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Variation for winter hardiness in Brachypodium distachyon (L.) Beauv. (3).

R. Kosina.

Comparative data on plant reaction to different environmental stresses proved that resistance to various stimuli can be correlated. Winter survival and heat resistance were correlated in oat varieties. Resistances to ice encasement, low temperature flooding, and freezing were positively correlated (r = 0.72 to 0.75) in strains of winter wheat (Hoffmann and Parsons 1991). In a pool of different accessions of *B. distachyon*, almost 50% appeared to be winter forms (Schwartz et al. 2010). Many these forms were diploid and collected in Turkey. Colton-Gagnon et al. (2014) did not detect broad genetic variation in winter hardiness among diploid forms of *B. distachyon*, despite earlier classification as spring or winter. A group of accessions expressed a facultative growth habit. Li et al. (2012) found that the genetic background of low temperature response in *B. distachyon* is different from that in the Triticeae cereals. Because *B. distachyon* is considered as a model grass for cereals, these differences justify further studies, especially for winter hardiness, vernalization, and weedy potential.

This report is a continuation of earlier data provided by Kosina and Tomaszewska (2014) and Kosina (2015). To recognize winterhardy forms in our grass collection, 26 accessions of various geographical origin (Italy, Iran, Pakistan, Turkey, Morocco, Spain, Greece, Bulgaria, Afghanistan, France, Iraq, Portugal, and Australia) and their 26 homozygous selections were sown in September 2015. All accessions germinated after one week. The temperature diagram (Fig. 3) shows that the first night frosts occurred at the beginning of October and simultaneously the maximum day temperature exceeded 20°C (green versus red arrows; Fig. 3). Frosts around –5°C were recorded in November, but temperatures above 0°C prevailed in November and December. Fluctuations of temperature near the end of 2015 did not stimulate plants to get frost resistance metabolically. Severe frosts occurred in January 2016, and most of the plants died thereafter. Only some accessions and their selections from Pakistan, Turkey, Spain, Bulgaria, and Iraq appeared to be frost resistant. Overwintered seedlings started to head around 12 May, 2016. The habit of the overwintered plants was very different (Figs. 4 and 5). Only two dwarf plants from accession PAK2B from Pakistan overwintered (Fig. 4A). Similar dwarfs were observed in accession ESP2 (Spain, Fig. 4B). This dwarfism was maintained up to maturity (Figs. 5A and B, p. 49). A selection (BGR2s) from accession BGR2 (Bulgaria, Fig. 4C) appeared to be a winter form, in which heading and ripening was about three weeks later than that for the other overwintered types. After overwintering, accessions from Turkey and Iraq developed similar habits to that in the same accessions cultivated in 2014 as spring forms (Figs. 5C and D, p. 49). Field experiments will be continued to identify that nature of dwarfing in frost-selected types from Pakistan and Spain.

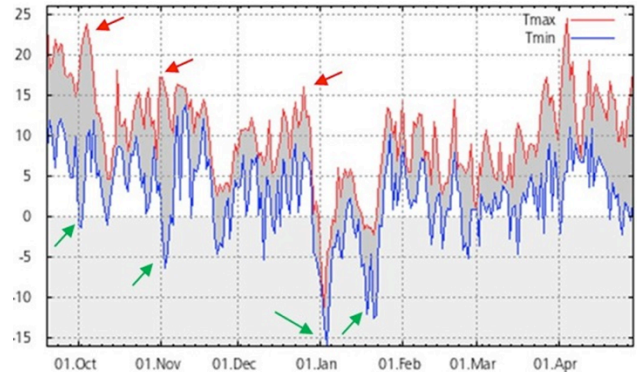

Fig. 3. Minimum (Tmin) and maximum (Tmax) temperatures during the autumn–winter–spring 2015–16 in the area of *Brachypodium distachyon* cultivation. Arrows point to some extreme temperatures (according to weatheronline.pl).

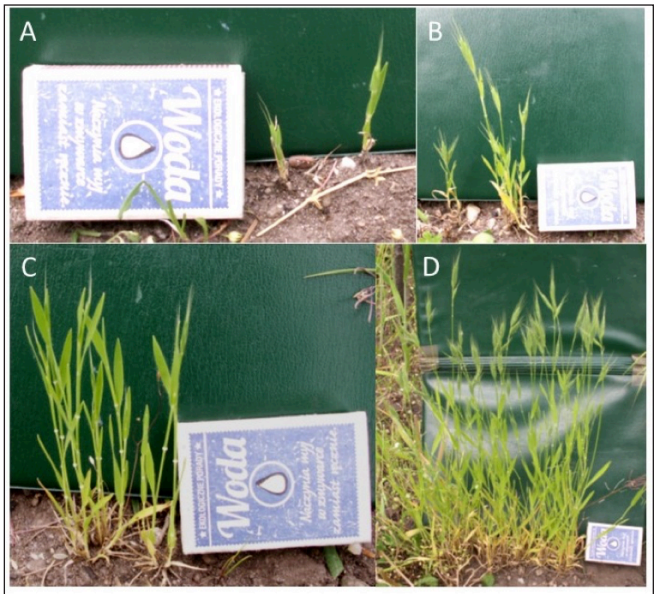

Fig. 4. Habit of overwintered forms of *Brachypodium distachyon* before and at heading stage: A – two dwarf plants from accession PAK2B (Pakistan); B – dwarf plants from accession ESP2 (Spain); C – plants from the selection BGR2s (Bulgaria) before heading; D – plants from the accession IRQ (Iraq) at late heading (a matchbox is shown for size comparison).

Considering the invasive status of *B. distachyon* in California, Bakker et al. (2009) pointed to its narrow genetic variation there. Mild winters (see Fig. 3 and Kosina 2015) in southwestern Poland and elsewhere allow Mediterranean species to invade northern regions. Such a

situation can be possible due to natural selection of a few frost-resistant plants in *B. distachyon*.

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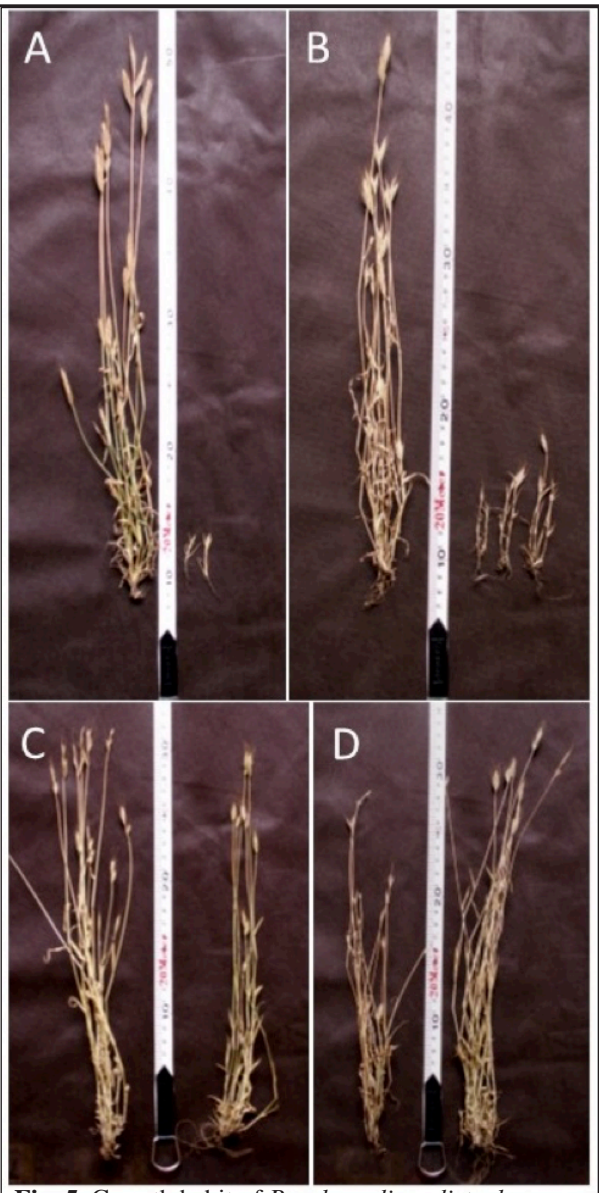

Fig. 5. Growth habit of *Brachypodium distachyon* plants cultivated as spring types and harvested in 2014 (to the left of the measuring tape) compared with plants overwintered during 2015–16 and harvested in June/July 2016 (to the right of the tape): A – accession PAK2B (Pakistan); B – accession ESP2 (Spain); C – accession TUR2 (Turkey); and D – accession IRQ (Iraq).

Variability of cell phenotypes expressed in the grass aleurone layer.

R. Kosina, M. Florek, A. Koźlik, M. Świetlikowska, P. Tomaszewska, and D. Zając.

Becraft and Asuncion-Crabb (2000) discovered that the starchy and aleurone endosperm are of common lineage origin in maize. The fate of the aleurone is determined by the position of aleurone cells within the tissue. Development of the aleurone layer is under the control of the *dek1* gene. Defects in *dek1* cause starchy cells to develop in the aleurone layer. However, a single aleurone cell has been found within the starchy endosperm of *Brachypodium distachyon* (Kamińska 2013). The position of this cell is different from those commonly observed in the aleurone layer. Thus, expression of the aleurone phenotype also can be triggered by stimuli other than the cell position.

Programmed cell death (PCD) is a common process that occurs during endosperm development (Becraft 2001). PCD can distinctly modify the final status of the aleurone layer. The disappearance of the already differentiated aleurone cells by means of PCD was previously noted in a '*Triticum turgidum* subsp. *dicoccum*/*Aegilops tauschii*' amphiploid, where starchy cells situated in the aleurone layer (Kosina et al. 2015). Thus, a type of 'aleurone-starch' mosaic may be caused by a *dek1* gene mutation or PCD of aleurone cells.

Becraft (2001) pointed to positional effects, cell cycle changes, genomic imprinting, and PCD as important events that modify the endosperm development. An example of a cell cycle change in the aleurone layer is found in Triticale. Normal aleurone cells are seen adjacent to both small and large (Fig. 6A; arrows). These two groups differ by at least two subsequent cytokineses (short versus long cell cycle). No expression of the aleurone phenotype is seen in a '*Triticum*/*Aegilops*' amphiploid (Fig. 6B). A large, single starch cell is developed within the aleurone layer. Tge size of this cell is evidence of a higher ploidy level and cytokinetic dysfunction. Aleurone cells also can be differentiated by the development of large vacuoles (Fig. 6C) and/or distinct globoids (Fig. 6D). The vacuolated cells develop in the form of large spots within the aleurone layer, whereas 'globoid cells' form smaller spots indicating their clonal origin (Kosina and Zając 2010).

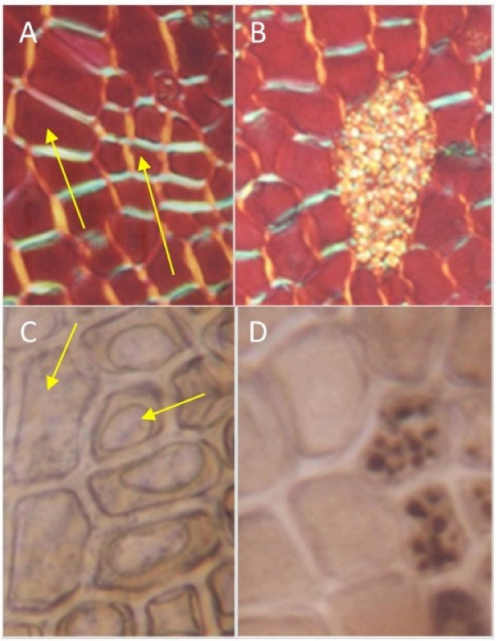

Fig. 6. Various aleurone cell phenotypes in a tangential view. A – cells of long (left arrow) and short cell cycle (right arrow) in Triticale; B – no expression of aleurone phenotype in a polyploid starch cell in a '*Triticum turgidum* subsp. *dococcoides*/*Aegilops tauschii*' amphiploid; C – nonvacuolated (left arrow) and vacuolated (right arrow) aleurone cells in *Leymus arenarius* (L.) Hochst.; and D – aleurone cells with large globoids (dark spots) in aleurone grains in a '*Triticum timopheevii* subsp. *timopheevii*/*Aegilops longissima*' amphiploid.

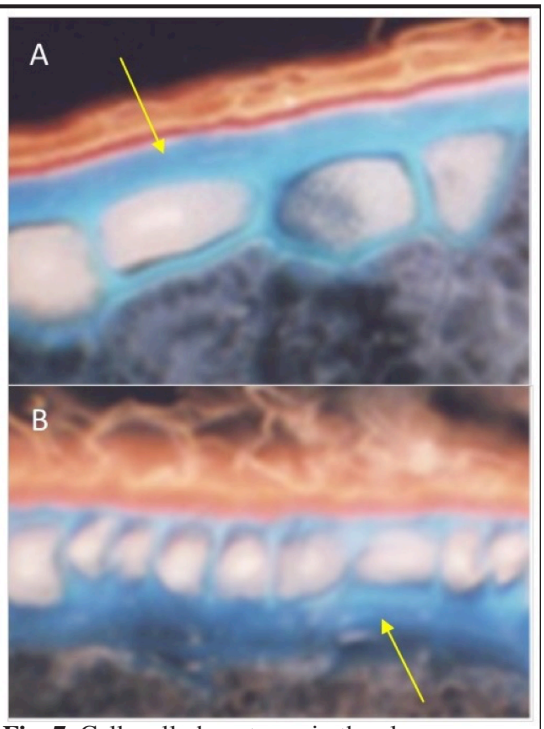

Fig. 7. Cell wall phenotypes in the aleurone layer (caryopsis cross-section). A – thick outer tangential walls in a '*Triticum timopheevii* subsp. *timopheevii*/*Aegilops umbellulata*' amphiploid. An arrow indicates the outer tangential cell wall adjacent to remnants of nucellar epidermis (both components exhibit a blue fluorescence of cell wall polysaccharides). B – thick inner tangential cell walls in *Leymus racemosus* (Lam.) Tzvelev.

Another phenotypic change in the aleurone layer is related to synthesis of cell wall polysaccharides (Fig. 7A and B). Most often cellulose and hemicelluloses are synthesized in the cell walls, but intensity of this synthesis is different. Two variants of cell wall synthesis are in the outer tangential wall (Fig. 7A) versus the inner tangential wall (Fig. 7B). Dif-

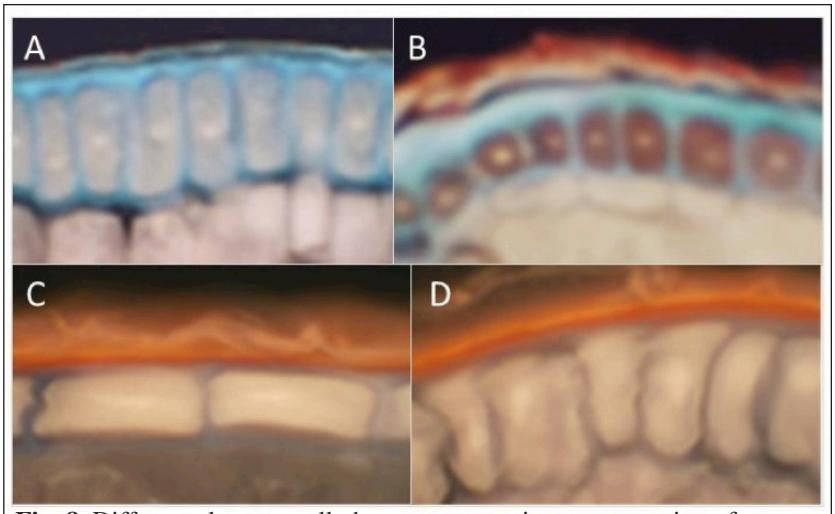

Fig. 8. Different aleurone cell phenotypes seen in a cross-section of caryopses. A – a phenotype of light protein in the aleurone cells in *Avena magna* Murphy et Torrell; B – a phenotype of dark protein in the aleurone cells in *A. magna*; C – a phenotype of dominant tangential growth of the aleurone cells in a '*Triticum timopheevii* subsp. *timopheevii*/*Aegilops umbellulata*' amphiploid; and D – a phenotype of dominant anticlinal growth of the aleurone cells in a '*T. timopheevii* subsp. *timopheevii*/*A. umbellulata*' amphiploid.

ferent storage metabolism in the aleurone protoplast forms various 'protoplast' phenotypes (Fig. 8A and B, p. 50). In both cases, the aleurone proteins are different, maybe with respect to globoids synthesis (such as in Fig. 6D, p. 50). Such different phenotypes were found in a single fruit. Two phenotypes of the cell wall growth were detected (Fig. 8C and D, p. 50). They can be visualized by a dominance of tangential wall growth, 'tangential phenotype' (Fig. 8C, p. 50) or a dominance of anticlinal wall growth, 'anticlinal phenotype'(Fig. 8D, p. 50). Both phenotypes can be detected in a single caryopsis. 'Thick anticlinal cell wall phenotypes' are presented (Fig. 9A and B) in an *Avena* amphiploid. The cell wall polysaccharides are synthesized mostly, but not always, in an anticlinal position, as was shown by Kosina et al. (2014). All walls of the aleurone cell can be thickened; large, polyploid cells, which vary each other in the diameter of aleurone grains (Fig. 9A and B). In both cells, assimilates are stored in the form of aleurone proteins and hemicelluloses in thick cell walls. An empty thick wall aleurone cell also was observed, and this phenotype has been called 'a-aleurone' (Florek and Kosina, unpbl.). The last type of the aleurone cell phenotype is a product of multidirectional cytokineses (Fig. 9C and D). The aleurone cells behave like callus, and cell walls are formed in various directions (Fig. 9C). The cells can be of very irregular shapes (Fig. 9D). Similar behavior was observed when external pressure was active against the aleurone layer, but this stimulus mostly induces the setting of periclinal walls (Kosina 2015). Irregular cell shapes are expressed in the wheat ventral aleurone layer, where the cells were described as amitotic (Morrison et al. 1978), however, data related to the creation of cell clones in the endosperm of *Thinopyrum distichum* proved that cytokineses in the ventral region are present, but less frequent (Kosina 2012). The aleurone mutants *dil1* and *dil2* discovered in maize are additional examples of multidirectional cytokineses (Lid et al. 2004). Thus, the creation of these aleurone phenotypes depends on the synthesis of storage products (aleurone protein, globoids, hemicelluloses, and vacuolization), rate and direction of cytokineses, length of the cell cycle, direction of growth of cell wall, and level of cell polyploidy.

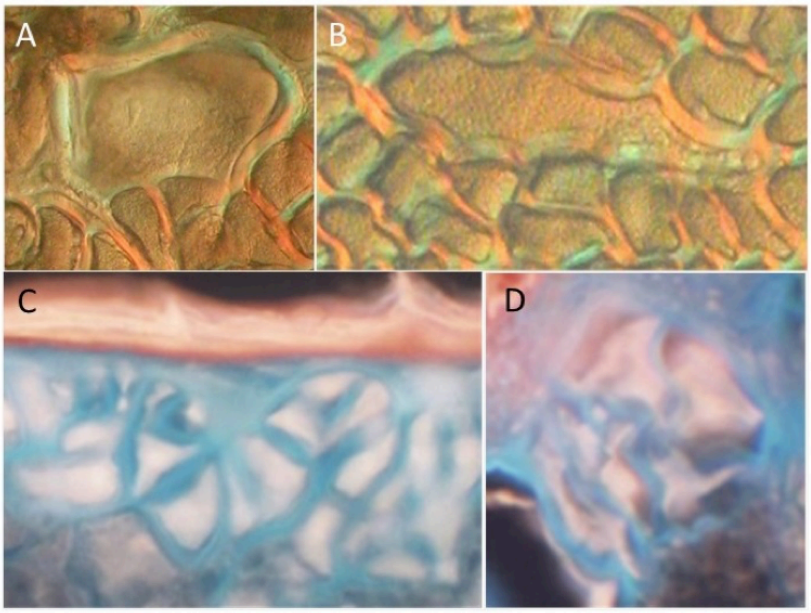

Fig. 9. Phenotypes of aleurone cells in a tangential view (A and B) and in a cross-section of the caryopsis (C and D). A and B – a phenotype of thick hemicellulosic anticlinal walls in polyploid aleurone cells in a '*Avena barbata*/*A. sativa* subsp. *nuda*' amphiploid; C – a phenotype of multidirectional cytokinesis and chaotic, callus-like growth of aleurone cells in a '*Triticum timopheevii* subsp. *timopheevii*/*Aegilops longissima*' amphiploid; and D – the same as in C in a '*Pseudoroegneria libanotica*/*Elymus yezoënsis*' amphiploid.

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ITEMS FROM ROMANIA

AGRICULTURAL RESEARCH & DEVELOPMENT STATION—S.C.D.A.
401100, Turda, Agriculturii street 27, Jud. Cluj, Romania.

CODRU – a new winter wheat cultivar.

Rozalia Kadar, V. Moldovan, I. Racz, and A. Ceclan.

Codru, a hard red winter wheat cultivar (*Triticum aestivum* L. subsp. *aestivum,* var. *erythrospermum*) developed by the Agricultural Research & Development Station of Turda, was released in 2015 because of its high yield performance associated with improved bread-making quality. Codru was selected from the cross 'Fundulea 4 / T56-95' using a pedigree selection method. The single cross between Fundulea 4 and T56-95 was made in 2000. The aim of this cross was obtaining descent recombinants with the superior yield potential of Fundulea 4 and with good quality from our breeding line T57-90. The individual selection began in the F_2 generation, following our breeding procedure presented previously (Ann Wheat Newslet 48:113-115). After some subsequent reselection, we obtained the line T136-03, which was advanced to the Official Yield Trials at the State Institute for Variety Testing and Registration (ISTIS) in the autumn of 2011. After three years of evaluation (2012–14) in seven locations, the line T136-03 was registered under the name 'Codru', and released to growers due to its good yield performance and broad adaptation to Transilvania's environments as well as improved bread-making quality.

Codru is an awned, white-spiked, semidwarf wheat. Juvenile growth is semierect. The foliage is green at the boot growth stage. Plant height (75–90 cm) is similar to that of Fundulea 4 and shorter than that of T56-95. Spikes are awned and lax, with red glumes. Kernels are red, ovate, with a midsized germ; the kernel crease is midwide and mid-deep, with rounded cheeks. The kernel size is quite large; 1,000-kernel weight is 47 g on average and has a quite good test weight (volume weight) of 77 kg/hectoliter.

Codru is medium-early in maturity (265 days), similar to Ariesan. The winterhardiness of Codru is adequate for most Transilvanian growing conditions. The cultivar has excellent straw strength, which confers good lodging resistance. For diseases resistance, Codru is moderately resistant to yellow rust and powdery mildew, but is moderately susceptible to leaf rust. Codru also showed moderate resistance to Fusarium head blight.

Codru has shown good yield performance in most of Official test sites (ISTIS). Averaged across three years (2012–14) and seven locations (21 location-years) Codru realized 6,507 kg/ha, 7% above the check cultivar Dropia, but did not differ widely in grain yield from the highest-yielding entry in the trials. However, the average grain yield of Codru in 2012 was 6,225 kg/ha, 12% higher than that of Dropia. In 2013, Codru averaged 6,742 kg/ha over seven locations, exceeding the Dropia check by 14%. In 2014, the average grain yield of Codru was 6,555 kg/ha, 3% below that of the Dropia check. The maximum grain yield of Codru was 9,297 kg/ha, obtained at the Center for Testing Varieties (CTS), Sibiu, in 2014.

Codru meets domestic quality criteria for high-quality bread floor production. The quality characteristics of Codru are reflected by a grain protein content up to 14.3% associated with a gluten content of 26.1% and a 52.5 mL Zeleny sedimentation index. According to quality parameters, Codru can be classified as a B_2 quality wheat.

Breeder and foundation seed of Codru will be maintained by the Agricultural Research & Development Station Turda.

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.

Using of the gene pool of bread wheat wild relatives for production of collection of newly identified introgressive spring bread wheat lines resistant to the main pathogens.

S.N. Sibikeev and A.E. Druzhin; E.D. Badaeva (Institute of General Genetics, Gubkina St. 3, Moscow, Russian Federation); and A.S. Rouban (Russian State Agrarian University, Moscow Timiryazev Agricultural Academy, Timiryazevskaya St. 49, Moscow, Russian Federation).

Triticum turgidum subsp. dicoccum lines k10456, k12133, k13659, k19352, k19357, k21433, k40030, and k45926 were selected as resistant to leaf rust; k10456, k13659, and k19352 have an IT of 0 to the pathogen, and two others, k12133 and k40030, were heterogeneous with ITs = 0; and 3. In spring bread wheat lines with *Lr* genes from *T. aestivum* subsp. *compactum*, resistance to leaf rust is inherited by two recessive genes, whereas in hybrids between Saratov-bred wheat cultivars, Saratovskaya 70 and Saratovskaya 74, and the triticale cultivar Satu, the resistance is inherited in a monogenic recessive manner. In lines of spring bread wheat with the *Lr* genes from *T. turgidum* subsp. *durum* var. *melanopus*, *T. dicoccum* cv. Vernal emmer, *T. turdigum* subsp. *dicoccoides* k46216 and k7507, *T. timopheevii*, and *T. aestivum* subsp. *presicum,* we identified dominant-monogenic control of resistance to leaf rust. These conclusions were based on the analysis of the segregation in F_2 and F_3 hybrid populations for resistance to leaf rust, as well as analyzing crosses. In the set of spring bread wheat lines, 'Saratovskaya 68 / *Aegilops biuncialis* (k2511)' and 'Saratovskaya 70 / *Ae. biuncialis* (k2511)' we identified the substitutions 3D (3Ae1) and 3D (3Ae2L) that have an IT of 0; and 2, respectively. Chromosomal instability was observed in both lines. In the set of spring bread wheat lines from crosses of Saratovskaya 68, L503, and Dobrynya with *Ae. columnaris* k1193, we identified three *Ae. columnaris* chromosomes, 3Ae2, 5Ae2, and 6Ae2, that control resistance to leaf rust. Furthermore, spring bread wheat lines resistant to leaf rust (IT=0;) carrying a combination of alien genes from *Thinopyrum intermedium* (6D(6Ag^{i})) and *Ae. speltoides* (2B (2S^{s})) and a translocation from *S. cereale* (T1BL·1RS) were detected.

Evaluating spring bread wheat introgression lines of the Genetics and Cytology Laboratory ARISER under drought conditions in 2015.

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

The conditions of the 2015 growing season led to a reliable estimate of abiotic stressors (drought) in introgression lines in the absence of leaf and stem rust epidemics. In 2015, the drought began at germination, continued until flowering and the start of grain filling, and was accompanied by high air temperatures (30°C and higher). Under these conditions, the grain yield of near-isogenic introgression lines containing combinations of translocations (T7DS·7DL-7Ae? + ? (*Thinopyrum elongatum* k-1587)) and double substitutions (3B (3Age) + 3D (3Age) (*Th. elongatum* k-1587)) significantly exceeded the recipient cultivar. At the same time, a productivity level equal to the recipient cultivar was noted in the lines with a combination of translocations, including T7DS·7DL-7Ae#1L (*Th. elongatum*) + T3DS°3Dl-3Ae#1L (*Th. elongatum*), T7DS·7DL-7Ae#1L (*Th. elongatum*) + T2AL·2AS-2MV#1 (*Ae. ventricosa*.), T7DS·7DL-7Ae#1L (*Th. elongatum*) + T1BL·1R#1S (*S. cereale*), and T7DS·7DL-7Ae#1L (*Th. elongatum*) + T4BS·4BL-2R#1L (*S. cereale*), but significantly

reduced grain yield was observed in the line with T7DS·7DL-7Ae#1L (*Th. elongatum*) + T6BS·6BL-6U#1L (*Ae. umbellulata*). In the introgression lines significantly exceeding the productivity of the recipient cultivar were lines with T2D·2S (*Ae. speltoides*) and the combination T2D·2S and T7DS·7DL-7Ae#1L.

Among lines obtained from crosses of CIMMYT synthetics and Saratov-breed cultivars, three lines significantly exceeded the grain yield of the cultivar Favorit. Two have alien substitutions, '6D (6Agi (*Th. intermedium*)) / synthetic Altar 84 / *Ae. tauschii* (224)', and third line is 'T7DS·7DL-7Ae#1L (*Th. elongatum*) / synthetic CROC / *Ae. tauschii* (224)', with grain yields of 2,973, 3,074, and 2,991 kg/ha, respectively, compared to 2,535 kg/ha for Favorit. The highest grain yield among the cultivars, introgression, and perspective spring bread wheat lines were three lines carrying the substitution 6D (6Agi (*Th. intermedium*)), giving 3,318, 3,244, and 3,141 kg/ha. Interestingly, one of these lines (Saratovskaya Golden*3 // Favorit) carries the cytoplasm of the durum wheat cultivar Saratovskaya Golden. Anlyzing the bread making quality in 2014 revealed excellent alveograph evaluations of the lines with T7DS·7DL-7Ae#1L (*Th. elongatum*) + 4BS·4BL-2R#1L (*S. cereale*) and T7DS·7DL-7Ae#1L (*Th. elongatum*) + T2AL·2AS-2MV#1 (*Ae. ventricosa*.) and some lines from crosses of CIMMYT synthetics and Saratov-bred cultivars. These introgression lines have a high flour strength (307–386) and bread volume (840–860 mm^3).

The drought conditions in 2015 did not allow us to evaluate the introgression lines for resistance to biostressors. However, the introgressive lines resistant to leaf rust (according evaluations in the 2014) and the drought resistance confirmed in 2015 recommends their use in breeding new bread wheat cultivars and, thereby, reducing significant yield losses from abiotic and biotic stresses.

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Protective effects of selenium and silicon under different durations of oxidative stress.

L.V. Osipova, I.V. Vernichenko, P.A. Yakovlev, and I.A. Bikovskaya.

Intensifying climate instability and increasing weather anomaly in recent years have resulted in redeucing plant metabolism and performance. Studies of plant response to the stresses that arise during the growing season are necessary in order to develop measures that reduce their negative impact.

An analysis of the current state of the problems connected with sustaining and implementing the adaptive capacity of plants indicates that there is a general reaction mechanism against stress that decreases energy costs for the establishment of specialized adaptation. One of the early impacts of stress on plants is the excessive accumulation of reactive oxygen intermediate (ROI) and oxidative stress development. Similar plant responses to various stress factors were detected in the studies dealing with soil drought, heat, and salinity. A primary, nonspecific plant reaction to the damaging effects of heavy metals, low temperature, UV radiation, herbicides, and flooding is ROI formation as well. Development of a common plant mechanism under various stresses conditions suggests that there is a single way to reduce the negative stress impact. Selenium and silicon are elements of the plant antioxidant system and are included in its different units. This fact became the basis for the study of selenium and silicon effects on spring wheat resistance to abiotic stresses impact.

The vegetative experiment was conducted in a sod-podzolic medium loamy soil culture with average macronutrient availability. The soil was limed to a full dose Ng. Selenium and silicon were used for a presowing seed treatment (PST). Experiments were according to Zhurbitskii (1968). Oxidative stress was modelled by ceasing irrigation at the VI organogenesis stage, which is critical in relation to water availability during the developmental period for generative organs.

Lada wheat was used to evaluate the effects of stresses of different duration; I, before the permanent wilting point (PWP) and II, 7 days after reaching the permanent wilting point. Plant performance and physiological status were evaluated by photosynthetic pigment content (chlorophyll a and b and carotenoids) and the reduction of malondialdehyde (MDA) content, indicating free radical processes in the plants. The MDA content, a product of lipid peroxidation, was determined by the thiobarbituric acid reaction.

The tracer test method was used to evaluate the protective effect of micronutrients. Nitrogen intake in wheat plants was determined both during the stress and repair process periods. Before and after the stress, labelled nitrogen, in the form of $Ca(^{15}NO_3)_2$ with 95AT% supplementation, was added to the vessel. After a short exposure time, plant samples were collected to assess the absorption capacity of the root system and assimilation of nitrogen (^{15}N) in vegetable protein. The samples were analyzed with a Delta Vadvantage isotope mass spectrometer.

We found that, at the early stages of organogenesis, in the transition from growth in the dark to growth in the light, abiotic stresses inhibit development, chlorophyll pigments form slower, and malondialdehyde content increases. Malondialdehyde is a product of membrane lipid peroxidation that damages membrane integrity and function. Under stress during the formation of generative organs, ww observed the reduction of flowering rudiments, a change of photosynthetic pigment content, malondialdehyde accumulation, and an inhibition of nitrate uptake in the roots and its incorporation with surface organ protein leading to a reductin in plant productivity (Table 1). The protective effects of selenium and silicon are due to a decrease in oxidative stress, pigment complex optimization that is a result of an increase in chlorophyll b and the carotenoids protecting the photosynthetic apparatus from free radical damage, maintaining the absorptive capacity of the root system during the stress period (Table 2), and activating nitrogen absorption for use in protein synthesis during the repair period (Table 1). Treated with micronutrients, plants are more resistant to possible stress, less injured, and better able to recover afterwards.

Table 1. Intensity of ^{15}N absorption by wheat plants during an increase in soil drought (mg/vessel over a 24-hour period).

Variant	Absorption period					
	Optimum			Drought I		Drought II
	0–1	1–4	4–11	0–1	1–4	4–11
H_2O	2.64	0.64	0.62	1.80	0.45	0.08
Se	3.40	1.30	0.39	2.70	1.08	0.09
Si	5.89	1.04	0.47	3.10	0.18	0.15

Table 2. Impact of selenium and silicon on ^{15}N absorption by plants during the repair process period after droughts of different duration and on spring wheat performance.

Variant	^{15}N absorption period (24 hr, mg/vessle)						Grain wieght (g/vessle)		
	Drought I			Drought II				Drought	
	1	6	9	1	6	9	Optimum	I	II
H_2O	0.55	5.95	6.35	0.24	3.23	3.85	0.95	0.50	0.34
Se	0.77	5.85	6.77	0.30	2.39	4.93	1.02	0.71	0.42
Si	0.77	5.88	6.24	0.62	4.89	5.62	1.00	0.64	0.46

The effectiveness of selenium and silicon is different and depends on the intensity of the stress. A prolonged, nonirrigated period reducess the protective effects of selenium, whereas those of silicon increase, which results in a change in the absorption rate of nitrate, its assimilation into proteins, and plant performance. In a record drought, the enzyme pool containing selenium may be inactivated, while the role of silicon in the antioxidant protection system increases under these conditions. Thus, application of selenium and silicon can be recommended for wheat seed pretreatment to enhance plant resistance and maintain performance.

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Endogenous formation of nitrates in wheat and the role of some stress factors and selenium.

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Abstract.
We present the results of previous studies obtained using ^{15}N-labelled substances under sterile conditions and experimental data proving the formation of endogenous nitrates in plants and the environmental impact. The physiological feasibility of the oxidation of reduced nitrogen compounds to nitrate and the role of nitrate in plant stress resistance are discussed. The increase in the fomation of endogenous nitrates in sterile wheat seedlings is shown. The effect of increased salt concentrations, some stress factors, and the ultra microelement selenium on the process was found.

Introduction. Pryanishnikov's (1945) classic research suggested the importance of nitrates, which are the main form and core plant food lessened to their in-between role as a nitrogen source. Recently, nitrates have been found to be more than subtracts and have broader irreplaceable physiological significance.

Until now there has been generally accepted opinion that ions NO_3^- are the only nitrate accumulation source for plants absorbed exogenously that is applied with fertilizers or formed by nitrification of nitrogen fertilizers and soil.

In previous studies with compounds labelled with the stable nitrogen isotope ^{15}N using nitrification inhibitors, under sterile conditions and in tissue culture experiments, nitrate formation from absorbed ^{15}N was recorded in the plants themselves (Vernichenko 1975, 1982, 2002; Vernichenko et al. 1976; Yagodyn et al. 1982, 1984, 1991).

The biological expediency of nitrate formation in plants appears to be due to several reasons. First, the nitrate form of nitrogen is needed in photosynthesis (Lipps 1997). Second, the nitrate form of nitrogen improves mitochondrial respiratory processes in plant cells, serving as an electron acceptor (Igamberdiev and Hill 2009; Vartapetyan et al. 2012). Third, NO_3^- ions possibly may signal the beginning of synthesis and functioning of a wide variety of enzymes of nitrogen, carbohydrate, and other plant metabolism types, particularly of the antioxidant enzyme group, which protects plants from the adverse effects of various stresses (Krapp et al. 2014; Vidal et al. 2015).

Delledonner et al. (1998), Wehdehenne and Hancook (2011), and Mur et al. (2013) proved evidence of a potential indirect influence of nitrate on increased plant tolerance to different stress factors through the synthesis of nitric oxide, another very important signaling molecule, which largely determines stress resistance of both animal and plant cells (Mamaeva et al. 2015).

Endogenous nitrate formation was suggested to be a necessity for plants caused by certain adverse environmental conditions due to their direct or sacrificial role as precursors for NO molecule synthesis. In addition, endogenous nitrate formation in plants also can be connected with the detoxification process of the increased number of nitric oxide molecules developed under unfavorable external conditions.

A lack of original NO_3^- in germinating plants (where the nitrate content is low) may initiate a variety of antistress responses of plant cells exposed to various adverse external factors. In this case, an increased accumulation of nitrates formed endogenously is likely. By using sterile seedlings in these studies, results from low initial nitrate content in seeds and the lack of nitrate in young plants during the first 7 days after germination (Oaks 1997) make it easier to detect nitrates formed endogenously.

Materials and Methods. Sterile sprouts frown in petri dishes were used in the studies. Wheat seeds were decontaminated and laboratory glassware and solutions were sterilized in order to prevent microbiological activity. Only whole-grain seeds were sampled for the experiment. Seeds were washed with running water and those that surfaced removed. The seeds were soaked in 96% ethanol for 5 min. and then in a 0.05% chlorhexidine solution for 20 minutes. After each soaking, the seeds were washed with sterile distilled water. Fifty seeds were put onto moist filter paper in each Petri dish. In

the selenium variant, the filter paper was moistened with a Na_2SeO_3solution. The petri dishes were covered and placed in an incubator at 20°C for 3 days. Seedlings obtained were moved aseptically into other environments to simulate stresses: a 3.8% saccharose solution (simulated drought) and 0.5% solutions of NaCl, NH_4Cl, Na_2SO_4 and $CdCl_2$ 300 mcm/ l. Distilled water was used as a control. Elevated temperature (37 °C) also was one of the stresses. Seedling exposure under stress conditions was 5 days. At the end of exposure time, nitrate content in seedlings was measured with a nitrate ion-selective membrane electrode 'Elite 021' on an ANION-4110 (pH meter– ionomer–conductometer) together with a silver chloride reference electrode. Nitrate extraction was in a 1% potash alum solution.

Discussion. Results of the research are presented (Table 1). The formation of endogenous nitrates in plant seedlings was confirmed. Nitrate content in germinated wheat increased from 4.5 μg/petri dish to 34 μg within 7 days. We found a different artificial stress effect on the amount of nitrate formed endogenously in 7-day-old wheat seedlings. Experiments with high salt concentrations showed that the greatest nitrate amount is from the oxidation of reduced nitrogen forms in plants. The maximum nitrate formed endogenously was found in the treatment with 0.5% NaCl solution. At the same time, simulated drought and Cd contamination slightly reduced the production of endogenous nitrate in wheat seedlings compared that of to control but, under these conditions, the nitrate content was significantly higher compared with the initial content of dry seed.

Table 1. Amount of nitrates in wheat seedlings after 7 days under different abiotic stress (* original nitrate content in seed was 4.5 μg/dish).

Treatment	NO_3^- content/Petri dish			NO_3^- amount formed endogenously/Petri dish		
	μg	% from initial content in seed*	% from check (without stress)	μg	% from initial content in seed*	% from check (without stress)
Check (without stress)	33.8	750	100	29.3	650	100
+ NH_4Cl	39.6	880	117	35.1	780	120
+ NaCl	51.3	1,140	152	46.8	1,040	160
+ Na_2SO_4	42.3	923	125	37.6	830	130
Drought (3.7% saccharose)	23.8	530	71	19.3	430	66
+ Cd	22.3	500	67	17.8	395	61
$HCP_{0.95}$	4.6	–	–	4.1	–	–

The effect of selenium (Table 2 p. 58) was evaluated as a factor that might increase plant resistance to adverse environmental conditions in the next set of sterile experiments (Hasanuzzaman et al. 2012; Vernichenko et al. 2015). The presence of endogenous nitrates also was found in wheat seedlings. A significant increase in the intensity of endogenous nitrate formation in treatments with NH_4Cl and NaCl are shown (Table 2). In experiments with Na_2SO_4, endogenous NO_3^- formation was not observed (Table 2). Simulated drought, elevated temperature, and Cd completely suppressed the formation of endogenous nitrate in the wheat seedlings. Apparently, these stresses influence the enzymatic systems involved in the oxidation of reduced nitrogen forms to nitrates. This problem requires further study.

The effect of selenium was different. Selenium addition promoted a 3-fold or more increase of endogenously formed nitrates. The effect of selenium effect on nitrate formation in wheat seedlings may be explained by the fact that, without other stress conditions, selenium becomes a stress for young plants even at low concentrations. A similar effect of elevated selenium concentration on the formation of endogenous nitrogen oxide in plants is closely related to nitrate metabolism was recently found by Chen et al. (2014). At the same time, under salt stress from increased NH_4Cl and, particularly, NaCl content, application of selenium significantly reduced endogenous nitrate formation, perhaps due to the sacrificial role of trace elements. Thus, NH_4Cl endogenous nitrate formation on addition of selenium decreased by 35%, but an excess of NaCl reduced the process by 4-fold.

Conclusion. Our data once again highlight the sacrificial role of selenium in adverse environmental conditions. However, explanating the mechanism of impact of various stresses on the intensity of endogenous nitrate and/or nitrogen oxide formation in plants, and the anti-stress effect of selenium, will require further in-depth consideration.

Table 2. The amount of nitrates in wheat seedlings after 7 days under different abiotic stresses on addition of selenium 9 (* original nitrate content in seed was 4.5 μg/dish).

Treatment	Se application	NO_3^- content/Petri dish		NO_3^- formed endogenously/Petri dish		
		μg	% from check	μg	% from original*	% from check
Check (without stress)	–	11.1	100	6.6	150	100
	+	25.1	225	20.6	460	310
+ NH_4Cl	–	14,9	135	10.4	230	160
	+	11.5	105	7.0	155	105
+ NaCl	–	51.9	470	47.4	1050	720
	+	16.1	145	11.6	260	175
+ Na_2SO_4	–	11.1	100	6.6	150	100
	+	7.1	65	2.6	50	40
drought (3.8% saccharose)	–	4.5	40	–	–	–
	+	4.6	41	–	–	–
+ Cd	–	3.3	30	–	–	–
	+	3.5	32	–	–	–
elevated temperature (37°C)	–	6.6	60	2.1	47	32
	+	4.6	41	0.1	2	2
$HCP_{0.95}$		2.3		1.6		

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ITEMS FROM UKRAINE

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Presowing seed treatment of winter bread wheat for protection against root rots.

N.V. Kuzmenko and A.Ye. Litvinov.

Root rots are one of the least visible, but more harmful, diseases. They damage primary and secondary roots and the base of the stalk. As a result, plants can die during sprouting; while producing shoots, tubers, and flowering; and spike-bearing production (Peresypkin 1979). In the chemical protection of winter wheat, especially at the first stages of organogenesis, a presowing seed treatment is ecologically safe for the environment, technologically easy, and economically profitable. Our investigation studied the phytosanitary role of chemical seed treatment of winter wheat with systemic and contact rungicides for reducing disease loss to the root rots and increasing grain yield.

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 2012–14. The soil was a typical medium-humus black earth soil on loess with up to 5.4% humus in the plowing layer. Black fallow and dried peas were used as forecrops of winter bread wheat. Winter wheat was sown during at an optimal time (12–29 September). The sowing rate of winter wheat on black fallow was 4.0 x 10^6 viable seeds/ha and 5.0 10^6 viable seeds/hectare after dried peas. 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 applies by root feeding during the spring tillering stage and by root feeding at flowering. Agrotechniques were in general use. Wheat seeds were pretreating prior to sowing with systemic and contact fungicides. The intensity of root rot development was studied using conventional methods (Omelyuta 1986).

The experiment included the following treatments

– Control (without protection or fertilizers).
– Vitavaks 200 FF (standard) (active agents: karboksin (200 g/l) + tyram (200 g/l) – 3.0 l/t,
– Rankona 15 (active agent: ipkonazol (15 g/l) – 1.0 l/t,
– Kinto Duo (active agents: trytikonazol (20 g/l) + prochloraz (60 g/l) – 2.5 l/t,
– Maksym Forte 050 FS (active agents: azoksystrobin (10 g/l) + tebukonazol (15 g/l) + fludioksonil (25 g/l) – 2.0 l/t,
– Inshur Perform FS (active agents: trytikonazol (80 g/l + pyraclostrobin (40 g/l) – 0.5 l/t,
– Selest Top 312,5 FS (active agents: dyfenokonazol (25 g/l) + fludioksonil (25 g/l); and insecticide active agent tiametoksum (262.5 g/l) – 1.25 l/t, and

– Yunta Kvadro 373.4 FS (active agents: protiokonazol (33.3 g/l) + tebukonazol (6.7 g/l); insecticide active agents: imidaklopryd (166.7 g/l) + klotianidyn (166.7 g/l) – 1.6 l/t.

Results. Averaged over the years (2012–14), the field germination capacity of plants in the Control (without protection and fertilizer) was 79% (Table 1). Fungicides reduced this index from 75% (Kinto Duo) to 65% (Yunta Kvadro 373.4 FS). Chemical treatment of winter wheat seed with fungicides and application of organic/mineral fertilizer contributed to a 26% increase (Inshur Perform FS) in total tillering during the spring tillering stage and up to a 44% increase (Vitavaks 200 FF). The number of tillers/m^2 in treatements with a chemical pretreatment during the spring tillering stage was greater by 15–29% than that of the control (1,080 tillers/m^2). The number of tillers/m^2 with the Maksym Forte 050 FS chemical treatment was 1,150, practically equal to that of the control treatment. Productive tillering at wax ripeness stage in the control was 1.7, whereas it was 23–29% greater in variants with chemical treatments and fertilizer applications. The number of productive spike-bearing stems/m^2 in the chemical treatments ranged between 540 (Yunta Kvadro 373.4 FS) and 620 (Vitavaks 200 FF), whereas the control had 500 spike-bearing stems.

Table 1. Tillering ability and stem density of winter bread wheat depending on presowing seed treatment, averaged over the years 2012–14. The control treatment is without fungicide protection or fertilizer.

Treatment	Field germination	At spring tillering stage		At wax ripeness stage	
		Total tillering	Number of tillers/m^2	Productive tillering	number of productive spike-bearing stems/m^2
Control	79	3.4	1,080	1.7	500
Vitavaks 200 FF (standard)	69	6.1	1,310	2.4	620
Rankona 15	69	4.8	1,350	2.4	600
Kinto Duo	75	5.4	1,330	2.2	580
Maksym Forte 050 FS	69	4.7	1,150	2.3	580
Inshur Perform FS	73	4.6	1,270	2.4	580
Selest Top 312.5 FS	72	4.9	1,520	2.2	580
Yunta Kvadro 373.4 FS	65	5.4	1,400	2.2	540
LSD 05	5.5	1.0	260	0.6	130

The intensity of root rot development (*Helminthosporium–Fusarium*) at spring tillering stage varied during the study. In 2012 and 2014, disease development was 1.7% and 6.7 %, respectively, and 4.2% and 15.2%, respectively, for percent diseased plants, in the control. In 2013, disease development was 19.9% and spread was 48.7%, exceeding the economic threshold of harmfulness by 1.3 times (the economic threshold of harmfulness = 10–15%) (Table 2). On average, over the three years, disease spread and development were 22.7% and 9.4%, respectively. Under meteorological and phytosanitary conditions during the study, pretreating seed with fungicides did not always protect the wheat plants against root rots. In 2012, in the Kinto Duo, Inshur Perform FS, Maksym Forte 050 FS, and Yunta Kvadro 373.4 FS treatments, the degree of root rot development was low, ranging between 0.0–0.4%. In 2012, all fungicides reduced

Table 2. The development of root rots at spring tillering stage of winter bread wheat depending on presowing seed treatment. The control treatment is without fungicide protection or fertilizer.

Treatment	Spread (%)				Development (%)				Technical effectiveness (%)			
	2012	2013	2014	2012–14 average	2012	2013	2014	2012–14 average	2012	2013	2014	2012–14 average
Control	4.2	48.7	15.2	22.7	1.7	19.9	6.7	9.4	—	—	—	—
Vitavaks 200 FF (standard)	4.8	14.6	22.8	14.1	1.8	6.0	8.0	5.3	0.0	69.8	0.0	23.3
Rankona 15	5.6	21.0	16.4	14.3	2.1	8.0	5.4	5.2	0.0	59.8	19.4	26.4
Kinto Duo	0.0	2.7	10.7	4.5	0.0	0.9	3.2	1.4	100.0	95.5	52.2	82.6
Maksym Forte 050 FS	0.6	6.7	10.1	5.8	0.3	2.6	2.8	1.9	82.3	86.9	58.2	75.8
Inshur Perform	0.0	19.8	15.0	11.6	0.0	8.4	5.1	4.5	100.0	57.8	23.9	60.6
Selest Top 312.5 FS	4.2	19.5	6.6	10.1	1.7	8.1	2.1	4.0	0.0	59.3	68.7	42.7
Yunta Kvadro	0.8	11.3	1.0	4.4	0.4	4.1	0.3	1.6	76.5	79.4	95.5	83.8
LSD 05					2.8	6.4	5.8					

the intensity of disease from 57% (Inshur Perform FS) to 95% (Kinto Duo). In 2014, the efficiency of the fungicides was Yunta Kvadro 373.4 FS (95.5%), Selest Top 312.5 FS (68.7%), Maksym Forte 050 FS (58.2%), Kinto Duo (52.2%), Inshur Perform FS (23.9%), Rankona 15 (19.4%), and Vitavaks 200 FF (0.0%). Averaged over the years 2012–14, systemic fungicides Yunta Kvadro 373.4 FS (83.8%), Kinto Duo (82.6%), and Maksym Forte 050 FS (75.8%) provided a high level of efficiency. The efficiency of Inshur Perform FS and Selest Top 312.5 FS was 60.6% and 42.7%, respectively. The efficiency of Rankona 15 and Vitavaks 200 FF (fungicides with a contact-systemic effect) was 26.4% and 23.3%, respectively.

At wax ripeness, root rot development in winter wheat decreased only in 2013, compared with that at spring tillering. In the control, development of root rots was 11.1% and spread was 30.8% (Table 3). In 2012 and 2014, the degree of disease development 4.3% and 17.3% and spread was 11.8% and 49.6%, respectively.

Table 3. The development of root rots at the waxy ripe stage of winter bread wheat depending on presowing seed treatment. The control treatment is without fungicide protection or fertilizer.

	Spread (%)				Development (%)				Technical effectiveness (%)			
Treatment	2012	2013	2014	2012–14 average	2012	2013	2014	2012–14 average	2012	2013	2014	2012–14 average
Control	11.8	30.8	49.6	30.7	4.3	11.1	17.3	10.9	—	—	—	—
Vitavaks 200 FF (standard)	11.3	22.1	53.4	28.9	3.8	8.1	19.5	10.5	11.6	27.0	0.0	12.9
Rankona 15	11.6	29.9	51.4	31.0	3.8	11.3	17.9	11.0	11.6	0.0	0.0	3.9
Kinto Duo	8.3	23.9	48.9	27.0	2.8	8.9	17.0	9.6	34.9	19.8	1.7	18.2
Maksym Forte 050 FS	10.1	25.6	55.8	30.5	3.4	8.9	20.5	10.9	20.9	19.8	0.0	13.6
Inshur Perform	8.5	25.0	42.6	25.4	2.8	9.6	14.1	8.8	34.9	13.5	18.5	22.3
Selest Top 312.5 FS	9.1	24.9	53.0	29.0	2.8	8.9	19.2	10.3	34.9	19.8	0.0	18.2
Yunta Kvadro	10.1	25.8	46.7	27.5	3.0	9.7	16.8	9.8	30.2	12.6	2.9	15.2
LSD 05					1.8	3.7	5.8					

The effect of fungicide treatments at wax ripeness considerably decreased. Averaged over the three years, the efficiency ranged from 3.9% (Rankona 15) to 22.3% (Inshur Perform FS).

Meteorological conditions and the phytosanitary state of winter wheat influenced the grain yield. Averaged over the years (2012–4), grain yield was 4.83 t/ha in the control with a 1,000-kernel weight of 43.34 g. With a presowing fungicide and the use of organic/mineral fertilizers, the saved grain yield was from 0.36 t/ha (Kinto Duo) to 0.49 t/ha (Selest Top 312.5 FS) averaged over three years. The 1,000-kernel weight increased from 44.03 g (Vitavaks 200 FF) to 45.06 g (Maksym Forte 050 FS), compared with that of the control.

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ITEMS FROM THE UNITED STATES OF AMERICA

KANSAS

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Soil chemical properties after growth of six winter cover crops.

Oliver W. Freeman and M.B. Kirkham.

In Kansas, winter cover crops have a new interest with the development of corn (*Zea mays* L.) and forage sorghum (*Sorghum bicolor* (L.) Moench) for biofuel. When they are harvested for bioenergy, the residue is removed leaving the soil prone to erosion during the winter fallow period. Winter cover crops may allow maximum biomass harvest by protecting the soil from wind and water erosion. In the 2014 *Annual Wheat Newsletter* (Vol. 60), we reported that leguminous winter cover crops winter-killed and that winter cover crops such as wheat or triticale should be grown. In that study, we

Table 1. The pH, organic matter (OM), nitrogen, and carbon in the 0 to 0.3 m depth of a Bismarckgrove-Kimo complex soil at Manhattan, KS, and a Funmar-Tarver loam soil at Hutchinson, KS, in the autumn of 2010 before planting of three leguminous cover crops. Soil again was sampled in the autumn of 2011. Two soil samples were taken within each of the four blocks (replications). See text for details. The values for soil properties are the averages and standard deviations of four replications. The far right column shows the averages of each row and standard deviations (n = 6).

Soil property	Sample 1 within each block			Sample 2 within each block			Average
	Winter legume cover crop			Winter legume cover crop			
	Alfalfa	Clover	Pea	Alfalfa	Clover	Pea	
Manhattan, KS, Autumn 2010							
pH	5.7±0.2	5.7±0.6	5.6±0.2	5.5±0.1	5.5±0.2	5.6±0.2	5.6±0.1
OM (%)	1.2±0.1	0.9±0.2	1.0±0.1	1.1±0.2	1.0±0.2	1.1±0.1	1.1±0.1
N (%)	0.06±0.01	0.05±0.01	0.07±0.01	0.06±0.02	0.05±0.1	0.07±0.01	0.06±0.01
C (%)	0.47±0.13	0.32±0.06	0.47±0.08	0.41±0.12	0.34±0.05	0.48±0.05	0.41±0.07
Manhattan, KS, Autumn 2011							
pH	6.4±0.1	6.5±0.1	6.5±0.1	6.6±0.2	6.4±0.1	6.4±0.2	6.5±0.1
OM (%)	2.2±0.2	2.4±0.2	2.3±0.2	2.3±0.1	2.4±0.2	2.3±0.2	2.3±0.1
N (%)	0.14±0.01	0.14±0.01	0.15±0.01	0.14±0.01	0.14±0.01	0.14±0.1	0.14±0.01
C (%)	1.43±0.07	1.50±0.12	1.47±0.12	1.43±0.11	1.47±0.06	1.45±0.15	1.46±0.03
Hutchison, KS, Autumn 2010							
pH	5.8±0.4	5.6±0.6	6.2±0.5	6.1±0.4	5.5±0.4	5.5±0.4	5.8±0.4
OM (%)	1.5±0.1	1.1±0.4	0.8±0.5	1.2±0.3	1.2±0.3	1.4±0.2	1.2±0.2
N (%)	0.09±0.01	0.07±0.02	0.09±0.01	0.07±0.01	0.08±0.02	0.09±0.02	0.08±0.01
C (%)	0.83±0.09	0.69±0.24	0.78±0.13	0.68±0.17	0.68±0.17	0.86+0.17	0.75±0.08
Hutchinson, KS, Autumn 2011							
pH	5.8±0.4	5.8±0.2	5.8±0.4	5.7±0.4	5.9±0.3	5.6±0.4	5.7±0.1
OM (%)	1.5±0.2	1.2±0.3	1.3±0.2	1.3±0.1	1.5±0.2	1.3±0.2	1.3±0.1
N (%)	0.08±0.01	0.07±0.02	0.08±0.01	0.08±0.01	0.07±0.01	0.08±0.01	0.08±0.01
C (%)	0.78±0.09	0.68±0.11	0.73±0.05	0.75±0.12	0.68±0.16	0.78±0.09	0.73±0.05

did not report the soil chemical properties as affected by the presence of the cover crops. Therefore, the objective of this research is to report the changes in pH, organic matter, nitrogen, and carbon in the soil as a result of growing the cover crops.

Six cover crops were studied, including 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, triticale (X *Triticosecale*; *Triticum* x *Secale*), winter oats (A*vena sativa* L.), and winter wheat. The plants grew at two locations in Kansas: Manhattan, in the northeastern part of the state, and Hutchinson, in the south-central part of the state. The cover crops were planted at times to simulate plantings in rotations with corn and forage sorghum. However, they were not in rotation with these crops, and corn and forage sorghum never grew in the experiment. 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. Details of the experiment are given in Freeman (2014).

The cover crops were planted in the autumns of 2009, 2010, and 2011. In the springs of 2010, 2011, and 2012, the cover crops were chemically terminated and the residue left on the surface of the ground. The soil was sampled at the 0–30 cm depth in the autumn of 2010 before planting the 2010–11 winter cover crops and in the autumn of 2011 before planting the 2011–12 winter cover crops. The soil, therefore, when sampled in the autumn of 2010 had one year's growth of cover crops (2009–10 season) and the soil in the autumn of 2011 had two year's growth of cover crops (2009–10 and 2010–11 seasons). 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.

In Manhattan, the soil is a Bismarckgrove-Kimo complex, a complex of two different soils that cannot be distinguished. The Bismarckgrove series is classified as a fine-silty, mixed superactive mesic Fluventic Hapludolls. At a 0–18

Table 2. The pH, organic matter (OM), nitrogen, and carbon in the 0 to 0.3 m depth of a Bismarckgrove-Kimo complex soil at Manhattan, KS, and a Funmar-Tarver loam soil at Hutchinson, KS, in the Autumn of 2010 before planting of three non-leguminous cover crops. Soil again was sampled in the Autumn of 2011. Two soil samples were taken within each of the four blocks (replications). See text for details. he values for soil properties are the averages and standard deviations of four replications. The far right column shows the averages of each row and standard deviations (n = 6).

Soil property	Sample 1 within each block			Sample 2 within each block			Average
	Winter non-legume cover crop			Winter non-legume cover crop			
	Oats	Triticale	Wheat	Oats	Triticale	Wheat	
Manhattan, KS, Autumn 2010							
pH	5.5±0.1	5.5±0.1	5.7±0.2	5.5±0.1	5.5±0.4	5.7±0.2	5.6±0.1
OM (%)	1.3±0.4	1.1±0.3	1.2±0.1	1.3±0.3	1.1±0.3	0.9±0.2	1.1±0.1
N (%)	0.07±0.02	0.06±0.02	0.06±0.01	0.07±0.02	0.06±0.01	0.05±0.01	0.06±0.01
C (%)	0.52±0.21	0.42±0.16	0.43±0.05	0.57±0.24	0.41±0.12	0.35±0.08	0.45±0.08
Manhattan, KS, Autumn 2011							
pH	6.5±0.05	6.6±0.1	6.5±0.1	6.5±0.1	6.4±0.1	6.4±0.2	6.5±0.1
OM (%)	2.2±0.2	2.3±0.2	2.3±0.2	2.2±0.1	2.3±0.3	2.2±0.2	2.3±0.1
N (%)	0.14±0.01	0.14±0.01	0.13±0.02	0.14±0.02	0.14±0.01	0.14±0.01	0.14±0.01
C (%)	1.43±0.09	1.44±0.08	1.46±0.14	1.42±0.13	1.49±0.09	1.47±0.10	1.45±0.03
Hutchison, KS, Autumn 2010							
pH	6.1±0.5	6.1±0.7	5.9±0.7	6.1±0.3	6.4±0.5	6.4±0.3	6.2±0.2
OM (%)	1.3±0.3	1.2±0.2	1.4±0.4	1.2±0.2	1.3±0.1	1.4±0.1	1.3±0.1
N (%)	0.09±0.01	0.08±0.02	0.09±0.02	0.08±0.02	0.09±0.02	0.09±0.01	0.08±0.01
C (%)	0.77±0.17	0.69±0.15	0.81±0.23	0.77±0.18	0.79±0.13	0.85±0.13	0.78±0.05
Hutchinson, KS, Autumn 2011							
pH	5.7±0.3	5.6±0.4	5.6±0.3	5.7±0.3	5.5±0.2	5.6±0.05	5.6±0.1
OM (%)	1.3±0.1	1.3±0.1	1.3±0.1	1.3±0.2	1.4±0.1	1.2±0.1	1.3±0.1
N (%)	0.08±0.02	0.08±0.02	0.09±0.01	0.08±0.02	0.08±0.01	0.08±0.01	0.08±0.01

cm depth, the soil is a silt loam and at a 18–51 cm depth, the soil is a silty clay loam. The Kimo series is classified as a clayey over loamy, smectic, mesic Fluvaquentic Hapludolls. At a 0–18 cm depth, the series is a silty clay loam, and at a 18–38 depth, the soil is a silty clay. In Hutchinson, the soil was a Funmar-Tarver loam (fine-loamy, mixed, superactive, mesic Pachic Argiustolls).

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). These plots were split into two '3 m x 12 m' plots that were planted and sampled at corn or forage sorghum harvesting and planting times. The two side-by-side plots varied in biomass due to differences in growth time (see *Ann Wheat Newslet* 60:127-128). The two side-by-side plots provided two soil samples for each cover crop in each block. We call these two samples 'Sample 1 within each block' and 'Sample 2 within each block' in the tables. Plots were assigned anew each year, so no one plot got consistently the same cover crop during the three years of the study.

Data for pH, organic matter, nitrogen, and carbon in the soil that grew the three leguminous winter cover crops (Table 1) and that grew the three non-leguminous winter cover crops (Table 2) are given. Differences in soil properties due to individual cover crops were not evident, so the chemical properties were averaged across treatments, and these averages are given in the far-right columns of the two tables. At Manhattan, all chemical properties increased in the one year between analyses in the autumn of 2010 and autumn 2011. The pH increased by about 1 point (5.6 to 6.5); organic matter increased by over two times (1.1 to 2.3%), as did the nitrogen (0.06 to 0.14%). Carbon increased by over three times (0.41 to 1.46%). Changes in chemical properties of the soil at Hutchinson were not evident between the two analyses, except for pH in the plots with non-leguminous cover crops, where the pH decreased from 6.2 to 5.6. The results showed that, on the Bismarckgrove-Kimo soil in Manhattan, two year's growth of cover crops increased pH, organic matter, nitrogen, and carbon.

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News.

Dr. Oliver W. Freeman II accepted a new job in late 2015. He is Agronomist at the Rose Lake Plant Materials Center, USDA, Natural Resources Conservation Service, 7472 Stoll Road, East Lansing, Michigan 48823 USA.

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

A 'Fitbit' for plants? A low-cost, portable platform to gauge plant health.

Jared Crain and Jesse Poland.

Kansas State University student and Phenocart developer Jared Crain collects data using the Phenocart in drought stress wheat trials at the Norman E. Borlaug Research Station, Cd. Obregon, Mexico.

Plant breeders test their experiments by growing the seeds of their labor. They cross two different plants that have desirable traits. They sow the resulting seeds and evaluate the results, hoping to find a candidate variety that is better than anything currently available. The 'laboratory' is often an outdoor field with thousands of plants. Farmers have monitored their fields for millennia by simply walking among the rows of plants, observing changes over time, and noting which plants do better. But as plant breeding technology becomes more complicated, farmers and scientists want specific data. They want to know exactly how tall the plants are, or exactly how green the leaves are. In a large test field, getting exact numbers means hours or even days of labor for a plant breeder. Because it is such a labor intensive process, we are working to develop technology that makes phenotyping much easier. The tool is called the Phenocart, and it captures essential plant health data. The Phenocart measures plant vital signs, such as growth rate and color, the same way a Fitbit monitors human health signals, such as blood pressure and physical activity.

In a field experiment with thousands of plots, the Phenocart is a quick way to evaluate plant health. The Phenocart also can help plant breeders design larger experiments. A larger sample size gives you more power. Measuring phenotypes is very labor-intensive, and really limits how big an experiment can be. The new tool will allow for faster measurements and accelerate the breeding process.

The Phenocart is a collection of sensors. The sensors are attached to a repurposed bicycle wheel and handles that a plant breeder can easily push among plants in a field. The Phenocart rapidly collects data as it is pushed among the plots. The Phenocart can be outfitted with different sensors depending on what needs to be measured, such as how green the plants are. This measure of vegetation index or 'greenness' is really the easiest and more straightforward way to measure the overall health status of the plant.

A thermometer can be used to check leaf temperature. Leaf temperature is also a good predication for crop yield. A global position system (GPS) can pinpoint exactly where the Phenocart measures, which helps organize data. The data is processed by software included in the Phenocart package. One of the best aspects about the Phenocart is that it's portable and can be packed up and takeen anywhere in the world, making an impact across the global plant breeding community and affordable technology for a broad group. As plant breeding becomes more sophisticated, so does measuring the results of large field experiments. The Phenocart is a low-cost, mobile way to gauge the health of thousands of plants quickly and accurately.

New technologies quicken development of climate-resilient wheat in South Asia.

Jared Crain, Daljit Singh, Trevor Rife, and Jesse Poland.

Crippling climate changes, coupled with a growing population, threaten food security, economic welfare and social harmony in South Asia, a region heavily dependent on wheat for its nutrition and income. But in the race to fight hunger, the development of new wheat cultivar that can withstand harsh growing conditions is severely hindered by traditionally laborious and time-consuming breeding processes. The Feed the Future Innovation Lab for Applied Wheat Genomics, led by Kansas State University, works with the International Maize and Wheat Improvement Center (CIMMYT) and the Borlaug Institute for South Asia to address this issue. The partnership is creating new solutions and technologies to get high-yielding, climate-resilient wheat cultivars into the hands of farmers in India and Pakistan years sooner.

Daljit Singh and Jared Crain from Kansas State University assist with phenotyping using a modified Phenocart in India.

In this effort, the Applied Wheat Genomics Innovation Lab has developed three new data collection technologies that are designed to speed up phenotyping, the process of gathering field data on plant characteristics, thereby enabling breeders to develop climate-resilient varieties at a much faster pace. These innovations are some of the first affordable technologies that could be developed on a large scale and implemented in states, countries and research locations throughout the world.

Phenocart. An inexpensive, locally adapted technology that collects and analyzes phenotypic data via computer instead of by hand. The Phenocart can be modified, using readily available items like bicycles, to fit the needs of Indian scientists where fields are inaccessible by tractors. This technology will allow researchers to collect data to assist in crop breeding and identify lines that are best suited for target environments.

Unmanned aerial vehicle (UAV). Another high-throughput and inexpensive phenotyping platform that greatly accelerates the breeding cycle. The UAV can facilitate the development of climate-resilient and resource-efficient varieties, promoting environmentally friendly agriculture.

Field Book. A simple and free app for Android devices that will help the breeding community to significantly reduce time and mistakes, resulting in better selections. The Field Book developers estimates that the app can save researchers and breeders one-third the time of hand-written notes. Researchers at CIMMYT, for example, may have 10,000 plots in a field trial, so a one percent error rate is pretty substantial. Field Book can eliminate human errors and speed up the turn-around time for analysis.

As a whole, the Applied Wheat Genomics Innovation Lab is working to use affordable, consumer-grade equipment to tackle some of the world's largest problems, like feeding nine billion people by the year 2050.

Kansas State University's leadership in wheat research recognized with $1.6M grant.

Jesse Poland and Bikram S. Gill; Sunish Sehgal (South Dakota State University, Brookings, SD, USA); and Gary Muehlbauer (Plant Genetics Department, University of Minesota, St. Paul, MN, USA.

Kansas State University wheat researchers are leading efforts to develop a better understanding of the wheat genome. The National Science Foundation's Plant Genome Program awarded the researchers a three-year, $1.6 million grant to fund projects and collaborations to help train new generations to answer challenging plant genomics questions.

The project is GPF-PG: Genome Structure and Diversity of Wheat and Its Wild Relatives. The project will focus on ways to improve the current wheat genome assembly by using genetic information. Currently, the use of molecular markers in wheat breeding is limited because of their size, which is five times larger than the human genome.

If we think about the genome as a book, with lots of letters that need to be organized into words and sentences and ordered pages that make a story, we are at the point with the wheat genome of having sentences organized on a page, but not clear what order the pages should go. To really understand the whole story, we need to get the pages in order.

The project has the support of Kansas Wheat. According to Justin Gilpin, COE of Kansas Wheat, wheat farmers are excited about the work going on at Kansas State University and the advances that this project will mean to wheat genetics and leveraging diversity. Resources from important agencies such as the National Science Foundation that support Kansas State University will really make a difference. The project also will partner with the Kansas Foundation for Ag in the Classroom to develop education and training opportunities for future researchers. Kindergarten through 12th grades will receive information for plant science careers. Undergraduate students and postdoctoral researchers also will have education and training in genomics and bioinformatics.

With the generation of huge datasets, the computational approaches of bioinformatics to understand biological data are critical. The goal is to integrate more computer science into agriculture classrooms. Because data sets have grown larger, good levels of computer skills are needed.

Sequencing the wheat genome to help feed the world: a high-quality, bread wheat reference sequence is on the horizon.

Jesse Poland.

Kansas State University, in collaboration with the International Wheat Genome Sequencing Consortium (IWGSC), has announced the production of an improved, whole-genome assembly of bread wheat. Using NRGene's DeNovaMAGICTM software and Illumina's sequencing data for assembly, the team is well on its way to sequencing Chinese Spring bread wheat. A high-quality, whole-genome reference sequence (a complete map of the entire genetic make-up from one end of the chromosome to the other, for all 21 bread wheat chromosome pairs) is less than two years away and will dramatically accelerate global research into crop improvement of the world's most staple crop.

The public-private collaborative project is coordinated by the IWGSC and led by Jesse Poland, Nils Stein of IPK Gatersleben in Germany, Curtis Pozniak of the University of Saskatchewan's Crop Development Centre in Canada, and Andrew Sharpe of the Global Institute for Food Security in Canada. Project participants also include researchers from Illumina, Inc.; NRGene in Israel and the United States; Tel Aviv University in Israel; and the French National Institute for Agricultural Research (INRA).

This improved assembly of the wheat genome is an excellent resource to move forward with genomics assisted breeding. With wheat being such an important crop for Kansas, projects like this will continue to enable world-class research efforts in wheat at KSU to understand the wheat genome and produce better cultivars.

To understand the significance of this achievement, it is important to understand why sequencing the wheat genome continues to be such a massive undertaking. The wheat genome itself is huge, with a total of 16 billion base pairs of DNA, especially compared to other significant staple crops such as rice and corn, which have 430×10^6 and 2.5×10^9, respectively. Building a full reference sequence with that many pieces has traditionally been virtually impossible. With the help of NRGene's DeNovaMAGICTM technology and Illumina's sequencing technology, the reality is in sight.

Having the whole genome sequence is like providing an instructional manual for building better plants. Until now, the pages in the manual were out of order and 40% of them were missing. Having a complete manual, with everything in the right order will allow us to quickly identify genes responsible for traits such as pest resistance, yield, and quality. With this genomic information we could potentially make the breeding cycle 2–3 times faster, and bring better varieties to farmers in a fraction of the time.

According to the United Nations, 70% more food will be needed by 2050. As global populations grow and available land and water become scarcer, the pressure is on crop and trait improvement to meet the wheat productivity increase that is needed. This high quality reference genome sequence will provide the genomic keys necessary to ensure an abundant supply of wheat for the years to come.

This project was coordinated through the International Wheat Genome Sequencing Consortium with funding from Genome Canada; Genome Prairie; the Saskatchewan Ministry of Agriculture, the Saskatchewan and Alberta Wheat Development Commissions, and the Western Grains Research Foundation through the Canadian Triticum Applied Genomics (CTAG2) project; Kansas State University through the US National Science Foundation Plant Genome Research Program; and Illumina, Inc.

Better bread: how researchers are using genomics to predict bread quality and accelerate wheat cultivar development.

Sarah Battenfield, Allan Fritz, and Jesse Poland; Susanne Dreisigacker, Carlos Guzman, Roberto J. Peña, and Ravi P. Singh (CIMMYT Int., Mexico); and R. Chris Gaynor (Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Scotland, UK).

A team of breeders and geneticists at Kansas State University and the International Maize and Wheat Improvement Center, or CIMMYT, has come up with a new approach to determine if new varieties of bread wheat will have what it takes to make better bread. With funding from the U.S. Agency for International Development Feed the Future Initiative, the team is using DNA markers to predict important quality traits for bread wheat, such as dough strength and loaf volume.

Historically, the main focus of wheat breeding has been grain yield and the selection of lines with the best performance and disease resistance. In many breeding programs, quality traits are evaluated at the very end of the selection cycle for candidate wheat varieties because of the high cost and the large quantity of grain needed for testing. Because the typical wheat breeding cycle takes eight to 10 years, waiting to test for bread quality until the final years often results in what were thought to be promising wheat lines being discarded because they can't produce a good loaf of bread.

The team used wheat quality data generated in the test baking lab and built prediction algorithms for determining quality traits in new generations of candidate wheat varieties using DNA markers. Using the prediction algorithm, they were able to advance wheat quality screening by at least a year and predict over 10 times more candidate varieties than can be tested in the quality lab. Traditionally, about 1,500 samples/year are tested in the CIMMYT quality lab, but because quality was predicted by DNA markers alone, all 10,000 first-year yield trials were screeded for quality, which is more than would be possible to physically handle, at roughly the same cost. The team believes there is potential to advance the process by up to three years.

Wheat quality testing starts with analyzing grain morphology, hardness and protein content. The procedure continues milling wheat kernels into flour then determining protein content and how much water is optimal for dough-making in different rheological tests. Then the flour is mixed with water in a mixograph, which is like a miniature mixing bowl with pins that can measure resistance of the dough while it is being developed. The curve tells us how strong a dough from one candidate cultivar is relative to another and what is the optimum mixing time to get that dough. Kansas hard red winter wheat needs to have really strong dough because most goes to industrial bakeries, so it needs to be able to withstand industrial processing.

Dough strength, amount of mixing time and extensibility are all measured and bread is baked as a final test of performance. From all this data, a decision can be made on whether the wheat line is good enough to keep, but this question cannot come until six to eight years into the breeding cycle. Using DNA from single plants, these new prediction models can be used to get an assessment of the quality much earlier in the breeding cycle, whiich is long before there is sufficient seed for quality testing. Decreasing breeding cycle time has the biggest impact in breeding on return on invest-

ment, according to the researchers. These adjustments indicate that selection for quality could increase two to three times above what is currently possible. The results also show that wheat breeding programs can use genomic selection for wheat quality, along with their traditional breeding pipeline, to more effectively and efficiently use resources, including time and money.

This prediction method allows the elimination of many lines, which will not be able to pass the final test of wheat quality. Accurate processing and end-use quality prediction models, such as genomic selection, will allow breeding programs to cull unacceptable lines or target specific lines before time and resources are invested in lines that will not pass the final test.

Additional sources of funding for the study were provided by the Monsanto Beachell-Borlaug International Scholars Program, the Bill and Melinda Gates Foundation, CGIAR CRP WHEAT and the Durable Rust Resistance Project.

Jesse Poland receives national award for early career plant breeding work.

Jesse Poland has received the National Association of Plant Breeders' 2016 Early Career Scientist Award, which recognizes a young scientist who is active in the field of plant breeding.

Award nominees must exhibit the ability to: establish strong research foundations, such as experimental techniques and publications; interact with multidisciplinary teams; and participate in professional societies relevant to their discipline. Poland has contributed to the study of plant breeding through publications, teaching and communicating his research at meetings, conferences, workshops and field days. In less than six years as a research geneticist at Kansas State University, Poland has

- Advised ten doctoral students and seven post-doctoral students and served as a committee member for other students in plant breeding and genetics.
- Welcomed and trained visiting students and scientists from India, Italy, Mexico and Uruguay.
- Served as the adviser to K-State's Plant Breeding and Genetics Club since its founding.
- Secured more than $12 million in competitive grants.
- Authored more than 50 publications with 4,000 total citations.

Two of his most significant achievements are the development and refinement of genotyping-by-sequencing, or GBS, a novel method for genetic characterization of wheat and other species, and the development of portable high-throughput phenotyping, or HTP, platforms. GBS has become an innate component of breeding programs around the world that allows low-cost, whole-genome, marker profiling. HTP platforms are helping breeders and researchers to maximize the amount of data available to them to make more accurate selections.

Poland also contributed to the development of the first physical sequence of barley, as well as the draft sequence of hexaploid wheat under international sequencing consortiums.Poland's nomination package, submitted by Trevor Rife and Narinder Singh, both doctoral students in genetics, chronicles his outstanding progress and significant achievements. Since joining Poland's research team as his first doctoral student in 2011, Rife has seen Poland assemble an impressive research team of students and scientists from a variety of academic backgrounds.

Molecular cytogenetic mapping of satellite DNA sequences in Aegilops geniculata and wheat.

Dal-Hoe Koo, Vijay K. Tiwari, Bernd Friebe, and Bikram S. Gill; and Eva Hřibová and Jaroslav Doležel (Institute of Experimental Botany, Centre of the Region Haná for Biotechnological and Agricultural Research, CZ 78371, Olomouc, Czech Republic).

Fluorescent in situ hybridization (FISH) provides an efficient system for cytogenetic analysis of wild relatives of wheat for individual chromosome identification and elucidation of homoeologous relationships and for monitoring alien gene transfers into wheat. We developed cytogenetic markers for the identification of wheat and *Ae. geniculata* ($U^gU^gM^gM^g$) chromosomes using satellite DNAs identified from flow-sorted chromosome $5M^g$. FISH was used to localize the satellite DNA on chromosomes of wheat and selected Aegilops species.

The FISH signals for satellite DNAs on chromosome 5M^g generally were associated with constitutive heterochromatic regions corresponding to C-band-positive chromatin including telomeric, pericentromeric, centromeric, and interstitial regions of all the 14 chromosome pairs of *Ae. geniculata*. Most satellite DNA also generated FISH signals on wheat chromosomes and provided diagnostic chromosome arm-specific cytogenetic markers that significantly improved chromosome identification in wheat. The newly identified satellite DNA CL36 produced localized M^g-genome chromosome-specific FISH signals in *Ae. geniculata* and in the M genome of the putative diploid donor species *Ae. comosa* subsp. *subventricosa* but not in *Ae. comosa* subsp. *comosa*, suggesting that the M^g genome of *Ae. geniculata* probably was derived from *Ae. comosa* subsp. *subventricosa*.

A new T2DS·2RL Robertsonian translocation transfers stem rust resistance gene Sr59 into wheat.

Mahbubjon Rahmatov and Brian J. Steffenson (Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108, USA); Jayaveeramuthu Nirmala and Matthew N. Rouse (USDA–ARS Cereal Disease Laboratory, St. Paul, MN 55108, USA); Tatiana Danilova and Bernd Friebe; and Eva Johansson (Department of Plant Breeding, Swedish University of Agricultural Sciences, PO Box 101, 23053 Alnarp, Sweden).

Emerging new races of the wheat stem rust pathogen from Africa threaten global wheat production. To broaden the resistance spectrum of wheat to these widely virulent African races, additional resistance genes must be identified from all possible gene pools. From the screening of a collection of wheat–rye chromosome substitution lines developed at the Swedish University of Agricultural Sciences, we described the line 'SLU238' 2R (2D) as possessing resistance to many races of *P. graminis* f. sp. *tritici*, including the widely virulent race TTKSK (isolate synonym Ug99) from Africa. The breakage-fusion mechanism of univalent chromosomes was used to produce a new Robertsonian translocation: T2DS·2RL. Molecular marker analysis and stem rust seedling assays at multiple generations confirmed that the stem rust resistance from SLU238 is present on the rye chromosome arm 2RL. Line TA5094 (N101)was derived from SLU238 and found to be homozygous for the T2DS·2RL translocation. The stem rust resistance gene on chromosome 2RL arm was designated *Sr59*. Although introgressions of rye chromosome arms into wheat have most often been facilitated by irradiation, this study highlights the utility of the breakage-fusion mechanism for rye chromatin introgression. *Sr59* provides an additional asset for wheat improvement to mitigate yield losses caused by stem rust.

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

Marsha Boswell.

Kansas Hard Red Winter Wheat Tour 2016.

Day 1. Twenty vehicles with 78 participants headed west from Manhattan, KS, on 3 May on the Hard Winter Wheat Tour 2016. Scouts stopped in 306 locations on the six routes between Manhattan and Colby. The Wheat Quality Council's wheat tour is held every year to get an idea of the yields and production of the crop. Crop scouts take measurements in fields across their routes, using a formula developed by USDA/NASS to estimate the yield for each field. These estimates are averaged in each car, and then combined with all cars to get a yield estimate each day. The average calculated yield for day 1 was 47.2 bushels per acre, compared with only 34.3 bushels per acre along the same route last year.

On 3 May, scouts reported seeing some stripe rust, barley yellow dwarf virus, early season drought stress, and freeze damage. Overall, wheat looked as good or better than expected. Almost all wheat was between late boot stage and early flowering stage. The NASS report on Monday rated Kansas winter wheat condition 2% very poor, 8% poor, 38% fair, 46% good, and 6% excellent. Winter wheat was 97% jointed and 49% headed, ahead of 34% last year and well ahead of the 28% average. A small group of scouts began the tour in Colorado and headed east to Colby, KS. They reported an average yield of 39 bushels/acre in Colorado and estimated production at 78 x 10^6 bushels for the state.

Nebraska reported that 95% of the state's crop is currently rated good to excellent, with an average yield of 55 bushels/acre. They are estimating 70.4 x 10^6 bushels of production this year, up from only 46 x 10^6 bushels last year.

Although scouts anticipated seeing a lot of stripe rust, reports came in that many of the fields had been sprayed with fungicide to prevent the spread of the disease. Aaron Harries, Kansas Wheat VP of Operation and Research, commended farmers for their management practices stateing 'Farmers need a round of applause for taking care of rust issues before they became a huge issue.' Jeanne Falk Jones, Kansas State University multi-county agronomy specialist, concurred. She discussed what extension is doing to educate producers about what they could do to get out in front of stripe rust. Romulo Lollato, Kansas State University wheat and forages extension specialist, discussed three major freeze events that occurred this spring, including one in northwest Kansas earlier this week. Falk Jones said 'We had cold temperatures Monday morning. It will take us 10 days to 2 weeks to know if we have any damage from that.'

Day 2. After day two of the Hard Winter Wheat Quality Tour 2016, scouts had visited 606 stops and calculated an average yield of 48.2 bushels/acre, up from the 34.4 bushel/acre estimate in 2015. The 20 vehicles traveled on six routes between Colby and Wichita, KS, on 4 May. While they ran into increased disease pressure as they moved south and east, the crop looked better than last year. Southwest portions of the state showed some signs of autumn drought stress, but with recent rains, the prospects for the crop have increased.

Most years on this route of the tour, the groups see little sign of moisture in the fields, but topsoil moisture was adequate this year, and some areas even had some water standing in the field. Many fields have been sprayed for stripe rust, and that has definitely made an impact on the crop. Today, scouts reported seeing more viral disease than fungal diseases, and overall, stands are good. Mark Hodges, from Plains Grains, Inc., reported that estimated yields for Oklahoma are 33.6 bushels/acre, with 3.82 x 10^6 acres harvested resulting in production of 128.5 x 10^6 bushels for the state, making it an above average crop.

Final projection. The 2016 Hard Red Winter Wheat Tour was uplifting for participants because calculated yields were higher than anticipated, disease pressure was lower than expected, and the three days of the tour had some of the best weather so far this spring. The three-day average was 48.6 bushels/acre, nearly a 13 bushel increase from last year.

The official tour projection for total production numbers of hard red winter wheat to be harvested in Kansas is 382.4 x 10^6 bushels. This number was calculated based on the average of estimated predictions from tour participants who gathered information from 655 fields across the state.

Even though the crop is about 10 days to two weeks ahead of average, harvest still won't begin for 30 to 45 days. A lot can happen during that time, and none of it is good. The wheat still needs additional moisture and cool temperatures to realize that yield potential. The last time yield reached 48 bushels/acre was in 2003, but at that time 10.5×10^6 acres were planted to wheat. Planted acres this year are the lowest since 1957 at 8.5×10^6. 'There are less acres planted this year, but we are seeing wheat become a higher managed crop than in the past; that's allowing us to see higher yields,' said Justin Gilpin, Kansas Wheat CEO. 'One thing that was a little surprising was how many fields had been treated with fungicide to help with stripe rust,' said Gilpin. 'Last year, stripe rust became a big yield inhibitor in Kansas, so farmers should be commended for taking steps to control the disease this year.'

MINNESOTA

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Wheat Rusts in the United States in 2015.

Significant spring rainfall in the Great Plains effectively ended the persistent drought conditions there. The ample precipitation, in combination with cooler than average temperatures, created conditions very conducive for stripe rust development throughout the Great Plains. The Atlantic coastal states generally experienced drier than average conditions during the late growing season, thus greatly limiting rust development there. Much warmer and dry conditions in the Pacific Northwest hastened crop development and contributed to reduced stripe rust levels.

Wheat stem rust (caused by *Puccinia graminis* f. sp. *tritici*). Wheat stem rust was not widespread or severe in the U.S. in 2015, only reported in Texas, Louisiana, Kansas, Nebraska, Ohio, Michigan, and North Dakota. All collections and observations were from nurseries, with the exception of collections from fields in northeastern and west-central Texas and a field in northwestern Ohio. Wheat stem rust was first reported on 4 March at Weslaco in Lower Rio Grande Valley, southern Texas. Race QFCSC was the most commonly identified wheat stem rust race in 2015 and in recent years. Race RFCSC, similar to QFCSC with added virulence to *Sr7b*, was found in a low frequency in collections from Nebraska. Stem rust infections on barley in the intermountain region in northern California and barley nursery near Monterey Bay were identified as BBLBB. Further testing of the isolates on host specificity determined that it belongs to the rye stem rust pathogen, *Puccinia graminis* f. sp. *secalis*. Wheat stem rust was not isolated from aecial samples of *Berberis vulgaris* collected from Minnesota and Wisconsin.

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

Wheat leaf rust (caused by *Puccinia triticina*). Wheat leaf rust was found throughout the Great Plains in 2015, but the cool temperatures and high rainfall in Texas and Oklahoma were more conducive for stripe rust development. Additionally, the loss of leaves to stripe rust combined with fungicide applications (to control stripe rust) contributed to the limited leaf rust development. Leaf rust did not develop to any great extent in the Gulf Coast states, and there was very little or no rust found in the Atlantic Coast states where conditions were dry. The limited development of leaf rust in the southern Great Plains region greatly reduced the amount of urediniospores carried to the northern states. Wheat leaf rust was found in the Willamette Valley in Oregon, where it has rarely been observed for the last 10–15 years. Warm spring and summer weather and adequate moisture created conditions for leaf rust development in the northern Great Plains and Ohio Valley, however, the limited inoculum arriving from the southern regions reduced leaf rust incidence and severity in the northern states. Leaf rust was found in Minnesota, Wisconsin, and Ohio, but severities were generally low. In 2015,

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2015 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, *Lr39*, and *Lr42*.

Pheno-type	Virulences	LA, MS, TN, VA		IL, IN, MI, OH, WI		OK, TX		KS, NE		MN, MT, ND		AZ		OR		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
MBDSB	1,3,17,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	5.3	0	0.0	2	0.2
MBDSD	1,3,17,B,10,14a,39	4	7.1	1	1.9	33	21.3	18	25.4	16	9.6	9	47.4	0	0.0	81	15.4
MBPSB	1,3,3ka,17,30,B,10, 14a	0	0.0	0	0.0	4	2.6	2	2.8	1	0.6	0	0.0	0	0.0	7	1.3
MBPSD	1,3,3ka,17,30,B,10, 14a,39	0	0.0	0	0.0	3	1.9	2	2.8	1	0.6	1	5.3	0	0.0	7	1.3
MBPTB	1,3,3ka,17,30,B,10, 14a,18	1	1.8	0	0.0	4	2.6	0	0.0	0	0.0	0	0.0	0	0.0	5	1.0
MBSDS	1,3,3ka,11,17,14a, 21,28,39	0	0.0	0	0.0	0	0	3	4.2	0	0	0	0.0	0	0	3	0.6
MBTNB	1,3,3ka,11,17,30,B, 14a	35	62.5	27	50.0	0	0.0	3	4.2	1	0.6	0	0.0	0	0.0	66	12.5
MBTSB	1,3,3ka,11,17,30,B, 10,14a	2	3.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
MCDSB	1,3,26,17,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	66.7	2	0.4
MCDSD	1,3,26,17,B,10,14a, 39	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
MCJSB	1,3,26,11,17,B,10, 14a	1	1.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MCPSB	1,3,26,3ka,17,30,B, 10,14a	1	1.8	0	0.0	3	1.9	0	0.0	0	0.0	0	0.0	0	0.0	4	0.8
MCPSD	1,3,26,3ka,17,30,B, 10,14a,39	0	0.0	0	0.0	2	1.3	1	1.4	1	0.6	0	0.0	0	0.0	4	0.8
MCPTB	1,3,26,3ka,17,30,B, 10,14a,18	0	0.0	0	0.0	6	3.8	0	0.0	0	0.0	0	0.0	0	0.0	6	1.1
MCTNB	1,3,26,3ka,11,17,30, B,14a	5	8.9	14	25.9	2	1.3	1	1.4	0	0.0	0	0.0	1	33.3	23	4.4
MDDSB	1,3,24,17,B,10,14a	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	5.3	0	0.0	2	0.4
MDJSB	1,3,24,11,17,B,10, 14a	0	0.0	0	0.0	0	0.0	1	1.4	0	0.0	0	0.0	0	0.0	1	0.2
MDPSB	1,3,24,3ka,17,30,B, 10,14a	0	0.0	0	0.0	0	0.0	0	0.0	4	2.4	0	0.0	0	0.0	4	0.8
MFDSB	1,3,24,26,17,B,10, 14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	10.5	0	0.0	2	0.4
MFGJG	1,3,24,26,11,10,14a, 28	2	3.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
MFJSB	1,3,24,26,11,17,B,10, 14a	0	0.0	0	0.0	2	1.3	0	0.0	2	1.2	0	0.0	0	0.0	4	0.8
MFPSB	1,3,24,26,3ka,17,30, B,10,14a	0	0.0	0	0.0	1	0.6	0	0.0	4	2.4	3	15.8	0	0.0	8	1.5
MFPSD	1,3,24,26,3ka,17,30, B,10,14a,39	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MFTSB	1,3,24,26,3ka,11,17, 30,B,10,14a	0	0.0	0	0.0	0	0.0	1	1.4	0	0.0	0	0.0	0	0.0	1	0.2
MGBJJ	1,3,16,10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
MLDSB	1,3,9,17,B,10,14a	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MLDSD	1,3,9,17,B,10,14a,39	0	0.0	0	0.0	11	7.1	3	4.2	7	4.3	0	0.0	0	0.0	21	4.0
MLPSB	1,3,9,3ka,17,30,B,10, 14a	0	0.0	0	0.0	0	0.0	1	1.4	1	0.6	0	0.0	0	0.0	2	0.4
MLPSD	1,3,9,3ka,17,30,B,10, 14a,39	1	1.8	0	0.0	16	10.3	4	5.6	11	6.6	2	10.5	0	0.0	34	6.5
MLTSD	1,3,9,3ka,11,17,30,B, 10,14a,39	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MMDSD	1,3,9,26,17,B,10,14a, 39	0	0.0	0	0.0	4	2.6	9	12.7	3	1.8	0	0.0	0	0.0	16	3.0
MMPSD	1,3,9,26,3ka,17,30,B, 10,14a,39	2	3.6	0	0.0	14	9.0	4	5.6	5	3.0	0	0.0	0	0.0	25	4.8

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2015 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1, Lr2a, Lr2c, Lr3, Lr9, Lr16, Lr24, Lr26, Lr3ka, Lr11, Lr17, Lr30, LrB, Lr10, Lr14a, Lr18, Lr21, Lr28, Lr39,* and *Lr42*.

Pheno-type	Virulences	LA, MS, TN, VA		IL, IN, MI, OH, WI		OK, TX		KS, NE		MN, MT, ND		AZ		OR		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
MNDSD	1,3,9,24,17,B,10,14a, 39	0	0.0	0	0.0	0	0.0	0	0.0	2	1.2	0	0.0	0	0.0	2	0.4
MNPSD	1,3,9,24,3ka,17,30,B, 10,14a,39	0	0.0	0	0.0	3	1.9	2	2.8	4	2.4	0	0.0	0	0.0	9	1.7
MPDSD	1,3,9,24,26,17,B,10, 14a,39	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
MPPSD	1,3,9,24,26,3ka,17, 30,B,10,14a,39	0	0..0	0	0.0	1	0.6	2	2.8	0	0.0	0	0.0	0	0.0	3	0.6
PBDGJ	1,2c,3,17,10,28,39	0	0.0	0	0.0	5	3.2	0	0.0	0	0.0	0	0.0	0	0.0	5	1.0
TBBGD	1,2a,2c,3,10,39	0	0.0	0	0.0	0	0.0	0	0.0	2	1.2	0	0.0	0	0.0	2	0.4
TBBGJ	1,2a,2c,3,10,28,39	0	0.0	0	0.0	9	5.8	1	1.4	4	2.4	0	0.0	0	0.0	14	2.7
TBBGS	1,2a,2c,3,10,21,28,39	0	0.0	0	0.0	0	0.0	0	0.0	52	31.1	0	0.0	0	0.0	52	9.9
TBBJJ	1,2a,2c,3,10,14a,28, 39	0	0.0	0	0.0	2	1.3	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TBRKG	1,2a,2c,3,3ka,11,30, 10,14a,18,28	1	1.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TBSQB	1,2a,2c,3,3ka,11,17, B,10	0	0.0	0	0.0	0	0.0	1	1.4	0	0.0	0	0.0	0	0.0	1	0.2
TCPSB	1,2a,2c,3,26,3ka,17, 30,B,10,14a	0	0.0	2	3.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TCRKG	1,2a,2c,3,26,3ka,11, 30,10,14a,18,28	0	0.0	2	3.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TCTQB	1,2a,2c,3,26,3ka,11, 17,30,B,10	1	1.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TCTSB	1,2a,2c,3,26,3ka,11, 17,30,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
TDBGJ	1,2a,2c,3,24,10,28,39	0	0.0	0	0.0	2	1.3	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TDBJJ	1,2a,2c,3,24,10,14a, 28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	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	1	0.6	0	0.0	0	0.0	1	0.2
TDPSB	1,2a,2c,3,24,3ka,17, 30,B,10,14a	0	0.0	1	1.9	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.2
TDTSB	1,2a,2c,3,24,3ka,11, 17,30,B,10,14a	0	0.0	0	0.0	4	2.6	1	1.4	0	0.0	0	0.0	0	0.0	5	1.0
TFBJQ	1,2a,2c,3,24,26,10, 14a,21,28	0	0.0	0	0.0	0	0.0	0	0.0	2	1.2	0	0.0	0	0.0	2	0.4
TFPSB	1,2a,2c,3,24,26,3ka, 17,30,B,10,14a	0	0.0	2	3.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.4
TFTSB	1,2a,2c,3,24,26,3ka, 11,17,30,B,10,14a	0	0.0	1	1.9	4	2.6	0	0.0	0	0.0	0	0.0	0	0.0	5	1.0
TNBGJ	1,2a,2c,3,9,24,10,28, 39	0	0.0	1	1.9	14	9.0	9	12.7	15	9.0	0	0.0	0	0.0	39	7.4
TNBGS	1,2a,2c,3,9,24,10,21, 28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
TNBJJ	1,2a,2c,3,9,24,10, 14a,28,39	0	0.0	3	5.6	2	1.3	5	7.0	19	11.4	0	0.0	0	0.0	29	5.5
TPBGJ	1,2a,2c,3,9,24,26,10, 28,39	0	0.0	0	0.0	0	0.0	0	0.0	2	1.2	0	0.0	0	0.0	2	0.4
TPBJJ	1,2a,2c,3,9,24,26,10, 14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
TPBSJ	1,2a,2c,3,9,24,26,B, 10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
Total		56		54		156		71		167		19		3		526	

Table 2. Number and frequency (%) of isolates of *Puccinia triticina* in the United States in 20145virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance gene	LA, MS, TN, VA		IL, IN, MI, OH, WI		OK, TX		KS, NE		MN, MT, ND		AZ		OR		Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	56	100.0	54	100.0	156	100.0	71	100.0	167	100.0	19	100.0	3	100.0	526	100.0
Lr2a	2	3.6	12	22.2	37	23.7	17	23.9	102	61.1	0	0.0	0	0.0	170	32.3
Lr2c	2	3.6	12	22.2	42	26.9	17	23.9	102	61.1	0	0.0	0	0.0	175	33.3
Lr3	56	100.0	54	100.0	156	100.0	71	100.0	167	100.0	19	100.0	3	100.0	526	100.0
Lr9	3	5.4	4	7.4	68	43.6	39	54.9	72	43.1	2	10.5	0	0.0	188	35.7
Lr16	0	0.0	0	0.0	0	0.0	0	0.0	1	0.6	0	0.0	0	0.0	1	0.2
Lr24	2	3.6	8	14.8	36	23.1	21	29.6	59	35.3	6	31.6	0	0.0	132	25.1
Lr26	12	21.4	21	38.9	41	26.3	18	25.4	23	13.8	5	26.3	3	100.0	123	23.4
Lr3ka	49	87.5	49	90.7	69	44.2	25	35.2	34	20.4	6	31.6	1	33.3	233	44.3
Lr11	47	83.9	44	81.5	13	8.3	8	11.3	4	2.4	0	0.0	1	33.3	117	22.2
Lr17	53	94.6	48	88.9	127	81.4	56	78.9	65	38.9	19	100.0	3	100.0	371	70.5
Lr30	49	87.5	49	90.7	69	44.2	24	33.8	34	20.4	6	31.6	1	33.3	232	44.1
LrB	53	94.6	48	88.9	122	78.2	56	78.9	66	39.5	19	100.0	3	100.0	367	69.8
Lr10	16	28.6	13	24.1	154	98.7	67	94.4	166	99.4	19	100.0	2	66.7	437	83.1
Lr14a	55	98.2	53	98.1	126	80.8	60	84.5	91	54.5	19	100.0	3	100.0	407	77.4
Lr18	2	3.6	2	3.7	10	6.4	0	0.0	0	0	0	0.0	0	0.0	14	2.7
Lr21	0	0.0	0	0.0	0	0.6	0	0.0	56	33.5	0	0.0	0	0.0	56	10.6
Lr28	3	5.4	6	11.1	34	21.8	15	21.1	100	59.9	0	0.0	0	0.0	158	30.0
Lr39	7	12.5	5	9.3	124	79.5	60	84.5	150	89.8	12	63.2	0	0.0	358	68.1
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	56		54		156		71		167		20		3		526	

Table 3. Estimated losses in winter wheat due to rust in 2015 (T = trace, less than 1% loss statewide; — no state estimates 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
AL	220	68.0	14,960	0	0	0	0	0	0
AZ	2	103.0	206	—	—	—	—	—	—
AR	240	56.0	13,440	0	0	0	0	T	T
CA	150	70.0	10,500	0	0	0	0	3	269
CO	2,140	37.0	79,180	0	0	T	T	25	26,393
DE	65	65.0	4,225	0	0	T	T	0	0
FL	15	43.0	645	—	—	—	—	—	—
GA	145	43.0	6,235	0	0	1	47	T	T
ID	700	82.0	57,400	0	0	0	0	3	1,775
IL	520	65.0	33,800	—	—	—	—	—	—
IN	260	68.0	17,680	0	0	1	179	2	269
IA	15	52.0	780	—	—	—	—	—	—
KS	8,700	37.0	321,900	T	T	T	T	15	58,596
KY	440	73.0	32,120	—	—	—	—	—	—
LA	92	39.0	3,588	T	T	T	T	T	T
MD	270	64.0	17,280	0	0	T	T	T	T
MI	475	81.0	38,475	T	T	1	389	T	T
MN	43	58.0	2,494	0	0	T	T	15	440
MS	120	48.0	5,760	0	0	T	T	T	T
MO	610	53.0	32,330	0	0	T	T	2	492
MT	2,220	41.0	91,020	0	0	0	0	2	1,858
NE	1,210	38.0	45,980	0	0	T	T	12	6,270
NV	6	90.0	540	—	—	—	—	—	—
NJ	20	50.0	1,000	—	—	—	—	—	—
NM	190	25.0	4,750	—	—	—	—	—	—
NY	110	63.0	6,930	0	0	T	T	0	0

Table 3. Estimated losses in winter wheat due to rust in 2015 (T = trace, less than 1% loss statewide; — no state estimates 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
NC	570	53.0	30,210	0	0	T	T	0	0
ND	190	44.0	8,360	0	0	0	0	0	0
OH	480	67.0	32,160	T	T	T	T	—	—
OK	3,800	26.0	98,800	0	0	4	4,117	25	32,933
OR	735	47.0	34,545	0	0	T	T	T	T
PA	175	65.0	11,375	—	—	—	—	—	—
SC	160	46.0	7,360	0	0	0	0	0	0
SD	970	44.0	42,680	T	T	T	T	15	7,532
TN	395	68.0	26,860	0	0	T	T	T	T
TX	3,550	30.0	106,500	0	0	4	4,438	25	35,500
UT	110	48.0	5,280	—	—	—	—	—	—
VA	210	66.0	13,860	—	—	—	—	—	—
WA	1,590	56.0	89,040	0	0	0	0	1	899
WV	4	60.0	240	—	—	—	—	—	—
WI	210	74.0	15,540	T	T	1	157	2	317
WY	130	32.0	4,160	—	—	—	—	—	—
U.S. % loss				T		0.7		12.7	
U.S. total	32,257	42.5	1,370,188		T		9,325		173,545

Table 4. Estimated losses in spring and durum wheat due to rust in 2015 (T = trace, — = no state estimate available, N/A = data not available, * U.S. 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
CA	NA	NA	NA	0	0	0	0	0	0
CO	7	65.0	455	0	0	T	T	25	152
ID	425	70.0	29,750	0	0	0	0	6	1,899
MN	1,430	60.0	85,800	0	0	T	T	15	15,141
MT	2,440	31.0	75,640	0	0	1	764	1	764
NV	2	55.0	110	—	—	—	—	—	—
NY	NA	NA	NA	0	0	T	T	0	0
ND	6,650	48.0	319,200	0	0	0	0	5	16,800
OR	93	50.0	4,650	0	0	T	T	T	T
SD	1,260	48.0	60,480	T	T	T	T	12	8,247
UT	9	55.0	495	—	—	—	—	—	—
WA	625	36.0	22,500	0	0	0	0	T	T
U.S. % loss				T		0.1		7.2	
U.S. total *	12,941	46.3	599,080		T		764		43,003

DURUM WHEAT

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
AZ	140	101.0	14,140	—	—	—	—	—	—
CA	60	103.0	6,180	0	0	0	0	1	62
ID	10	70.0	700	0	0	0	0	0	0
MT	605	31.0	18,755	0	0	0	0	1	189
ND	1,075	39.5	42,463	0	0	0	0	0	0
SD	6	41.0	246	T	T	T	T	T	T
U.S. % loss				0		0		0.31	

yield losses of 4% due to leaf rust were estimated in the hard red winter wheat cultivars in Texas and Oklahoma, with trace levels of loss in all other states (see Table 3, pp. 76-77).

In the soft red winter wheat region of the southeastern states and Ohio Valley, *P. triticina* race MBTNB with virulence to *Lr1, Lr3, Lr11, Lr3ka, Lr17, Lr30, LrB,* and *Lr14a* was the most common race. In the hard red winter wheat region of Texas, Oklahoma, Kansas, and Nebraska, race MBDSD, with virulence *to Lr1, Lr3, Lr17, LrB, Lr10, Lr14*, and *Lr39,* was the most common race. In the hard red spring wheat region of South Dakota, North Dakota, and Minnesota, race TBBGS, with virulence to *Lr1, Lr2a, Lr2c, Lr3, Lr10, Lr21, Lr28,* and *Lr39,* was the most common race. As in past years, wheat cultivars with specific leaf rust resistance genes have likely selected the most common and virulent races of *P. triticina* in the different regions of the U.S.

Wheat stripe rust (caused by *Puccinia striiformis* f. sp. *tritici, Pst*). Stripe rust appeared early in 2015 (January and February) in Oregon, Louisiana, Arkansas, Mississippi, and Texas. Oregon experienced a very mild winter, whereas the Gulf States areas had a wet winter. Stripe rust, however, was particularly severe in the Great Plains and was found all the way to the Canadian border in North Dakota by early June. Cool, wet conditions in the spring in the Plains states were very conducive for stripe rust development. Wheat production in Texas, Oklahoma, Kansas, Colorado, Nebraska, and South Dakota was significantly impacted by stripe rust in 2015 (see Table 3 and 4, pp. 76-77); the heaviest recorded stripe rust year in Colorado and also in Nebraska. Stripe rust was still active and developing in South Dakota, North Dakota and Minnesota in late June. Although stripe rust was found in the Gulf States, Southeast, and mid-Atlantic areas, the impact was minimal in these areas. The onset of warm weather in the Gulf States limited stripe development there, whereas dry conditions in the Mid-Atlantic states limited development there. Warm, dry conditions in Washington hastened crop development and contributed to reduced stripe rust levels in the state.

Stripe rust resulted in significant losses in Great Plains states (see Tables 3 and 4, pp. 76-77) with an estimated national winter wheat loss of 12.7%, a 7.2% spring wheat loss, and 0.3% durum wheat loss due stripe rust in 2015.

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

For more information. For more details on the cereal rust situation in the U.S. as well original reports from CDL staff and cooperators, the bi-weekly Cereal Rust Bulletins and cereal rust observation maps, please visit: http://www.ars.usda.gov/Main/docs.htm?docid=9757.

ITEMS FROM NEBRASKA

UNIVERSITY OF NEBRASKA
Department of Agronomy & Horticulture, Department of Plant Pathology, and the USDA–ARS Grain, Forages and Bioenergy Research Unit, Lincoln, NE, 68583, USA.

Growing conditions.

The 2014–15 growing season would be considered being very heterogeneous for production. Western Nebraska was planted into generally acceptable moisture, and then had a very unusual winter with highly fluctuating temperatures leading to more winterkill than normal. Most Nebraska lines fared well. Rains at harvest delayed the harvest and weathered the grain. Southwestern Nebraksa had generally good growing conditions throughout the year and produced very good quality grain. Eastern Nebraska had a normal growing season with the exception of very heavy rains right after planting for early planted wheat, which hurt emergence. At flowering, excessive moisture lead to severe epidemics of stripe (yellow) rust and Fusarium head blight (scab).

Wheat production.

In the 2014–15 season, Nebraskans planted 1,490,000 acres of wheat and harvested 1,210,000 acres with an average yield of 38 bushels/acre for a total production of 45,980,000 bu. This production was much lower than the production in 2014, but higher than that in 2013. The high level of planted acres that were not harvested is likely due to winterkilling in western Nebraska due to fluctuating temperatures. In the 2013–14 season, Nebraskans planted 1,550,500 acres of wheat and harvested 1,450,000 acres with an average yield of 49 bushels/acre for a total production of 71,050,000 bu. In the 2012–13 season, 1,470,000 acres of wheat were planted in Nebraska and 1,130,000 were harvested with an average yield of 35 bu/a for a total production of 39,550,000 bu. The 2012–13 crop was one of the smallest crops in the last 50 years and certainly highlighted the effect of drought. In 2012, 1,380,000 acres of wheat were planted in Nebraska and 1,300,000 were harvested with an average yield of 41 bu/a for a total production of 53,300,000 bu. Despite continued genetic improvement, the main determinant in wheat production seems to be acres harvested, government programs, the price of corn, and weather (which also affects disease pressure and sprouting). This is an economic reality in understanding wheat yields and productivity in Nebraska.

New wheat cultivar NE10589.

NE10589 was released in 2015. A full description and data can be found at: http://agronomy.unl.edu/Baenziger/NE-10589SignedRelease.pdf. Briefly, NE10589 is a hard red winter wheat cultivar developed cooperatively by the Nebraska Agricultural Experiment Station and the USDA–ARS. NE10589 was released primarily for its superior adaptation to rainfed wheat production systems throughout Nebraska and in adjacent wheat producing states. NE10589 will be marketed as Husker Genetics Brand 'Ruth' Hard Red Winter Wheat, named in honor of our greenhouse manager who was a huge aid to the breeding program and who died far too young. Genetically, NE10589 is a semi-dwarf wheat, containing the *RhtB1b* allele (formerly known as *Rht1*). NE10589 was selected from the cross 'OK98697/Jagalene//Camelot' where the pedigree of OK98697 is 'TAM 200/HBB313E//2158'. The final cross was made in 2004. This line seems to be very broadly adapted and was selected using both phenotypic and genomic selection.

NE10589 was evaluated in Nebraska replicated yield nurseries starting in 2010, in the USDA-ARS coordinated Northern Regional Performance Nursery in 2013 and 2014, in the Southern Regional Performance Nursery in 2014, and in the University of Nebraska Fall Sown Wheat Performance Trials in 2014 to 2015. In the Nebraska Intrastate Nursery (2012 to 2015), NE10589 performed extremely well across Nebraska in head-to-head comparisons for grain yield with the currently popularly available wheat cultivars. These data are supported by the 2013 and 2014 USDA–ARS Northern Regional Performance Nursery where NE10589 ranked 9th and 2nd region-wide of the 37 and 40 entries tested in those years (data available at http://www.ars.usda.gov/Research/docs.htm?docid=11932). For a more northern adapted wheat cultivar, it also performed well in the 2014 Southern Regional Performance Nursery where it ranked 19th of the 40 lines tested in that year. In the last two years, NE10589 was tested in the Nebraska State Variety Trials across 25 environments. NE10589 (3,436 kg/ha) had higher grain yield than all currently popular winter wheat cultivars that were tested state-wide (e.g., Overland, 3,275 kg/ha; Freeman, 3,214 kg/ha; and Wesley, 2,947 kg/ha). Based upon these data, NE10589 is adapted to all rainfed wheat production in Nebraska. NE10589 is moderately late in maturity, which is very similar to that of Overland, two days later than that of Freeman, and one day later than that of Settler CL. The mature plant height of NE10589 is similar to that of Robidoux, but shorter than Camelot, Goodstreak, Panhandle, and Overland. NE10589 is taller than Wesley, Settler CL, and Freeman. NE10589 has moderate straw strength for a semi-dwarf wheat with little lodging reported in the years it has been tested. The winter hardiness of NE10589 is good and comparable to other winter wheat cultivars grown in Nebraska.

NE10589 is resistant to *Soilborne wheat mosaic virus* in field nurseries in Nebraska and is moderately resistant to stem rust in field nursery tests at St. Paul, MN, and stripe rust in field nurseries in Nebraska. The cultivar is moderately susceptible to susceptible for leaf rust. By molecular markers, NE10589 is believed to carry the *Lr37/Sr38/Yr17* translocation. NE10589 is moderately susceptible to Fusarium head blight (data from greenhouse and field observations in Nebraska and Kansas) and moderately susceptible to DON accumulation. Cultivar NE10589 is moderately resistant to moderately susceptible to Hessian fly, but its reaction can be quite variable among greenhouse seedling tests. NE10589 is susceptible to *Barley yellow dwarf virus* and *Wheat streak mosaic virus* (data obtained from the USDA–ARS Northern Regional Performance Nursery and field observations in NE).

NE10589 has high grain volume weight, which is similar to most high grain volume weight wheats. The overall end-use quality characteristics for NE10589 (scored as 4.0, where 3 is fair, 4 is good, and 7 is excellent) was lower than that of Wesley, but higher than that of Overland and similar to many commonly grown wheat cultivars. NE10589 should be acceptable to the milling and baking industries.

In positioning NE10589, based on performance data to date, it should be well adapted to most rainfed wheat production systems throughout Nebraska and in adjacent areas of the Great Plains. NE10589 is not recommended for irrigated wheat production, due to its not having similar straw strength and comparable yield potential to the best available irrigated wheat cultivars (data not shown). Where adapted, NE10589 should be a replacement for Overland (under rainfed production). NE10589 is genetically complementary to virtually all wheat cultivars grown in Nebraska, with the exception of Camelot and Jagalene.

NE10589 is an awned, tan-glumed cultivar. The field appearance is most similar to that of Wesley, but is easily separated because Wesley has a bronze chaff. After heading, the canopy is moderately closed and erect to inclined. The flag leaf is recurved and twisted at the boot stage. The foliage is green with a waxy bloom on the leaf sheath, with little waxy bloom on the spike at anthesis and on the leaves. The leaves are glaborous. The spike is tapering, narrow, and lax. The glume is short and wide, and the glume shoulder is square to elevated. The beak has an acuminate tip. The spike is predominantly inclined at maturity with some recurved spikes. Kernels are red colored, hard textured, and mainly ovate in shape. The kernel has no collar, a medium brush of short length, rounded cheeks, midsize germ, and a narrow and shallow crease.

NE10589 was developed with partial financial support from the Nebraska Agricultural Experiment Station and the Nebraska Wheat Development, Utilization, and Marketing Board. Partial funding for P.S. Baenziger is from Hatch project NEB-22-328; USDA–IFAFS competitive grant 2001-04462; USDA, NRICGP 00-353000-9266, 2004-35300-1470, and 2007-51300-0375; USDA CSREES NRICAP grant 2006-55606-16629; USDA OREI 2007-51300-03785; AFRI/2011-68002-30029; the CERES Trust Organic Research Initiative; and USDA under Agreement No. 59-0790-4-092, which is a cooperative project with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the USDA. Cooperative investigations of the Nebraska Agricultural Research Division, University of Nebraska, and the USDA–ARS.

New winter triticale cultivars.

P. S. Baenziger (breeder-inventor), K. Vogel, R. Mitchell, S. Wegulo, T. Regassa, D. Santra, and G. Hein.

In 2015, seven winter triticale (*xTriticosecale* Wittmack) lines **NT05421**, **NT07403**, **NT09423**, **NT11406**, **NT11428**, **NT12414**, and **NT12434**, developed cooperatively by the Nebraska Agricultural Experiment Station and the USDA–ARS and recommended for release in 2016 by the developing institutions. The lines were developed for grain or forage production primarily in the Great Plains and to provide triticale growers with greater diversity to select winter triticale lines for grain, forage, or cover crop. However, the University of Nebraska has commercial triticale partners who have tested these lines in regions beyond Nebraska and our testing network that also includes locations beyond Nebraska. Proprietary data from our cooperators are not shown and only data developed from Nebraska are presented. The previously released winter triticale (NE426GT) that is good for both grain and forage production (Baenziger et al. 2005) was used for head-to-head comparisons. NE422T (Baenziger and Vogel 2002), also previously released, was included in the comparisons because of it is an excellent forage triticale (4% better forage yielding than that of NE426GT). However, NE422T is a lower grain yielding line (16%) than NE426GT, which increases the cost of seed production. Hence, the two previously released cultivars represent the current grain and forage yield of commercially available winter triticale lines in Nebraska. In reviewing the forage data, no lines were significantly better than NE426GT, but two lines (NE11406 and NT12434) were significantly lower forage yielding than NE426GT. For grain yield, two lines (NT07403 and NT09423) were significantly better than NE426GT. No new line was significantly lower grain yielding than NE426GT. Thus, most of the modern triticale lines were similar in forage yield and equal or better for grain yield to the currently commercially available lines. Considering other attributes, for flowering date, NE422T was significantly later than NE426GT, which was expected. Only NT07403 was significantly earlier than NE426GT. The remaining lines were not significantly different from NE426GT. For plant height, NE422T, NT05421, and NT11428, were significantly taller than NE426GT, whereas NT07403 and NT12414 were significantly shorter than NE426GT.

Triticale has few diseases in Nebraska and there are no regional nurseries, hence there is little disease or insect data to report. Historically, triticale is very resistant to most diseases commonly found in Nebraska, such as the rusts, and many of the virus diseases, such as *wheat streak mosaic virus,* which is prevalent in western Nebraska. For example in 2012, David Marshall evaluated in Kenya using field races (TTKSK and its derivatives; personal communication) and had stem rust infections of 10% (NT05421), 1% (NT07403), and 1% (NT09423), with infection types of S, S, and S, respectively, whereas in the same nursery, Jagger wheat ranged from 50–70% infection and infection type of S. For stripe rust, NT05421, NT07403, NT09423, and Jagger were all rated as having an infection type of moderately susceptible. In 2013, NT11406 and NT11428 were evaluated for stem rust resistance in Kenya using field races, and both lines were rated as being resistant, whereas Jagger ranged from 15–60% infected with a susceptible infection type of dead (killed by the disease). Stripe rust was not present in 2013. In Nebraska, when leaf, stripe, or stem rust were present on wheat, NT05421, NT07403, NT09423, NT11406, NT11428, NT12414, and NT12434, would be considered as resistant. In years of high infection of ergot (caused by *Claviceps purpurea* (Fr.) Tul.), NT05421, NT07403, NT09423, NT11406, NT11428, NT12414, and NT12434, had very low infections. During its selection, lines with ergot are routinely discarded. Triticale is susceptible to bacterial streak disease (incited by *Xanthomonas campestris* pv. *translucens* (Jones et al.) Dye). No significant differences were detected among the lines tested. Note, bacterial streak disease was absent in the year that NT12414 and NT12434 were evaluated, so no data are presented for those lines.

Considering each line separately, NT05421 is a winter triticale with prostrate growth habit in the winter. NT05421 was derived from a complex cross mainly involving NE422T which the final cross was made in 1999. The F_1 was grown in the greenhouse in 2000, and the F_2 seed was planted as a bulk at Lincoln, NE, harvested with a combine in 2001, and replanted that autumn at Lincoln, NE, as an F_3 bulk. In 2002, $F_{3:4}$ heads were snapped from the F_3 bulk and planted in Lincoln, NE, that autumn as individual short rows (approximately 75-cm long with 25 cm between rows). In 2003, based upon visual selection for the absence of disease, good straw strength, and agronomic appearance, the better rows were selected. The harvested seed was visually inspected for seed quality and ergot, and those samples with poor seed quality (shriveled grain) and ergot were discarded. The remaining lines ($F_{3:5}$) were planted at Lincoln, NE, in four row plots that were 3-m long with 25 cm between rows in the autumn of 2003 and combine harvested in 2004. The center two rows were cut and threshed using a plot thresher. No further selection was made thereafter. Based upon grain yield, seed quality, and agronomic and resistance to disease, $F_{3:6}$ lines were advanced for planting in the autumn of 2004 and harvesting in 2005 in a multilocation trial at Lincoln (single replication), Mead (two replications), and Sidney, NE (single replication). The name NT05421 is derived from the line being selected in Nebraska (N) being a triticale (T) in 2005 (hence 05) and being derived from plot 421. Thereafter, NT05421 was tested in multilocation trials with three replications at the same three Nebraskan locations. Plant color at boot stage is blue-green, and the stem is without anthocyanin. The neck is moderately hairy and straight. The flag leaf is upright, not twisted, and with a waxy bloom. The auricle is colorless. The seed is amber in color, oval, wrinkled, and with a large and long brush.

NT07403 is a winter triticale with prostrate growth habit in the winter. NE07430 was derived from the cross 'NE98T424/Flood//NT00418', which was made in 2001. The pedigree of NE98T424 is 'Presto/NE91T409' and the pedigree of NT00418 is 'RAH-123/NE94T409'. The same breeding procedure described for NT05421 was used, beginning with the cross being made two years later. The plant color at boot stage is green and the stem is without anthocyanin. The neck is hairy and straight. The flag leaf is drooping, twisted and with a waxy bloom. The auricle is colorless. The head is mid-dense, clavate, awned, and the color is tan. The glumes at maturity are pubescent, mid-long, narrow, with a wanting shoulder. The beak is acute. The seed is amber in color, oval, slightly wrinkled, and with a large and long brush.

NT09423 is a winter triticale with prostrate growth habit in the winter. NE09423 was derived from the cross 'NE426GT/NT01417', which was made in 2003. The pedigree of NT01417 is 'NE85T121/NE87T148//RAH-123'. The same breeding procedure described for NT05421 was used beginning with the cross being made four years later. The plant color at boot stage is green and the stem is without anthocyanin. The neck is hairy and straight. The flag leaf is upright, not twisted and with a waxy bloom. The auricle is colorless. The head is mid-dense, fusiform, awned, and the color is tan. The glumes at maturity are glabrous, mid-long, narrow, with a wanting shoulder. The beak is acuminate. The seed is amber in color, ovate, wrinkled, and with a large and long brush.

NT11406 is a winter triticale with prostrate growth habit in the winter and derived from the cross 'NT04427// NE92T422/NE426GT sib/3/NT02458//CTM86.101/GWT 88-12', which was made in 2005. The pedigree of NT04427 is 'NE422T/TX95V71'1, the pedigree of NE92T422 is '85LT401/NE83T24', and the pedigree of NT02458 is 'RAH-123/NE90T413'. The same breeding procedure described for NT05421 was used beginning with the cross being made six years later. The plant color at boot stage is yellow-green and the stem is without anthocyanin. The neck is hairy and

straight. The flag leaf is upright, twisted and with a waxy bloom. The auricle is colorless. The head is mid-dense, oblong, awned, and the color is yellow. The glumes at maturity are slightly pubescent, mid-long, and mid-wide with a wanting shoulder. The beak is obtuse. The seed is amber in color, oval, slightly wrinkled, and with a mid-sized and short brush.

NT11428 is a winter triticale with prostrate growth habit in the winter and derived from the cross 'NE03T413/3/NT02458//CTM86.101/GWT 88-12', which was made in 2005. The pedigree of NE03T413 is 'NE426GT sib//TRICAL 2700'. The same breeding procedure described for NT05421 was used beginning with the cross being made six years later. The plant color at boot stage is green and the stem is without anthocyanin. The neck is hairy and straight. The flag leaf is upright, twisted and with a waxy bloom. The auricle is colorless. The head is mid-dense, fusiform, awned, and the color is yellow. The glumes at maturity are slightly pubescent, mid-long, and mid-wide with a wanting shoulder. The beak is obtuse. The seed is amber in color, oval, slightly wrinkled, and with a large and long brush.

NT12414 is a winter triticale with prostrate growth habit in the winter. NT12414 was derived from the cross 'NT05433//NE426GT', which was made in 2006. The pedigree of NT05433 is 'NE426GT/TX95VT7117'. The same breeding procedure described for NT05421 was used beginning with the cross being made six years later. The head is mid-dense, fusiform, awned, and the color is tan. The glumes at maturity are slightly pubescent, long, and mid-wide with a wanting shoulder. The beak is acuminate. The seed is amber in color, oval, slightly wrinkled, and with a mid-size and mid-long brush.

NT12434 is a winter triticale with prostrate growth habit in the winter derived from the cross 'NT01451/NT05434', which was made in 2005. The pedigree of NT01451 is 'OMI-4MI-3MI/NE91T410//RAH-123' and the pedigree of NT05434 is 'NE98T424/PLAI'. The same breeding procedure described for NT05421 was used beginning with the cross being made six years later. The neck is hairy. The head is mid-dense, oblong, awned, and the color is tan. The glumes at maturity are slightly pubescent, long, and wide with a wanting shoulder. The beak is acuminate. The seed is amber in color, ovate, wrinkled, and with a large and long brush.

The lines have been uniform and stable since 2014. Less than 2.0% of the plants were rogued from the Breeder's seed increase in 2014–15. Rogued plants were taller in height or were awnless. Up to 3% off types may be encountered in future generations. The Nebraska Foundation Seed Division, Department of Agronomy and Horticulture, University of Nebraska–Lincoln, Lincoln, NE 68583 had foundation seed available to qualified certified seed enterprises in 2015 with the first sale of certified seed in 2016. The U.S. Department of Agriculture will not have commercial seed for distribution. The seed classes will be Breeder, Foundation, Registered, and Certified. All lines will be submitted for plant variety protection under P.L. 10577 with the certification option. A fee will be assessed on all certified seed sales. Small quantities of seed for research purposes may be obtained from Dr. P. S. Baenziger and the Department of Agronomy and Horticulture, University of Nebraska–Lincoln, for at least 5 years from the date of this release. In addition, a seed sample has been deposited in the USDA-ARS National Small Grains Collection, Aberdeen, ID, and this seed is freely available to interested researchers.

The lines were developed with partial financial support from the Nebraska Agricultural Experiment Station. Partial funding for P.S. Baenziger is from Hatch project NEB-22-328 and the Nebraska Wheat Development, Utilization, and Marketing Board. Cooperative investigations of the Nebraska Agricultural Research Division, University of Nebraska, and USDA–ARS.

The effect of Fusarium head blight and stripe rust on grain yield of hard winter wheat in Lincoln, NE.

Javed Sidiqi, P.S. Baenziger, S.N. Wegulo, and G. Bai.

To determine the effect of fungal plant pathogens on grain yield in eastern Nebraska, we initiated a study in 2015 to compare fungicide treated and untreated plots using our elite nursery. Although it is well-documented that diseases reduce grain yield and fungicide use is becoming more common, growers still debate the cost and value of using fungicides. This experiment was to provide growers with information on the value of fungicides, so they can make informed decisions and also learn about our advanced breeding lines and how they respond to fungicides in the presence of disease. The Nebraska elite nursery contains 60 lines (two historic check cultivars, six cultivars, and 52 unreleased elite lines).

Two fungicide regimens, treated vs. untreated, were utilized. In the treated plots, Cruiser Max® was used to treat the seed before planting, then at early spring green-up, the plots were sprayed with Priaxor®. At flag leaf, the plots were sprayed with Twinline® followed by Caramba® at flowering. Seed treatments and fungicides were not applied to the untreated plots. Each fungicide treatment (treated and untreated) had 60 genotypes replicated twice in an alpha lattice design with an incomplete block size of five entries. Grain yield was harvested using a small plot combine and the grain was weighed after drying in the seed house.

Eastern Nebraska receives on average 65 to 75 cm of rainfall annually. In 2015, the Lincoln research station received 42 cm of precipitation from 1 May to 15 June. The average flowering date for winter wheat in our elite trial was 24 May with a range from 20 May to 29 May. Hence, the conditions were ideal for Fusarium head blight (FHB). The other major disease present was stripe rust. Other diseases that are favored by cool moist conditions were present, but not to the extent of FHB and stripe rust. Average FHB index in the untreated plots was 56% (range 4–96%) compared to 10% in the treated plots (an 82% reduction in index; range 0–68%). Yield in the treated plots averaged 3,460 kg/ha (range 1,360– 4,860 kg/ha) compared to 1,940 kg/ha (a 44% reduction in yield; range 340–3,500 kg/ha). On average, the diseases caused a 44% reduction in yield (excluding the two historic check cultivars which actually yielded higher in the untreated plots; yield loss due to disease ranged from 15% to 86%). Significant negative correlation between FHB index and yield in the untreated plots ($R = –0.38$; $P = 0.0034$) indicated that some lines had good FHB resistance whereas others were susceptible. In contrast, there was no correlation between FHB index and yield in the treated plots ($R = 0.04$; $P = 0.7454$), indicating the effectiveness of Caramba® applied at flowering in suppressing FHB. The stripe rust reactions varied among lines from highly resistant to highly susceptible. In looking at those lines that had infection scores of 1–3 (on a 1= resistant to 9= susceptible scale) for stripe rust, the grain yield loss averaged 30%, presumably due to FHB. In looking at those lines with infection scores of 7–9 for stripe rust, the grain yield loss averaged 50%. In both the resistant and susceptible to stripe rust groups, lines varied in their response to FHB, with the best lines having only a 15% or 27% yield loss. Although not measured, the effects on grain volume weight and seed germination were obvious in preparing and planting seed this autumn. This experiment will be repeated to provide multi-year disease loss information and to ensure having high quality seed for planting. Growers in eastern Nebraska were warned of the FHB epidemic, and many decided to use fungicides despite the low price of wheat. Clearly, this year fungicides were economically beneficial, especially when coupled with cultivars that also had some tolerance or resistance to FHB and stripe rust.

In previous research, we found *Fhb1*, a major gene for FHB tolerance, was not pleiotropic or linked to genes that reduce grain yield. We are using high yielding *Fhb1* lines from segregating populations and Wesley *Fhb1 or* Overland *Fhb1* in our crossing block. For the first time, we are seeing lines in our multiplelocation observation nursery that contain *Fhb1*, indicating our breeding strategy is beginning to work. The backcrossing approach is probably the best way to move needed genes into adapted line for further wheat improvement.

Response of a collection of waxy *(reduced amylose) wheat breeding lines to Fusarium graminearum.*

D.L. Funnell-Harris and R.A. Graybosch.

Loss of function mutations in the *Waxy* (*Wx*) gene, encoding granule-bound starch synthase I (GBSSI) that synthesizes amylose, result in starch granules containing mostly amylopectin. Wheat grain with this trait has increased usability for some foods due to the ability to modify starch composition and nutritional value in the end product. However, impaired GBSSI activity may alter grain and starch structure and, consequently, responses to pathogens. There are no published reports on response of *waxy* wheats to Fusarium head scab. A screen of colonization by *Fusarium graminearum* of *waxy* breeding lines and wild-type and *waxy* checks was conducted at Mead, NE, in 2014. Grain was either surface disinfested before plating or directly plated onto medium semiselective for *Fusarium* spp., indicating internal or both internal and superficial infections, respectively. Grains with fungal growth were enumerated for each line and grain treatment. Nondisinfested *waxy* grains (69.5%) were significantly less colonized as compared with wild-type (78.9%) ($P < 0.01$). Surface disinfested grains of both phenotypes had similar levels of infection (14.4% for wild-type versus 10.0% for *waxy*; $P = 0.07$). Fungal colonies growing onto the medium were transferred and morphologically identified as similar to *Fusarium graminearum*, *Fusarium* spp., or other fungi. Along with *F. graminearum*, *F. verticillioides, F. equiseti,* and *F. acuminatum*, were common in wild-type grain, whereas the most commonly detected species in *waxy* grain was *F. verticilliodes*. These preliminary results indicated that *waxy* wheats are not more susceptible to *F. graminearum* than

wild-type. Analyses of mycotoxins such as deoxynivalenol will be needed to confirm whether these promising *waxy* lines in development are not more susceptible to *F. graminearum* than non-*waxy* lines.

Prospects for selecting wheat with decreased cadmium concentration in grain.

M. Guttieri, C. Liu, P.S. Baenziger, D. Rose, and B. Waters.

Wheat is a primary staple cereal and a significant source of mineral nutrients in human diets. Therefore, decreasing concentration of the toxic mineral, cadmium (Cd), could significantly improve human health. Previously, we found that grain Cd concentration of some genotypes grown in Nebraska trials were above the Cd Codex guidance level (> 0.2 mg kg/L), and highly repeatable differences in grain Cd were found between pairs of low and moderate Cd commercial cultivars. Grain Cd concentration was predicted by Cd concentration in above ground plant tissues at anthesis. Genome-wide association scans using high-density SNP markers identified markers on 5AL associated with grain Cd in a region homoeologous to the *Cdu1* locus on 5BL in durum wheat. Our current work is to study the level of Cd in mill streams, the uptake of Cd, and ways to select for lower Cd.

Hybrid wheat.

N. Garst, A. Easterly, and P.S. Baenziger; A. Ibrahim and J. Rudd (Texas A&M University), and Bhoja Basnet (CIMMYT Int, Mexico).

One of the great opportunities and challenges for wheat improvement is the development of hybrid wheat. Currently. numerous companies have hybrid wheat breeding efforts with Saaten-Union Recherche France be one of a few companies that markets hybrid wheat. Our belief is that the public sector needs to have a public, transparent hybrid wheat breeding effort to advance the science and educate the next generation of plant breeders. As such, we have been working on hybrid wheat for the past 5 years.

In order for hybrid wheat to be commercially successful, a number of characteristics must be considered. First, we must find effective hybridization system on a large scale. For this, the small grains program at UNL will be developing and examining potential hybrids developed through use of chemical hybridizing agents (CHAs), then evaluating the potential for a cytoplasmic-male sterility system to produce commercial hybrids. Crossing blocks were planted in the autumn of 2014 and treated with CHA (thanks to a collaboration with Saaten-Union Recherche, France) in 2015 to develop 650 experimental hybrids. To measure CHA-induced sterility, we visually assessed gaping heads (routinely seen in genetic and cytoplasmic male sterility) and phytotoxicity, induced male sterility using bagged heads, and then harvested yield. Over 85% of the bagged heads had three seeds or less, indicating over 90% sterility. However, this is likely a conservative estimate, because rains throughout flowering delayed head bagging, allowing for some cross pollination, and fertile florets inside a bag could pollinate sterile florets within the bag. Phytotoxicity was measured and appeared to be higher in the Nebraska germplasm than in the Texas germplasm. We believe this was most likely due to a staging error prior to the application of the CHA. The Nebraska and Texas lines were very similar in immature head length in the early spring when we sprayed; thus, we sprayed all of the lines in the female block on the same day. However, the Nebraska lines flowered three days later than the Texas lines, indicating we may have sprayed the Nebraska lines too early. Phytotoxicity with the CHA was low in the Texas material, which indicated that when CHA is properly applied, we see low incidence and severity of phytotoxicity. Anther extrusion was important in the crossing blocks where the male lines averaged from four to eight (with nine indicating a line with excellent anther extrusion) for this trait. The correlation between harvested grain yield and anther extrusion in the male pollinator line was $r=0.59$, $P < 0.01$). The average grain yield on the female plots pollinated by Freeman, one of our best anther-extruding lines (anther extrusion score: eight), was 768 g/plot. The seed set on the female lines pollinated by Freeman also was helped because Freeman is a moderately late line; thus, the maximum amount of pollen would be shed while the female lines were 'gaping' (proper nick for hybrid seed production).

Greenhouse work to identify R lines is underway, in conjunction with the introgression of male sterile cytoplasm into Nebraska-adapted winter wheat lines. Most current wheat breeding is done for the development of inbred cultivars and, as such, no true heterotic pools have been identified. Through utilization of modern genomic systems, we will work to build reliable and high-performing heterotic pools for hard winter wheat.

Genotype-by-sequencing for SNP discovery and genotyping; field trial analysis by incorporating spatial trends; and integration of genomic selection in the Nebraska Wheat breeding program.

Vikas Belamkar, Mary J. Guttieri, Ibrahim El-basyoni, Waseem Hussain, Jesse Poland, Diego Jarquín, Aaron J. Lorenz, and P. Stephen Baenziger.

The Nebraska wheat breeding program has released ~36 cultivars to date, and has a vital role in feeding millions of people. In order to meet the global food demand, wheat yields need to increase by 1.7% a year. However, the current increase in yield is only 0.9% a year. Genomic selection (GS) can rapidly increase genetic gain over time by increasing selection intensity and selection accuracy and reducing generation interval time in a breeding program. Our objectives are to (1) build a pipeline to analyze genotype-by-sequencing (GBS) data for SNP discovery and genotyping; (2) incorporate spatial trends while analyzing field trials to generate accurate best linear unbiased predictions (BLUPs) or estimates (BLUEs); and (3) inspect whether GS can (a) predict performance of new lines in a trial, (b) improve accuracy of selection decisions, (c) recycle elites line earlier to the crossing block, (d) reduce costs by phenotyping a subset of lines, and (e) predict performance of lines across locations.

This work was comprised of 1,100 entries from four independent $F_{3:6}$ nurseries (also known as DUP trials) evaluated during 2012–15 at 27 environments (year x location combinations). Each year, the $F_{3:6}$ nursery was composed of ~267 entries and three checks, which were grown in a single replicate augmented design at five to eight locations in Nebraska. Yield (kg/h) was analyzed using a mixed model analysis pipeline built for analyzing augmented trials while accounting for global-trends (experimental design), local-trends (spatial variation within the trial), or both. For 22 of the 27 environments, models adjusting for spatial variation provided better fit to the data. Spatially corrected BLUPs from the best performing mixed model were generated and used in the downstream analysis.

Genotype-by-sequencing was used to discover and genotype SNP markers. A SNP database was built for the breeding program by analyzing GBS data of ~3,300 unique genotypes sequenced from 2012–15. The average accuracy of SNP calling tested using lines sequenced multiple times was >95%. Nearly 206,622 SNPs were identified in the breeding program and are available for multiple projects in the breeding program. Filtering the SNPs with maximum missing percentage of less than 80% reduced the SNPs to 79,118. These SNPs were then processed through the imputation algorithm, and the genotype calls were successively imputed. Further filtering of SNPs by applying filtering relevant to GS (SNPs with minor allele frequency greater than 0.05 and imputation accuracy value of allelic R^2 greater than 0.5) provided 26,925 high-quality SNPs across the 1,100 lines for GS.

Genomic estimated breeding values (GEBVs) were generated using BGLR package and customized R-scripts, and Reproducing Kernel Hilbert Space Regression (RKHS) model. For each of the years (2012–15), genomic prediction ability (PAB) was estimated by randomly marking entries as missing in steps of 10%, from 10% to 90% of dataset. For example, 50% of the lines are marked as missing in 2012, and the remaining 50% of the entries in 2012 and all of the entries from 2013, 2014, and 2015 are used to predict the performance of the 50% of the entries marked as missing in 2012. This process is repeated 10 times by randomly marking 50% of the entries missing in the 2012 trial. The correlation value between GEBVs and observed phenotypic values (BLUPs) for each of the run is recorded. This correlation value is referred to as the prediction ability (PAB). We also estimated prediction ability (PAC) by marking 100% of the entries missing in a year, and using the data from rest of the years to make predictions. This scenario is similar to predicting performance of new lines in a trial using the data from previous years. Average PAB calculated using 10-fold cross validation ranged from 0.229 to 0.552, and PAC varied from 0.167 to 0.282.

The prediction ability values may not be truly helpful from a practical breeding perspective. They do not provide enough confidence for ranking lines based on GEBVs instead of spatially corrected BLUPs, or observed phenotypic values. In order to address this question, we tracked entries from each of these four nurseries that were advanced, and it was remarkably apparent that lines with 'above average GEBV and BLUPs' were being retained for longer times in the breeding program. This suggests using GEBV together with BLUPs can improve accuracy of selection decisions and recycle elite lines earlier to the crossing block.

Prediction ability estimated with 50% of the entries missing in each year, found more winners (entries) with above average GEBV and BLUPs. Hence, evaluation of only 50% of the entries in a year to make accurate selections seems possible. Improving PAC from the current value of ~0.20 to >0.37 will trigger examining skipping of a field trial year.

Currently, we are exploring GS models integrating G x E information; utilizing multi-year, multi-location evaluation of $F_{3:6}$ nurseries (DUP trial) to assist in selecting entries suitable for advanced multi-location yield trials from the $F_{3:5}$ nursery (also known as WS4R8 nursery), which has ~1,800 entries and is tested at a single location. Genomic seletcion for quality traits also is in progress.

Enhancing wheat drought tolerance using SNP markers based on high-throughput genotyping by sequencing technology.

Waseem Hussain, P. Stephen Baenziger, Vikas Belamkar, Mary Guttieri, Amanda Easterly, Jorge Venegas, and Jesse Poland.

Globally, drought is the most wide-spread limitation to wheat productivity and stability in rainfed systems. The Great Plains wheat belt has been battling drought for years. Consequently, developing wheat cultivars with enhanced drought tolerance and high yield has been the focus of many wheat improvement programs. Improving drought tolerance is challenging due to its complex nature, and previous studies conducted in identifying key genes/quantitative trait loci (QTL) were based mostly on low-density markers and not able to provide precise information about the numbers and locations of QTLs controlling the traits related to drought. To increase the power and precision of QTL mapping in wheat, high-density linkage maps are needed. Genotyping-by-sequencing (GBS) is one of the next generation sequencing method that allow sequencing, discovery, and genotyping of thousands of SNPs in cost effective manner and quickly. The SNPs generated through GBS can be used to develop the high-density linkage maps for precision QTL mapping in wheat. High-density linkage maps may be useful to genetically dissect and find the key genes underlying complex traits such as grain yield in wheat. This project will (i) determine the genetic variability of the recombinant inbred lines (RILs) derived from contrasting parents Harry and Wesley for several morpho-physiological traits under multiple rainfed environments, (ii) develop a high-density, linkage map based on GBS-generated SNPs in 204 RILs, (iii) determine the reliability of the newly constructed map with known tagged genes of chaff color and wax/glaucousness, and (iii) identify QTL and the 'QTL x environment' interaction for several morpho-physiological traits.

After stringent filtering, a high-density linkage map was constructed with 2,923 SNPs distributed on 36 linkage groups.The total length of linkage map spanned 5,269.34 cM with an average distance of 1.79 cM between adjacent markers. The high accuracy and reliability of this map was illustrated by finding and co-localizing the genes for chaff color and wax/glaucousness to correct and previously mapped genomic regions. For plant height, a total of 18 QTL were identified across all locations on linkage groups 2DS, 2BL, 3A, 3B.3, 6A.2, 7AL, and 7B.2, and the phenotypic variance explained by these QTL ranged from 4.9 to 16.8%. Six QTL revealed significant interactions with environment and accounted for 1.11–2.73% of the phenotypic variation. Interestingly, a major QTL, *qph.hw.2DS,* was found in all the five environments and explained 7.4–16.4% of the phenotypic variation. A height-reducing allele for this QTL was contributed by Wesley. QTL mapping for grain yield revealed in total 14 QTL across all locations on linkage groups 2D, 3A, 4A, 4B, 5B, 6B, 6D, and 7A. The phenotypic variance explained by these QTL ranged between 3.9– 19.5 %. QTL *qyld.hw.6B.2* was stable and detected in three locations followed QTL *qyld.hw.6B.1* detected in two locations. Favorable alleles for grain yield were contributed by both the parents. Digenetic interactions between QTL was evident, however, none of the interactions were stable across locations. Six QTL revealed significant interactions with environment and accounted for 1.94% to 18.46% of the total phenotypic variation.

Biofortification of winter wheats by incorporating low phytate and Gpc-B1 traits.

J.P. Venegas, R.A. Graybosch, and P.S. Baenziger.

Approximately 60% of the world's population are iron (Fe) deficient and over 30% are zinc (Zn) deficient. This situation is attributed to production areas with low mineral phytoavailability and consumption of staple crops with low tissue mineral concentrations and/or high concentrations of antinutrients such as oxalate, tannins, or phytic acid (IP6). To alleviate this situation, developing wheats with higher grain Fe and Zn concentrations and low phytic acid (LPA) content are needed. For this study, two types of RIL populations were created; one population from '*Gpc-B1*/LPA' straight crosses and ten populations from '*Gpc-B1*/*LPA*//adapted cultivars' three-way crosses, in which F_1 derived from the initial '*Gpc-B1*/LPA' crosses were mated with Nebraska-adapted winter wheat materials to enhance agronomic adaptation to the target growing environments. After the F_4, all RILs were classified as either wild type (WT) or LPA using the high inorganic

phosphate (HIP) protocol. HIP results from the two- and three-way cross populations showed differences in the amount of LPA RILs in both crossing methods. Fifty LPA RILs out of 400 were identified in the two-way cross population and 24 LPA RILs out of 200 were identified in one of the families from the three-way cross populations. The observed segregation suggests that the trait is controlled by two or more genes. Several, single LPA mutations were isolated, mainly in maize, barley, and rice. This study confirms the results of a previous segregation analysis using a different population and the polygenic inheritance of the wheat LPA mutation.

Temperature-dependent Wsm1 and Wsm2 gene-specific blockage of viral long-distance transport provides resistance to Wheat streak mosaic virus and Triticum mosaic virus in wheat.

Satyanarayana Tatineni, Everlyne N. Wosula, Melissa Bartels, Gary L. Hein, and Robert A. Graybosch.

Wheat streak mosaic virus (WSMV) and *Triticum mosaic virus* (TriMV) are economically important viral pathogens of wheat. Wheat cultivars Mace, carrying the *Wsm1* gene, and Snowmass, with *Wsm2,* are resistant to WSMV and TriMV, and WSMV, respectively. Viral resistance in both cultivars is temperature-sensitive and effective at 18ºC or below but not at higher temperatures. The underlying mechanisms of viral resistance of *Wsm1* and *Wsm2*, nonallelic, single dominant genes, are not known. We found that fluorescent protein-tagged WSMV and TriMV elicited an approximately similar number and sized foci at 18°C and 24ºC on inoculated leaves of resistant and susceptible wheat cultivars. These data suggest that resistant wheat cultivars at 18ºC facilitated efficient cell-to-cell movement. WSMV and TriMV efficiently replicated in inoculated leaves of resistant wheat cultivars at 18ºC but failed to establish systemic infection, suggesting that *Wsm1*- and *Wsm2*-mediated resistance debilitated viral long-distance transport. Neither virus was able to enter the leaf sheaths of inoculated leaves or crowns of resistant wheat cultivars at 18ºC but both were able to do so at 24ºC. Thus, wheat cultivars Mace and Snowmass provide resistance at the long-distance movement stage by specifically blocking virus entry into the vasculature. Taken together, these data suggest that both *Wsm1* and *Wsm2* genes similarly confer virus resistance by temperature-dependent impairment of viral long-distance movement.

Observations on the quality characteristics of waxy (amylose-free) winter wheats.

R.A. Graybosch (USDA–ARS, Lincoln, NE) and Jae-Bom Ohm and Linda Dykes (USDA–ARS, Fargo, ND).

Previous investigations have suggested waxy (amylose-free) wheats possess weak gluten properties and may not be suitable for commercial gluten extraction, limiting the use of waxy wheat as a source of unique starch, because gluten is a by-product of the wheat starch purification process. Fifty waxy wheat lines were used to determine to what extent gluten protein and other grain quality related traits might vary and, consequently, allow the development of waxy wheat with acceptable gluten properties. Among the waxy lines, significant variation was observed for all measured quality traits with the exception of flour protein concentration. No waxy entries statistically equaled the highest ranking nonwaxy entry for grain volume weight, falling number, flour yield, or mixograph mix time. No waxy lines numerically exceeded or equaled the nonwaxy mean for falling number, flour yield, or mixograph mix time. For grain and flour protein related variables, however, many waxy lines were identified well within the range of acceptability, relative to the nonwaxy controls used in this study. Approximately 50% of the waxy lines did not differ from the highest ranking nonwaxy cultivar for grain and flour protein concentrations. Forty-three (86%) of the tested waxy lines were not significantly different from the nonwaxy line with the highest mixograph mixing tolerance, and 22/50 (44%) of the waxy wheat lines did not differ from the highest ranking nonwaxy line in gluten index scores. All waxy experimental lines tested produced gluten via Glutomatic washing. The quality of the gluten, as measured both by mixograph and gluten index, varied widely among the waxy lines tested, and waxy lines not statistically different from the highest ranking control nonwaxy cultivars were identified. These observations suggest that weak gluten is not a natural consequence of the waxy trait, and waxy cultivars with acceptable gluten properties can be developed.

Comings and goings.

All projects are more than crosses, selections, evaluations, data, and seed. At its heart, it is the people who make this research possible. Dr. Mary Guttieri completed her PhD. degree and continued to help the project immensely while working as a postdoc with Dr. Brian Waters before accepting a position with the USDA–ARS in Manhattan, KS. Dr. Kath-

erine Frels, Dr. Juthamas Fakthongphan, and Dr. Santosh Rajput successfully completed their PhDs. Dr. Hanaa Abouzeid returned home after working in the project as a Fulbright visiting scholar. Jorge Venegas and Madhav Bhatta joined the project as new graduate students. Ms. Amira Mourad and Dr. Ahmed Sallam joined the project as visiting scientists. Mr. Rich Little, after 7 years of leading our organic research project, accepted another position and works part time leading the organic triticale research. We are extremely grateful for the excellent work that the team has done and continues to do.

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SOUTH CAROLINA

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The quest for celiac-safe wheat.

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In the last decade, a wide array of gluten-free products became available for gluten sensitive, intolerant, and allergenic individuals. Market for these products is burgeoning and expected to touch a $2.34 x 10^9 sales mark by 2019. Generally speaking, gluten-free products are not an ideal choice for consumption by individuals with no medical necessity. A gluten-free diet is standard therapy for the 'gluten syndrome', albeit there are a number of associated issues, such as: *i*) resent research provided compelling evidence that strict adherence to a diet totally devoid of gluten-containing grains, or based on foods specifically manufactured for celiac patients, deteriorates the gut health of consumers by its negative influence on gut microbiota. The gluten-free diet also is shown to increase the risk of colon cancer in consumers, because of the reduced content of dietary fiber and bioactive compounds, such as antioxidants (Gil-Humanes et al. 2014; De Palma et al. 2009 and references cited therein). *ii*) Adaption to the gluten-free diet is shown to initially improve the patient condition, but long-term adherence to it results in multiple deficiencies and changes in a patients body mass index (BMI), which increases their vulnerability to other disorders (Theethira et al. 2014). In view of these facts, and other benefits associated with wheat intake, a number of countries recommend consuming 250–350 g of bread per day (depending on national food habits), and the World Health Organization recommends eating bread several times per day (World Health Organization 2003).

In a nutshell, developing potential alternatives to the gluten-free diet by modifying the composition of wheat grains to make them suitable for consumption by celiac patients is imperative. As reported previous ly in the *Annual Wheat Newsletter*, so far we have characterized wheat genotypes with 45.2% to 76.4% reductions in their respective gluten contents. These genotypes accumulate fairly reduced amounts of gliadins and low-molecular-weight glutenin subunits. However, their release for general consumption by celiac patients cannot be considered due to labeling issues and the inability of the current medical system to diagnose sensitivity of individual patients to the specific gluten proteins. The conceivable solution to this problem will be to develop celiac-safe wheat genotypes, which are completely devoid of immunogenic prolamins. In this direction, we received a re-investment grant from the Life Sciences Discovery Fund (LSDF) to employ cutting-edge genome editing procedures to simultaneously silence two epigenetic regulators of prolamin accumulation in wheat endosperm. The approach undertaken in the LSDF research grant involves use of reduced gluten wheat genotypes for genetic retransformation with the newly developed genome editing constructs to pyramid their effects on gluten accumulation in these genotypes. Preliminary results obtained in this direction are discussed below.

Likely reasons for the incomplete elimination of immunogenic prolamins in wheat transformants expressing the *DEMETER* targeting hairpin and artificial micro RNAs. Accumulating evidences of our own and parallel research suggested that *DEMETER* (*DME*) expression starts early during grain development, with low-level expression before fertilization to medium- to high-level expression 1 to 15 days after pollination (our unpublished results and Kapazoglou et al. 2013). On the other hand, the endosperm-specific, wheat high-molecular-weight (HMW) glutenin gene *1Dy*

promoter, which we used to drive expression of the *DME* silencing hairpin- and artificial micro RNAs, triggers expression of the native gene 6–8 days after pollination (Thilmony et al. 2014). These observations, to some extent, explained the reason behind incomplete silencing of the *DME* homoeologues in >400 transformants screened so far (Rustgi et al. 2014, 2015). The concomitant effect of incomplete silencing of *DME* homoeologues also was observed on the accumulation of gliadins and glutenins in developing endosperm, especially on the γ-gliadins, which accumulate early during grain development (cf. Piston et al. 2009).

Approach adapted to develop celiac-safe wheat genotypes. Recent characterization of a knockout mutant in the iron-sulfur (Fe–S) cluster biogenesis gene of *Arabidopsis* with an accompanying silencing effect on the DME targeted genes, sparked new possibilities. This gene is reported to facilitate installation of the Fe–S cluster on the DME enzyme, which is vital for its interaction with genomic DNA and its subsequent demethylation. The emerging knowledge about DEMETER's structure, function, and regulation has prompted us to target this gene for site-directed mutagenesis in selected reduced-gluten wheat genotypes, formerly reported by in Rustgi et al. (2014, 2015). Taking advantage of the new findings in *Arabidopsis* and the advent of genome editing procedures, we made the following two changes to our strategy: *i*) retransform selected wheat transformants with a DME-specific, TALE repressor driven by a maize endosperm specific promoter, which exhibits an expression pattern similar to that of the wheat *DME* gene; and *ii*) integrate the *DME* TALE repressor in the Fe–S cluster biogenesis gene homologs in wheat. Integration of the DME TALE repressor in the Fe–S cluster biogenesis gene is expected to have an additive effect on the silencing of the wheat *DME* genes in the reduced-gluten wheat genotypes used for genetic retransformation.

Collectively, simultaneous silencing of the *DME* and the Fe–S cluster biogenesis genes in the formerly characterized gluten-deficient wheat transformants will check DME activity at three time points: 1) transcriptional, by DME-specific TALE repressor, 2) post-transcriptional, by DME targeting hp-/amiRNAs), and 3) post-translational, by insertional mutagenesis of the Fe–S cluster biogenesis genes. This approach is expected to provide desired level of DME suppression with concomitant effect on the accumulation of immunogenic prolamins in developing grains.

Cloning of the Fe–S cluster biogenesis gene from common wheat. To target Cas9 nucleases to the wheat homologs of the Fe–S cluster biogenesis gene, full-length genomic copies of the gene were cloned and sequenced from the target wheat genotype. Similar to *DME* homoeologues, the Fe–S cluster biogenesis genes exist in three copies located on the long arms of wheat group-2 chromosomes (2AL, 2BL, and 2DL). The three homoeologous copies are transcriptionally active, for which cDNA sequences are available in the public domain. In order to obtain full-length genomic sequences of the Fe–S cluster biogenesis genes from wheat cultivar Brundage 96, PCR primers were designed based on sequences of cDNA clones and the available genomic DNA sequences of this gene from wheat cultivar Chinese Spring. Brundage 96 is a wheat genotype we formerly used for genetic transformation with the *DME*-specific RNA interference constructs. Transformants developed in the Brundage 96 background currently are being used as explant source for genetic retransformation with DME TALE repressor and CRISPR Cas9 nuclease constructs.

Construction of dTALE repressor (donor) and CRISPR Cas9 nuclease constructs. In order to achieve complete endosperm-specific silencing of the three homoeologous wheat *DME* genes, a donor construct flanked on either side by the sequences of the Fe–S cluster biogenesis gene was developed. A 16.5-repeat, TALE array specifically designed to target a 17-nucleotide sequence, in the promoter region of the *DME* homoeologues, was assembled following a stepwise procedure described in Cermak et al. (2011). In this construct, the *DME* TALE repressor is cloned under the control of a maize endosperm-specific promoter and a nopaline synthase (*nos*) terminator.

A second nuclease construct, specifically targeting a conserved region of 20 nucleotides in the wheat homologs of the *Arabidopsis* Fe–S cluster biogenesis gene, was developed. The purpose of this construct is to introduce double-stranded breaks at the target site in the gene of interest, which increases the possibility of homologous recombination mediated DNA repair at the desired genomic site. In order to develop the desired CRISPR Cas9 constructs, a readymade rice CRISPR Cas9 construct was procured from Addgene (Cambridge, MA), and modified for the gene of interest.

Delivery of DEMETER TALE repressor (donor) and CRISPR Cas9 nuclease constructs. Selected, reduced-gluten wheat genotypes for genetic retransformation were grown in the greenhouse, and spikes at Feeke's stage 10 to 10.1 were collected (Large 1954). The spikes were pretreated to induce embryogenesis in uninucleate microspores following Brew-Appiah et al. (2013). The isolated androgenic microspores were regenerated into calli and will be co-transformed with the *DME* TALE repressor and CRISPR Cas9 construct following Rustgi et al. (2016). The scheme of events leading to the first crop of putative transformants is shown (Fig. 1, p. 91). Once wheat genotypes with TALE repressor

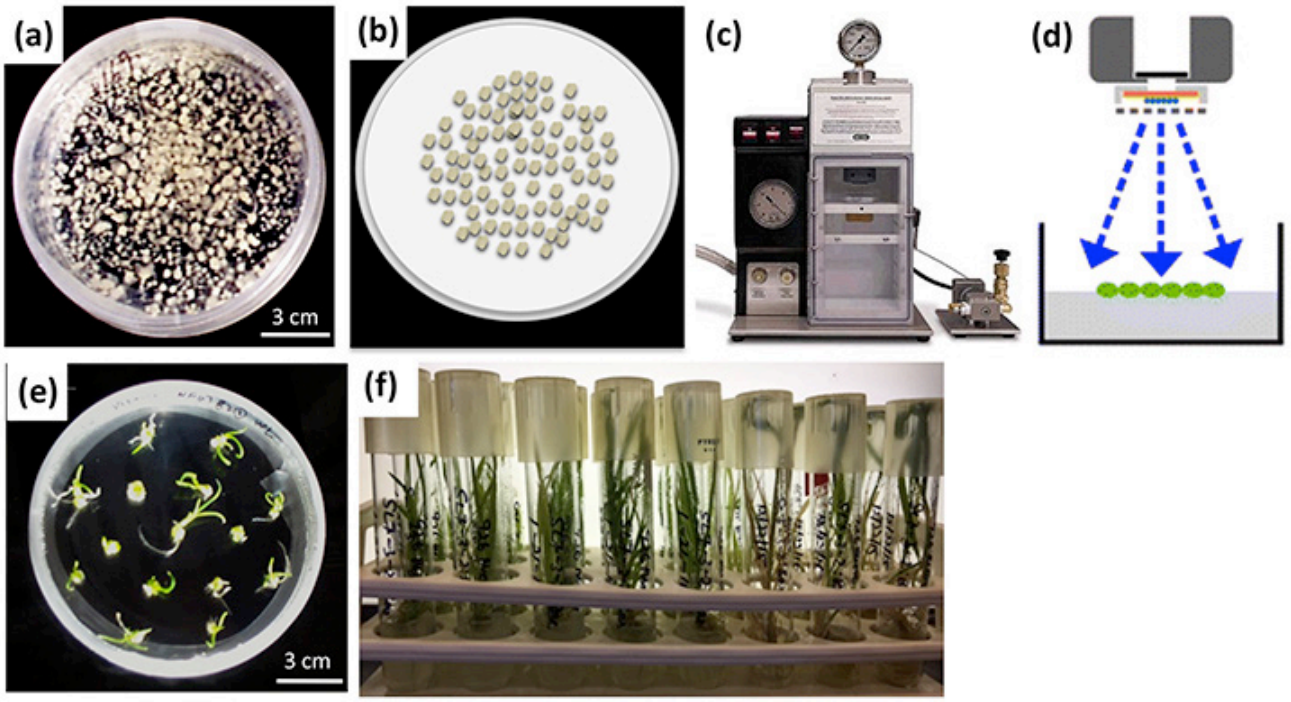

Fig. 1. Biolistic transformation of microspore embryoids. (a) 20- to 21-day-old microspore embryoids in induction medium. (b) Diagrammatic representation of 35- to 40-day-old microspore embryoids transferred to the regeneration media in a '60 × 15 mm' Petri dish and arranged in the center of plate prior to bombardment. (c) Gene gun. (d) Diagrammatic representation of the micro-carrier launch assembly and the bombardment process. (e) Plantlets growing on regeneration media. (f) First batch of wheat regenerants co-transformed with the DME TALE repressor and CRISPR Cas9 nuclease constructs.

introgression(s) in the Fe–S cluster biogenesis gene are identified, these lines will be selected against the introgression of Cas9 expression cassette in the genome.

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2015 Wheat Production in the Commonwealth of Virginia.

Growing conditions. Temperature and rainfall in September and October were generally near the 30-year means and mostly conducive for wheat seeding, although some areas were delayed due to excess moisture. In late November, soil moisture was mostly adequate and wheat was rated 76% good and 21% fair. December was mild for most areas of the commonwealth, and rainfall of 2–3 inches was widespread. Temperatures in early January and much of February and early March were colder than the long-term average, which definitely reduced winter growth and tillering in many fields. Mostly due to this delayed development, only 64% of wheat acres were rated good or excellent. By early April, conditions and crop ratings improved statewide, however development was 5–10 days behind most years. Widespread rain and cool weather persisted in most of the state through mid-April. Freeze damage from earlier cold nights was observed in some fields, especially in the southern counties, but little yield loss was experienced. Early May brought much warmer weather and less rainfall. Although Fusarium head scab was reported in some areas, the overall occurrence was low due to the general absence of rain during flowering. By 24 May, wheat heading was reported in 85% of fields, compared to the 5-year average of 95% by this date. Timely harvested wheat generally had good test weight and grain quality, however many areas experienced frequent rains prior to harvest causing reduction in quality and an increase in dockage.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service (http://quickstats.nass.usda.gov), in the autumn of 2014, Virginia farmers planted 260,000 acres (105,300 ha) of wheat. The following spring, 210,000 acres (85,050 ha) were harvested. The average yield was 66 bu/A (4,435 kg/ha). Overall, 13,860,000 bushels (377,207 metric ton) of wheat were produced in 2015.

Disease incidence and severity. Entries in Virginia's 2015 state wheat variety trials were rated (0 = no infection to 9 = severe infection) for disease severity at four diverse locations. The 127 entries in the 2015 trial had mean powdery mildew (*Blumeria graminis*) ratings that varied from 0 to 5 (mean of 1.1) in Virginia's southern Piedmont region (Nottoway County), 0–6.8 (mean of 1.9) in the northeastern region (Richmond County), and 0–3.8 (mean of 0.9) on the Eastern Shore (Accomack County). *Barley/Cereal Yellow Dwarf Virus* infection was moderate at the southern Piedmont test site (0.3–4) and at the southwestern test site (0.3–2.5) near Blacksburg, VA. Leaf rust (*Puccinia triticina*) was prevalent in several regions and was moderately severe at the northeastern (0–8.5) and southwestern (0–7.8) sites with mean trial ratings of 2.0 and 2.6, respectively. Race surveys, conducted by Dr. James Kolmer at the USDA–ARS Cereal Disease Lab on eight *P. triticina* collections from Blacksburg and Warsaw, VA, identified 10 races of leaf rust and only race MCTNB was common at the two locations (Richmond and Montgomery counties). The other races identified from Montgomery county included MCJSB, MMPSD, TCBQL, and TCTQS and races MBTNB, MFGJG, TBRKQ, and TCTQB from Richmond county. Stripe rust (*Puccinia striiformis*) was noted on a few plots of the cultivar Tribute wheat at Warsaw,

VA. Samples sent to Dr. Xianming Chen at the USDA–ARS in Pullman, WA, identified race PSTv-52 (virulence for *Yr6*, *7*, *8*, *9*, *17*, *27*, *43*, *44*, and *YrExp2*).

State cultivar tests. Wheat trials were planted as no-till at Holland and Shenandoah Valley sites at 48 seed/ft^2. Tests at Blackstone, Blacksburg, Orange, Painter, and Warsaw were planted as conventional-till at 44 seed/ft^2. Past seasons across Virginia have provided the opportunity to evaluate day length sensitivity, spring freeze damage, glume blotch, Fusarium head blight, and general plant health. Many newer wheat cultivars and lines performed well in all tested environments. Cultivars that yielded significantly higher than the statewide mean in 2015 were Pioneer Brand 26R59, VA10W-119, Pioneer Brand 26R10, USG 3895, MAS #32, VA12FHB-8, VA11W-106, USG 3612, VA11W-279, AgriMAXX Exp 1450, AgriMAXX 446, SS 8513, and MAS #7. VA10W-119, VA11W-106, VA11W-279, and SS 8513 also had test weights that were significantly higher than the mean of all lines tested. Average yield of all lines tested in 2014–15 was 67 bu/acre. Pioneer Brand 26R10 had the highest two-year average yield. USG 3404, AgriMAXX 446, SS 8360, Shirley, AgriMAXX 434, USG 3523, Hilliard, USG 3612, MAS #37, Pioneer Brand 26R20, USG 3251, VA11W-106, and AgriMAXX 427 all had grain yields significantly above the mean over the 2014 and 2015 harvests. Hilliard, Pioneer Brand 26R20, and VA11W-106 also had test weights that were significantly higher than the two-year mean of all tested lines. The two-year average grain yield over all locations and cultivars was 71 bu/acre.

Virginia Wheat Yield Contest results. The 2015 contest was conducted statewide and the results can be found in the table below. Congratulations to our winners!

Table 1. 2015 Virginia Wheat Yield Contest results.

Place	Grower	Farm	County	Yield (bu/acre)	Cultivar
Soft wheat					
1st	John Shepherd	Shepherd Grain Farm	Nottoway	110.5	Shirley
2nd	Brett Wightman		Shenandoah	100.9	Featherstone 73
3rd	Boogie Davis	Davis Produce	New Kent	100.2	USG 3404
4th	Evan Perry	Corbin Hall Farm	Middlesex	95.7	Pioneer 26R20
Hard wheat					
1st	Paul Davis	Davis Produce	New Kent	86.5	Vision 45
2nd	Craig Brann		Northumberland	81.5	Vision 30

Newly released cultivar. Soft red winter (SRW) wheat cultivar **Hilliard** (tested as VA11W-108) was developed and released by the Virginia Agricultural Experiment Station in May 2015. Hilliard was derived from the cross 'Pioneer Brand 25R47 (PI 631473) / Jamestown (PI 653731)'. Hilliard is a widely adapted, mid-season wheat cultivar with good winter hardiness. Hilliard has high grain yield potential, good straw strength, and has performed well over most of the U.S. eastern SRW wheat production areas. With the exception of stem rust, Hilliard has expressed moderate to high levels of resistance to diseases prevalent in the SRW wheat region; these include powdery mildew, leaf rust, stripe rust, leaf and glume blotch, bacterial leaf streak, *Soil Borne Mosaic Virus, Barley and Cereal Yellow Dwarf Viruses*, Fusarium head blight, and Hessian fly.

Evaluating wheat nitrogen water use efficiency (NUE) by ground and aerial remote sensing. Dr. Maria Balota and research associate Joseph Oakes are half way through with field measurements in 2015–16 wheat NUE tests 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 nondestructively evaluate NUE in wheat in the field. For this project, 12 wheat cultivars are being evaluated under two nitrogen fertility treatments: a low fertility treatment with a total of 60 pounds N/acre and a normal fertility treatment with a total of 120 pounds 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 unmanned aerial vehicle (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 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, and saturation, along with vegetation indices derived from them, i.e., Green Area (GA) and Greener Area (GGA), and UAV-based NDVI and CT. Both the GA and GGA indices were significantly correlated ($R^2 = 0.7$) with ground NDVI at GS 30. We also have learned that biomass can be successfully estimated from the RGB indices (Fig. 1). Measurements that would have taken hours to measure by hand can now be done in a matter of minutes with the assistance of the UAV. Research is on-going with the other UAV sensors (Fig. 2) throughout the growing season to compare aerial versus ground taken measurements at subsequent growth stages.

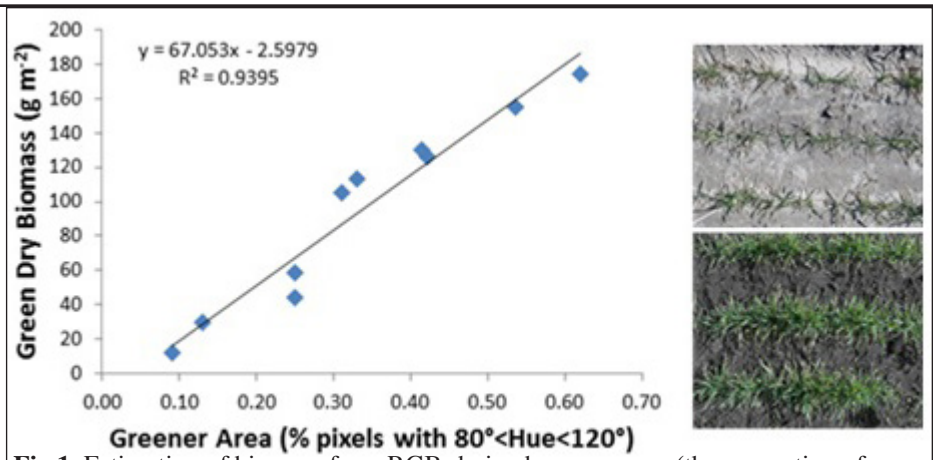

Fig 1. Estimation of biomass from RGB-derived greener area (the proportion of green pixels, Hue angle from 60 to 120°).

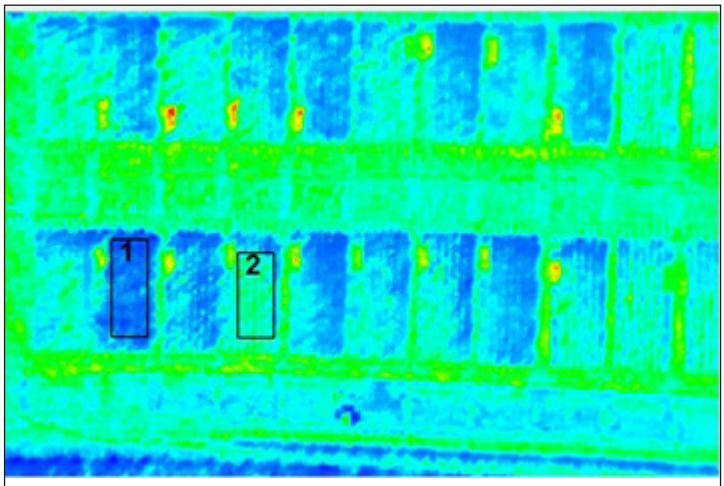

Fig 2. Estimation of canopy temperature (CT) from thermal images taken by a UAV platform. Plot 1 received 120 pounds of N and it is cooler and healthier (18°C) than plot 2 than received only 60 pounds of N, for which CT is 24°C.

Foliar disease control.

Dr. Hillary Mehl.

Disease pressure varies by location and year, and the profitability of foliar fungicide applications in wheat varies based on yield response, cost of application, and price received for the wheat crop. Thus, assessing efficacy of foliar fungicides in different years and environments is important for making data-based fungicide recommendations in wheat. Different fungicide chemistries and application timings were evaluated for foliar disease control in wheat in 2015. Trials were planted in Suffolk and Warsaw, VA. Leaf blotch was present in trials at both locations, and low levels of powdery mildew were observed in Suffolk. A cold winter and relatively dry conditions in April and May slowed down disease development, and leaf blotch symptoms were not observed on the flag leaf until flowering in Suffolk and after flowering in Warsaw. Flowering applications of a triazole (e.g., Prosaro) resulted in reduced disease severity on the flag leaf during grain development, but earlier applications (jointing and flag leaf) did not reduce disease compared to the untreated control. All application timings resulted in a yield response in Suffolk, but yield gains were greatest for late fungicide applications. Late onset of disease and low disease severity in Warsaw resulted in no yield response to fungicide applications. Environmental conditions in 2015 slowed down disease development, and fungicide trials demonstrated the benefit of late season triazole applications for the control of foliar diseases. Triazoles, including Prosaro, Caramba, and Proline, are the recommended fungicides for *Fusarium* head blight control and should be applied at flowering if scab risk is high. If onset of foliar diseases is late, a single application of a triazole can be made at flowering for both *Fusarium* head blight and foliar disease control. However, as the 2016 growing season has shown, foliar disease in wheat can develop much earlier if conditions are wet and warm, and in these years earlier foliar fungicide applications may be beneficial.

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

Morris and Engle lead the Pacific Northwest Wheat Quality Council, a consortium of collaborators who evaluate the quality of new cultivars and advanced breeding lines. We also conduct the U.S. Wheat Associates' Overseas Varietal Analysis Program for Soft White and Club Wheat. Our current activities and projects include grain hardness and puroindolines, waxy wheat, polyphenol oxidase (PPO), arabinoxylans, SDS sedimentation test, and soft durum wheat.

Publications.

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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*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
674791 PVPO	*Triticum aestivum* subsp. *aestivum*	Redstone	United States	Colorado
674792 PVPO	*Triticum aestivum* subsp. *aestivum*	W040511B1	United States	Indiana
674997	*Triticum aestivum* subsp. *compactum*	GE.2013-06	Georgia	
674998	*Triticum aestivum* subsp. *spelta*	GE.2013-07	Georgia	
674999	*Triticum timopheevii* subsp. *timopheevii*	GE.2013-09	Georgia	
675000	*Triticum aestivum* subsp. *aestivum*	GE.2013-12	Georgia	
675001	*Triticum monococcum* subsp. *monococcum*	GE.2013-14	Georgia	
675002	*Triticum aestivum* subsp. *macha*	GE.2013-15	Georgia	
675003	*Triticum aestivum* subsp. *macha*	GE.2013-16	Georgia	
675004	*Triticum aestivum* subsp. *macha*	GE.2013-17	Georgia	
675005	*Triticum turgidum* subsp. turgidum	GE.2013-18	Georgia	
675007 PVPO	*Triticum aestivum* subsp. *aestivum*	Curiosity CL+	United States	Washington
675008 PVPO	*Triticum aestivum* subsp. *aestivum*	Mela CL+	United States	Washington
675010	*Triticum turgidum* subsp. *durum* Kronos-(*gw2-a1* wild type)	United Kingdom	England	
675011	*Triticum turgidum* subsp. *durum* Kronos-(*gw2-a1* mutant)	United Kingdom	England	
675012	*Triticum turgidum* subsp. *durum* Kronos-(*gw2-a1* wild type)	United Kingdom	England	
675013	*Triticum turgidum* subsp. *durum* Kronos-(*gw2-a1* mutant)	United Kingdom	England	
675014	*Triticum aestivum* subsp. *aestivum* Paragon-(*gw2-a1* wild type)	United Kingdom	England	
675015	*Triticum aestivum* subsp. *aestivum* Paragon-(*gw2-a1* mutant)	United Kingdom	England	
675152	*Triticum turgidum* subsp. *durum*	Kandur 1170	United States	Kansas
675154JPR	*Triticum aestivum* subsp. *aestivum*	ND 810	United States	North Dakota
675155JPR	*Triticum aestivum* subsp. *aestivum*	ND 812	United States	North Dakota

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
675337PVPO	*Triticum aestivum* subsp. *aestivum*	Focus	United States	South Dakota
675456PVPO	*Triticum aestivum* subsp. *aestivum*	KanMark	United States	Kansas
675457PVPO	*Triticum aestivum* subsp. *aestivum*	Hot Rod	United States	Kansas
675458PVPO	*Triticum aestivum* subsp. *aestivum*	LCS Compass	United States	Virginia
675464	*Triticum aestivum* subsp. *aestivum*	CDLSr24Sr31	United States	Minnesota
675465	*Triticum aestivum* subsp. *aestivum*	CDLSr31Sr36	United States	Minnesota
675466	*Triticum aestivum* subsp. *aestivum*	CDLSr24Sr36	United States	Minnesota
675510	*Triticum aestivum* subsp. *aestivum*	03LNK 6034-73	United States	Nebraska
675511	*Triticum aestivum* subsp. *aestivum*	03LNK 6034-5	United States	Nebraska
675512	*Triticum aestivum* subsp. *aestivum*	03LNK 6034-8	United States	Nebraska
675513	*Triticum aestivum* subsp. *aestivum*	03LNK 6034-87	United States	Nebraska
675514	*Triticum aestivum* subsp. *aestivum*	03LNK 6053-8	United States	Nebraska
675515	*Triticum aestivum* subsp. *aestivum*	03LNK 6053-13	United States	Nebraska
675516	*Triticum aestivum* subsp. *aestivum*	03LNK 6053-50	United States	Nebraska
675517	*Triticum aestivum* subsp. *aestivum*	03LNK 6053-46	United States	Nebraska
675518	*Triticum aestivum* subsp. *aestivum*	2004Y 2113	United States	Nebraska
675564	*Triticum aestivum* subsp. *aestivum*	Pembroke 2014	United States	Kentucky
675634PVPO	*Triticum aestivum* subsp. *aestivum*	SY Drifter	United States	Iowa
675635PVPO	*Triticum aestivum* subsp. *aestivum*	SY Flint	United States	Iowa
675636PVPO	*Triticum aestivum* subsp. *aestivum*	SY Sunrise	United States	Iowa
675637PVPO	*Triticum aestivum* subsp. *aestivum*	SY Viper	United States	Iowa
675638PVPO	*Triticum aestivum* subsp. *aestivum*	SY 100	United States	Iowa
675639PVPO	*Triticum aestivum* subsp. *aestivum*	122082W	United States	Iowa
675640PVPO	*Triticum aestivum* subsp. *aestivum*	Yurok	United States	California
675641PVPO	*Triticum aestivum* subsp. *aestivum*	UI Castle	United States	Idaho
675643PVPO	*X Triticosecale* spp.	SY TF135	United States	Iowa
675644JPR	*Triticum aestivum* subsp. *aestivum*	Lassik SBEII a/b-AB	United States	California
675645JPR	*Triticum aestivum* subsp. *aestivum*	Lassik SBEIIa/b-A, SBEIIa-D	United States	California
675646JPR	*Triticum aestivum* subsp. *aestivum*	Lassik SBEIIa/b-B, SBEIIa-D	United States	California
675647JPR	*Triticum aestivum* subsp. *aestivum*	Lassik SBEIIa/b-AB, SBEIIa-D	United States	California
675998	*Triticum aestivum* subsp. *aestivum*	NE10589	United States	Nebraska
676026PVPO	*Triticum aestivum* subsp. *aestivum*	Northern	United States	Montana
676042PVPO	*Triticum aestivum* subsp. *aestivum*	LCS Pistol	United States	Colorado
676043PVPO	*Triticum aestivum* subsp. *aestivum*	Savoy	United States	Georgia
676044PVPO	*Triticum aestivum* subsp. *aestivum*	Southern Harvest 555	United States	Georgia
676052	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn1)	United States	Washington
676053	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn1)	United States	Washington
676054	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn1)	United States	Washington
676055	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn1)	United States	Washington
676056	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn1)	United States	Washington
676057	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN1)	United States	Washington
676058	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN1)	United States	Washington
676059	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN1)	United States	Washington
676060	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN1)	United States	Washington
676061	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN1)	United States	Washington
676062	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn2)	United States	Washington
676063	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn2)	United States	Washington
676064	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn2)	United States	Washington

Table 1. Recent PI assignments in *Triticum, X Triticosecale*, *Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
676065	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn2)	United States	Washington
676066	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn2)	United States	Washington
676067	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN2)	United States	Washington
676068	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN2)	United States	Washington
676069	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN2)	United States	Washington
676070	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN2)	United States	Washington
676071	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN2)	United States	Washington
676072	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn3)	United States	Washington
676073	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn3)	United States	Washington
676074	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn3)	United States	Washington
676075	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn3)	United States	Washington
676076	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn3)	United States	Washington
676077	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN3)	United States	Washington
676078	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN3)	United States	Washington
676079	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN3)	United States	Washington
676080	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN3)	United States	Washington
676081	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN3)	United States	Washington
676082	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn4)	United States	Washington
676083	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn4)	United States	Washington
676084	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn4)	United States	Washington
676085	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn4)	United States	Washington
676086	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (vrn4)	United States	Washington
676087	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN4)	United States	Washington
676088	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN4)	United States	Washington
676089	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN4)	United States	Washington
676090	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN4)	United States	Washington
676091	*Triticum aestivum* subsp. *aestivum*	Nugaines NIL (VRN4)	United States	Washington
676108PVPO	*Triticum aestivum* subsp. *aestivum*	Emerson	Canada	Saskatchewan
676251	*Triticum aestivum* subsp. *aestivum*	Skagit 1109	United States	Washington
676252	*Triticum aestivum* subsp. *aestivum*	Edison	United States	Washington
676254	*Triticum aestivum* subsp. *aestivum*	Skagit 1209	United States	Washington
676255	*Triticum aestivum* subsp. *aestivum*	Pactole	France	
676269JPR	*Triticum aestivum* subsp. *aestivum*	vrn-2	United States	California
676270PVPO	*Triticum aestivum* subsp. *aestivum*	Joe	United States	Kansas
676271PVPO	*Triticum aestivum* subsp. *aestivum*	Hilliard	United States	Virginia
676284PVPO	*Triticum aestivum* subsp. *aestivum*	122173W	United States	Idaho
676285PVPO	*Triticum aestivum* subsp. *aestivum*	SY Selway	United States	Idaho
676286PVPO	*Triticum aestivum* subsp. *aestivum*	SY Coho	United States	Idaho
676287PVPO	*Triticum aestivum* subsp. *aestivum*	SY Teton	United States	Idaho
676288PVPO	*Triticum aestivum* subsp. *aestivum*	Chet	United States	Washington
676289PVPO	*Triticum aestivum* subsp. *aestivum*	Alum	United States	Washington
676290PVPO	*Triticum aestivum* subsp. *aestivum*	Seahawk	United States	Washington
676291PVPO	*Triticum aestivum* subsp. *aestivum*	Bentley	United States	Oklahoma
676292PVPO	*Triticum aestivum* subsp. *aestivum*	TCG-Cornerstone	United States	North Dakota
676293PVPO	*Triticum aestivum* subsp. *aestivum*	TCG-Spitfire	United States	North Dakota
676294PVPO	*Triticum aestivum* subsp. *aestivum*	TCG-Wildfire	United States	North Dakota
676295PVPO	*Triticum aestivum* subsp. *aestivum*	AgriMAXX 462	United States	Virginia
676977PVPO	*Triticum aestivum* subsp. *aestivum*	Avery	United States	Colorado
676978JPR	*Triticum aestivum* subsp. *aestivum*	Lanning	United States	Montana
677023PVPO	*Triticum aestivum* subsp. *aestivum*	122024W	United States	Iowa
677024PVPO	*Triticum aestivum* subsp. *aestivum*	122581W	United States	Iowa

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale*.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
677025PVPO	*Triticum aestivum* subsp. *aestivum*	122816W	United States	Iowa
677026PVPO	*Triticum aestivum* subsp. *aestivum*	122950W	United States	Iowa
677027PVPO	*Triticum aestivum* subsp. *aestivum*	LCS Prime	United States	Colorado
677028PVPO	*Triticum aestivum* subsp. *aestivum*	LCS Trigger	United States	Colorado
677131	*Triticum aestivum* subsp. *aestivum*	MNR220	United States	Montana

IV. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2015–16 SUPPLEMENT

R.A. McIntosh[1], J. Dubcovsky[2], W.J. Rogers[3], C. Morris[4], R. Appels[5] and X.C. Xia[6].

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The most recent version of the Catalogue, compiled for the 12Th International Wheat Genetics Symposium held in Yokohama, Japan, and a 2013–14 Supplement are 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.

Laboratory Designators

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Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics
1.2. Club/Compact spike
Insert above QTL:

C$_g$ {11114}. 2BL {11114}. **bin:** 2BL-0.48-0.89, near breakpoint 0.69.
v: Akage Gumbai {11114}; Akage Gumbai 22 {11114 }; Gumbai 22 {11114}; Kiroshita Komugi {11114}; Nakote Gumbai {11114}.
ma: *Xhbg410/Xhbg440-2B* – 18.1 cM – *C$_g$* – 15.3 cM – *Xgwm47-2B* {11114}.

9. Brittle Rachis
Following the introductory sentence add:
Wedge (W) type disarticulation is associated with the *Br-1* gene set, whereas barrel (B) type disarticulation is caused by a different gene and is limited to species with the D genome {15033}.

Insert after *Br-D1*:
Br-S1 {11080}. 3SS {11080}. **v:** Iranian spelts {11080}.
tv: *Triticum timopheevii* subsp. *timopheevii* {11080}.
dv: *Aegilops tauschii* {11080}.
ma: *Xpsr1196-3S* 32.3 cM – *Br-S1* – 1.5 cM – *Xabg471-3D* {11080}.

Br-D2 {11080}. 3DS {11080}. **v:** Common wheat {11080}; European spelts {11080}.
dv: Al8/78 (shattering 11080}; TA1604 (non-shattering) {11080}.
ma: *Xwmg2013-3D* – 1.5 cm – *Br-D2* – 2.9 cM – *Xpsr170-3D* {11080}.

17. Dormancy (Seed)

17.1. Germination index

TaSdr. 2B {11119}.

TaSdr-B1a {11119}. **v:** Yangxiaomai {11119}.
c: GenBank KF021990 {11119}.

This allele is associated with lower germination index.

TaSdr-B1b {11119}. **v:** Zhongyou 9507 {11119}.
c: GenBank KF021991 {11119}.

This allele is associated with higher germination index.

17.2. Vivipary

17.3. Pre-harvest sprouting

27. Glaucousness (Waxiness/Glossyness)

27.2 Epistic inhibitors of glaucousness

Iw1. Add: **bin:** 2BS3-0.84-1.00.
v: WE74 {11094}. Shamrock {11090}.
ma: *JIC007* – 1.47 cM – *Iw1* – 0.18 cM – *JIC010*/*JIC011* {11090}. Co-segregation with BF474014, CJ876545, and CD927782 and flanked by BE498358 and CA499581 within a 0.96-cM interval {11094}.

Iw2. Add: **bin:** DS5-0.84-1.00.
v: TA4152-60 {11094}.
ma: Co-segregation with BF474014 and CJ876545 and flanked by CJ886319 and CJ519831 within a 4.4-cM interval {11094}.

NEW SECTION

33. Grain Traits

Variation in grain traits based on gene homology with other species

TaGASR7-A1 {11115}. Snakin/GASA gene family. 7AL {11115}.
ma: *Xwmc301-7A* – 17.9 cM – *TaGASR7* – 10.6 cM – *Xwmc9-7A* {11115}.
c: GenBank KJ000052 {11115}.

Hap1c in Lumai 14 and Xiaoyan 81 conferred higher grain length and grain weight than *Hap1g* in Hanxuan 10 and Xinmai 10 {11115}.

TaGS-D1 {11116}. 7DS {11116}. **ma:** *TaGs-D1* – 8.0 cM – *Xbarc184* {11116}.

TaGs-D1a {11116}. **v:** Doumai {11116}; Jingdong 8 {11116}.
c: KF687956 {11116}.

Associated with higher TKW and grain length {11116}.

TaGs-D1b {11116}. **v:** Shi4185 {11116}; Yumai 21 {11116}.
c: KF687957 {11116}.

Associated with lower TKW and grain length {11116}.

TaSAP1-A1 {11117}. Stress association protein gene family.
7A {11117}. **ma:** *Xwmc530-7A* – 2.1 cM – *TaSAP1-A1* – 13.9 cM – *Xbarc174-7A* {11117}.
c: GenBank KC193579 {11117}.

Variation at this locus was associated with 1,000-kernel weight, number of grains/spike, spike length, peduncle length and total number of spikelets/spike, but different haplotypes had different effects various traits {11117}.

41. Height

41.1. Reduced Height: GA-insensitive

41.2. Reduced Height: GA-sensitive

***Rht18*.** Add note:
Hexaploid derivatives in the backgrounds of Fengchan 3, Jinmai 47 *Rht8*, and Xifeng 20 are reported in {11096}.

Rht23 {11077}. 5DL {11077}. **v:** NAUH164 {11077}.
ma: *Xgdm63-5D* – 4.7 cM – *Rht23* – 11.1 cM – *Xbarc110-5D* {11077}.
NAUH164 is an EMS-derived mutant of Sumai 3 {11077}.

43. Hybrid Weakness

43.1. Hybrid necrosis

***Ne2m*.** Add: **ma:** *Xbarc55-2B* – 1.1 cM – *Xkwh37* – 4.9 cM – *Lr13/Ne2* – 5.8 cM – *Xgpw1109* – 3.7 cM – *Xbarc18-2B* {11068}.

47. Leaf Tip Necrosis

Ltn3 {11070}.
i: RL6077 {11070}.
v: Chapingo 48 {11070}.
c: This multiple disease resistance/necrosis locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

67. Response to Vernalization

***Vrn-D1b*.** **v:** Add: Additional Chinese germplasm {11072}.

Add immediately following the *vrn-D1* listing:
Vrn-D1a, Vrn-d1b, and *Vrn-D1* were present in 27.3%, 20.6%, and 52.1%, respectively, of 689 Chinese wheat accessions {11072}.

82. Proteins

82.3. Endosperm storage proteins

82.3.1. Glutenins

82.3.1.1 *Glu-1*

***Glu-A1*.** Add:

Glu-A1ba {11106}. [*Glu-A1g* {11106}]. 1.1 {11106}. **v:** Barbela 28 {11106}.
The sequence encoding subunit 1Ax1.1 shows high nucleotide identity with other *Glu-A1* alleles, with the main difference being an insertion of 36 amino acids in the central repetitive region. It is the largest and most acidic subunit currently known at this locus and has been implicated in high dough extensibility in some cv. Barbela wheat lines, although this contrasts with other data showing a similar effect to that of subunit 1Ax1 {11107}.

Pathogenic Disease/Pest Reaction

84. Reaction to Barley Yellow Dwarf Virus

***Bdv2*.**
Add note at end of section:
Small recombinant segments are described in a pontin series of lines: recombinants were obtained with *Lr19* but not with *Sr25* {11097}.

86. Reaction to *Blumeria graminis* DC.

86.1. Designated genes for resistance

Pm2

Pm2a {11049}. [*Pm2* {130}], [*Mlu* {1175}, *Mlx* {1088}].
Remainder as now listed for *Pm2*.

Pm2b {11049}. Putatively derived from *Agropyron cristatum*. *PmKM2939* {11049}; *PmPB3558* {11075}.

bin: C-5DS1-0-0.63.
v: KM2939 {11049}; PB3558 {11075}
ma: *Xscar112* – 0.5 cM – *Pm2b* – 1.3 cM – *Xscar203*/*Xmag6176*/*Xcfd81-5D* {11049}; *Xcfd81-5D* – 5.5 cM – *PmPB3558* – 3.9 cM – *Xbwm25* – 0.9 cM – *Xbwm21* – 0.9 cM – *Xbwm20* {11075}.

Pm2c {11061}. *PmNM* {11061}. 5DS {11061}.
bin: 5DS-1-0-0.63
v: Niaomai {11061}.
ma: *Xcfd81-5D* – 0.4 /0.1 cM – *Pm2c* – 7.5/4.9 cM – *Xcfd78-5D* {11061}.

Allelism with *Pm2a* and *Pm2b* was based on more than 7,600 F_2 plants.

Pm46. Add:

v: Chapingo 48 {11070}.
c: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

Pm51. Correct to:

ma: *Xwmc332-2* – 3.2 cM – *Pm51* – 1.5 cm – *BQ246670* {11026}.

Pm54 {11050}. *PmA2K* {11050}. 6BL {11050}. **bin:** 6BL-0.450-1.00.
v: AGS 2000 PI 612956 {11050}.
ma: *Xgpw2344-6B* – 1.00 cM – *wPt-9256* – *Pm54* – 1.2 cM – *Xbarc134-6B* {11050}.

Pm55 {11108}. Derived from *Dasypyrum villosum*. *Pm5VS* {11108, 11109}.
5AS (T5VS·5AL) {11108}. **v:** NAU421 {11108}
5DS (T5VS·5DL) {11109}. **v:** NAU415 (11108, 11109}.
ma: A 730-bp 5EST-237 band is associated with chromosome 5VS {11109}. 5VS also carries puroindoline genes; therefore all lines with this gene will be soft (T5VS·5DL) or supersoft (T5VS·5AL).

The backgrounds of NAU415 and NAU421 are Chinese Spring. The PM resistance conferred by this gene gradually increases from the third leaf stage and reaches an immunity level by the seventh leaf stage.

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

MlIW172 {11095}. 7AL {11095}. **bin:** 7Al-16-0.86-0.90.
tv: *T. turgidum* subsp. *dicoccoides* IW172 {11095}.
ma: *WGGC4664*/*WGGC4665*/*WGGC4668* – 0.44 cM – *MlIW172* – 0.7 cM – *WGGC4659* {11095}.

86.4. QTL for resistance to *Blumeria graminis*

PmSE5785 {11084}. Recessive. 2DL {11084}.
v: SE5785, Snipe / Yav79 // Dack / Teal /3/ Ae. tauschii 877 11084}; NO7728-1 {11084}; NO7728-2 {11084}.
ma: *Xbarc59-2D* – 3.6 cM – *PmSe5785* – 4.6 cM – *Xwmc817-2* {11084}.

Correct spelling:
Reaction to *Colletotrichum cereale*

90. Reaction to *Diuraphis noxia* (Mordvilko)

Dn6. 7D.

Dn2401 {M14031}. 7DS {11078}. **v:** CI2401, PI 97812 {11078}.
ma: *Xbarc214-7D* – 1.1 cM – *Dn2401* – 1.8 cM – *Xgwm473-7D* {11078}.

91. Reaction to *Fusarium* spp.

91.1. Disease: Fusarium head scab, scab

Fhb1. Add: **v:** Alsen {11071}; Rollag {11071}.

Fhb5.

Fhb6 {11048}. Derived from *Elymus tsukushiensis* syn. *Roegneria kamoji*. 1AS {11048}.
T1AL·1AS-1E^{ts}#1S {11048}. **v:** TA5660, KS14WGRC61 {11048}; TA5093 {11048}.
ma: Three CAPS and one KASPar SNP (*wg1S-snp1*) markers were developed {11048}.
TA5660 is in Chinese Spring background; TA5093 is in Everest background.
TW·1E^{ts}#1S {11048}. **v:** TA5655 {M11048}.

Fhb7 {11060}. Derived from *Thinopyrum ponticum*. *FhbLoP* {11118}.
T7DS.7Dl-7el$_2$L {11060}. **v:** SDAU1881 {11060}; SDAU1886 {11060}.
ma: Flanked by 7el$_2$ markers *Xcfa2240* and *XsdauK66* in a 1.7-cM interval {11060}.
T7DS·7el$_2$ {657}. **v:** KS24-2 {657}.

Tetraploid wheat

Add:

'T. turgidum subsp. *dicoccoides* Mt. Gerizim#36 /*2 *T. turgidum* subsp. *durum* Helidur' F$_6$ lines: two QTL for type-2 resistance located on chromosomes 3A (*Xbarc45-3A – Xbarc67-3A*) and 6B *Xs13m22_2 – Xgwm626-6B* {11088}.

92. Modify title to:
Reaction to *Heterodera avenae* Woll., *H. filipjeva* (Madzhidov) Stelter

Cre 5. Add: **v:** Madsen {11102}.

Cre8. **ma:** Add: The map in {10343} was reversed: *Cre9* was located closer to the end of chromo-aomw 6BL (11081}. Six markers that can be screened by KASP™ and *wri15* developed from a SNP were reported {11081}.

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

Rmg7. Add: 2AL {11083}. **ma:** *Xcfd50-2A* – 5.6 cM – *Rmg7* – 15.1 cM – *Xhbg327-2A* {11083}.

Rmg8 {11083}. 2BL {11083}. **v:** S615 {11083}. **bin:** 2BL6-0.89-1.00.
ma: *Xwmc317-2B* – 12.1 cM – *Rmg8* – 22.4 cM – *Xbarc159-2B* {11083}.
According to {11083} markers linked to *Rmg8* were independent of those linked to *Rmg7*.

94. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

H16. Add: , 1AS {15011}. **bin:** 1AS-3-0.86-1.00. **v:** P921682 {11058}.
ma: Add: *Xpsp2999-1A* – 3.7 cM – *H16* – 5.5 cM – *Xbarc263*/*Xwem6B-1A* {11058}.

H17. Add: , 1AS {11058}. **bin:** 1AS-3-0.86-1.00. **v:** P921680 {11058}.
ma: Add: *Xpsp2999-1A* – 6.27 cM – *H17* – 5.1 cM – *Xbarc263*/*Xwem6B-1A* {11058}.

99. Reaction to *Puccinia graminis* Pers.

Sr9h. **v:** Matlabas {10057}. **ma:** Add: *wPt-3132* – 1.9 cM – *Sr9h* – 1.9 cM – *wPt-8460* {11010}. S*r9h* – 20.7 cM – *Sr28* {11010}.

Sr12. Modify and add: 3BS or centromeric region {1332, 682, 11103}; 3BL (11104}.
v2: Condor *Sr8a*{11105}; Celebration *Sr9gSr16* (939}; Condor Thatcher *Sr5Sr9gSr16* {939}; RL6058 (a Thatcher derivative) {11104}.
ma: *IWA6086 – Sr12 – IWA4613* {11104}.

Add to note section. Although the association of field resistance and *Sr12* was not definitive allelism or close linkage is clearly involved (11104}.

Sr21. Add:

dv: After einkorn, add: CI 2433, i.e. Einkorn CI 2433 {1460, 11110}.
ma: *FD52726* – 0.25 cM – *Sr21* – 0.05 cM – *EX594406* {11110}.

Sr42. **v:** PI 595667 {11087}. **v2:** PI 410954 *Sr24* {11087}.
ma: Add: *Xcfa49-6D* – *Sr42*/*IBW31561*/*IWB30767* – *FSDRSA* {11087}.

Add notes: *Sr42* co-locates with *SrCad, SrNini, SrSh7*, and *SrTmp*. Three haplotypes were identified in {11087}: C–C–T, AC Cadillac, Peace, PI 595667; T*–C–T, Norin 40, Eagle 10, Ember, Guard, Ripper, Shield; T–C–T, Triumph 64, CnS-SrTMP64, Blouk, Digalu, Pfunye, Robin, PI 410954.

Sr43. 7DL· Add: , 7DS-7el$_2$S·7el$_2$L {11076}.

Add note: Derivatives RWG33 and RWG34 with shortened alien segments are reported in {11076}.

Sr49. Replace current entry with: **v:** Mahmoudi AUS 28011 {10704}.
and replace current entry with: **ma**: *sun479* – 0.9 cM – *Sr49* – 1.5 cM – *sun209* – 0.5 cM – *Xwmc471-5B* {10704}.

Sr55. Add: **v:** Chapingo 48 {11070}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

Sr59 {11066}. Derived from *Secale cereal*e. 2D (T2DS·2RL) {11066}.
v: TA5094 {11066}. **su:** SLU238 (2R(2D)) {11066}.
al: VT828041 (6X triticale) {11066}.

SrND643 {11092}. 4AL {11092}. **bin:** 4AL4-0.8-1.00.
v: Kenya Sunbird {11092}; Kenya Tai {11092}; ND643/2*Weebill1 GID6302736 {11092}.
tv: ND643 {11092}.
ma: *Xwmc776-4A* – 2.9 cM – *Xgwm350-4A* – 0.5 cM – *SrND643* – 4.1 cM – *Xwmc219-4A* {M14045}.

SrTm4 {11111}. Recessive. 2A^{m}L {11111}.
dv: *T. monococcum* subsp. *monococcum* PI 306540 {11111}.
bin/contig: IWGS_2AL_contig 6401556
ma: *BQ461276* – 1.6 cM – *SrTm4* – 0.5 cM – *DR732348*/*Xgwm526*/*Xgdm93-2A* {11111}.

SrTmp. Add: *SrSha7* {11057}. 6DS.
v: Digalu {11057}; Kenya Robin {11057}.

100. Reaction to *Puccinia striiformis* Westend.

100.1. Designated genes for resistance to stripe rust

Yr18. Add note at end of section:

Forty-three Chinese land varieties predicted to have *Yr18* based on markers had high rust severities. Genetic analyses of four of these landraces (Sichuanyonggang 2, Baikemai, Youmai, and Zhangsihuang) indicated the presence of an independent suppressor {11101}.

Yr26. **v:** Guinong 22 {11098}.

Yr46. **v:** Chapingo 48 {11070}.
c: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

Yr51. Revisions:

v2: AUS 27858 *Yr57* {10850}. **ma:** *sun106* – 0.6 cM – *owm45F3R3* – 1.2 cM – *Yr51* – 2.5 cM – *sun104* – 1.8 cM – *Xgwm160-4A* {10850}.

Yr57. Correction:

ma: Replace present entry with: *sts3B15* – 4.5 cM – *BS00062676* – 2.3 cM – *Yr57* – *Xgwm389-3B* – 2.0 cM – *Xbarc75-3B* {10963}.

Yr58. Correction:

Yr58 was previously located in chromosome 3BL. The location was revised to 3BS. The corrected listing for this gene becomes:

Yr58 {10964}. 3BS {10964}. **bin:** 3BS3-0.87-1.00.
v: Sonora W195 AUS 19292 {10964}.
ma: *1121669*/*3023704* – 3.9 cM – *Yr58* – 4.6 cM – *100016328*/*1233292* {10964}.

Yr68 {11051}. Adult-plant resistance. 4BL {11051}. **bin:** 4BL1-0.86-1.00.
i: AGG91587WHEA1 = csAvYr4BL = Avocet S*5 / Undesignated International Nursery ex New Zealand Entry 03.25 {11051}.
v: Undesignated International Nursery ex New Zealand 03.25 {11051}.
ma: *IWB74301* – 0.5 cM – *Yr68*/*IWA4640* – 0.5 cM – *IWB28394* {11051}.

Yr69 {11052}. *YrCH86* {11052}. 2AS {11052}. **bin:** 2AS5-0.78-1.00
v: CH7086 {11052}.
ma: *Xwmc25-2A* – 2.7 cM – *X2AS33* – 1.9 cM – *Yr69* – 3.1 cM – *Xmag3807-2A* {11052}.
Linkage with *Yr17*: (F_2 seedling test) 30.0 cM {11052}.

Yr70 {11055}. Derived from *Ae. umbellulata*. *YrUmb* {11055}. 5DS {11055}.
v: IL 393-4 {11055}, *T. turgidum* subsp. *durum* cv. WH890 / *Ae. umbellulata* Pau 3732 // CS Ph^I /3/ 2*WL711 {11055}.
al: *Ae. umbellulata* Pau 3732 {11055}.
ma: *Yr70* – 7.6 cM – *Xgwm190-5D* {11055}; A co-segregating 450 bp *Lr57–Yr40–* CAPS16 marker was present in IL 393-4, but not in many Australian wheat cultivars {11055}.
Yr70 behaves as an allele of *Yr40* derived from *Ae. geniculata*. The low infection types are also different.

Yr71 {11056}. Adult-plant resistance. *YrSA3* {11056}. 3DL {11056}.
v: AGG91588WHEA, 'Sunco / Avocet S' RIL4667.153.11.1 {11056}.
v2: Sunco *Yr18* {11056}.
ma: *Yr71* – 1.6 cM – *IWB17207*/*IWB10438*/*IWB23615*/*IWB63653* – 0.5 cM – *IWB57983* – 0.9 cM – *IWB23518* – 2.4 cM – *Xgwm114b-3D* – 5.6 cM – *Sr24*/*Lr24* {11056}.

Yr72 {11059}. *YrAW4* {11059}. 2BL {11059}. **bin:** 2BL-5-0.59-0.89.
v: AUS27507 {11059}; AUS27894 {11059}.
ma: *Xsun481-2BL* – 1.8 cM – *Yr72* – 1.2 cM – *IWB12294* – *Xsun482-2BL* – 1.5 cM – *Xsun482-2BL* – 1.5 cM – *IWB69000* {11059}.

Yr73 {11062 Complementary gene involved in the *YrA* specificity. 3DL {11064, 11062}.
v2: Avocet R {11063}; Anza = WW15 {11062}; Banks R {11063}; Condor R {11063}; Egret R {11063}; Funo {11062}; Jupateco 73 {11062}; Lerma Rojo-64 {11062}.
ma: Located and mapped by DArT-Seq markers {11062}.

Yr74 {11062}. Complementary gene involved in the *YrA* specificity. 5BL {11062}.
v2: Avocet R {11063}; Anza = WW15 {11062}; Banks R {11063}; Condor R {11063}; Egret R {11063}; Funo {11062}; Jupateco 73 {11062}; Lerma Rojo-64 {11062}.
ma: Located and mapped by DArT-Seq markers {11062}.

The cross 'Avocet R / Teal' used to map *Yr73* and *Yr74* included a T5BL-7BL reciprocal translocation. Susceptible lines carrying the individual genes will be permanently accessioned after screening candidate lines for the Avocet R = Chinese Spring chromosome configuration. The translocated chromosomes are present in Teal and do not involve *Yr74*.

Yr75 {11065}. Adult-plant resistance. *YrAxe* {11065}. 7AL {11065}.
bin: 7AL16-0.86-0.90.
v: 'Axe / Nyabing-3' RIL#5 {11065}.
v2: Nyabing-3 *Yr29* {11065}.
ma: *Xcfa2016-7A* – 1.0 cM – *Yr75* – 0.3 cM – *IWB36240* {11065}.

Yr76 {11067}. *YrTye* {186}. 3AS {11067}, 6D {186}.
bin: 3AS4-0.45–1.00 {11067}.
i: AvS*4 / Tyee {11067}.
v: Tyee CItr 17773 {11067}; ARS-Amber {11067}; Cara {11067}; Chukar {11067}.
v2: Hyak *Yr17* {11067}.
ma: *Xbarc321-6D* – 6.2 cM – *Xbarc57-6D* – 4.3 cM – *Xwmc11-6D* – 2.6 cM – *Yr76* – 3.4 cM – *Xwmc532-6D* – 6.9 cM – *Xgwm369-6D* – 2.6 cM – *Xbarc12-6D* {11067}.

100.2. Temporarily designated genes for resistance to stripe rust

YrC591. Add: **bin:** 7BL-3-0.85-1.00. **ma:** *Xmag1714-7B* – 1.2 – *YrC591* – 0.4 cM – *Xbarc182-7B* {11099}.

YrHA {11100}. 1AL {11100}. **v:** H901414-121-5-5-9 {11100}.
ma: *Xwmc469-1A* – 3.4 cM – *YrHA* – 4.6 cM – *Xgwm497-1A* {11100}.

YrSD {11085}. 5BL {11085}.
i: Taichung 29*6 / Strubes Dickkopf 11085}.
v: Strubes Dickkopf {11085}.
ma: *Xwmc640-5B* – 3.6 cM – *YrSD* – 2.4 cM – *Xbarc59-5B* – 3.0 cM – *Xwmc783-5B* {11085}.
The authors concluded that this gene was different from *Yr25*, which was located in chromosome 1D {158}.

YrSP. Add: **bin:** 2BL-C-0.5. **ma:** *IWA638* – 0.6 cM – *YrSP* – 1.5 cM – *dp269-2* – 1.9 cM – *Xwmc332-2B* {11091}.

100.3. Stripe rust QTL

At the end of section add:
A summary of published QTL locations is provided in {11089}; 49 chromosome regions on 20 of the 21 wheat chromosomes were proposed.

101. Reaction to *Puccinia triticina*

101.1. Genes for resistance

Lr3. Add:
Lr3d {11054}. **i:** RL6062, Thatcher*6 / PI 268316 {11054}.
v: PI 268316 {11054}.

Lr11. Add:
LrBP2 {11074}. Add: ',2DS {11074}'. **v2:** Buck Poncho Lr10 {11074}.
ma: *Lr11* – 0.3 cM – *SCAR32/35* – 1.6 cM – *Xgwm614-2D* {11074}.

Lr13. Add:
ma: *Xbarc55-2B* – 1.1 cM – *Xkwh37* – 4.9 cM – *Lr13/Ne2* – *Xgpw1109* – 3.7 cM – *Xbarc18-2B* {11068}.

Lr21. **v:** Add: Barlow {11093}; Faller {11093}; Prosper {11093}.

Lr28. **v:** Sunland {11069}.
ma: *Xbarc343-4A* – 7.7 cM – *Lr28*/*Psr119*/*SCS421*/*mag3092* – 1.1 cM – *Xwmc219-4A* – 2.2 cM – *Xwmc219-4A* {11069}.

Lr39. **v:** Add: Armour {11086}; Bullet {11086}; PostRock {11093}; TAM 112 {11086}; Winterhawk {11086}.

Lr48. Add: **ma:** *Xgwm429b-2b* – 4.2 cM – *Sun563*/*Sun497* – 0.6 cM – *IWB31002*/*IWB39834*/*IWB34324*/*WB72894*/*Lr48* – 0.3 cM – *IWB70147* – 2.0 cM – *Xbarc67-2B* {11112}.
Based on haplotype analysis *Lr48* was postulated in 13 Australian Condor relatives {11112}.

Lr67. Add: **v:** Chapingo 48 {11070}.
c: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

The following is a revised entry for *Lr74*.
Lr74 {11031}. Adult-plant resistance. 3BS {11031}. **bin:** 3BS8-0.78-0.87.
v1: AGG91583WHEA = BT-Schomburgk Selection {11031}; Spark {11031}.
ma: *Xcfb5006-3B* – 1.9 cM – *Lr74* – 2.2 cM – *BS00009992* – 2.7 cM – *Xgwm533-3B* {11031}.

Lr75 {11053}. Adult-plant resistance. *QlrP.sfr-1BS* {10066}. 1BS {10066, 11053}.
v1: ArinaLr75, Arina*2 // Forno / Arina#F7NIL85 {11053}, IPKXXXXX, C14.20 {11053}.
v2: Forno *Lr34* {10066; 11053}.
ma: *Lr75* – 2.74 cM – *Xgwm18-1B* {11053}.

Lr76 {11055}. Derived from *Ae. umbellulata*. *LrUmb* {11055}. 5DS {11055}.
v: IL 393-4 {11055}, *T. turgidum* subsp. *durum* cv. WH890 / *Ae. umbellulata* Pau 3732 // CS Ph^I /3/ 2*WL711, C14.21 {11055}.
al: *Ae. umbellulata* Pau 3732 {11055}.
ma: *Lr76* – 7.6 cM – *Xgwm190-5D* {11055}.
Lr76 behaves as an allele of *Lr57* derived from *Ae. geniculata*. The low infection types are also different. A co-segregating 450-bp *Lr57-Yr40*-CAPS16 marker was present in IL 393-4, but not in many Australian wheat cultivars {11055}.

LrBi16. Add: **bin:** 7BL-10.
ma: *Xcfa2257-7B* – 2.8 cM – *LrBi16* – 2.5 cM – *Xgwm344-7B* {11082}. A closer AFLP marker could not be converted to a STS/SCAR marker {11082}.
Allelic with *Lr14c*, but showed different reaction patterns compared to lines with *Lr14c* and *LrFun* {11082}.

Add after *LrZh84*:
Lr6Ai#2 {11079}. 6Ai#2 {11079}.
v: Tulaikoskaya 5 {11079}; Tulaikoskaya 10 {11079}; Tulaikoskaya 100 {11079}.

116. Reaction to Wheat Yellow Mosaic Virus
QTL:
RIL population: 'Xifeng (R) / Zhen 9523' (S): Three QTL, *Qym.njuy5A.1* (R^2 = 0.26-0.54), *Ym.njau-3B.1* (R^2 = 0.03-0.01), and *QYm.njau-7B.1* (R^2 = 0.03-0.05 in some trials). The chromosome 5A gene was closely associated with *Xwmc415.1*, *CINAU152*, and *CINAU153* and was phenotyped as a single Mendelian gene {11073}.

References.

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

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VIII. VOLUME 63 MANUSCRIPT GUIDELINES.

The required format for Volume 63 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 44–62 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 63 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. 37–62) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.