ANNUAL WHEAT NEWSLETTER

Volume 65

Contribution no. 20-044-B from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

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Volume 65

Edited by W. John Raupp Jr., Department of Plant Pathology, Kansas State University, Manhattan, KS 66506-5502 USA. Facilities during manuscript editing were provided by the Plant Pathology Department and the Wheat Genetics Resource Center, Kansas State University, and the Kansas Wheat Innovation Center, 1990 Kimball Avenue, Manhattan, KS 66502.

1 September, 2019.

Contribution no. 20-044-B from the Kansas Agricultural Experiment Station, Kansas State University, Manhattan.

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IN DEDICATION TO
MERLE G. EVERSMEYER

Merle G. Eversmeyer, age 83, passed away on Monday, 4 February, 2019, at the Ascention-Via Christi Hospital, Manhattan, Kansas.

Dr. Eversmeyer was born on 9 December, 1935, in Waterville, Kansas, the son of Gideon F. and Susie E. (Kintigh) Eversmeyer. On 14 March, 1982, he was united in marriage to Beverly Ringey.

Merle earned a B.S in Agronomy and M.S. and Ph.D. degrees in Plant Pathology all from Kansas State University. Following completion of his Ph.D. in 1971, he joined the USDA–ARS Plant Science and Entomology Research Unit, which was housed within the Kansas State Department of Plant Pathology as the Cereal Rust Epidemiology Project Leader. In 1972, he became the Research Leader for the Plant Science and Entomology Research Unit, a position he held until his retirement in 2002. He also held a faculty appointment as an adjunct associate professor within the KSU Department of Plant Pathology.

Merle specialized in the epidemiology and ecology of wheat diseases, particularly leaf rust. He spent much of his time surveying for leaf rust each spring to determine if it had overwintered in Kansas (which always resulted in the most severe epidemics) and then entering the data for use in simulation models. His career was spent developing and improving these models for the improved forecasting of rust epidemics and yield losses. He also was actively involved in screening wheat germplasm for resistance to wheat rust and searching for new sources of resistance.

Merle enjoyed gardening, planting flowers, and bringing flowers home to Beverly. He also loved Christmas and was known for starting the Christmas music in July and having the house fully decorated. He also loved watching the K-State Wildcats and the Kansas City Royals and Chiefs. He and Beverly traveled extensively through his work, traveling to over 26 different countries.

Dr. Eversmeyer was a lifelong member of the United Methodist Church and together, he and Beverly led an adult singles group that traveled all over; at one time they had 85 members.

I. SPECIAL REPORTS

INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM.

The first fully annotated reference genome sequence of bread wheat – IWGSC RefSeq v1.0.

On 17 August, 2018, the International Wheat Genome Sequencing Consortium (IWGSC) published in the journal *Science* a detailed description and analyses of the reference sequence of the bread wheat genome. The article, entitled 'Shifting the limits in wheat research and breeding using a fully annotated reference genome' (DOI: 10.1126/science.aar7191), is the culmination of 13 years of collaborative international research coordinated by the IWGSC.

Authored by more than 200 scientists from 73 research institutions in 20 countries, the article presents an annotated reference genome sequence (IWGSC RefSeq v1.0) of the bread wheat cultivar *Chinese Spring*. IWGSC RefSeq v1.0 represents 94% of the hexaploid wheat genome assembled in 21 chromosome-like pseudomolecules. It is the highest quality genome sequence produced to date for wheat and the first fully annotated sequence for bread wheat.

In addition to the sequence expressed in pseudomolecules of the 21 chromosomes, the *Science* article reports the precise location of 107,891 high confidence genes, along with more than 4.7 x 10^6 molecular markers. The genes and markers are identified in context, i.e., they have been positioned on their specific sub-genomes. The sequence information in between the genes and markers is also described, providing a comprehensive view of the organization of the genes and the regions important for their regulation.

The article, and a companion article published in the same issue (DOI: 10.1126/science.aar6089) also presents a transcription atlas from 850 RNA-Seq datasets representing all stages of wheat phenological development, which reveals novel co-expression networks including some with relevance to flowering time.

The potential for IWGSC RefSeq v1.0 to accelerate the identification of candidate genes underlying important agronomic traits was illustrated with two examples: the mapping of a quantitative trait conferring resistance to drought stress and insect damage, and the design of targets for genome editing of genes implicated in flowering-time control.

Prepublication access to the IWGSC RefSeq v1.0 and associated data has been provided to the scientific community since January 2017 and the data have been widely used since, as exemplified by the number of download and BLAST searches at the IWGSC data repository (Fig 1). The IWGSC's reference sequence of the bread wheat genome is already having a significant impact on wheat improvement and research as evidenced by the number of articles describing studies which used or cited IWGSC RefSeq v1.0 and associated resources (Fig 2). In 2018 alone, IWGSC RefSeq v1.0 was used for analyses and cited in more than 265 published research articles.

Fig 1: Cumulative downloads and BLAST searches at the IWGSC data repository from 2012 to 2018

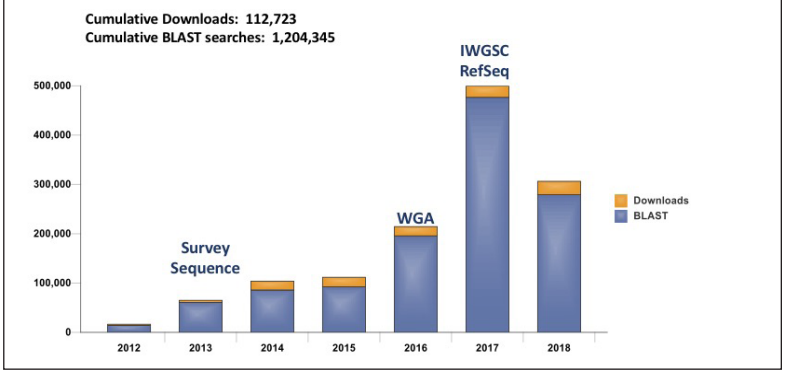
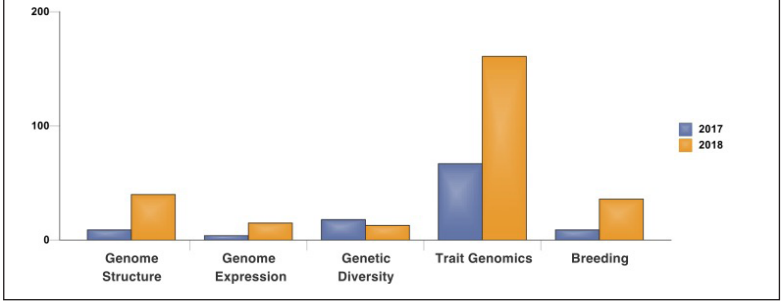


Fig 2: Number of research articles published in 2017 and 2018 that reference or use IWGSC RefSeq and associated resources



IWGSC RefSeq v1.0 lays the foundation for understanding the genetic basis of bread wheat and for genomics-based crop improvement in wheat in response to challenges imposed by population expansion and climate change.

The IWGSC has now moved into Phase II and focuses its efforts on four activities: (1) characterizing the breadth of wheat diversity by de novo sequencing and assembling multiple wheat genomes (landraces and elite cultivars); (2) producing the IWGSC Gold Standard reference sequence by gap filling and integrating manual and functional annotation to the reference sequence; (3) producing an IWGSC Exome Array based on the IWGSC RefSeq v1.0; and (4) developing user-friendly, integrated databases and tools to benefit public breeders and industry partners.

With these activities, the IWGSC will reach beyond the reference sequence to provide breeders and the broader scientific community with a full genome-sequence based tool box for wheat improvement.

References.

The International Wheat Genome Sequencing Consortium (IWGSC), et al. 2018. Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science. 2018 Aug 17; 361(6403), eaar7191 [doi: 10.1126/science.aar7191].

Ramírez-González, R.H., Borrill, P., et al. 2018. The transcriptional landscape of polyploid wheat. Science. 2018 Aug 17; 361(6403), eaar6089 [doi: 10.1126/science.aar6089].

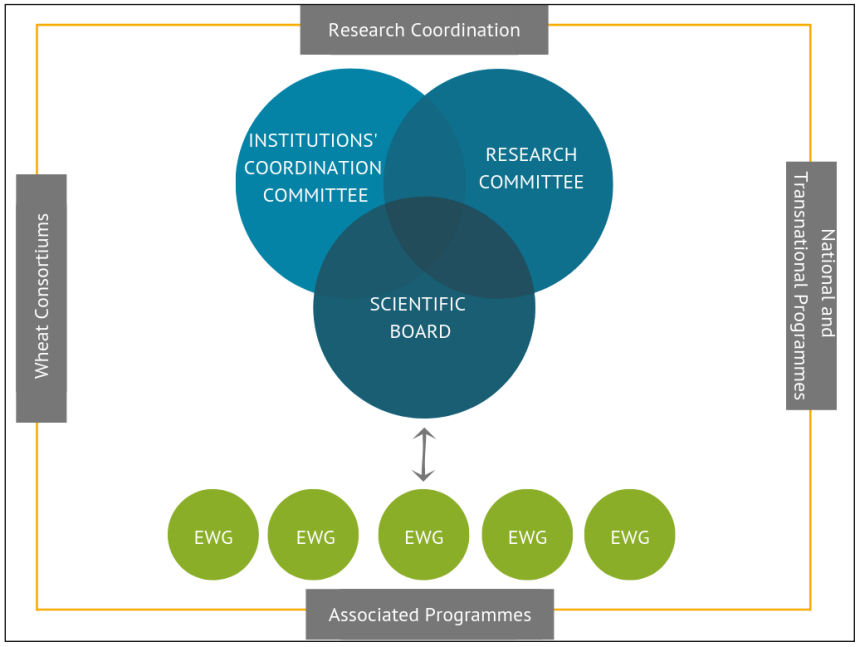
Data Access

All IWGSC RefSeq v1.0 and associated resources are publicly available at the IWGSC data repository at URGI-INRA Versailles, France [https://wheat-urgi.versailles.inra.fr/].

WHEAT INITIATIVE
Königin-Luise-Straße 19, Berlin, GERMANY.

Wheat Initiative at a glance.

Created in 2011 following endorsement from the G20 Agriculture Ministries, the Wheat Initiative provides a framework to establish strategic research and organisation priorities for wheat research at the international level in both developed and developing countries.



The Wheat Initiative fosters communication between the research community, funders, and global policy makers, and aims at securing efficient and long-term investments to meet wheat research and development goals. It also initiates and supports activities in order to enhance communication and increase global access to information, resources, and technologies.

The Wheat Initiative actions will lead to the creation of improved wheat cultivars and the dissemination of better agronomic practices worldwide. The combination of new cultivars and agronomic practices will, in turn, allow farmers to improve and stabilise wheat yields in diverse production environments.

Recent changes and developments.

We are delighted to report on the developments made during the past year, which was one of major change and transition for the Wheat Initiative.

The Wheat Initiative moved its offices to the Julius Kühn-Institute (JKI), the German Federal Research Centre for Cultivated Plants in Berlin-Dahlem, Germany. The relocation from France to Germany was welcomed with strong support from the German Federal Ministry of Food and Agriculture (BMEL). With the relocation to Berlin, the management structure was changed as Alisa-Naomi Sieber was appointed to the new role of overall Program Manager. Peter Langridge will remain as the Chair of the Scientific Board (SB).

The Institutions' Coordination Committee (ICC) appointed Nicole Jensen as the new Chair of the ICC. Nicole is the general manager for the Genetics and Enabling Technologies business group at the Australian Grains Research and Development Corporation. She has extensive experience in the seed industry, both in Australia and internationally. We also are pleased to note that Frank Ordon, the Chair of the Research Committee, on his new role as president of the JKI, which he began in January 2019.

The start of 2019 also brought a few changes within our Secretariat. Xuan Hinzmann worked as our Communications Manager for one year and is now on maternity leave. We wish her and her family the very best during this exciting time! Whitney Buchanan, our new Communications Manager, started the position at the end of February 2019 and is very enthusiastic about her role, particularly when it comes to creating new public relations strategies for the Wheat Initiative.

In June 2019, we also published our 2018 Annual Report, which can be found at the following link: https://drive.google.com/file/d/1V3Vj15yzHjup9a2PD3gySaKnyb3nJvsY/view. We aim to create second versions of our Strategic Research Agenda and our Vision Paper, titled 'An International Vision for Wheat Improvement' later in 2019.

Events in 2019.

Co-Hosted the 1st International Wheat Congress (IWC) in Saskatoon. We are delighted to announce that we were a co-host of the IWC in Saskatoon, Canada, from 21-26 July, 2019. The congress venue was the TCU Place, a world class facility in the heart of Saskatoon's vibrant downtown.

This was the first meeting of its kind and included a balanced program encompassing all areas of wheat research, including joint plenary sessions and concurrent sessions tailored to focus on specific disciplines. All plenary sessions were streamed live on the web and social media platforms. Furthermore, our Expert Working Groups are hosting internal and public satellite meetings. For further information, please visit the following: https://www.wheatinitiative.org/iwc-satellite-meetings

November Conference on Heat and Drought. There will be a two day conference on 'Genetic Diversity: The key for improving drought stress tolerance in crops' from 19–20 November in Berlin-Dahlem, Germany. The conference will consist of informative seminar and it is organized by JKI and IPK on behalf of the BMEL. We expect 150 international participants to attend the event.

Do not miss out on Wheat Initiative news.

For more information about the Wheat Initiative and our current activities, please be sure to follow us on Twitter at @WheatInitiative and by using the hashtag #WheatTheWorld.

You also can sign up for our free quarterly newsletter, which includes reading suggestions from wheat experts, a 'Wheat Story', dates of meetings and workshops, and much more: http://eepurl.com/ducc15.

We also are pleased to announce that we are making huge changes to our website. Be sure to visit and provide us with your feedback at www.wheatinitiative.org.

II. WHEAT WORKERS' 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.

BRS Parrudo: wheat cultivar from Embrapa.

Pedro Luiz Scheeren, Vanderlei da Rosa Caetano (Embrapa Clima Temperado. C.P. 403, 96010-971 Pelotas, Rio Grande do Sul, Brazil), Eduardo Caierão, Márcio Só e Silva, Luiz Eichelberger, Martha Zavariz de Miranda, Alfredo do Nascimento Junior, Douglas Lau, Flávio Martins Santana, Leila Maria Costamilan, Márcia Soares Chaves, Maria Imaculada Pontes Moreira Lima, Paulo Roberto Valle da Silva Pereira, José Pereira da Silva Júnior, Leandro Vargas, Eliana Maria Guarienti, João Leonardo Fernandes Pires, Gilberto Rocca da Cunha, Ricardo Lima de Castro, and Sirio Wiethölter.

The release of BRS Parrudo aimed to offer farmers a wheat cultivar with a new plant ideotype, a plant with medium plant height; short, narrow, and upright leaves; solid stem at the basal internodes; and high spike fertility, which can be cultivated in the usual the field conditions used by the farmers.

For some time, several breeding strategies were used in Brazil to improve wheat grain yield, focused mainly on lodging and disease resistance. Parallel to the development of cultivars by the conventional breeding methods described by Allard (1971) and used by various breeding institutions in the late 1970s and early 1980s (Riede et al. 2015; Caierão et al. 2016), an innovative method, the systemic approach (Scheeren et al. 2011) was introduced into wheat breeding. In co-evolution with the current production system, improvements in disease resistance were sought, while maintaining or even increasing the crop yield potential. As of 1990, the systemic selection was addressed in partnership between Embrapa Trigo and Embrapa Clima Temperado. In this approach, also used in the selection of BRS Parrudo, the selection is made in the first generations, in a great number of crosses and backcrosses (4,000–5,000 combinations/year), with intense elimination of individuals. The method was improved by applying selection to multiple stresses already in the F_1 generation of multiple crosses (single double crosses including only four parents or in complex F_1, including F_1/F_1 crosses, using a large number of different parents), rather than initiating selection only in the F_2 population. After obtaining close to ideal plants, they were crossed to get desired new lines. Artificial inoculation of diseases (for example: powdery mildew, leaf rust, fusarium head blight) were used in order to obtain rapid solutions for several selected traits. Simultaneously, a new plant ideotype with industrial suitability characteristics of bread wheat was sought as key objective. Acting this way, a large number of highly resistant lines to several diseases were obtained in a short period of time and as a final result of the breeding efforts of 30 years, cultivar BRS Parrudo was released. The purpose of this study was to describe the yield performance, main agronomic characteristics and industrial suitability for the end use of the Embrapa wheat cultivar BRS Parrudo.

BRS Parrudo was created using the principles of the systemic selection, as described above, and this work was made in a partnership between Embrapa Trigo and Embrapa Clima Temperado. To obtain the parents of BRS Parrudo, many selections were made in early generations, in a great number of populations derived from crosses and backcrosses (4,000–5,000 combinations/year), with intense elimination of individuals. In the F_1 generations, many traits for strong plant type were selected in the screen house, such as solid stem and short and erect leaves. Then, initiating selection in the field in the F_2 populations and continuing until the F_7 generations, an intense selection for multiple stresses (most of the diseases occurred naturally in the field and some were artificially inoculated, like powdery mildew and leaf rust) was applied. During the process, after obtaining close to desired plants, new crosses were made to get desired new lines. Cultivar BRS Parrudo was derived from single cross F70465, made in summer 2000–01, in a screen house at of Embrapa Trigo, in Passo Fundo, Rio Grande do Sul (RS). As parents we used the lines WT 98108, originated from selections performed in Passo Fundo and in Warta, Londrina, Paraná (PR), and TB 0001, bred and selected at Embrapa Clima

Temperado, in Pelotas, RS. WT 98108 present high grain yield potential and TB 0001 has the desired characteristics of plant type. In 2001, the F_1 were self-pollinated in a screen house in Passo Fundo to produce F_2 seeds. Beginning in 2002, the segregating populations from F_2 to F_7, composed of 200 individuals selected in the previous generation, were space planted in the experimental field under natural conditions to permit individual plant selection, without use of fungicides, or in screen house, at Embrapa Trigo. In all generations were selected individual plants. After threshing individually the selected plants, a strong visual selection of the grains was carried out keeping the best plants in terms of grain filling, red and glassy grains, and absence of yellow berry. In the winter of 2007, all the plants from one field plot, already in the F_8 generation, were harvested and named PF 070478.

In 2008, line PF 070478 was evaluated in the preliminary test series of special lines of Embrapa. Thereafter, it was included in the tests of value for cultivation and use (VCU) in 2009, 2010 and 2011. All tests were arranged in a randomized complete block design with three replications. Each experimental unit, consisting of one genotype, was sown in five rows of 5 m long, spaced 0.2 m apart, resulting in a total evaluated area of 5 m^2. As recommended by the Brazilian government rules for registration of wheat cultivars (Brazilian Ministry of Agriculture, Livestock and Supply (MAPA) – Brazil (2010) two cultivars, from the Brazilian recommended list of wheat cultivars were chosen as checks, including BRS Guamirim, as an early cycle cultivar, and Quartzo, as a medium cycle cultivar, and both presenting high yield potential. All cultural treatments were applied according to the technical recommendations of the National Wheat and Triticale Commission (Fronza 2008, Castro 2009, Marchioro 2011). Prior to sowing, seeds were treated with triadimenol + imidacloprid. Tests were carried out in the states of RS, Santa Catarina (SC), and in southern PN, in the Wheat Adaptation Regions 1 (cold/wet/high altitude) and 2 (moderately hot/humid/low altitude; Embrapa Trigo (2006)). In RS, the tests were carried out in Vacaria (28°30'44" S, 971 m; Latossolo Bruno Aluminoférrico); Passo Fundo (28°15'46" S, 687 m; Latossolo Vermelho Distrófico húmico) at two sowing dates, early and late, to avoid frost; São Borja (28°39'38" S, 123 m, Nitossolo Vermelho Distroférrico latossólico); Três de Maio (27°46'24" S, 343 m, Latossolo Vermelho Distroférrico); and Victor Graeff (28°15'46" S, 411 m; Latossolo Vermelho Distrófico férrico); in SC in the counties of Abelardo Luz (26°33'53" S, 760 m, Latossolo Vermelho), Canoinhas (26°10'38" S, 839 m, Latossolo Bruno Aluminoférrico) and Chapecó (27°05'47" S, 674 m, Latossolo Vermelho Distroférrico); and in PN, in Guarapuava (25°25'36" S, 1,098 m; Latossolo Bruno Ácrico Húmico) and Ponta Grossa (25°05'42" S, 969 m; Latossolo Vermelho Distroférrico). In the VCU trials, cultivar BRS Parrudo was compared with the control cultivars BRS Guamirim and Quartzo (which are two cultivars from the recommended list, as postulated by Brazilian Ministry of Agriculture, Livestock and Supply (MAPA) – Brazil 2010. In terms of grain yield, BRS Parrudo produced 106% (2009), 102% (2010), and 103% (2011), when compared with the mean of the two control cultivars in each year, and a mean of 103% in relation to the controls in the three evaluation years. In 2010, cultivar BRS Parrudo produced 5,459 kg/ha, whereas the mean of the control cultivars was 5,367 kg/ha (Table 1).

Table 1. Grain yield (kg/ha) of BRS Parrudo and the control cultivars BRS Guamirim and Quartzo. % = percentage in relation to the mean of the control cultivars BRS Guamirim and Quartzo, MC = mean of the control cultivars BRS Guamirim and Quartzo. Locations in 2009: Passo Fundo, Rio Grande do Sul (RS) (two growing seasons, early and medium sowing date to avoid frost), São Borja (RS) (two growing seasons), Três de Maio (RS) (two growing seasons), Chapecó, Santa Catarina (SC) and Canoinhas (SC). Locations in 2010: Passo Fundo (RS) (two growing seasons), São Borja (RS) (two growing seasons), Três de Maio (RS) (two growing seasons), Vacaria (RS), and Abelardo Luz (SC). Locations in 2011: Passo Fundo (RS) (two growing seasons), São Borja (RS) (two growing seasons), Três de Maio (RS), Vacaria (RS), Victor Graeff (RS), Chapecó (SC), Canoinhas (SC), Ponta Grossa, Paraná (PR) and Guarapuava (PR).

	2009		2010		2011		Mean	
Genotype	kg/ha	%	kg/ha	%	kg/ha	%	kg/ha	%
Number of locations	8		8		11		27	
BRS Parrudo	4.574	106	5.459	102	4.860	103	4.964	103
Quartzo	4.717	109	5.604	104	4.728	100	5.016	104
BRS Gurmirim	3.952	91	5.130	96	4.709	100	4.597	96
MC	4.334	100	5.367	100	4.719	100	4.807	100

BRS Parrudo (Fig. 1A, p. 9) is a low to medium-tall cultivar (mean of 85 cm in Passo Fundo, RS) and of a short cycle (average of 85 days-to-heading and 135 days-to-maturity in Passo Fundo). The stem is solid in the first internode

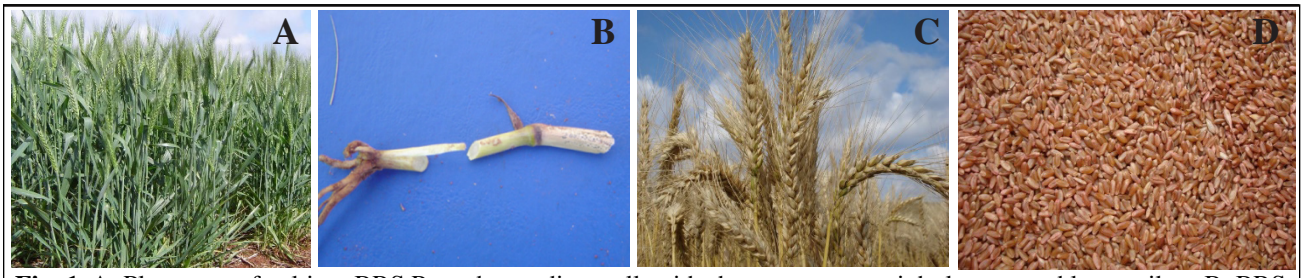


Fig. 1. A. Plant type of cultivar BRS Parrudo; medium-tall, with short, narrow, upright leaves, and long spikes. B. BRS Parrudo presents a solid stem at the basal internode until the flowering period. C. Spikes of BRS Parrudo at maturity. D. Seeds of BRS Parrudo are hard red vitreous. Passo Fundo, 2011. Photos by Pedro Luiz Scheeren.

during the early stages (Fig. 1B). The grains are hard red vitreous (Fig. 1D) is resistant to lodging and soil acidity and moderately resistant to frost in the vegetative phase. In relation to biotic stresses, it is resistant to soilborne wheat mosaic virus and powdery mildew (*Blumeria graminis*); moderately resistant to Fusarium head blight (*Fusarium graminearum*), Septoria glume blotch *(Stagonospora nodorum),* spot blotch (*Bipolaris sorokiniana*), wheat tan spot (*Pyrenophora tritici-repentis*, and leaf rust (*Puccinia triticina*); moderately susceptible to preharvest sprouting; and moderately tolerant to barley yellow dwarf virus.

Regarding the industrial suitability in the homogeneous wheat adaptation Regions 1 and 2 of RS and SC, cultivar BRS Parrudo was classified as strong gluten wheat suitable for bread making according to Regulation no. 38 (Brazil 2010) by the Brazilian Ministry of Agriculture, Livestock and Supply (MAPA). Sixty percent of the samples from Region 1 and 62.5 percent of samples from Region 2 reached this classification. Samples of BRS Parrudo from the homogeneous adaptation Region 1 of RS and SC, analyzed between 2009 and 2011 at the Grain Quality Laboratory of Embrapa Trigo, had mean gluten strength (W) of 345 x 10^{-4} J in the Alveography test and a mean elasticity index (EI) of 60.4% (Table 2). Samples of BRS Parrudo from the homogeneous adaptation Region 2 of RS and SC, analyzed in the same period, had a mean gluten strength (W) of 324 x 10^{-4} J and a mean EI of 57.9%, with a variation of 46 to 65%. Classified as strong gluten wheat, this cultivar is recommended for the production of bread, dry pasta, cracker cookies, industrial baking and can be blended with weaker gluten wheat for baking in general.

Table 2. Industrial suitability traits of cultivar BRS Parrudo in the Brazilian Wheat Adaptation Regions. Samples = the number of samples per region; Region 1: Passo Fundo, Rio Grande do Sul (RS), Vacaria (RS), Victor Graeff (RS), Canoinhas, Santa Catarina (SC), Ponta Grossa, Paraná (PR), and Guarapuava (PR); Region 2: São Borja (RS), Três de Maio (RS), Chapecó (SC), and Abelardo Luz (SC).

Traits	Mean of Region 1	Mean of Region 2	Overall mean or sum
Number of samples/region	9	9	18
Mean of falling number	339	337	338
Mean of gluten strength (x10^{-4} Joules)	345	324	334
Mean of lightness (0 = black, 100 = white (Minolta))	93.1	92.2	92.6
Mean of color b (+ = yellow hues, – = blue hues (Minolta))	10.9	11.7	11.3
Mean of tenacity or resistance to extension	120	123	122
Mean of extensibility or average abscissa at dough rupture (mm)	77	71	74
Mean of tenacity/extensibility ratio	1.6	1.9	1.8

Wheat cultivar BRS Parrudo also responded with significant grain yield increase to the application of high nitrogen rate, without lodging in the farm fields. In 2013, in the mean of the best 22 fields (40 ha/farmer), BRS Parrudo produced more than 4 t/ha and reached 6.3 t/ha at the best site. In the Alveograph test, the mean W value was 368 x 10^{-4} J and the mean stability 29 minutes (Farinograph test); the highest values were 495 x 10^{-4} J and 62 minutes, respectively. In average of nine locations, BRS Parrudo presented a mean of 40.7 mg Fe/kg, 53.3% superior to the mean iron value of cultivar Quartzo (26.6 mg Fe/kg), which presented the largest acreage in the South Brazilian wheat region in 2013 (Table

3). Considering the high (level of) iron concentration in the grains, BRS Parrudo can be classified as a natural biofortified wheat cultivar. BRS Parrudo was registered and protected by the Ministry of Agriculture, Livestock and Supply (MAPA) under the numbers 29434 and 20120242, respectively.

Table 3. Iron concentration (mg/kg) in grains of BRS Parrudo in comparison with Quartzo and percentage of increase in nine locations in 2013. Quartzo is the most planted cultivar in the South Brazilian Wheat Region. [1] First sowing date (early June); [2] Second sowing date (late June) (RS = Rio Grande do Sul, SC = Santa Catarina, and PR = Paraná states).

Location	Quartzo	BRS Parrudo	% difference of increase
Três de Maio, RS	28.3	41.1	45.2
Passo Fundo, RS [1]	21.5	32.1	49.3
Passo Fundo, RS [2]	22.1	31.5	42.5
São Luiz Gonzaga, RS	31.8	46.3	45.6
São Borja, RS	30.5	53.1	74.1
Chapecó, SC	25.5	40.5	58.8
Canoinhas, SC	24.3	37.6	54.7
Campos Novos, SC	26.4	40.4	53.0
Ponta Grossa, PR	28.7	44.0	53.3
Mean	26.6	40.7	52.9

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Performance of wheat cultivars in the state of Rio Grande do Sul, Brazil, 2017.

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

The Brazilian Commission of Wheat and Triticale Research (BCWTR) annually conducts the State Test of Wheat Cultivars in the state of Rio Grande do Sul (STWC–RS), aiming to support the indications of cultivars. This work had the objective to evaluate wheat cultivar grain yield performance of STWC–RS, in 2017. The grain yield performance of 30 wheat cultivars (Ametista, BRS Guaraim, BRS Marcante, BRS Parrudo, BRS Reponte, CD 1303, CD 1705, Celebra, FPS Certero, Inova, Jadeíte 11, LG Cromo, LG Oro, LG Supra, Marfim, ORS 1401, ORS 1402, ORS 1403, ORS 1405, ORS Vintecinco, Quartzo, TBIO Alpaca, TBIO Iguaçu, TBIO Mestre, TBIO Noble, TBIO Sintonia, TBIO Sinuelo, TBIO Sossego, TBIO Toruk, and Topazio) was studied in 12 environments (Coxilha, Cruz Alta, Não-Me-Toque, Passo Fundo – season 1; Passo Fundo – season 2; Vacaria – season 1; Vacaria – season 2; and Augusto Pestana, Ijuí, Santo Augusto, São Borja and Três de Maio), in Rio Grande do Sul in 2017. The experiments were carried out in a randomized block design with three or four repetitions. Each plot consisted of five rows of 5 m in length with 0.2 m spacing between rows. The plant density was approximately 330 plants/m^2. Grain yield data (kg/ha) were subjected to individual analysis of variance (for each environment) and to grouped analysis of variance (for all environments). The grouped analysis of variance was performed employing the mixed model (fixed cultivar effect and randomized environment effect). The grain yield performance of wheat cultivars was evaluated by analysis of adaptability and stability, employing the method of distance from the ideal cultivar, weighted by the coefficient of residual variation, proposed by Carneiro (1988). In this analysis, the ideal cultivar was considered as the cultivar with high grain yield, high stability, low sensitivity to adverse conditions of unfavorable environments and ability to respond positively to improvement of favorable environments. The general average of STWC–RS in 2017 was 3,544 kg/ha. The experiment conducted in Santo Augusto had the highest average of wheat grain yield: 4,845 kg/ha. The maximum wheat grain yield was 5,610 kg/ha, in Santo Augusto (cultivar CD 1303).

The Inova, FPS Certero, Topázio, ORS Vintecinco, and TBIO Mestre cultivars had adaptability and stability in favorable environments (environments with average of wheat grain yield higher than the general average). Cultivars Topázio, FPS Certero, LG Oro, BRS Reponte, and Inova had adaptability and stability in unfavorable environments (environments with average of wheat grain yield lower than the general average). The general average of all environments, cultivars FPS Certero (3,963 kg/ha), Topázio (3,920 kg/ha), Inova (3,948 kg/ha), LG Oro (3,818 kg/ha), and ORS 1401 (3,780 kg/ha) came closest to the ideal cultivar.

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Wheat crop in the state of Rio Grande do Sul, Brazil, 2017.

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

The state of Rio Grande do Sul (RS) is one of the main wheat-producing states in Brazil. The objective of this study was to analyze the wheat crop in Rio Grande do Sul state, in the year 2017. In 2017, RS harvested 690,233 ha of wheat (36.4 % of the total area harvested in Brazil), producing 1,192,918 tons of wheat (27.6% of Brazilian production), with an average of grain yield of 1,728 kg/ha (552 kg/ha below the Brazilian average: 2,280 kg/ha). Among the geographical mesoregions of RS (Fig. 2), the Northwest mesoregion harvested the largest wheat area: 550,973 ha (79.8% of the cropped area in the state) and had the largest production: 884,908 tons of wheat grain (74.2% of state production, Table 4). However, the average of wheat grain yield obtained in this mesoregion was the lowest of the state: 1,606 kg/ha (122 kg/ha below the state average, Table 4). The Northeast mesoregion harvested 36,730 ha of wheat (5.3% of the cropped area in the state), produced 115,001 tons of wheat grain (9.6% of state production), and had the highest average of wheat grain yield of the state: 3,131 kg/ha (1,403 kg/ha above the state average, Table 1). The wheat crop in the state of RS in 2017 had unfavorable weather conditions, with (i) lots of rain at the beginning of the sowing period, resulting in delayed sowing; (ii) rain lack in the crop growing period, resulting in the reduction of tillering and plant density; (iii) late frosts in some regions, especially in the Northwest mesoregion, damaging the grain formation and filling; and (iv) excessive rainfall in spring, resulting in high incidence of *Fusarium* head blight, the most important wheat disease in RS. Comparing the wheat crop data with the results of the State Test of Wheat Cultivars in RS (STWC–RS) in 2017, the average of wheat grain yield of commercial crops was 1,816 kg/ha below the average of STWC–RS (3,544 kg/ha).

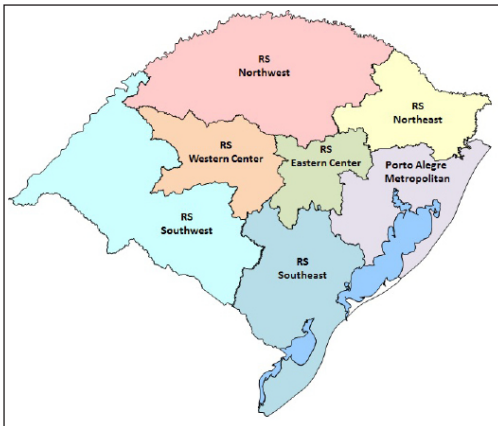

Fig. 2. Mesoregions in the state of Rio Grande do Sul, Brazil.

Table 4. 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 2017 (Source: IBGE. 2019).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	550,973	79.8	884,908	74.2	1,606
RS Northeast	36,730	5.3	115,001	9.6	3,131
RS Western Center	44,729	6.5	77,948	6.5	1,743
RS Eastern Center	8,591	1.2	14,116	1.2	1,643
Porto Alegre Metropolitan	1,140	0.2	3,075	0.3	2,697
RS Southwest	43,150	6.3	87,154	7.3	2,020
RS Southeast	4,920	0.7	10,716	0.9	2,178
Rio Grande do Sul State	690,233	100.0	1,192,918	100.0	1,728

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A. Börner, A.M. Alqudah, D.Z. Alomari, W. Berrueta, M. Cardelli, A.C. Castro, A.M. Castro, Yu.V. Chesnokov, J. del Río, K. Eggert, D. Giménez, M. Jayakodi, T. Kartseva, U. Lohwasser, G. Lori, I. Malbrán, S. Misheva, Q.H. Muqaddasi, M. Nagel, M.S. Röder, L. Saldúa, M. Schierenbeck, V.P. Shamanin, M.R. Simón, R. Tarawneh, J.P. Uranga, N. von Wirén, M. Yanniccari, and K. Zaynali Nezhad.

Identification of large-effect, consistent QTL for anther extrusion in doubled-haploid, spring wheat populations developed from German Federal ex situ gene bank accessions.

In order to establish a robust hybrid wheat breeding system, varieties harboring alleles that promote outcrossing have to be developed. In this study, we developed two doubled haploid (DH) populations of hexaploid spring wheat accessions taken from IPK gene bank. The phenotypic data of anther extrusion (AE) based on three years of field trials in both populations showed a wide variation and approximated a normal distribution. Both populations were genotyped with a 15k Infinium single nucleotide polymorphism (SNP) array resulting in 3,567 and 3,457 polymorphic SNP markers for DH population-1 and -2, respectively. Composite interval mapping identified quantitative trait loci (QTL) on chromosomes 1D, 2D, 4A, 4B, 5A, and 6B; with consistent QTL (that are detected in all the years) on chromosome 4A in DH population-1, and on chromosomes 2D and 6B in DH population-2. The consistent QTL explained 17.2% (4A), 32.9% (2D), and 12.3% (6B) of phenotypic variance. Genic scan of the chromosome 2D QTL showed that the wheat gene *TaAP2-D*, an ortholog of *Cleistogamy1,* which promotes AE via swelling of the lodicules in barley, lies within the QTL region. Moreover, a diagnostic marker developed for *TaAP2-D* also showed co-segregation with the AE phenotype. This study shows the use of gene bank diversity as a reservoir to find alleles that are otherwise difficult to detect in elite populations. The identification of large effect consistent QTL for AE is expected to help form efficient male parental lines suitable for F_1 hybrid seed production, and a source for map-based cloning.

Genome-wide association study of iron and zinc accumulation in wheat grains.

After the green revolution and improving crop yield production, nutritional qualities in many cases dropped. Therefore, improving the nutritional quality became an imperative need particularly in the developing countries where malnutrition is spreading and one of the most important crops is wheat.

Discovering the genetic factors underlying the natural variation of minerals in wheat is the main goal of the project. A genome-wide association study (GWAS) of iron (Fe) and zinc (Zn) concentrations in wheat grains using a European wheat diversity panel of 369 varieties and phenotypic data based on three years of field experiments has been used. Inductively coupled plasma optical emission spectrometry (ICP–OES) was used to measure Fe and Zn concentrations in wheat grains. High genotyping densities of single-nucleotide polymorphism (SNP) markers were obtained by the application of the 90k iSELECT ILLUMINA array and 35k Affymetrix array resulting in 15,523 polymorphic markers and additionally a subpanel of 183 genotypes was analyzed with a novel 135k Affymetrix marker array resulting in 28,710 additional polymorphic SNPs. Best linear unbiased estimates for Fe and Zn were calculated across the years and ranged from 24.42 to 52.42 µg/g and 25.05 to 52.67 µg/g, respectively, with a moderate heritability values for both.

GWAS revealed 41 and 40 significant SNPs ($-\log_{10}$ (*P*-value) ≥3.0) for Fe and Zn, respectively in the complete panel, whereas the number of significant SNPs was increased to 137 and 161 in the subpanel. The most significant associations for grain Fe concentration were located on chromosome 2A (763,689,738–765,710,113 bp) and within this region we detected candidate genes that are associated with Fe uptake or transportation such as NAC transcription factors and transmembrane proteins. The most significant and consistent associations for grain Zn concentration were located on

chromosomes 3B (723,504,241–723,611,488 bp) and 5A (462,763,758–466,582,184 bp), and within this genomic region we found candidate genes involved in Zn uptake and transport or potential regulatory factors, such as bZIP transcription factors and mitogen-activated protein kinase genes.

Oxidative stress response in semidwarf wheat.

A study was performed to elucidate the effect of wheat height reducing (*Rht*) genes on plant response to oxidative stress in dependence of the genotypic background. Six near-isogenic lines (*Rht-B1a+-D1a, Rht-B1b, Rht-B1c, Rht-D1b, Rht-B1b+ -D1b,* and *Rht-B1c+-D1b*) in four cultivar backgrounds were used. The oxidative stress was provoked by exposing seedlings to 15% polyethylene glycole-induced osmotic stress for 8 days. Main growth parameters and leaf content of free proline, hydrogen peroxide, and malondialdehyde were measured to assess plant stress tolerance and the corresponding level of oxidative stress. Treatment, *Rht* allele, cultivar, and their interactions had significant effects on the growth parameters and stress indicators. The observed general effect of individual *Rht* alleles varied depending on the genotypic background. This information accentuates the need for an accurate choice of an *Rht* allele when introducing them into a specific genetic background to develop a drought tolerant cultivar.

How foliar diseases affect gluten content of wheats from diverse origin.

Wheat gluten content is an important quality parameter that defines the product end-use. Foliar diseases affect wheat quality differentially according to the nutritional habit of the pathogen involved. The aim of this study was to evaluate the influence of foliar diseases on gluten content in spring wheat genotypes from diverse origin. The experiments were carried out in the field at the National University of La Plata using a split-plot design. The main plot was the fungicide treatment: with fungicide or without fungicide. The subplots were 110 wheat genotypes from different origin. Grain samples were conditioned and milled with Bühler MLU 202. Gluten content was determined by Glutomatic 2200. The pathogen frequency showed significant differences among genotypes. The genotypes were affected by *Puccinia triticina*, the causal agent of leaf rust (57.2%), A*lternaria* spp. including pathogenic and saprophytic species (32.7%), *Fusarium* spp. in the leaves (5.5%), *Zymoseptoria tritici*, the causal agent of Septoria tritici blotch (2.7%), and *Pyrenophora tritici repentis* the causal agent of tan spot (1.8%). The glutent content was affected by fungicide applications and the 'fungicide × cultivar' interaction indicated that genotypes more affected by leaf rust showed significant decreases in gluten content whereas genotypes mainly affected by Septoria tritici blotch, *Fusarium* spp., and TS registered significant increases. A particular case was observed with genotypes mainly affected by *Alternaria* spp., where the gluten content showed increases or decreases, probably due to the presence of pathogenic and nonpathogenic species of *Alternaria*, causing that the others nonprevalent pathogens determine the fluctuation in the gluten content. These results could be explained according to the different behavior of the nutritional habit of the pathogens involved. It has been mentioned that when classic biotrophs are controlled by fungicides, the grain protein concentration often increases, as the pathogen has a more damaging effect on the accumulation and partitioning of N to the grain than on the accumulation and partitioning of the dry matter. Conversely, most reports of the effect of controlling necrotrophic found that fungicide use is associated with a reduction in protein concentration, as the pathogen interrupts the supply of assimilates by reducing the photosynthetic capacity of the plant via destruction of leaf tissue and, therefore, having a much larger effect on carbon accumulation than N. Results indicate the importance of knowing the susceptibility of genotypes to the most prevalent pathogens to infer their impact in gluten content when fungicides are applied. The position of molecular markers conditioning gluten content is being investigated.

Genome-wide association mapping for several agronomical traits and grain architecture in a winter wheat population.

The future productivity of wheat will be of utmost importance for global food security, because it is the most widely grown crop worldwide. Our primary aim is to identify loci that influence several agronomical traits related to yield potential and grain architecture of a winter wheat population through association mapping. An experiment was performed at Leibniz Institute of Plant Genetics and Crop Plant Research (Gatersleben, Germany) during 2017. A winter wheat panel consisting of 265 accessions from 28 countries and five continents were analyzed. Flowering date, flag leaf area, plant height, peduncle length, and spike length were recorded under field conditions. Thousand-kernel weight, grain length and

grain width were measured using a MARVIN Seed Analyzer. A genome-wide association analysis was performed using the Wheat 90K Illumina iSelect SNP array that consisted of 81,587 SNPs. Mixed linear model using the Q + Kinship matrix was employed to calculate the associations between the markers and the traits evaluated (TASSEL 5.1). Significant markers were reported ($P \leq 0.001$; $LOD > 3$).

Field experiments showed 41 molecular markers related to flowering date (2 on chromosome 1A, 27 on 2A, 3 on 2D, 4 on 3A, 1 on 4B, 1 on 5B, 1 on 6A, 1 on 7A, and 1 on 7D); 19 related to flag leaf area (2 on 2A, 1 on 2B, 4 on 3A, 3 on 3B, 1 on 4A, 4 on 4B, and 4 on 5B); 38 to plant height (8 on 1B, 2 on 2A, 4 on 2D, 2 on 3A, 2 on 3B, 5 on 4B, 1 on 4D, 5 on 6A, 5 on 6B, 2 on 7A, and 1 on 7B); 32 markers related to peduncle length (3 on 2A, 1 on 2B, 2 on 3B, 1 on 4A, 4 on 4B, 1 on 4D, 7 on 5B, 2 on 6A, 3 on 6B, 1 on 7A, and 7 on 7B); and 16 markers related to spike length (1 on 1A, 1 on 1B, 4 on 2A, 1 on 2B, 4 on 2D, 3 on 4B, and 2 on 5B). For grain architecture, 36 molecular markers were related to 1,000-kernel weight (1 on 1A, 4 on 1B, 4 on 2B, 2 on 3A, 5 on 3B, 2 on 4A, 2 on 4B, 1 on 4D, 6 on 5B, 1 on 6A, 3 on 7A, 4 on 7B, and 1 on 7D); 26 markers were associated to grain length (2 on 1A, 3 on 1B, 4 on 2B, 1 on 3B, 1 on 4A, 2 on 4B, 2 on 5A, 4 on 5B, 1 on 6A, 1 on 6B, 4 on 7A, and 1 on 7B); and 65 related to grain width (4 on 1B, 8 on 2B, 4 on 3A, 7 on 3B, 2 on 4A, 2 on 4B, 3 on 5A, 4 on 5D, 1 on 6B, 3 on 7A, 24 on 7B, and 3 on 7D). New studies are being done to confirm these associations. Markers linked to the loci obtained through this project could then be used for marker-assisted selection in wheat breeding programs for improving yield.

Quantative trait loci mapping in hexaploid soft wheat in the west Siberian plain.

Mapping QTL is a modern approach to study their genetic variability. Therefore, mapping QTL, which determine economically valuable traits and their effective use in the marker-assisted selection, are of practical interest. We evaluated a set of 114 recombinant inbred lines of the ITMI (International Triticeae Mapping Initiative) spring wheat mapping population in the conditions of the west Siberian plain, Russian Federation. The ITMI mapping population was obtained by crossing spring wheat cultivar Opata 85 with a synthetic hexaploid W7984, the amphidiploid which was produced by crossing *Aegilops tauschii* (DD) sample CIGM86.940 and tetraploid wheat *T. turgidum* subsp. *durum* cultivar Altar 84 (AABB). In total, 42 different economically valuable traits were evaluated during the vegetation period, and 55 QTL were identified. The dependence fidelity between the identified loci and trait polymorphism was estimated based on the threshold of the likelihood ratio of LOD-score (logarithm of odds). For 35 identified QTL, an $LOD \geq 3.0$ was found. Identified QTL were dispersed on 19 different chromosomes and expressed in environment conditions of southern forest-steppe zone of west Siberian plain with varying certainty. The manifestation of the identified QTL may be environmentally dependent or independent, and the investigated quantitative traits correlated and were interrelated. To determine the nature of the relationship between the evaluated traits, the correlation coefficients r_{xy} were calculated. We revealed different correlations between expression of the evaluated economically valuable traits studied, which stresses on the complex nature of their manifestation. We established that the genetic variability of most of the traits evaluated is usually controlled by several QTL with broad effects, which correlate with one another or by a large number of QTL with small effects. The detected QTL and linked molecular markers may be of interest for further studies of the genetic control of economically valuable traits determined by identified QTL and for implementing marker-assisted selection in bread wheat.

Quantification of mycotoxins in wheat grains determined tolerance to Fusarium head blight elicited by phytohormone treatments.

Fusarium head blight (FHB) is a very important wheat disease provoking economical damage in Argentina, mainly it causes loss of grains and synthesis of mycotoxins. When deoxynivalenol (DON) toxin levels are higher than 1 ppm, those wheats are discarded for human consumption. Because only a few resistance sources are available, we tested synthetic hexaploids as a donor for FHB resistance several years ago. Several lines showed induced resistance against FHB after phytohormone treatments. The current study included two novel lines (L and M) and a commercial cultivar (ACA 315), which were tested in two different localities (La Plata and Tres Arroyos) during three years. A split-plot design was used in order to compare the responses to the following hormone pretreatments: jasmonic acid (JA), giberellic acid (GA), a solution with a strain of *Pseudomonas fluorescens* (Pf), or water (control); which were sprayed at anthesis. Twenty-four hours later, half of the plots of every pretreatment of each genotype were inoculated. Spikes were harvested manually, and the number of total grains, damaged kernels, and 1,000-kernel weight (TKW) were recorded. Afterwards,

every sample was ground in a coffee grinder and following the protocol of ELISA RIDASCREEN® the content of DON was assessed in the lines L, M, and ACA315, with and without inoculation with *F. graminearum,* pretreated with JA, GI, Pf, or water and harvested in La Plata or Tres Arroyos during 3 years. There were significant differences between wheat lines (L and M) and commercial A315, the latter showed the highest levels of DON. Regardless, the hormonal pretreatments received, the year, or the locality, when commercial wheat was inoculated, this cultivar showed the highest levels of DON, despite mycotoxin levels were not correlated with the number of damaged kernels or TKW. Lines L and M showed significant differences between pretreatments in both localities during the 3 years. When the line M was inoculated it showed significantly lower DON values after the Pf pretreatment, the rest of the hormonal treatments allowed lower values of damaged grains with a higher TKW, but the DON content exceeded 2 ppm. Line L showed the lowest DON content, when it was inoculated after receiving pretreatments of JA, GI, or Pf consistently in both localities and in the 3 years of trials. The elicitation of SAR in the experimental line L increased the tolerance to FHB with a scarce number of damaged kernels, a higher TKW, and an extremely low content of DON.

Natural evaluation of 15 different bread wheats segregating populations for salinity stress in the field.

Salinity is one of the most defective abiotic stresses for some bead wheat growing areas. Developing new cultivars harboring tolerance to this stress is important. Current study aims to evaluate 15 RILs populations in order to find suitable lines. These segregating populations were derived from different crosses among bread wheat pure lines selected form landrace accessions. The landraces were received kindly from IPK-Gatersleben Genebank in Germany in 2010. After the first two years field evaluations, many pure lines were selected, which resulted in a genebank collection of pure lines in Gorgan University originated from landrace accessions of different origins. Then, some of the lines from different origins were crossed to develop new sources for variation. The 15 populations were developed from F_2 to F_6 via single-seed descendent approach. Based on the filed observation, there are huge intra- and inter-population variations morphologically and phonologically. This year, these population will be grown and evaluated on a salty land to select the most tolerant ones naturally. Because each population has about 10,000 different lines, we expect to test 150–1,000 lines in this experiment.

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ITEMS FROM INDIA

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Nuclear Agriculture & Biotechnology Division
Mumbai-400085, India.

Gamma-ray induced mutants with enhanced resistance to yellow (stripe) rust in elite wheat cultivars of the North Western Plain Zone (NWPZ) of India.

G. Vishwakarma and B.K. Das (Nuclear Agriculture & Biotechnology Division); Satish Kumar, M.S. Saharan, and C.N. Mishra (ICAR–Inidan Institute of Wheat & Barley Research, Karnal, Haryana, India); and A. Saini (Moleuclar Biology Division).

The North Western Plains Zone (NWPZ) is a major wheat producing zone in India with ~10 m/ha land under cultivation, which contributes ~50% of Indian wheat production. Wheat production in NWPZ is affected by various biotic and abiotic stresses, of which yellow (stripe) rust caused by *Puccinia striiformis* f. sp. *tritici* is the most serious threat. Due to the rapid emergence of new virulent pathotypes in this zone most of the wheat cultivars are becoming susceptible to prevalent stripe rust races. Breeding for resistance for yellow rust by conventional approach leads unwanted variability in genetic architecture of the high-yielding cultivars; hence, in such a scenario, to achieve enhanced resistance to yellow rust of wheat, a radiation-induced, mutation-breeding approach was initiated in the popular bread wheat cultivar DBW-88. Healthy seeds were irradiated with gamma rays and M_1 was raised at Trombay in 2014–15, subsequently the M_2 was screened under artificial epidemic conditions for yellow rust at IIWBR–Karnal; selected resistant mutants were confirmed in the M_3 generation and then carried forward for stability in subsequent generations. In 2017–18 (*rabi* season), the M_6 generation was screened for stripe rust resistance at IIWBR–Karnal, mutant lines showed resistance to stripe rust in artificial field epidemic conditions (immune–5MS) compared to the parent cultivar (60S–80S). The resistant lines will be further evaluated for agronomic and yield traits and advanced for national trials if found suitable. The mutants will provide additional germplasm resource for resistance to stripe rust and can be used directly after yield trials or be used indirectly as donor in other high-yielding backgrounds.

Two other high-yielding cultivars, HD-2967 and WH-1105 (highly popular in NWPZ), were irradiated with gamma rays. The M_1 generation was raised at IIWBR–Karnal in 2016–17. A plant-to-row progeny of ~1,800 individual M_1 plant harvests were raised at IIWBR–Karnal (2017–18) and screened for resistance to prevalent races of yellow rust under artificial epidemic conditions. Putative mutants showing enhanced resistance to yellow rust (immune–20MS) compared to that of the parent (60S–80S) were identified and will be confirmed in subsequent generations. These studies have generated novel germplasm resources for resistance to yellow rust and demonstrate a suitable strategy for breeding for rust resistance using mutation breeding to complement conventional breeding approach.

Development of improved plant types in elite Sharbati wheat cultivars of India using gamma ray-induced mutation breeding.

G. Vishwakarma and B.K. Das (Nuclear Agriculture & Biotechnology Division), J.B. Singh and S.V. Sai Prasad (ICAR–Inidan Institute of Wheat & Barley Research, Karnal, Haryana, India), and D.A. Gadekar (MPKV–Agriculture Research Station, Niphad, Nashik, India).

The Central Zone (CZ) of India, is one the important zones of India primarily for its high end-use quality wheat cultivars. Sharbati wheat cultivars are very popular among farmers and consumers due to its excellent Chapatti-making quality and, hence, fetch a premium price for farmers. HI-1500 (Amrita) and HI-1531 (Harshita) are two widely grown Sharbati wheat cultivars in the CZ with good yield and rust resistance that provide better returns to farmers. However, these cultivars are medium-tall in nature and medium-late in maturity. As a result, heavy irrigation and fertilizer application conditions or unseasonal rains/storms during later crop stages lead to severe lodging and significant yield loss. To develop plant types with improved agronomic traits such as reduced height, early maturity, and increased tillering, mutation

breeding was initiated in these elite Sharbati wheat cultivars. Healthy seeds of the two cultivars were irradiated and the M_1 generation raised at Trombay and Indore. Subsequently, the M_2 generation plants were screened for improved traits at Indore and Niphad; putative mutants with improved agronomic traits such as semidwarf height, early maturity, and high tillering were identified. These mutants were further evaluated in the M_3 at Indore and Niphad for improved phenotypes and will be carried forward for further stabilization and use in breeding programs.

Mutation breeding for improvement of two other popular wheat cultivars of the CZ, C-306, and HW-2004, also was initiated using gamma rays; the M_1 was raised at Indore. The mutant population will be screened for desirable agronomic traits, i.e., semidwarf habit, early maturity, and rust resistance. Overall, using mutation breeding, a broad spectrum of variability for selection and use within the genetic architecture of the well-adapted cultivars was created that will be useful for developing cultivars with better adaptability to environment.

Improvement of earliness and rust resistance in the excellent, Chapatti-making quality cultivar C-306 using mutation and molecular breeding.

G. Vishwakarma and B.K. Das.

The wheat cultivar C-306 (released in 1969) is well-known for its Chapatti-making quality and is cultivated in most of the wheat-growing zones owing to its high demand in flour industry. However, C-306 is susceptible to prevalent races of stem and leaf rust; in addition, because of its medium-late maturity, it is exposed to terminal heat stress. To improve these two important constraints in the C-306 background, mutation breeding was initiated using gamma rays and a ~25-day, early maturing mutant (TWM-89) was obtained. The early maturing mutant escapes terminal heat stress and, hence, yield loss is not affected due to poor grain filling. In addition, the mutant has quality traits similar to those of the parent. However, like C-306, the early maturing mutant (TWM-89) was susceptible to wheat rusts. Thus, to recombine early maturity with rust resistance, the *Sr24*/*Lr24* genes were transferred from HW-2004 (a near-isogenic line of C-306) so that the other genomic architecture contributing to quality and other traits remain the same. *Sr24*/*Lr24* is already deployed in Indian wheat cultivars and confers resistance to most of the prevalent stem and leaf rust races in central and peninsular zones of India. Many tightly linked markers are reported for the *Sr24* gene, and these markers ($SCS1302_{609}$ and *XBARC-71*) were used to select for *Sr24* carriers. Rust-resistant and early maturing plants were identified in the F_2 and carried forward in further generations (F_3–F_5). Stable, rust-resistant, early maturing lines in the F_5 were obtained, and these will be advanced for yield and agronomic traits in the next year. C-306, a popular cultivar even after more than 45 year of release, shows its preference for consumers and farmers. In addition, the cultivar also is well-known for its heat and drought tolerance. The improved version of C-306, with early maturity and rust resistance, can efficiently replace C-306 with better results and the ability to face climate change.

Molecular characterization and mapping of an early maturing locus in wheat cultivar C-306 using simple-sequence repeat markers.

G. Vishwakarma, Y. Haribabu, K. Suryavanshi, and B.K. Das (Nuclear Agriculture & Biotechnology Division); D.A. Gadekar (MPKV–Agriculture Research Station, Niphad, Nashik, India); and A. Saini (Moleuclar Biology Division).

Mutation breeding is a useful tool for creating additional variability for utilization in crop improvement. In addition, the mutants obtained are excellent models for genetic and molecular biology studies of the trait involved. In this aspect, an early maturing mutant (TWM-89) obtained in wheat cultivar C-306 using gamma ray irradiation at BARC, Mumbai, was characterized for the mutant trait. The mutant is ~25 days earlier maturing than that of the parent line, although other traits are similar. Three hundred SSR markers from the *Xgwm* and *WMC* series spanning all chromosomes of bread wheat were used to screen the parent and mutant for variability in allele size. Eleven SSR markers showing variable allelic status in the parent and the mutant were identified. These markers belonged to six different chromosomes, suggesting that more than one locus may be involved in earliness. The 11 SSR markers are being used to study segregation in an F_2 mapping population derived from crossing the early mutant with its parent. The information will help in molecular tagging of the mutant locus and further map-based cloning. This information will help to better understand maturity in wheat and also will help to develop molecular markers useful for transferring earliness trait in other wheat cultivars.

Genetic improvement of wheat in the Peninsular and Central zones of India for yield and quality traits.

A.S. Shitre, G. Vishwakarma, and B.K. Das (Nuclear Agriculture and Biotechnology Division); N.R. Potdukhe and B.D. Gite (Wheat Research Unit, Dr. PDKV, Akola., Maharashtra, India); and D.A. Gadekar (MPKV–Agriculture Research Station, Niphad, Nashik, India).

Quality improvement in wheat has two objectives: improvement in nutritional quality and improvement in processed product quality. The current R&D work on both aspects are being addressed by our group.

Genetic improvement for iron (Fe) and zinc (Zn) content. Wheat is the second most important staple food crop of the world after rice. In under-developed and developing countries malnourishment is a major problem. Among minerals, Fe and Zn are very important, required for the normal and healthy growth of human beings. Fortification of food by adding these minerals externally is difficult to follow in day-to-day life. So, biofortification of staple food-grains is one of the cheapest and long-term possible solutions. Initial screening of existing wheat genotypes for assessing the variability for Fe and Zn content was carried out to identify suitable genotypes for use in a crossing program for developing high-yielding wheat lines with increased Fe and Zn content. One hundred and fifty genotypes (including released cultivars and advanced stable lines developed for the Central and Peninsular zones of India) were screened for Fe and Zn content using a ICP–OES technique. Genotypes showing higher Fe and Zn content were identified and are being used in the crossing program. F_1 and F_2 generations are being raised.

Genetic improvement for lysine content. Work is initiated to standardize the protocol for lysine content. Twenty genotypes were screened for lysine content.

Improvement for processed product quality. Wheat is the second largest crop grown in India and is consumed in the form different end-products such as *Chapatti*, noodles, bread, and biscuits. In the south Asiatic segment, wheat is largely consumed as noodles and *Chapatti*. The organo-leptic quality of any food materials depends upon its colour, appearance and test. In the case of wheat, the color of the end-product, specifically noodles, pasta, *Chapatti,* and bread, depends upon the color of the dough. Polyphenol oxidase (PPO) is an enzyme located in bran layer of the wheat. The enzymatic activity of PPO is responsible for the discoloration of the dough and ultimately the end-product. Eighty genotypes including released cultivars were screened biochemically using L-DOPA as substrate for PPO activity. These genotypes also are screened using molecular marker (PPO 18 and PPO 33). Genotypes with low PPO activity were identified and will be used in a crossing program to develop high-yielding, low-PPO genotypes.

Improvement for yield and yield-related traits. One hundred new crosses were made to develop high-yielding, superior recombinant lines for the Central and Peninsular zones of India. Three advanced wheat genotypes (TAW-33, TAW-157, and TAW-159), which performed well in Preliminary Varietal Trial (PVT) at Dr. PDKV, Akola, will be promoted in a multi-location varietal trial in 2018–19.

Mutation-breeding program. Durum wheat occupies 5–7% area of wheat growing regions in India and has very good export potential to European countries due to a specific demand for pasta. The limited cultivation is due various reasons, such as low yield and tall-growth habit. A mutation-breeding program in durum wheat will develop semidwarf, high-tillering, and long-panicle genotypes, which will be utilized in a crossing program to increase yield and improve yield-related traits. Similarly, a mutation-breeding program in bread wheat and dicoccum wheat were initiated to identify early, semidwarf, and free-threshing mutants.

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CH. CHARAN SINGH UNIVERSITY, MEERUT

Molecular Biology Laboratory, Department of Genetics and Plant Breeding, CCS University, Meerut 250004, India.
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P.K. Gupta, H.S. Balyan, P.K. Sharma, Shailendra Sharma, Sachin Kumar, Kalpana Singh, Ritu Batra, Supriya Kumar, Jitendra Kumar, Gautam Saripalli, Tinku Gautam, Rakhi, Sunita Pal, Anuj Kumar, Irfat Jan, Kuldeep Kumar, Manoj Kumar, Divya Malik, Sourabh Kumar, Vivudh P Singh, Hemant Sharma, Deepti Chaturvedi, and Parveen Malik.

Genetic and epigenetic regulation of leaf rust resistance.

Rust diseases of wheat are among the oldest diseases and are highly devastating. Leaf rust alone causes severe yield losses. Thus, we carried out studies to understand the molecular basis of leaf rust resistance due to *Lr28* (a seedling resistance gene, SR) and *Lr48* (an adult-plant resistance gene) genes using genetic and epigenetic approaches. The genetic studies involved cDNA-AFLP/RNASeq (transcriptomics), and the epigenetic studies involved (i) MSAP/MeDIP-Seq for methylation, (ii) ChIP-qPCR/ChIP-Seq for histone modifications, and (iii) smRNA-Seq and degradome analysis for miRNAs and their targets, and (iv) analysis of long noncoding RNA (lncRNA). For this purpose, the following plant material was used: (i) a pair of NILs differing for *Lr28* (susceptible NIL HD2329 and resistant NIL HD2329+*Lr28*) and (ii) the resistant line CSP44 (selected from the Australian cultivar Condor) carrying *Lr48*. These lines were challenged by a virulent pathotype 77-5 of *Puccinia triticina*.

Transcriptome analysis (cDNA-AFLP and RNA-Seq). Transcriptome analysis using cDNA-AFLP for *Lr48* and *Lr28* and high-throughput RNA-Seq for *Lr28* allowed us to identify a large number of differentially expressed genes (TFs such as WRKYs; and protein kinases such as LRR, WAKs, and S/TPKs; and oxidative stress-response genes such as GSTs and peroxidases). Some of these genes were involved in providing resistance due to *Lr28*/*Lr48* genes and others contributed to leaf rust susceptibility (Dhariwal et al. 2011, 2015; Sharma et al. 2018). Some of the differentially expressed genes also were validated using qRT-PCR.

DNA methylation. In order to understand the role of DNA methylation in SR due to *Lr28*, two approaches (MSAP and MeDIP-Seq) were used. The MSAP analysis involved pairs of isochizomers (*Eco*RI + *Msp*I and *Eco*RI+ *Hpa*II) differing for their sensitivity to methylated cytosines. MeDIP-Seq, on the other hand, is an affinity-based technique involving enrichment of methylated cytosines using methylated cytosine specific antibodies followed by high-throughput sequencing. MSAP identified a number of differentially methylated fragments and also showed abundance of C^mG methylation in compatible interaction and C^mHG methylation in incompatible interaction suggesting change in methylation context. The MeDIP-Seq identified differentially methylated regions (DMRs) during compatible and incompatible interactions. These DMRs were distributed in different genomic regions, such as introns, exons, promoters, TTS (transcription termination sites), and intergenic regions. Some of these DMRs contained disease responsive genes such as genes with leucine rich repeat (LRR) containing domains or oxidative stress responsive genes. Transposable elements, such as gypsy and0 LTRs, also were identified in the DMRs. About 250 methylated genes also were found to be differentially expressed in RNA-Seq data providing some evidence of the role of DNA methylation in regulation of gene expression. Whole-genome, bisulfite sequencing also is being carried out to identify DMRs with changes in methylation contexts (CG, CHG, and CHH) at single-base resolution.

ChIP-qPCR and ChIP-Seq. The role of epigenetic modifications (histone methylation and acetylation) in leaf rust resistance due to *Lr28* also was examined using ChIP-qPCR and ChIP-Seq. ChIP-qPCR analysis for six differentially expressed defense-response genes (each containing an important disease responsive motifs in their promoter region) was carried out, and the results were compared with the RNA-Seq data. The promoter enrichment of H3K4/K9 acetylation

marks changed with time. Changes in expression of two of the six genes (*N-acetyltransferase* and *peroxidase12*) largely matched changes in the H3K4/K9 acetylation marks in the promoter regions. The remaining four genes also showed enrichment of H3K4/K9ac marks, but it did not perfectly match with their expression levels, suggesting complexity in regulation of expression of these genes, which probably is controlled by other genetic and epigenetic regulatory mechanisms. Genome-wide, histone modification also is studied in relation to two histone methylation marks H3K4me3 (activation mark) and H3K27me3 (repressor mark). ChiPped libraries for both the epigenetic marks were prepared for the pair of NILs for *Lr28* followed by high-throughput sequencing. In the absence of inoculation, the highest differential binding sites (DBS) were identified for H3K4me3 in the compatible interaction and for H3K27me3 in the incompatible interaction. The lowest DBS were found in the incompatible interaction for both the marks. The DBS identified for both marks mostly contained different categories of genes involved in (i) defense response, (ii) oxidative stress, (iii) metabolism, (iv) photosynthesis, (v) methylation, and (vi) chromatin modification. Some of the genes associated with modified histone also showed differential expression in RNA-Seq data, indicating a relationship between histone methylation and gene expression.

MicroRNA (miRNA) and their targets. Forty differentially expressed miRNAs in response to leaf rust infection in resistant and susceptible NILs were identified. Among these miRNAs, six were up-regulated in the incompatible interaction, whereas seven were up-regulated in compatible interaction. Seven of these 13 differentially expressed miRNAs were validated through qRT-PCR. Most of the up-regulating miRNAs in the incompatible interaction belonged to the same miRNA family. Degradome analysis identified target genes for the conserved and novel miRNAs, which included the following: bidirectional sugar transporter SWEET, NAC transcription factor, glutamate decarboxylase, transcription repressor VAL2, histone deacetylase 19, non-specific lipid transfer protein, sucrose transporter SUT1, and Myb repressor. Sugar transporter SWEET was targeted by a number of miRNAs in the compatible interaction, indicating that pathogen utilize host sugar transporters for their growth during compatible interactions. Most of the miRNAs have multiple targets. Targets for more miRNA families (59) were found in the incompatible interaction compared to targets for miRNA families (32) in the compatible interaction.

lncRNAs. Long non-coding RNAs (lncRNAs) are known to play a major role in regulation of gene expression at both transcriptional and translational levels. To gain insight into their role, if any, against leaf rust disease, 5,322 lncRNAs specific to *Lr28* were identified using transcriptome data (21,345 transcripts). Out of the total 5,322 lncRNAs, 3,498 lncRNAs were non-redundant, which were further classified as follows: overlapping (1,194), intronic (291), intergenic (1,176), antisense (733), and sense (104). Of the non-redundant lncRNAs, 1,802 were identified as differentially expressed. An interaction of lncRNAs with miRNAs showed that 16 lncRNA compete with 16 miRNAs for 39 target mRNAs. Seven lncRNAs were found as decoys/sponges of seven miRNAs. Furthermore, 67 lncRNAs were targets of 22 miRNAs, which could thus cleave these lncRNAs. Interaction of lncRNA with transcription factors (TFs) showed that 50 TFs (19 TF families) were identified within 108 lncRNAs. The TFs bHLH, ERF, HSF, MYB, MYB_related, NAC, Nin-like, SBP, and WRKY, co-expressed with lncRNAs in bread wheat. The above information revealed that these lncRNAs might be important regulators for leaf rust disease resistance.

Together, the transcriptome and epigenome data will help us establish a network of genes that are involved in the regulation of leaf rust infection/disease in wheat. This data will, in turn, serve as a resource for molecular breeding of leaf rust disease in wheat.

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QTL analysis for grain traits.

Grain traits are related to market value and milling yield. Thus, we identified QTL regulating grain traits. For this purpose, we utilized an RIL population derived from the cross 'NW1014/HUW468' that was evaluated at two locations (Meerut and Varanasi). Phenotypic data on seven grain traits and a linkage map of 55 simple-sequence repeat markers for eight wheat chromosomes was used for QTL analysis by composite interval mapping. A total of 18 QTL on eight chromosomes were identified. Five QTL for grain length:width ratio were found on chromosomes 1A, 6A, 2B, and 7B; three QTL for grain perimeter length were located on chromosomes 4A, 5A, and 7B; and three QTL for grain area size were mapped on 5D and 7D. Two QTL were identified on chromosomes 4A and 5A for grain length, and two QTL for grain width were identified on chromosomes 7D and 6A. Similarly, two QTL for factor form density were found on chromosomes 1A and 5D. A solitary QTL for 1,000-kernel weight (TKW) was identified on chromosome 2B. For several traits, QTL also co-localized on chromosomes 2B, 4A, 5A, 6A, 5D, 7B, and 7D. These QTL may be validated for specific crosses and then used for marker-assisted selection to improve grain quality in bread wheat.

Validation of QTL for TKW using MAS-derived pairs of NILs. Eight pairs of NILs for three grain weight QTL were developed; seven in the background of Raj3765 and one in the background of K9107. For this purpose, MAS was used to transfer of three grain weight QTL (*QGw.ccsu-1A.2*, *QGw.ccsu-1A.3,* and *QGw.ccsu-1B.1*) earlier reported by us. Two genotypes of each of the eight pairs of NILs differed for QTL alleles (QTL_{Hgw} derived from the donor parent and the QTL_{Lgw} derived from the recipient parent). Each pair of NILs involved a solitary QTL except in one NIL, which differed for all the three. The difference in TKW in two NILs of an individual pair ranged from 2.8 to 7.5 g, thus validating the effect of the QTL for TKW, although the quantum of difference did not always match the phenotypic variance of the corresponding QTL. As expected, the NILs that involved all the three QTL had the maximum difference of 7.5 g in TKW, and the NILs that involved QTL *QGw.ccsu-1A.2* had a minimum average difference of 2.8 g for TKW. The above NILs may be used in future for MAS and for fine mapping of TKW QTL.

QTL mapping for preharvest sprouting tolerance. Preharvest sprouting (PHS) is an importat factor for loss of grain quality and yield around the world, particularly in the regions where wet weather conditions occur at the time of grain maturity. Genotypes lacking adequate level of grain dormancy can be more prone to PHS. Breeding wheat genotypes with a balanced degree of seed dormancy is one of the preferences of breeders to control damage due to PHS. We are currently making efforts to map QTL for seed dormancy and PHS tolerance. A DH mapping population of 386 lines derived from a cross of two Canadian white-grained spring wheat genotypes, SC8021-V2 and AC Karma, is being used. The genotype SC8021-V2 is resistant to PHS and AC Karma is moderately susceptible. This population was imported from the Swift Current Research and Development Centre of Agriculture and Agri-Food Canada, Swift Current, Saskatchewan, Canada, under a collaborative research program. The DH population and parents have already been genotyped with an Infinium iSelect 90K SNP assay. Presently, the parents and DH lines are being evaluated in multi-location field trials for seed dormancy and PHS tolerance related traits. QTL analysis may provide important insight into the genetic control of PHS in white-grained wheat and will also allow identification of markers for use in breeding for PHS tolerance in wheat.

QTL analysis and marker-assisted selection for heat tolerance. High temperature or heat stress affects 40% of the wheat-growing area in the world. Every 1°C rise in temperature above the optimal temperature of 26°C decreases wheat yield by an estimated 3–4%. In India, the wheat crop mainly suffers from terminal heat stress due to delayed sowing of wheat at the end of December/beginning of January and the late harvest of preceding crops (rice, sugarcane, maize, or cotton). The sudden rise in temperature during anthesis causes significant reduction in grain number (due to floret sterility) and grain weight. Therefore, knowledge of the genetic and molecular basis of heat tolerance is essential for breeding high-yielding, heat-tolerant and climate-resilient wheat genotypes.

In view of this, we have undertaken the following two activities. First, a DH population consisting of 177 lines was derived from a cross involving cultivars Giza168 (heat tolerant) and PBW343 (heat sensitive). In 2017–18, the DH population, along with the two parents, was evaluated for 18 traits on three sowing dates (timely, late, and very late) at two different locations (Meerut and Lucknow). The phenotypic data suggested a significant decline in the mean performance of all the traits under late and very late sown conditions. Evaluation of the DH population and its parents is being repeated during the current crop season (2018–19). The SNP data obtained through genotype-by-sequencing (GBS) of the DH population and its two parents will soon become available. The phenotypic and genotypic data will be used for QTL mapping. Second, foreground MAS for 10 known QTL for different traits related to heat stress tolerance in the BC_2F_1 population (PBW343/Giza168//PBW343) is in progress to identify plants containing a maximum number

of desirable QTL alleles to be again backcrossed with cultivar PBW343. Third, 12 gene copies encoding large and small subunits of the AGPase enzyme (involved in starch biosynthesis), located on chromosomes of homoeologous groups 1, 5, and 7, have been identified and efforts to develop allele-specific markers for introgression (through MAS) of *AGPase* alleles imparting tolerance to heat stress have been initiated.

Genetic variability and QTL analysis for nitrogen use efficiency. Chemical fertilizers are applied in high doses to provide necessary nutrients for crop growth and development. Among the chemical nitrogen (N) fertilizers, urea is the most commonly used fertilizer in India. Currently, ~30.6 MMTs of urea are consumed accounting for 83% of total N fertilizer consumption in the country. However, use efficiency of urea-N by crop plants can be as low as 20% and it rarely exceeds 50%. The remaining N is lost to the environment, which contributes to environmental pollution. Hence, improving N-use efficiency (NUE) is desirable so that low doses of N fertilizer may help improve/maintain crop yields, reduce the cost of crop production, and also reduce environmental pollution. The need to assess the variability for NUE among wheat genotypes and conduct QTL analyses for NUE-related traits for use in marker-assisted breeding will enable improvement of NUE in wheat. Towards meeting these objectives, a set of 21 wheat cultivars and an RIL population were evaluated for different agronomic and NUE-related traits under four N doses (0 kg/h, 60 kg/h, 120 kg/h, and 180 kg/h). The 21 wheat cultivars were evaluated in a split-plot design with three replications. Data were recorded on 14 traits (yield and NUE-related traits) that are being analyzed to quantify the genetic variability for NUE and its related traits. Similarly, the mapping population (154 RILs) derived from the cross 'C306/HUW468', two parental genotypes and three check genotypes (NW1014, RAJ3765, and UP2387) were phenotyped in an augmented block design experiment under the above four different N doses. A genetic map of the above RIL population is being prepared using the SNP marker data. The phenotypic data and the genetic map will be used for QTL interval mapping and to identify the candidate genes underlying the identified QTL.

Genome-wide association studies (GWAS).

GWAS analysis for Fe, Zn, β-carotene, grain protein content, and yield traits. Wheat is consumed by more than 40% world population as a staple food and is the primary source of calories for millions of people worldwide. However, the crop is deficient for major micronutrients such as Fe, Zn, and β-carotene, which are present only as minor constituents of wheat grain. Over 3 x 10^6 people, including one third of the children in developing countries, suffer from micronutrient malnutrition or hidden hunger. We analyzed the genetic architecture of grain micronutrients (Zn, Fe, and β-carotene contents), grain protein content, and four yield traits in a spring wheat reference set comprised of 246 genotypes. Phenotypic data on these traits was recorded at two locations, and the genotyping data for 17,937 SNP markers were used for genome-wide association study. After Bonferroni correction using four different methods, we observed that (i) a single-locus, single-trait analysis gave 136 marker-trait associations (MTAs), (ii) the multi-locus mixed model gave 587 MTAs, (iii) a multi-trait mixed model gave 28 MTAs, and (iv) a matrix-variate linear mixed model gave 33 MTAs. As many as 73 epistatic interactions also were detected. Using these results, nine of the most important MTAs were selected for biofortification. These markers were associated with three traits, i.e., grain protein content, grain Fe content, and grain yield per plot. These MTAs can be used in wheat improvement programs either using marker-assisted recurrent selection or pseudo-backcrossing method.

GWAS for heat stress tolerance. Yield loss due to heat stress in wheat is mainly observed in the form of floret sterility and reduced grain size/grain weight. Temperature below 26°C is ideal for wheat grain development due to its temperate C3 nature. Even a slight deviation from this temperature leads to decline in yield (http://plantsinaction.science.uq.edu.au/book/export/html/158). Thus, we decided to conduct GWAS for heat stress tolerance traits. Phenotypic data on 12 traits related to heat tolerance on 273 genotypes of a spring wheat reference set was recorded at two locations (Meerut and Powerkheda) under timely sown and late-sown conditions over two years. The phenotypic and genotypic data on ~17,000 SNPs was used for GWAS using three different approaches (GAPIT, SUPER, and FarmCPU). All the 11 traits displayed normal distribution. A decline in average trait value was noticed under heat-stress conditions (late sown). A PCA analysis using GAPIT classified the population into six different sub-populations. Using each of three approaches, a greater number of significant MTAs (p value < 0.001) were identified at Powerkheda than at Meerut. Of the total 1,060 MTAs identified under late-sown conditions, 24 were identified by all the three approaches. Similarly, of the 1,064 MTAs identified under timely sown conditions, 25 were identified by all the three methods. The MTAs identified by all the three approaches of GWAS are important. Candidate genes underlying significant MTAs are being identified.

GWAS for resistance to two nematodes. Two parasitic nematodes, *Heterodera avenae* (cereal cyst nematode) and *Pratylenchus thornei* (root lesion nematode), cause severe losses to the wheat crop. *H. avenae* is the major parasitic nematode of wheat in India, whereas *P. thornei* is emerging as a potential threat to wheat/rice and legumes crops. *H. avenae* is an endemic problem and is distributed from the Northern Hill region to Central India. Therefore, a need exists for strong host–plant resistance against these two nematodes for deployment in wheat to effectively control the nematode population. We are undertaking GWAS using a diverse exotic (~200 genotypes) and indigenous (160 genotypes) wheat collection. The 200 exotic and 100 indigenous genotypes were screened for resistance to *H. avenae*. The genotypes showed a range of 03 to 40 cysts/plant, where a low number of cysts indicates resistance and a high number indicates susceptibility. The phenotypic data, along with genotyping data, will be used for determining marker-trait associations through GWAS. The above information will be supplemented with QTL interval mapping using one or more bi-parental mapping populations.

Pyramiding of rust resistance genes into high grain quality wheat lines.

We are attempting to pyramid QTL/genes for improved grain quality (grain protein content and preharvest sprouting tolerance) and resistance to all the three rusts using the following three genotypes in the backgrounds of HD2967 and Lok1 earlier developed using MAS: (i) HD2967 (*Gpc-B1/Yr36 + Lr24*), (ii) HD2967 (*Lr19/Sr25 + Yr10 + Lr34*), and (iii) Lok1 (*Gpc-B1/Yr36+ Lr24 + Sr2 + Qphs.dpivic.4A.2*). Using these three genotypes, the following two crosses were attempted: (1) 'HD2967 (*Gpc-B1/Yr36 + Lr24*) / HD2967 (*Lr19/Sr25 + Yr10 + Lr34*)' and (2) 'Lok1 (*Gpc-B1/Yr36+ Lr24 + Sr2 + Qphs.dpivic.4A.2*) / HD2967 (*Lr19/Sr25 + Yr10 + Lr34*)'. The F_2 from cross 1 comprised 1,950 plants, and 950 plants were in the F_2 from cross 2. Foreground MAS for all the QTL/genes was carried out in the two F_2 populations. Thirteen of the 1,950 F_2 plants from the cross 1 and five of the 950 F_2 plants from cross 2 contained all the QTL/gene combinations in either homozygous or heterozygous state. Foreground MAS in the F_3 progenies of the selected F_2 plants of each the two crosses is being carried out to identify plants homozygous for all the QTL/genes. The progenies derived from selected plants will be evaluated in station trials to determine their potential for use in future wheat breeding programs.

Marker-assisted backcross breeding for improvement of drought tolerance.

A major QTL (*Qyld.csdh.7AL*) contributing to > 20% higher yield/spike under stress environments (including drought stress) was introgressed from wheat genotype SQ1 into four popular Indian wheat cultivars (HUW234, HUW468, K307, and DBW17) using marker-assisted backcross breeding. A set of 62 BC_2F_5 progenies with desirable phenotypes were evaluated in randomized block design with two replications under irrigated and rainfed environments at Meerut (UP) and Niphad (Maharashtra) during the 2015 and 2016 crop seasons. The average decline in grain yield under rainfed environments at the two locations was 9% (Meerut) to 31% (Niphad), suggesting the suitability of the rainfed environments for evaluation of the derived progenies. Under rainfed environments, six progenies in the backgrounds of HUW234, HUW468, and K307 at Meerut and four progenies in the background of HUW234 at Niphad gave significantly higher grain yield (8% to 59%) than their respective recipient genotypes. One of the higher yielding progenies, in the background of HUW234, was common at both the locations. The high-yielding progenies also were significantly superior for two or more of the following seven traits: grain number/spike, grain weight/spike, tiller number/m^2, harvest index, biomass, canopy temperature, and chlorophyll content. All 62 progenies are being further evaluated to assess their mean performance and interaction with environments (including location and years). As a follow-up, introgressing the QTL *Qyld.csdh.7AL* into three (HD2967, WB2, and DBW88) high-yielding wheat cultivars has been initiated following marker-assisted backcross breeding. A set of 30 and 13 BC_2F_3 progenies in the backgrounds of HD2967 and DBW88, respectively, homozygous for *Qyld.csdh.7AL* were selected and currently being evaluated at Meerut location during the current crop season.

A web resource for nutrient use efficiency related genes/QTL and miRNA.

We have prepared a web resource [https://f1000research.com/articles/7-673/v1] containing information on nutrient use efficiency (NtUE)-related genes/QTL and the corresponding available microRNAs in four cereal crops wheat, rice, maize, and barley; two alien species related to wheat (*Triticum urartu* and *Aegilops tauschii*); and two model species (*Brachypodium distachyon* and *Arabidopsis thaliana*). Gene annotations integrated in web resource were manually cu-

rated from the existing databases and the available literature. Descriptions of the NtUE-related genes and their functional annotation is provided.

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Computational identification of genes in wheat and their comparative analysis with genes of monocot and dicot species.

Dormancy-related gene ***KNOX4*****.** Wheat production in large acreage is challenged by various abiotic stresses, mainly fluctuation in environmental conditions. Near Asian monsoon areas and high-moisture conditions at maturity induce germination of grain within spikes in genotypes that lack grain dormancy. Grain dormancy is generally developed during seed maturation and its conservation in mature seed is influenced by environmental and genetic factors. Recently, *KNOX4*, a class II KNOTTED-like homeobox gene, was identified in *Medicago truncatula* that controls seed dormancy by cuticle development in the seed coat. The structure and function of *KNOX4* and its role in controlling grain dormancy is not known in cereals. We identified putative orthologs of *M. truncatula KNOX4* gene in 13 different plant species involving six monocots and seven dicots. We revealed comprehensive molecular structure of *KNOX4* gene based on intron-exon architecture and its encoded proteins in above species with emphasis on wheat. At the sequence level, a large variation was found in number, size, and phase of introns, although exons were relatively conserved in all species. Three *KNOX4* genes, one each located on chromosomes 5A, 4B, and 4D, were detected in the wheat genome. The presence of a gene on 5A rather than on 4A as expected may be due to the known translocation between chromosomes 4A and 5A in wheat. In the wheat genes, the number of exons was largely conserved, with five exons per gene, except that located on chromosome 5A, which has only three exons. We believe that the gene on chromosome 5A is truncated, and this aspect needs further investigation. *In silico* expression analysis indicated that the level of gene expression was similar in all the species, however, it was tissue specific (e.g., coleoptile in monocots and seed coat in dicots). Primary, secondary, and tertiary structures of the protein of *KNOX4* genes also were predicted, showing a high level of similarity among the 13 examined species. This study provides the basic knowledge about the existence, structure, and putative function of *KNOX4* genes in wheat and other species.

SWEET **genes for sugar transport.** SWEET proteins represent one of the largest sugar-transporter families in the plant kingdom and play crucial roles in plant development and stress responses. A total of 108 *TaSWEET* genes distributed on all the 21 wheat chromosomes were identified by us using the latest whole-genome sequence. These 108 genes included 14 of the 17 types reported in *Arabidopsis* and also included three novel types. Tandem duplications (22) and segmental duplications (5) played a significant role in the expansion of the TaSWEET family. Cis-elements identified in the promoter regions of the *TaSWEET* genes indicate the response of *TaSWEET* genes during development and also during biotic/abiotic stresses. The TaSWEET proteins carried 4–7 trans-membrane helices showing diversity in structure. Phylogenetic analysis using SWEET proteins of wheat and eight other species gave four well-known clusters. Both *in silico* and *in planta* qRT-PCR expression analysis indicated relatively higher expression of *TaSWEET* genes in water/heat sensitive and leaf rust-resistant genotypes. The results provided insight into the functional role of TaSWEETs in biotic and abiotic stresses, which may further help in planning strategies to develop high-yielding wheat cultivars tolerant to environmental stresses.

RWP-RK transcription factor genes. RWP-RKs, a small family of transcription factors, are unique to plants and function particularly under conditions of nitrogen starvation. The RWP-RKs have been classified in two sub-families, NLPs (NIN-like proteins) and RKDs (RWP-RK domain proteins). NLPs are involved in regulating tissue-specific expression of genes that are involved in nitrogen-use efficiency (NUE), whereas RKDs are involved in regulating expression of genes involved in gametogenesis/embryogenesis. We identified 37 *RWP-RK* genes; 18 of these belonged to NLP sub-family (range: 2,865–7,340 bp with 4/5 exons) and 19 genes belonged to an RKD sub-family (range: 1,064–5,768 bp with 1 to 6 exons). TaNLP genes were distributed on 15 chromosomes from five homoeologous groups (with two genes each on 4B, 4D, and 5A), whereas *TaRKD* genes were distributed on 12 chromosomes from four homoeologous groups (except groups 1, 4, and 5). Two to three splice variants also were available in nine of the 37 genes. Sixteen genes also carried 24 SSRs, whereas 11 genes had targets for 13 different miRNAs. At the protein level, MD simulation analysis suggested their interaction with nitrate-ions. Nine representative genes were used for *in silico* expression analysis under varying

levels of N at post-anthesis stage; only two of these genes (*TaNLP1* and *TaNLP*2) showed significant differences in their expression. We also examined quantitative expression of four representative genes (*TaNLP2*, *TaNLP7*, *TaRKD6,* and *TaRKD9*) under different conditions of N supply in root and shoot tissues of two contrasting genotypes that differed in NUE (C306 with low NUE and HUW468 with high NUE). Significant differences in expression were noticed. In particular, the *TaNLP7* gene showed significant up-regulation in the roots and shoots of HUW468 (with higher NUE) during N-starvation. This gene has already been characterized in *Arabidopsis* and tobacco and is known to be involved in nitrate-signal transduction pathway.

***CCD8* genes involved in synthesis of strigolactones.** The *CCD8* (carotenoid cleavage dioxygenase 8) gene in plants is involved in the synthesis of strigolactones, which are important plant hormones and plays an important role in controlling plant growth and development. This gene has been well characterized in maize. Using the cDNA and protein sequences of *ZmCCD8*, we identified putative *CCD8* orthologs in six other monocots (including wheat) and eight dicots. The sequence similarity of all the orthologs with respect to maize, ranged from 52–75.9% at the gene level and 60.9–93.7% at the protein level. The average length of the gene was ~3.3 kb (range: 2.08–3.98 kb), although the number of introns within the genes differed (four or five in dicots and three or four in monocots, except in *T. urartu* with six introns). Several cis-acting regulatory elements were identified in the promoters of *CCD8* genes, which are known to respond to biotic and abiotic stresses. The N-terminal end (up to ~70 amino acids) of CCD8 proteins was highly variable due to insertions, deletions, and mismatches. The variation in genes and proteins were particularly conspicuous in *T. urartu* and *Ae. tauschii* among the monocots and *A. thaliana* and *P. persica* among the dicots. In CCD8 proteins, 12 motifs (including six novel motifs) were also identified; four of these novel motifs occurred in all the selected species. The 3D structures of proteins had the characteristic features of the related enzyme apocarotenoid oxygenase (ACO) of *Synechocystis* (a representative of cyanobacteria). The qRT-PCR in wheat revealed that relative to expression under optimum P, the expression under phosphorous (P)-starved condition increased ~37-fold in root tissue of the cultivar C306 and ~33-fold in shoot tissue of the cultivar HUW468 (the two cultivars differed in their P-use efficiency), suggesting that expression of *TaCCD8* genes is genotype-dependent and tissue-specific and is regulated under different levels of P-supply.

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

Technical efficiency in wheat production: Insights from farm households in Bihar.

R. Sendhil, Anuj Kumar, Satyavir Singh, Mangal Singh, J.K. Pandey, and G.P. Singh.

Introduction. Post Green-Revolution technological innovations and interventions facilitated a major quantum jump in wheat production (Sharma et al. 2014). The average national wheat productivity has reached an all-time record of 3,424 kg/ha with regional disparities (Sharma et al. 2015; Singh et al. 2017). However, in the recent past, yield levels among regions struck a plateau, which poses a concern for breaking yield barriers. Among the alternatives, raising crop productivity is possible through agronomic interventions that could be achieved by the optimal use of resources resulting in improved technical efficiency. Theoretically, technical efficiency is the effective combination of inputs and resource services to produce the maximum possible output, given the level of input bundle (Sendhil et al. 2006). An estimation of technical efficiency will give a clue to the existing level of resource use and suggest strategies to produce the potential output under the farmers' practice. In the milieu, an attempt has been made to analyze the resource use pattern, yield gaps, and technical efficiency in wheat production.

Data and methodology. Data on socioeconomic and crop production were collected from 200 randomly selected respondents in 2018 across two districts of Bihar, Muzzafarpur, and Vaishali (Fig. 1) through a structured, pretested interview schedule. The data pertains to the 2017–18 crop season. Bihar was purposively selected based on the extent of vulnerability in wheat production (Sendhil et al. 2017, 2018). Tabular, percentage, and graphical analyses were used for arriving at meaningful conclusions. A yield-gap analysis was done using methodology developed at the International Rice Research Institute, Philippines.

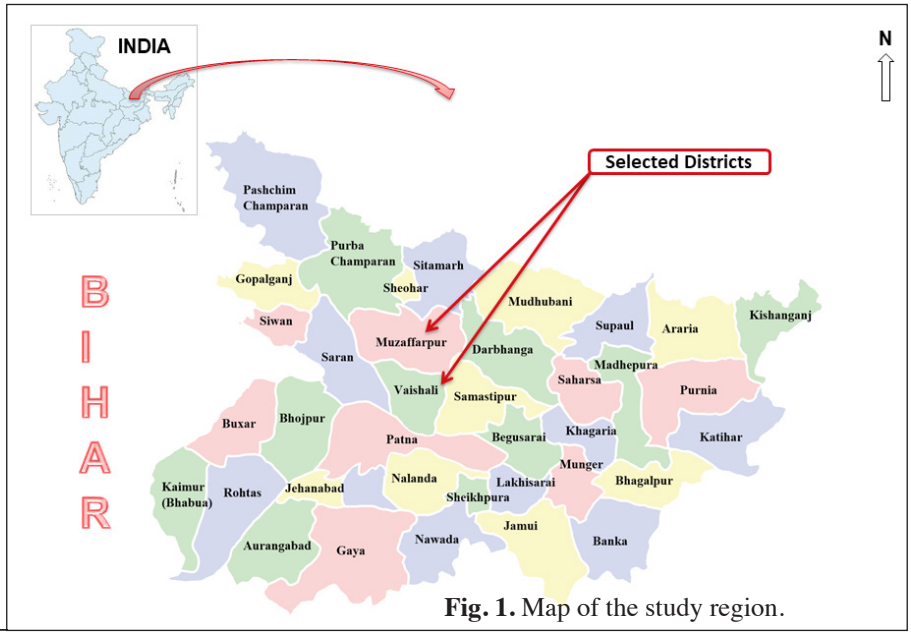

Fig. 1. Map of the study region.

The data envelopment analysis (DEA) was performed to estimate the technical efficiency of resource use in wheat production. The DEA is a popular, nonparametric method of estimating the productive efficiency of decision making units (DMUs, wheat farms in this case) empirically.

The following minimization (inputs bundle) objective function was used for the DEA as outlined in Sendhil et al. (2006) and Chandrasekar et al. (2017).

$$\min_{\Theta,\lambda} \Theta$$
$$\text{st } -y_i + Y\lambda \geq 0,$$
$$\Theta x_i - Y\lambda \geq 0,$$
$$\lambda \geq 0,$$

where Θ is a scalar and λ is a N x 1 vector of constants.

The above objective function, subject to constrains, was solved through a linear programming approach using DEAP software (Coelli 1996).

Results and discussion. The gap between potential yield and average level realized by a farmer gives an idea regarding the differences in adoption and management practices. A majority of the farmers cultivated HD 2967 for its higher yield. The potential farmer yield was 56.81 q/ha in Muzaffarpur and 51.87 q/ha in Vaishali. Analysis of the yield gap (YG) indicated that the YG–I, i.e., the difference between the experimental yield and a farmer's potential yield, was negative and highest in Muzzafarpur (–9.39 q/ha, –16.53%). YG–I arise due to difference in the package of practices adopted between farmers and researchers, and their management. However, YG–II, yield difference between the farmer's potential and average farmer, was positive in the study region. YG–II indicates the management gap in recommended package of practices between an average and a potential farmer (ICAR–IIWBR 2018).

In the post-YG analysis, the level of resource use pattern was examined to find differences among farmers and regions. The analysis indicated a significant difference in resource use in the study region. Seeds were used more than the recommended rate, whereas fertilizer nutrients (NPK) were either over used or under used, corroborating the findings of Ahmad et al. (2018). Seeds were over used by 21.18% in the Muzzafarpur district and 28.96% in the Vaishali district of Bihar. Only two irrigations were given in the study region. The NPK application was 223.75 kg/ha in the Muzzafarpur district and 237.76 kg/ha in the Vaishali district. The present analysis indicated a need for estimating the farm-wise technical efficiency in order to suggest optimal production given the level of resources.

Table 1. Estimates of technical efficiency using a data envelopment analysis (n = 200).

Range	Number of farmers	Efficiency score
Up to 0.60	32	0.5348
0.61–0.70	58	0.6614
0.71–0.80	43	0.7479
0.81–0.90	39	0.8813
0.91–1.00	28	0.9481
Overall	**200**	**0.7428**

Estimates of DEA showed that wheat producers are technically efficient by 74.28% (Table 1), indicating around 26% of additional output can be produced with optimal use of the input bundle (seed, fertilizer, irrigation, plant protection chemicals, and manure/biofertilizers). Using a stochastic frontier function, technical efficiency in wheat production was estimated by Ahmad et al. (2018) in Bihar and reported to be around 6% inefficient. The use of quality seed is one of the major factors in deciding the level of production efficiency. Furthermore, the DEA indicated that a majority of the farmers (58, 29%) fall under a 61–70% efficiency. Around 32 farmers (16%) were technically inefficient by 47%, indicating ample scope for yield enhancement. Overall, the study advocates for optimizing the resource use, especially seed and fertilizer, for ensuring incremental production.

Conclusions. Clearly, yield gaps and inefficiencies arise due to over-use or under-use of inputs owing to differences in the adoption of practices by farmers. Approximately 26% inefficiency was estimated in wheat production in the farmers' field, implying that the existing level of resources can be optimized for producing the same level of output. Alternatively, more output can be produced with the same level of resources. The study suggests increasing the level of awareness on the recommended package of practices (region-specific), using quality seed of improved or latest wheat cultivars, and increasing the rate of mechanization followed by a soil-test-based nutrient application.

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ITEMS FROM MEXICO

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

Validation of durum wheats in semi-commercial plots in southern Sonora during the 2010–11 crop season.

José Luis Félix-Fuentes and Guillermo Fuentes-Dávila.

Abstract. Grain yield potential of nine commercial durum wheat cultivars released by INIFAP, was evaluated in semi-commercial plots with a cooperating farmer in the Yaqui Valley, Sonora, Mexico during the 2010–11 crop season. Seed density was 150 kg/ha in 200 m long plots with 12 beds with double row. The variables evaluated were: grain yield, test weight, a 1,000-kernel weight (TKW), protein content, and pigment value. Cultivars CIRNO C2008 and Huatabampo Oro C2009 showed the highest average grain yield of 9.2 and 9.1 t/ha, respectively; they also showed 9.0% and 6.6% yellow berry. Huatabampo Oro C2009 and CIRNO C2008 produced the highest TKW with 49.4 and 49.0 g, respectively. The highest pigment value was shown by CEVY Oro C2008 with 30.9, followed by Patronato Oro C2008 with 29.5. There were no statistical differences in test weight or protein content.

Introduction. Wheat is the second most important cereal in Mexico, with an average per capita annual consumption of 57.4 kg. Durum wheat represents 59.79% of the wheat production in the country, and it has become the third world exporter of this product; however, Mexico imported 3.3 x 10^6 tons of the bread wheat in 2016–17 from the USA (Noltemeyer 2017). Durum wheat in Mexico is cultivated primarily in the northwestern region, whereas bread is scattered in 17 states throughout the country (SIAP 2018a). The area with durum wheat has increased in the last few years, reaching more than 250,000 ha, being the state of Sonora the main producer of this species (SIAP 2018b), and where the highest grain yields have been obtained. Although leaf rust and stripe rust are a constant threat to durum wheat production in the region, farmers continue the exploitation of this plant species with the expectation to export their product. Therefore, wheat breeding programs in the country are focused on generating promising lines and subsequently cultivars, that could meet the expectations of the producers. The objective of this work was to evaluate several durum wheat commercial cultivars in semi-commercial plots for grain yield, test weight (kg/hl), TKW, protein content, and pigment value.

Materials and methods. This work was carried out during the 2010–11 crop season in semi-commercial plots in Benito Juárez county (Yaqui Valley) in the state of Sonora. The durum wheat cultivars released by the National Institute for Forestry, Agriculture and Livestock Research (INIFAP) during the years 2000 to 2009 are shown (Table 1, p. 31). Seed density was 150 kg/ha in 200-m long plots with 12 double-row beds. Data were generated in a 2-m long x the 2 bed (the two central beds) experimental units with three replications per cultivar. The variables evaluated were grain yield, test weight, TKW, protein, and color. Statistical analysis was performed with SAS (Windows 9.0).

Table 1. Durum wheat cultivars evaluated during the 2010–11 crop season in the Yaqui Valley, Sonora, Mexico.

Cultivar	Selection history
Atil C2000	C091B1938-6M-030Y-030M-4Y-OM
Júpare C2001	CDSS95B00803M-D-OM-1Y-OB-3Y-OB
Samayoa	C2004CDSS95B00181S-0M-1Y-0B-1Y-0B-0Y-0B-14EY-0Y
CEVY Oro2008	CDSS02Y00381S-0Y-0M-19Y-0M
CIRNO C2008	CGS02Y00004S-2F1-6Y-0B-1Y-0B
Patronato Oro C2008	CDSS02Y00390S-0Y-0M-8Y-0M
Sawali Oro C2008	CDSS02Y00786T-0TOPB-0Y-0M-2Y-0M-0Y
Huatabampo Oro C2009	CDSS02B00562S-0Y-0M-2Y-1M-04Y-0B
Movas C2009	CDSS02B00720S-0Y-0M-8Y-1M- 04Y-0B

Results and discussion. Significant statistical differences in grain yield were found among cultivars, although the range fluctuated from 7.4 to 9.2 t/ha with an average of 9.5. CIRNO C2008 showed the highest grain yield with 9.2 t/ha, 1.7 t/ha higher than Samayoa C2004, which produced the lowest yield, and 117 kg higher than Huatabampo Oro C2009 which was the closest to CIRNO (Fig. 1). Huatabampo Oro C2009 showed a pigment (Minolta b) value of 27.5 (Fuentes-Dávila et al. 2012) whereas CIRNO C2008 was 21.5 (Félix-Fuentes et al. 2010). Atil C2000 and Júpare C2001 were partially affected by leaf rust and yielded 7.7 and 8.2 t/ha, respectively. Huerta-Espino and Singh (2000) reported that grain yield losses may be significant based on cultivar and the environmental conditions during the crop season. Rusts affect leaves, stems, and heads of plants with the consequent reduction in photosynthates available for grain development (Cox et al. 1997). Yield loss is mainly due to limitation in grain filling, but when the disease is severe before heading, the number of tillers might also be reduced (Roelfs et al. 1992).

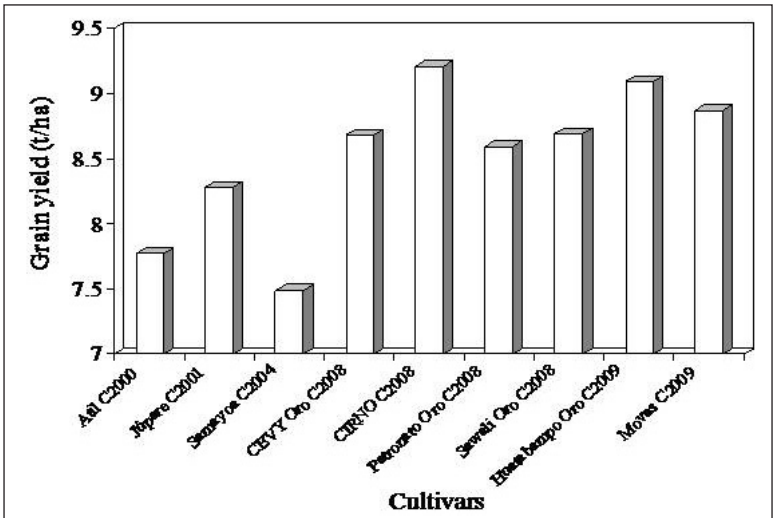

Fig. 1. Grain yield of the nine durum wheat cultivars during the 2010–11 crop season in the Yaqui Valley, Sonora, Mexico.

Despite the susceptibility to leaf rust, Júpare C2001 produced an acceptable grain yield. This cultivar occupied most of the area grown with wheat in southern Sonora from 2003–04 to 2008–09 (119,327.38 ha) (Fuentes-Dávila et al. 2010), and then it was replaced with cultivar CIRNO C2008 (Fig. 2, Camacho-Casas et al. 2004). Out of the cultivars referred to as 'Golden' (Oro), given that denomination for their high pigment content (Minolta b value) during their release for commercial cultivation, all of them showed high grain yield (see Fig. 1). Significant statistical differences were found in the TKW (Fig. 3A, p. 32); cultivars Huatabampo Oro C2009 and CIRNO C2008 produced the highest TKW with 49.4 and 49.0 g, respectively. Despite ranking fifth in grain yield, CEVY Oro C2008 showed the lowest TKW with 39.6 g. Cultivar Samayoa C2004, which produced the lowest grain yield, ranked fourth in TKW with 45.2 g. Hays et al. (2007) indicate that the reduction in number of grains per head and in the TKW is due to greater production of ethylene, when genotypes are subjected to stress rather when they are cultivated under optimum conditions. This greater production of ethylene causes seed dessication and an increase in the abortion rate as a consequence of an early aging. There were no statistical differences in test weight (Fig. 3B, p. 32), and the range was from 80.6 to 84.8; cultivar Huatabampo Oro C2009 showed the

Fig. 2. Durum wheat cultivar CIRNO C2008.

highest test weight, and at the time of its release for commercial cultivation in 2009, slightly overcame check cultivar Júpare C2000. The test weight is influenced by the correlation between fertilization and the environmental conditions that prevail during grain filling (Hewstone and Jobet 2001). There were no statistical significant differences in protein content, which ranged from 11.12 a 11.98% (Fig. 3C); cultivar Atil C2000 showed the highest content. Stone and Savin (1999) mention that the increase in nitrogen availability produce higher grain yield and a decrease in the percentage of protein, commonly known as dilution effect. Then, in a second phase, increases in the level of nitrogen in the soil render higher grain yield and higher protein content in the grain. In the last phase, the stabilization, the variations in yield and protein content scarcely fluctuate under changes of the edaphic offer of nitrogen. Smith et al. (1989) indicate that the protein content increases with the application of nitrogen-based fertilizers between anthesis and flowering, under different environments. Significant statistical differences for pigment were found among cultivars (Fig. 3D); with the exception of Movas C2009, the Golden cultivars were superior to the rest. The yellow color does not depend only on the presence of carotenoids, but it is also influenced by other factors such as the rate of extraction of semolina or flour (Matsuo and Dexter 1980) which can be explained for cultivar Movas C2009. This cultivar previous to its release for commercial cultivation, showed maximum values of 28.9, superior to Júpare C2001, which was the cultivar check at that time (Félix-Fuentes et al. 2011). The highest pigment value was shown by CEVY Oro C2008 with 30.9, followed by Patronato Oro C2008 with 29.5, whereas Atil C2000 showed the lowest value with 23.4. One of the most important parameters that determine the adoption of a particular cultivar by farmers is grain yield potential despite its susceptibility to diseases, because a high-yielding cultivar, even with two fungicide applications to control leaf rust, would make it profitable for the farmer. Therefore, some cultivars in the Yaqui Valley are still being cultivated despite losing their resistance to leaf rust. In the case of cultivar CIRNO C2008 and all those materials that yield more than 8 t/ha in demonstration plots, will undoubtedly be sown commercially by farmers during the following crop season.

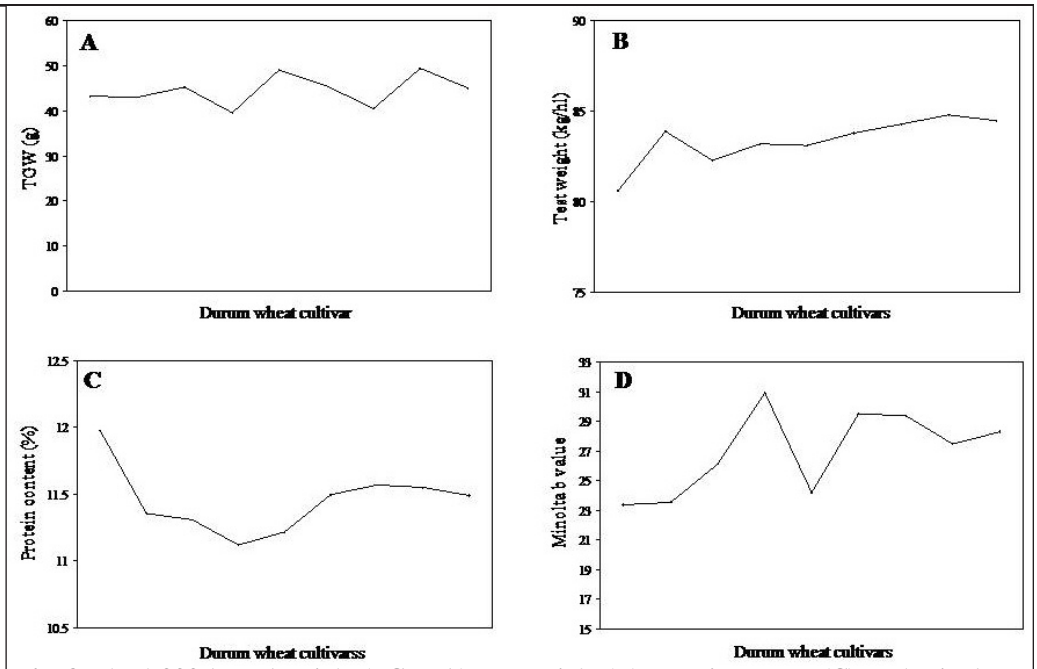

Fig. 3. The 1,000-kernel weight (TGW, A), test weight (B), protein content (C), and Minolta b values (D) of nine durum wheat cultivars during the 2010–11 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Conclusions. CIRNO C2008 showed the highest grain yield with 9.2 t/ha, followed by Huatabampo Oro C2009 with 9.1 in semi-commercial plots. Significant statistical differences were found in TKW; Huatabampo Oro C2009 and CIRNO C2008 produced the highest TKW with 49.4 and 49.0 g, respectively. The highest pigment value was shown by CEVY Oro C2008 with 30.9, followed by Patronato Oro C2008 with 29.5. No statistical differences were noticed in test weight and protein content.

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INSTITUTO TECNOLÓGICO DE SONORA
5 de Febrero 818 Sur, Col. Centro, Cd. Obregón, Sonora, México 85000.

JUNTA LOCAL DE SANIDAD VEGETAL DE NAVOJOA
Rafael Almada 2403, Col. Brisas del Valle, Navojoa, Sonora, México 85864.

JUNTA LOCAL DE SANIDAD VEGETAL DEL VALLE DEL YAQUI
Blvd. Rodolfo Elías Calles 711 Poniente, Sochiloa, 85150 Cd Obregón, Sonora, México 85150.

Presence of wheat stripe rust in southern Sonora during the 2018–19 crop season.

Guillermo Fuentes-Dávila, María Monserrat Torres-Cruz (Instituto Technológico de Sonora), Pedro Félix-Valencia, Benjamín Valdenebro-Esquer (Junta Local de Sanidad Vegetal de Navojoa), Germán Castelo-Muñoz (Junta Local de Sanidad Vegetal del Valle del Yaqui), and José Luis Félix-Fuentes.

Abstract. Stripe or yellow rust of wheat occurs in cooler climates (2–15°C), which are generally associated with higher elevations, northern latitudes, or cooler years. As a consequence of an early attack by the pathogen, stunted and weakened plants often occur. Losses can be severe (50%) due to shrivelled grain and damaged tillers. In extreme situations, stripe rust can cause a 100% loss. In southern Sonora, Mexico, stripe rust has occurred for several decades and its incidence has caused economic losses to farmers. During the 2018–19 crop season, through a pest-monitoring program carried out by the plant health agencies in the Mayo and Yaqui Valleys, stripe rust was detected in 11 and 25 wheat fields, respectively. In the first valley, nine fields with durum wheat cultivar CIRNO C2008, one with bread wheat cultivar Tacupeto F2001, and one with bread wheat Villa Juárez F2009 occupied 51,573, 343, and 100 ha, respectively. The average temperature from 1 January to 16 March, 2019, fluctuated between 15.3 and 17.1°C, the average minimum temperature was between 2.1 and 7.7°C, and the average maximum temperature was between 26.9 and 29.7°C. In the Yaqui Valley, 23 fields with cultivar CIRNO C2008, which occupied 101,014 ha, and only one field grown with cultivars Ónavas F2009 and Villa Juárez F2009, which occupied 750 and 607 ha, respectively, were affected by stripe rust. The average temperature between 1 February and 15 April fluctuated between 15.2 and 19.5°C, the average minimum temperature between 3.5 and 8.0, and the average maximum temperature between 28.1 and 34.2°C.

Introduction. Yellow or stripe rust caused by the fungus *Puccinia striiformis* f. sp. *tritici* Eriks. affects wheat (*Triticum aestivum* L. and *Triticum durum* Desf.), barley (*Hordeum vulgare* L.), rye (*Secale cereale* L.), and grasses (McIntosh 1998). This rust is currently one of the most damaging diseases of wheat on a global scale (Roelfs et al. 1992; Zwer and Qualset 1994). Roelfs et al. (*op. cit.*) reported that the fungus attacks members of the genera *Aegilops*, *Agropyron*, *Bromus*, *Elymus*, *Hordeum*, *Secale*, and *Triticum*. However, in southern Sonora, Mexico, apparently no investigations have been carried out related to this matter. The causal agent is a low temperature pathogen and represents an important problem in places where the prevailing climate is cool and moist, such as northeastern Europe, the mountainous regions of South America, and East Africa (Stubbs 1988). Since 2000, two new aggressive strains of yellow rust have been identified and these have spread across continents at a rapid rate. Virulence to important resistance genes, such as *Yr27,* has appeared and has been one factor in major disease epidemics that have occurred from North Africa to South Asia (RustTracker.org. 2019).

The minimum, optimum, and maximum temperatures for germination of the spores are 0, 11, and 23°C, respectively (Roelfs et al. 1992). In relation to rust survival, Hassan et al. (1986) reported that urediniospores of *P. recondita* showed a survival capacity for various periods of time when subjected to simulated summer temperature conditions in moist or dry soil, under a layer of soil, on dry leaves, and on excised leaves, and that dormant mycelium survived all conditions that the host tissue was capable of surviving. Fauzi (2009) reported that urediniospores of *Puccinia abrupta* var. *partheniicola* (H.S. Jackson) J. Parmelee, a potential biological control agent of the parthenium weed (*Parthenium hysterophorus* L.), during simulated summer conditions in the field, that were placed either on plant debris or on intact plants exposed to summer conditions and regularly tested for viability, could only survive for less than six weeks. Hassan et al. (1986) indicated that urediniospores of *P. recondita* f. sp. *tritici*, are able to over summer on volunteer wheat plants

and, therefore, are able to serve as a source of inoculum for the primary infection on autumn sown wheat. The rusts can be controlled with fungicide sprayings, but this increases the costs of cultivation and damage to the environment (Sandoval et al. 1999).

Fig. 4. Urediniospores of *Puccinia striiformis* f. sp. *tritici* and symptoms of the leaf and stem.

Genetic resistance is the safest, most economical, and environmental means of control (Ma et al. 1997), although the protection is often ephemeral, given that the fungal populations respond to the selection pressures generated by resistant cultivars, producing genotypes that overcome the resistance, particularly when genes of specific race are used. With changes in the populations of the pathogen, breeding for the genetic resistance of wheat should be a continuous activity (Schafer 1987). The reduction in yield due to stripe rust depends on the phenological stage in which 100% infection is reached; thus, between the seedling stage and tillering, the loss is 95%, during stalk formation, 70%, at booting, 50%, at flowering, 35%, at milky stage of the grain, 20%, and at dough stage of the grain 10% (Chester 1946). Rusts attack leaves, stems, and spikes of the plant (Fig. 4), reducing the quantity and composition ,of the photosynthetic products available for development of the grain (Cox et al. 1997). Yield losses are generally due to the lack of grain filling, but when the disease is severe prior to booting, the number of tillers also may decrease; as a consequence of an early attack by the pathogen, stunted and weakened plants often occur. Losses in yield can be as much as 30 to 75% (Torabi and Nazari 1998; Roelfs 1978). In extreme situations, stripe rust can cause a 100% loss. Early development of stripe rust probably affects the number of grains, while in late growth stages, grain weight is affected (Schultz and Line 1992).

In Mexico, stripe rust occurs in the region El Bajio (states of Guanajuato, Michoacan, Jalisco, and Queretaro) (Solís et al. 2007; Rodríguez et al. 2009), and it is important in the central high plain (state of Mexico, Hidalgo, Tlaxcala, and Puebla) (Salazar-Gómez 1992; Rodríguez-García et al. 2010), as well as in Sonora and North Baja California (Rodríguez et al. 2009). Roelfs et al. (1992) reported northwestern Mexico as a region where stripe rust is a local problem in irrigated wheat, which includes southern Sonora. According to Huerta-Espino and Singh (2000), the disease also occurs in rainfed wheat in Mexico, in cold areas characterized by long dew periods, such as the high valleys near the state of Toluca, and in the states of Tlaxcala and Puebla. They also indicate that the causal agent may survive as mycelium for long periods of time, and that there are some wild barley species that may serve as hosts to the fungus when no wheat is available.

In Mexico, there is little information with respect to the effect of rusts on grain yield of wheat; information is even scarcer for stripe rust. In the Bajio, the disease may reach 100% severity in some cultivars of commercially sown wheat. According to Buendía et al. (2019), this disease may cause 70% of shrivelled grains and the lowest a 1,000-kernel weight and test weight in susceptible bread wheat cultivars, such as Nana F2007. In Mexico, virulence studies have been carried out by Rodríguez et al. (2009), Rodríguez-García et al. (2010), and Huerta Espino et al. (2012). Solís et al. (2007) reported that in 1998 they conducted experiments to determine the effect of the disease on the phenology and yield of grain and its components in 250 wheat genotypes. During the last two decades, stripe rust incidence has had an important effect on the economics of wheat production in southern Sonora, because large areas had to be sprayed with fungicides in order to minimize losses due to this disease. Considering the cheapest fungicides in the market at that time, during the 2012–13 crop season, more than 1,500 x 10^6 dollars were invested in fungicide purchase and applications on 75,292 ha for stripe and leaf rust control. The durum wheat cultivars affected were CIRNO C2008, Movas C2009, and Atil C2000, and the bread wheat cultivar Tacupeto F2001 (personal communication, Plant Health Agency in the Yaqui Valley, PHAYV). During the 2013–14 crop season, more than 300,000 dollars were invested in fungicide purchase and applications for control of stripe rust on 15,598 ha. The durum wheat cultivars affected were CIRNO C2008, Movas C2009, and Atil C2000, and the bread wheat cultivars Tacupeto F2001, Kronstad F2004, Roelfs F2007, and Onavas F2009 (personal communication, PHAYV). In the region, media are well aware of the agricultural situation in the Mayo and Yaqui Valleys and provide information about the phytosanitary status frequently during the crop season, such as in 2015, when the presence of stripe rust was detected in Benito Juárez and Huatabampo Counties (Azteca Noticias 2015). In January of 2019, an alert warning by the secretary of agriculture and rural development was sent to farmers in the Valley of Mexica-

li about the possible presence of yellow rust in the region, given the environmental conditions that occurred and because of the presence of the disease in southern Sonora (SADER 2019).

Pest monitoring program in southern Sonora (PMPSS). This program was initiated in the 1980s, when Karnal bunt incidence increased notoriously, and later expanded in the 1990s, when an outbreak occurred in soybean with whitefly (*Bemisia tabaci* Gennadius). Since then, the program has increased to include other pests, such as Paratrioza (*Bactericera cockerelli* Sulc), wheat aphids, *Diaphorina citri* Kuwayama, pepper weevil (*Anthonomus eugenii* Cano), potato tuber moth (*Phthorimaea operculella* Zeller), and stripe and leaf rust, but emergency tasks also are put in place when an important plant insect or disease appears in the area. The monitoring is carried out by trained technicians in the Mayo and Yaqui Valleys, who visit 240 pilot fields in the Yaqui Valley and 102 in the Mayo on a weekly basis. Although funding is provided by the federal and state governments, the main source comes from the farmer's unions.

Stripe rust monitoring in southern Sonora during the 2018–19 crop season. Monitoring starts in January in both valleys, and the first wheat field with stripe rust was detected in the Mayo Valley during the week of 27 January–2 February (Fig. 5), then in three other fields during 3–9 February, two during 10–16 February, one during 17–23 February, one during 24 February–2 March, two during 3–9 March, and one during 10–16 March. The total number of fields affected by stripe rust according to the monitoring carried out by technicians of the PMPSS in the Mayo Valley was 11; nine with durum wheat cultivar CIRNO C2008, and one with bread wheat cultivars Tacupeto F2001 and Villa Juárez F2009, which occupied 51,573, 343, and 100 ha, respectively. Weather data were obtained from the automated meterological station network in Sonora (REMAS 2019) comprising 13 stations in the Mayo and 22 in the Yaqui Valleys. This network was built with the objective of generating, storing, processing, and distributing weather data in the state of Sonora, Mexico. Variables recorded are temperature, relative humidity (RH), precipitation, solar radiation, wind speed and direction, barometric pressure, and evapotranspiration, which are collected on a 10 minute frequency, every hour, and daily. Mean temperature during January in the Mayo Valley was 15.3°C, with a range of 2.1 to 26.9°C (Fig. 6), whereas the RH was 76.5% with a range of 23.3 to 99.3%. Although the highest temperatures reached 26.9°C, these occurred during 12:00 pm to 4:00 pm. In February, the mean temperature was 15.3°C, with a range of 3.3 to 28.8°C, and the RH was 76.5%, with a range of 35.6 to 98.8%. Similarly, as in January, although the highest temperatures reached 28.8°C, these occurred between 11 am to 3:00 pm. During the first 16 days of March, the mean temperature was 17.1°C, with a range of 7.7 to 29.7°C, with a RH of 75.6%, with a range of 35.4 to 97.8%. Similar to January and February, although the highest temperatures reached 29.7°C, these occurred from 12 pm to 3 pm. The average temperature between 1 January to 16 March fluctuated between 15.3 and 17.1°C, which are a few degrees higher than the optimum temperature for spore germina-

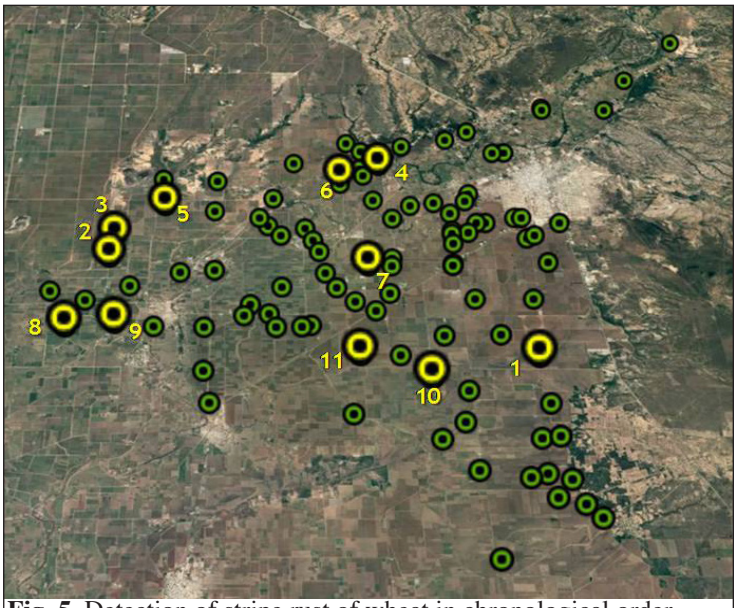

Fig. 5. Detection of stripe rust of wheat in chronological order from 27 January to 16 March in the Mayo Valley during the 2018–19 crop season. Green circles represent pilot wheat fields and the yellow those with the disease.

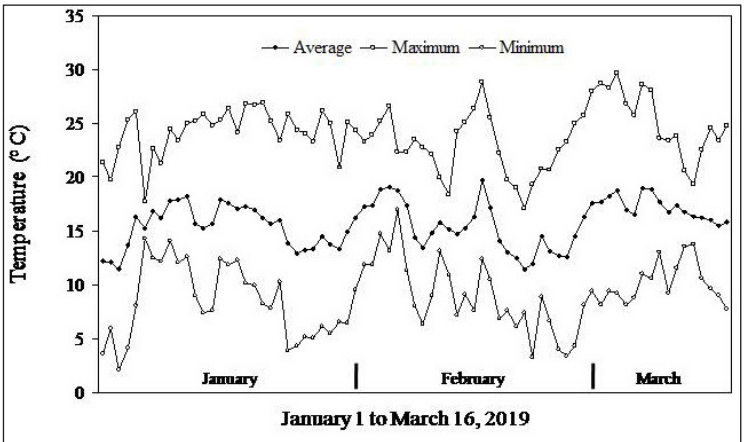

Fig. 6. Daily maximum, minimum, and mean temperatures recorded from 1 January to 16 March during the 2018–19 autumn–winter

tion reported by Roelfs et al. (1992); the average minimum temperatures fluctuated between 2.1 to 7.7, which are higher than the minimum (0°C) reported by the same authors as the limit for spore germination, and the average maximum temperatures fluctuated between 26.9 to 29.7°C, which are at least seven degrees above the maximum temperature for spore germination. Analyzing the data corresponding to the first week that one detection of stripe rust was reported and those three weeks when three and two detections were reported, the average temperature between 27 January–2 February was 15.3°C, 16.7°C between 3–9 February, 16.3°C between 10–16 February, and 17.8°C between 3–9 March (Fig. 7). The daily temperatures in the four weeks are very close and all above the optimum of 11°C reported by Roelfs et al. (*op. cit*.). Despite being higher than optimum temperatures for spore germination, they are within the range conducive for germination. Because this is a simple analysis that does not provide information about a possible interaction between a particular set of temperatures and the presence of stripe rust, bias in the monitoring must be taken into account as more fields could have been effected by stripe rust that were not detected by the technicians from the PMPSS. Given the presence of the fungus in the area, either by survival in plant debris, volunteer, other hosts, or wind currents from other areas, the fungus had temperatures conducive for infection, since the highest temperatures only prevail for a few hours during the day, primarily from 11 am to 3:00 pm. In addition, fluctuation of temperatures from 1 or 2°C to more than 30 is conducive for dew formation, which is common in southern Sonora at this time of the wheat season, and is beneficial to the fungus for spore germination.

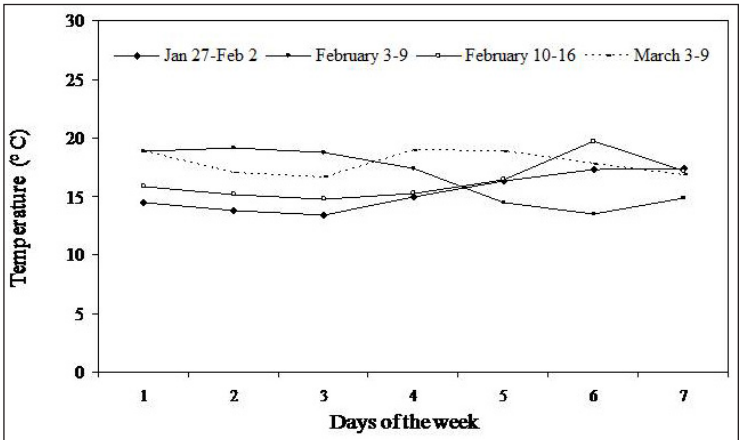

Fig. 7. Daily mean temperatures recorded during the weeks of 27 January–2 February, 3–9 February, 10–16 February, and 3–9 March, during the 2018–19 autumn–winter wheat season in the Mayo Valley, Sonora, Mexico.

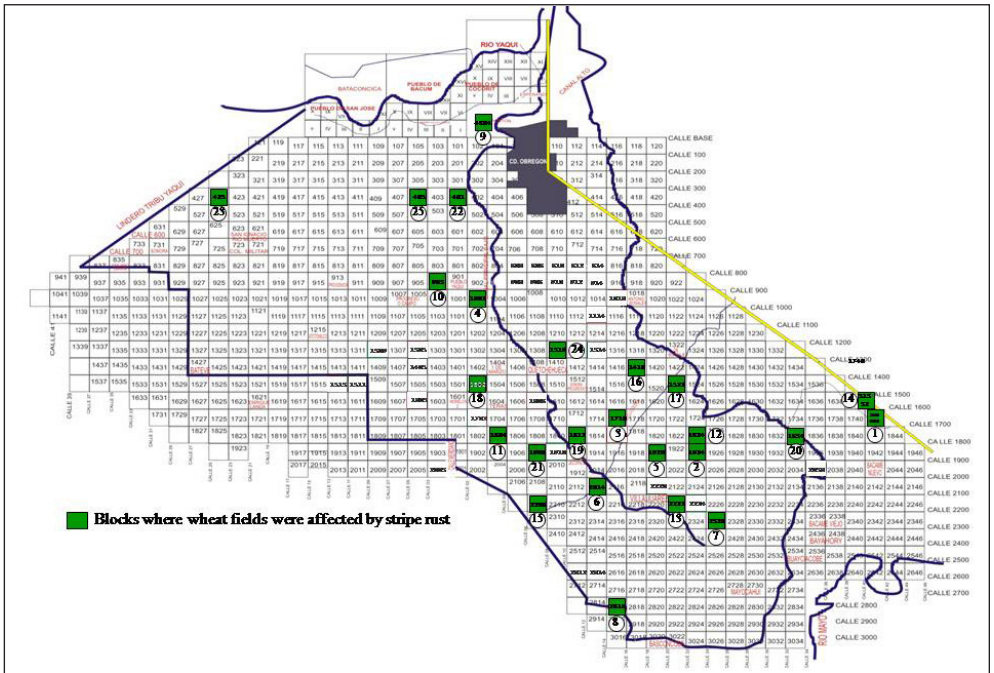

Fig. 8. Detections of stripe rust of wheat in chronological order from 10 February to 13 April in the Yaqui Valley during the 2018–19 crop season.

In the Yaqui Valley, 23 fields with durum wheat cultivar CIRNO C2008, which occupied 101,014 ha, were affected by stripe rust, and only one field grown with cultivars Ónavas F2009 and Villa Juárez F2009, which occupied 750 and 607 ha, respectively. In this valley, the first detection of the disease was during 10–16 February (Fig. 8), two weeks later than the first detection in the Mayo Valley, then one during 17–23 February, one during 24 February–2 March 2, seven during 3–9 March, four during 10–16 March, one during 17–23 March, two during 24–30 March, six during 31 March 31–6 April, and two during 7–13 April. Mean temperature during February in this valley was 15.2°C, with a range of 3.5 to 28.1°C (Fig. 9, p. 37), whereas RH was 73.1%, with a range of 32.2 to 94%. Although the highest temperatures reached 28.1°C, these occurred during 12:00 pm to 3:00 pm. In March, the mean temperature was 17.3 °C, with a range of 6.7 to 30.1°C, and the RH was 70.2%, with a range of 31.9 to 93.4%. Similar to February, although the highest temperatures reached 30.1°C, these occurred

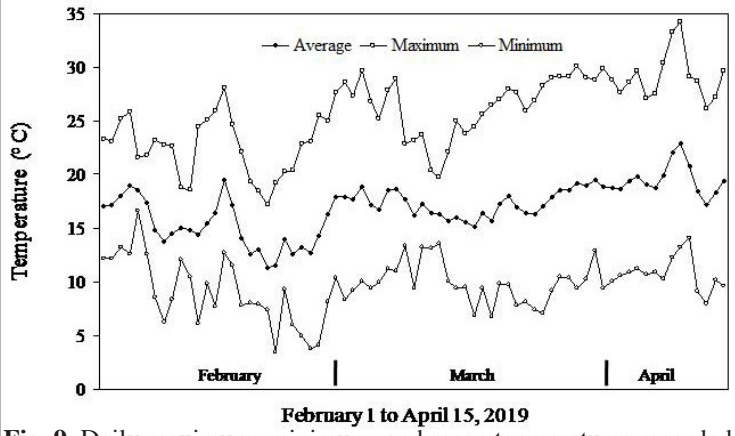

Fig. 9. Daily maximum, minimum, and mean temperatures recorded from 1 February to 15 April durn the 2018–10 autumn–winter wheat season in the Yaqui Valley, Sonora, Mexico.

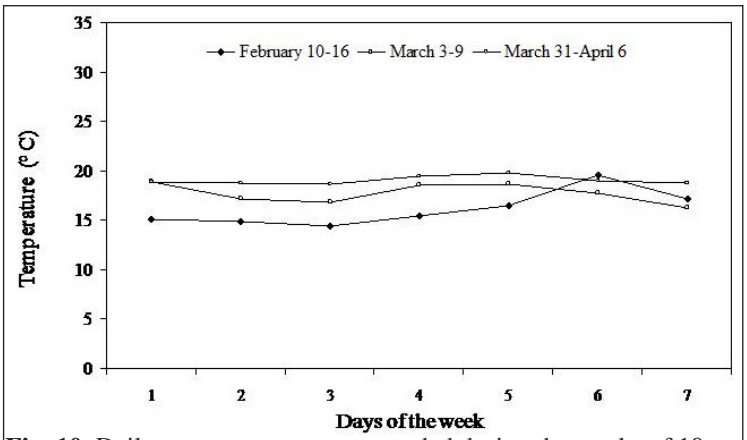

Fig. 10. Daily mean temperature recorded during the weeks of 10–16 February, 3–9 March, and 31 March–6 April, during the 2018–19 autumn–winter wheat season in the Yaqui Valley, Sonora, Mexico.

during 12:00 pm to 3:00 pm. During the first 15 days of April, the mean temperature was 19.5°C, with a range of 8 to 34.2°C, and the RH was 64.3%, with a range of 18.8 to 89.9%. Similarly as in February and March, although the highest temperatures reached 34.2°C, these occurred during 11:00 am 3:00 pm. The average temperature during 1 February to 15 April fluctuated between 15.2 and 19.5°C, which are a few degrees higher than the optimum temperature for spore germination reported by Roelfs et al. (1992). The average minimum temperatures fluctuated between 3.5 to 8, which are higher than the minimum (0°C) reported by the same authors as the limit for spore germination, and the average maximum temperatures fluctuated between 28.1 to 34.2°C, which are at least five degrees above the maximum temperature for spore germination. When comparing the average temperatures of the week of 10–16 February, when only one detection of stripe rust was reported, and the week of 3–9 March, when seven detections were reported, the temperatures are similar (16.1 and 17.7°C, respectively) (Fig. 10). In the week of 31 March to 6 April, the average temperature was 19.0°C which is 2.9 degrees higher than that of 10–16 February. As in the Mayo Valley, daily temperatures during the three weeks are very close and all above the optimum of 11°C reported by Roelfs et al. (*op. cit.*), but conducive for spore germination. Although average temperature in both valleys during the period indicated before was 16.6°C, which is above the optimum for spore germination according to Roelfs et al. (*op. cit.*), may indicate that the fungus has adapted to the climatic conditions that occur in this region, since for several decades, stripe rust has become an endemic disease in southern Sonora.

Conclusions. The total number of fields affected by stripe rust between 1 January and 16 March, 2019, according to the Pest Monitoring Program in southern Sonora in the Mayo Valley was 11; nine with durum wheat cultivar CIRNO C2008, one with bread wheat cultivar Tacupeto F2001, and one with bread wheat Villa Juárez F2009, which occupied 51,573, 343, and 100 ha, respectively. The average temperature during that period of time fluctuated between 15.3 and 17.1°C, the average minimum temperature between 2.1 and 7.7°C, and the average maximum temperature between 26.9 and 29.7°C.

In the Yaqui Valley, cultivar CIRNO C2008 occupied 101,014 ha, Borlaug 100 20,030, and Quetchehueca Oro C2013 6,371 ha. Twenty-three fields with CIRNO C2008 were affected by stripe rust, but only one field grown with cultivars Ónavas F2009 and Villa Juárez F2009, which occupied 750 and 607 ha, respectively. The average temperature between 1 February and 15 April fluctuated between 15.2 and 19.5°C, the average minimum temperature between 3.5 to 8.0°C, and the average maximum temperature between 28.1 and 34.2°C.

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Evaluation of advanced bread wheat lines for Karnal bunt resistance in the field during the 2013–14 crop season.

Guillermo Fuentes-Dávila, Ravi Prakash-Singh (CIMMYT Int, km45 Carret, México–Veracruz, El Batán, Texcoco, Edo. de México CP 56103), Ivón Alejandra Rosas-Jáuregui, Carlos Antonio Ayón-Ibarra, María Monserrat Torres-Cruz, Pedro Félix-Valencia, José Luis Félix-Fuentes, and Gabriela Chávez-Villalba.

Abstract. We evaluated 1,178 advanced bread wheat lines for resistance to Karnal bunt during the 2013–14 crop season. Sowing dates were 21 November and 3 December, 2013, using 8 g of seed for each 0.7-m row on a bed with two rows. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage, in five heads/line. Harvesting was done manually, and the percentage of infection was determined by counting healthy and infected grains. The range of infection of the advanced lines at the first date was 0.0–84.8%, with an average of 19.3%, and 0–71.1% at the second, with an average of 17.5%. The range of the average percentage of infection was 0.0-65.6% with a mean of 18.4%. Lines that did not show infected grains were KACHU/2*MUNAL#1, FRNCLN*2/BECARD, MON/IMU//ALD/PVN/3/BORL95 /4/OASIS/2*BORL95/5/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07, BECARD*2/PFUNYE#1, SAAR//INQALAB91*2/KUKUNA/3/KIRITATI/2*TRCH/5/BAV 92//IRENA/KAUZ/3/HUITES/4/DOLL, BABAX/LR42//BABAX/3/ER2000/4/BAVIS, and PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1. Ninety-one lines fell into the 0.1–2.5% infection category, 88 within 2.6–5.0%, 161 within 5.1–10.0%, 620 within 10.1–30%, and 211 with more than 30% infection. Lines with the highest percentage of infection were BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/BECARD with 84.8%, MELON//FILIN/MILAN/3/FILIN/4/PRINIA/PASTOR//HUITES/3/MILAN/OTUS//ATTILA/3*BCN/5/MELON//FILIN/MILAN/3/FILIN with 84.5%, and AGT YOUNG/3/1447/PASTOR// KRICHAUFF/4/SOKOLL/3/PASTOR//HXL7573/2*BAU with 77.4%, all at the first date. The average of the three highest levels of infection of the susceptible check was 99.02%.

Introduction. Karnal bunt of wheat, caused by *Tilletia indica* occurs, on bread wheat (Mitra 1931), durum wheat, and triticale (X *Triticosecale*) (Agarwal et al. 1977). This disease was first identified in India (Mitra 1931), and later in Mexico (Duran 1972), Pakistan (Munjal 1975), Nepal (Singh et al. 1989), Brazil, (Da Luz et al. 1993), the United States of America (APHIS 1996), Iran (Torarbi et al. 1996), the Republic of South Africa (Crous et al. 2001), and apparently in Afghanistan (CIMMYT 2011). In general, the fungus partially affects some grains in a plant (Bedi et al. 1949) (Fig. 11), and in some occasions they are totally destroyed. Although the fungus may penetrate the embryo, it does not necessarily cause damage (Chona et al. 1961; Mitra 1935). Partially infected grains may give rise to healthy plants, although it has reported that the percentage of germination decreases depending on the level of seed infection (Bansal et al. 1984; Rai and Singh 1978; Singh 1980), and that severely affected seed lose viability or show abnormal germination (Rai and Singh 1978). Another report indicates that seed with the greatest infection, but with the embryo intact, produce the highest number of tillers (Fuentes-Dávila et al. 2013). Control of this pathogen is difficult, because teliospores are resistant to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1985, 1988). Chemical control can be accomplished by applying fungicides during flowering (Fuentes-Dávila et al. 2005, 2016; Salazar-Huerta et al. 1997), however, this measure is not feasible when quarantines do not allow tolerance levels for seed production (SARH 1987). The use of resistant wheat cultivars is the best control method and also would reduce the possibilities of introduction of the disease into Karnal bunt-free areas. Since the 1940s, several species of *Triticum* have been evaluated for resistance to Karnal bunt (Bedi et al. 1949; Singh et al. 1986, 1988). Bread wheat is the species most affected by the disease; under artificial inoculation some lines may show more than 50% infected grain (Fuentes-Dávila et al. 1992, 1993); therefore, it is important to keep evaluating new advanced lines and wheat cultivars. Our objective was to evaluate the reaction of 1,178 advanced bread wheat lines for resistance to *T. indica* in the field.

Fig. 11. Wheat grains partially infected with *Tilletia indica*.

Materials and methods. We evaluated 1,178 advanced bread wheat lines for resistance to Karnal bunt during the 2013–14 autumn–winter crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, México, located in block 910 of the Yaqui Valley, Sonora, México, at 27°22'04.64"N latitude and 109°55'28.26"W longitude, 37 masl, with a warm climate (BW (h)) and extreme heat according to Koppen's classification, modified by García (1988).

Sowing dates were 21 November and 3 December, 2013, using 8 g of seed for each 0.7-m row in a bed with two rows in a clay soil at pH 7.8. For agronomic management, INIFAP›s technical recommendations were followed (Figueroa-López et al. 2011). Inoculum was prepared by isolating teliospores from infected grains, followed by centrifugation in a 0.5% sodium hypochlorite solution, and plating on 2% water–agar Petri plates. After teliospore germination, fungal colonies were transferred and multiplied on potato–dextrose-agar. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage in five heads from each line (Fig. 12). High relative humidity in the experimental area was provided by an automatic mist spray-irrigation system (Fig. 13) five times a day for 20 min each time. To avoid bird damage, an anti-bird net system was installed in the area used for evaluation of the wheat lines. Harvest was manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. Evaluated lines originated from the collaborative project between the Global Wheat Program of the International Maize and Wheat Improvement Center (CIMMYT) and the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP).

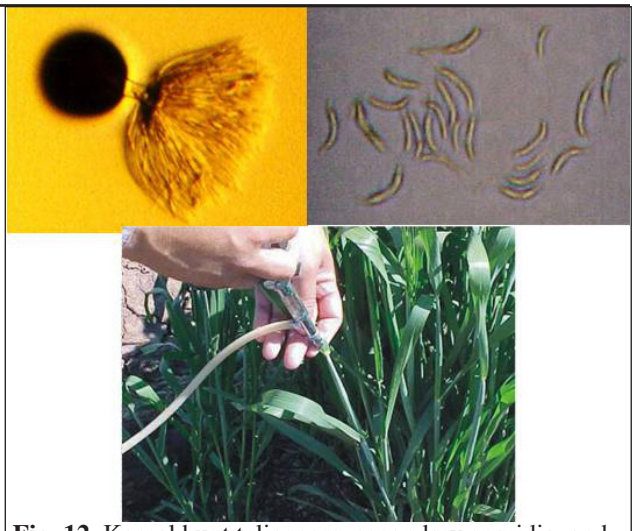

Fig. 12. Karnal bunt teliospore, secondary sporidia, and inoculation by injection during the boot stage of the wheat plant.

Fig. 13. Mist-irrigation system and anti-bird net system in the area used to evaluate advanced bread wheat lines for resistance to *Tilletia indica*.

Results. The percentage range of infection of the advanced lines at the first date was 0.0–84.8%, with an average of 19.3%, and 0.0–71.1% at the second, with an average of 17.5%. The average percentage range of infection was 0.0–65.6%, with an average of 18.4%. Overall (average of the two dates), seven lines did not show any infected grain (Table 2), 91 were in the 0.1–2.5% infec-

Table 2. Advanced bread wheat lines that did not show any infected grains with *Tilletia indica* at two dates, after artificial field inoculation, during the 2013–14 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, México.

Entry	Pedigree and selection history
168	KACHU/2*MUNAL #1
	CMSS09Y00817T-099TOPM-099Y-099ZTM-099NJ-099NJ-13WGY-0B
185	FRNCLN*2/BECARD
	CMSS09Y00838T-099TOPM-099Y-099M-099Y-17WGY-0B
355	MON/IMU//ALD/PVN/3/BORL95/4/OASIS/2*BORL95/5/HUW234+LR34/PRINIA// PBW343*2/ KUKUNA/3/ROLF07
	CMSA09Y00855S-050Y-050ZTM-050Y-3WGY-0B
675	BECARD*2/PFUNYE #1
	CMSS09B00804T-099TOPY-099ZTM-099NJ-099NJ-42WGY-0B
698	SAAR//INQALAB 91*2/KUKUNA/3/KIRITATI/2*TRCH/5/BAV92//IRENA/KAUZ/3/HUITES/4/DOLL
	CMSS09B00881T-099TOPY-099M-099Y-9M-0WGY
1129	BABAX/LR42//BABAX/3/ER2000/4/BAVIS
	CMSA09M00434S-050ZTM-0NJ-099NJ-7RGY-0B
1151	PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1
	CMSA09M00198T-050Y-050ZTM-0NJ-099NJ-2RGY-0B

Table 3. Advanced bread wheat lines with less than 0.5% infection with *Tilletia indica* at two dates, after artificial field inoculation during the 2013–14 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, México.

Entry	Pedigree and selection history	Range of infection	Average
354	MON/IMU//ALD/PVN/3/BORL95/4/OASIS/2*BORL95/5/ SOKOLL/3/PASTOR//HXL7573/2*BAU	0.0–0.40	0.20
	CMSA09Y00852S-050Y-050ZTM-0NJ-099NJ-11WGY-0B		
586	PAURAQ/6/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAY-ON/5/KACHU #1	0.0–0.41	0.20
	CMSS09B00531S-099ZTM-099NJ-099NJ-3WGY-0B		
716	ROLF07/KINGBIRD #1//MUNAL #1	0.38–0.41	0.40
	CMSA09M00147T-050Y-050ZTM-050Y-2WGY-0B		
1173	MUNAL #1*2/SOLALA	0.38–0.0	0.19
	CMSS09B01058T-099TOPY-099M-099Y-1M-0WGY		

tion category (four lines had less than 0.5% infection in both dates, Table 3), 88 within 2.6–5.0%, 161 within 5.1–10.0%, 620 within 10.1–30.0%, and 211 with more than 30% infection (Fig. 14). The average of the three highest infections of the susceptible check (KBSUS 1) was 99.02%. Fifty lines consistently showed a percentage of infection below 2.5% at both dates and 67 were below 5.0%. Lines with less than 5.0% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). Lines that did not show infected grain were KACHU/2*MUNAL#1, FRNCLN*2/BECARD, MON/IMU//ALD/PVN/3/ BORL95/4/OASIS/2*BORL95/5/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07, BECARD*2/PFUNYE#1, SAAR//INQALAB91*2/KUKUNA/3/KIRITATI/2*TRCH/5/BAV92//IRENA/KAUZ/3/HUITES/4/DOLL, BABAX/LR42//BABAX/3/ER2000/4/BAVIS, and PFAU/ MILAN/3/BABAX/LR42//BABAX*2/4/NIINI#1; those with the highest were BABAX/ LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/BECARD with 84.8%, MELON //FILIN/MILAN/3/FILIN/4/PRINIA/PASTOR//HUITES/3/MILAN/OTUS//ATTILA/3*BCN/5/MELON//FILIN/MILAN/3/FILIN with 84.5%, and AGT YOUNG/3/1447/PASTOR//KRICHAUFF/4/SOKOLL/3/PASTOR//HXL7573/2*BAU with 77.4%, all at the first date. In the group of advanced bread wheat lines evaluated during the 2013–14 crop season, 186 are worth evaluating in the following crop season in order to verify their resistance to *T. indica*, because they may be prospects for commercial release or at least used as parents in breeding programs.

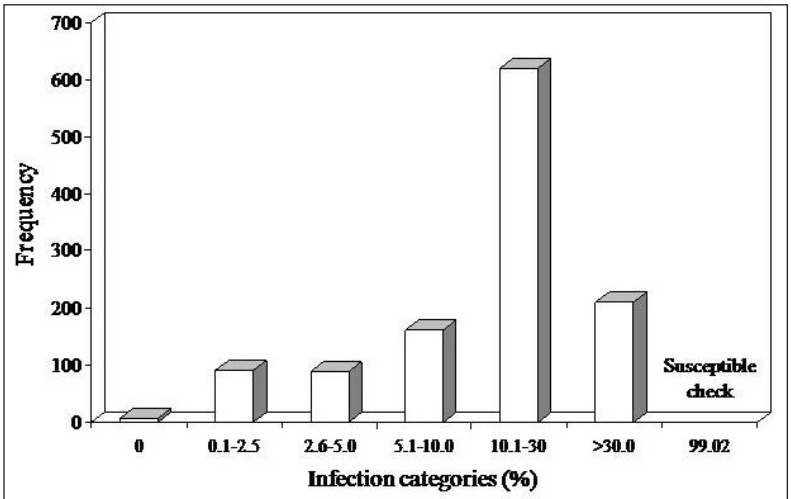

Fig. 14. Karnal bunt infection categories (%) in 1,178 advanced bread wheat lines artificially inoculated in the field at two planting dates during the 2013–14 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, México. The average of the three highest infection scores of the susceptible check was 99.02%.

Conclusions. The average range of percentage infection of 1,178 advanced bread wheat lines evaluated for resistance to Karnal bunt during the 2013–14 autumn–winter crop season was 0.0–65.6%, with an average of 18.4%. Seven lines did not show any infected grain at both dates. Fifty lines consistently showed an average percentage of infection below 2.5% at both dates and 67 were below 5.0%. Lines with the highest percentage of infection were BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/ BECARD with 84.8%, MELON//FILIN/MILAN/3/FILIN/4/PRINIA/PASTOR//HUITES/3/ MILAN/OTUS//ATTILA/3*BCN/5/MELON//FILIN/MILAN/3/FILIN with 84.5%, and AGT YOUNG/3/1447/PASTOR//KRICHAUFF/4/SOKOLL/3/PASTOR//HXL7573/2*BAU with 77.4%, all at the first date. The average of the three highest levels of infection of the susceptible check was 99.02%.

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ITEMS FROM THE RUSSIAN FEDERATION

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

Compensating ability of Ae. columnaris chromosomes in a set of substituted and additional lines of spring bread wheat.

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

As a result of research between 2007–17, the original collection of spring bread wheat lines with chromosomes or translocations from *Ae. columnaris* k1193 was obtained. The recipient cultivars were Saratovskaya 68, Dobrynya, and L503. The complete collection includes a set of substitution lines 2A(2U^c), 3D(3U^c), 3B(3U^c), 6D(6U^c), 6A(6U^c), 1D(1X^c), 1A(1X^c), 3B(3X^c), 5D(5X^c), and 6D(6X^c); multiple substitutions 3D(3X^c)6D(6X^c), 3D(3X^c)5D(5X^c)6D(6X^c), and 5D(5X^c)6D(6X^c); additional lines with chromosomes 2U^c and 3U^c; and several unidentified translocations for chromosomes 2D and 6D. Based on this collection, cooperative research with the Laboratory of Genetic Bases of the Plant Identification Institute of General Genetics by name N.I. Vavilov, the first genetic classification of chromosomes *Ae. columnaris* has been provided. The compensation ability of each of the substituted chromosomes for traits of spike productivity were detected. Chromosome 6U^c was found to be the least compensating, and the greatest were 3U^c and 5X^c. In general, a decrease in spike productivity and the 1,000-kernel weight for all chromosomes was observed. The effect of increasing the compensating capacity in lines with double substitutions was noted. The ability compensatory capacity on the level of the recipient cultivar was noted for the line 5D(5X^c)6D(6X^c), but line 3D(3X^c)6D(6X^c) has a greater effect. For SDS-sedimentation value, all *Ae. columnaris* chromosomes except 2U^c decrease the quantity of the sediment. The most significant (1.5–2.0 times) was observed in lines with chromosomes carrying gliadin and glutenin seed storage proteins 6U^c, 1X^c, and 6X^c.

Evaluation of spring bread wheat introgression lines for drought resistance in 2018.

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

A hard drought was observed during the 2018 vegetation season, which allowed us to evaluate original near isogenic lines (NILs) of spring bread wheat with a combination of alien translocations. Furthermore, in these conditions, we evaluated a set of introgression lines with genetic material from various bread wheat relatives and lines derived from CIMMYT synthetics after crosses with Saratov breeding cultivars. The set of NILs with combinations of T7DS·7DL-

7Ae#1L + T1BL·1R#1S translocations with recipient cultivars L503 and L2032 insignificantly increased grain productivity, but this effect was significant in lines with the cultivar Dobrynya. An insignificant increase in grain productivity was noted for T7DL-7Ae#1L + T2AL·2AS-2MV # 1 in Dobrynya-derived lines. The direct effect of the T7DL-7Ae#1L translocation on grain yield was positive (insignificant increase). The greatest effect on grain productivity was noted for the T4AS·4AL-7S#2S translocation (significant increase); this NIL had the maximum grain yield. The *Lr28* gene in the T4AS·4AL-7S#2S translocation is effective against leaf rust in the Lower Volga region. In addition, this translocation from *Ae. speltoides* is one of the sources of genes for heat and drought resistance. The substitution of chromosome 6D(6Ag^{i}) from *Th. intermedium* had a neutral effect on grain productivity under severe drought conditions, at the same time, an NIL with double substitution 3B(3Ag^{e}) 3D(3Ag^{e}) from *Th. elongatum* (2n=70) significantly increased grain yield. Thus, different chromosomes from the E genome of *Th. intermedium and Th. elongatum* (E genome of these species is common) effect drought resistance. Among the introgression lines, maximum grain productivity, 1,126 kg/ha, was obtained in line L293/17 (Saratovskaya 29/*Th. elongatum**5//Saratovskaya 29/3/Saratovskaya 68 (T7DL-?)) and a grain yield of 1,075 kg/ha were noted in line L167/18 (Favorit/*T. persicum**2//Favorit (substitution 6D (6Ag^{i}) plus genetic material from *T. persicum*)) (**Editors note:** according to van Slageren (1994), the correct name for *T. persicum* is *T. turgidum* subsp. *carthlicum*) compared with that of the donor cultivar Favorit (931 kg/ha) (substitution 6D (6Ag^{i}), and Saratovskaya 55 (drought-resistant)) (470 kg/ha). From crosses of the CIMMYT synthetic lines with cultivars from Saratov breeding, line L375 (L505/3/Croc/*Ae. tauschii* (205)/Weaver/4/L505/5/L505) was distinguished for grain yield, 1,132 kg/ha, and significantly exceeded the standard cultivar Favorit. A DNA marker analysis of line L375 showed the presence of the *Lr19*/*Sr25* + *Lr26*/*Sr31* + *Lr41* genes in the translocations T7DS·7DL-7Ae#1L + T1BL·1R#1S + T2DS·2DL (*Ae. tauschii*). In the addition to resistance to a complex of diseases (powdery mildew, leaf rust, and stem rust), this line also has good drought resistance.

Laboratory of Plant Immunity to Diseases, 7 Toulaikova St., Saratov, 410010, Russian Federation.

Puccinia triticina population structure in winter and spring wheat in the Saratov Region of Russia during 2013–17.

E.A. Konkova.

The analysis of the *Puccinia triticina* Ericss Saratov population's structure for virulence genes during 2013–17 is provided. Infectious material was collected from winter and spring bread wheat cultivars and lines bred at ARISER. These cultivars and lines have varying degrees of pathogen severity, from moderate (10–20%) to high (70–90%). The studies of virulence genes in the *P. triticina* population were performed on the set of near-isogenic lines in the cultivar Thatcher, which contains 52 lines with identified *Lr* genes. Ten monopustule isolates were isolated from pathogen populations. The composition of the pathogen populations for virulence genes was determined by its infection type on the NILs. We established that *P. triticina* populations in 2013–17 were characterized as highly virulent. The number of virulence genes ranged from 40 to 44, but the number of resistance genes varied from six to nine. The main difference between the population compositions were in the different types of reaction to the *Lr9, Lr19, Lr23, Lr24,* and *Lr29* genes. These genes showed resistance, then a susceptible type of reaction to *P. triticina*. During 2013–17, a high efficiency in genes *Lr41, Lr42, Lr43+Lr24, Lr47,* and *Lr53* was observed. The use of these genes in breeding will expand the genetic diversity of new cultivars and stabilize the pathogen population composition. These data indicate the need for continuous monitoring of the *P. triticina* population composition for the virulence gene frequency, which will allow us to develop a strategy for breeding resistant cultivars and their spread in regions of wheat cultivation.

ITEMS FROM UKRAINE

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

Grain quality of the tetraploid wheat Triticum persicum var. rubiginozum.

Editors note: according to van Slageren (1994), the correct name for *T. persicum* is *T. turgidum* subsp. *carthlicum*, however, we are using the authors original classification for clarity because it is itemized as *T. persicum* in the database of the National Centre for Plant Genetic Resources of Ukraine.

L.I. Relina, L.A. Vecherska, and R.L. Boguslavskyi.

Abstract. *Triticum persicum* Vav. is a tetraploid wheat that has promise for breeding, however, its grain quality is little studied. Our purpose was to evaluate the biochemical parameters, performance, and processing characteristics of *T. persicum* var. *rubiginozum* grain. The analyses were on *T. persicum* var. *rubiginozum* (*T. turgidum* subsp. *carthlicum*) from a collection of the National Center for Plant Genetic Resources of Ukraine. Plants were grown in a typical black soil in 2015, 2016, and 2017. The protein content was determined by Kjeldahl digestion. The carotenoid level was spectrophotometrically assessed in acetone extracts. Antiradical activity (ARA) was investigated in ethanol extracts by DPPH• assay. The iron, zinc, and copper contents were determined by atomic absorption spectrometry. Grain hardness was determined using a hardness tester measuring the force applied to crush kernels. The protein content in *T. persicum* var. *rubiginozum* grain ranged within 15.7–20.4%. Despite a year-to-year variation, high protein content in the grain seems to be a consistently expressed trait. The carotenoid content in *T. persicum* var. *rubiginozum* grain varied between 2.0 and 3.1 mg/kg. The average ARA (588.2±24 chlorogenic acid equivalents (CGAE)/g of seed) was higher than that in the reference durum wheat cultivar Spadshchyna (525.4±38.9 CGAE/g of seed). *T. persicum* var. *rubiginozum* grain contains 30.7–39.8 mg/kg and 31.1–43.9 mg/kg of iron and zinc, respectively, which is comparable to the levels in commercial durum wheat cultivars. *T. persicum* var. *rubiginozum* grain contained of 0.62–3.47 mg/kg of copper. We also measured performance and processing parameters of *T. persicum* var. *rubiginozum*. The 1,000-kernel weight was 26.0–29.0 g. The test weight was around 75–77 kg/hL, which is satisfactory; grade I grain has ≥75 kg/hL. Vitreousness was only 44–52% and grain hardness was 188–214 N. We showed that 1) *T. persicum var. rubiginozum* should be crossed with large-seeded and highly vitreous accessions to achieve grain of a larger size and greater vitreousness; 2) *T. persicum* var. *rubiginozum* could be used in wheat breeding as a source of high protein content and sufficient mineral content; 3) *T. persicum* var. *rubiginozum* could be a source of antioxidants; and 4) involving *T. persicum var. rubiginozum* in breeding for pasta qualities is inadvisable.

Introduction. *Triticum persicum* Vav. (*T. turgidum* subsp. *carthlicum*)is ancient tetraploid wheat discovered by N.I. Vavilov in 1912 with an area was described as the Trans-Caucasian region and adjoining areas of Turkey (Dorofeev 1987). *Triticum persicum* is an early-ripening, easily threshed analogue of *T. durum* that is cold tolerant, during both early growth and maturation. In addition to lodging resistance, *T. persicum* is tolerant to abundant rainfall during maturation and not prone to preharvest sprouting. This species is highly resistant to powdery mildew (dominant trait) (Vavilov and Yakushkina 1925) and loose smut, and relatively resistant to brown (depending on the form, those with black spikes are more resistant), yellow, and stem rust (polymeric inheritance) (Vavilov and Yakushkina 1925). High protein (up to 23%) makes it valuable for breeding, however, *T. persicum* has a number of disadvantages, such as low drought and heat resistance, susceptibility to soil drought, a small grain, and poor bread-making qualities.

Little used in breeding, a Swedish powdery mildew-resistant spring bread cultivar and Italian high-yielding forms with shortened vegetation periods and high grain vitreousness were created with the involvement of *T. persicum* (Bennett 1984). *Triticum persicum* can be used successfully in hybridization to boost the yield capacity. For example, a significant gain in grain yield was obtained in a line derived from a combination 'bread wheat Favorit/*T. persicum*' (4.808 kg/ha vs. 4.317 kg/ha in Favorit) (Sibikeev et al. 2018). Thus, *T. persicum* is a promising object for wheat breeding, though little studied in terms of grain quality, and these grain characteristics are of increasing interest. Grain

quality is determined by many factors, such as starch and protein contents and compositions, vitamin and antioxidant content, and micronutrient amount. Biofortification (enhancement in grain nutrient levels), either agronomically (via fertilization) or genetically (via breeding), is believed to be a promising and cost-effective approach to alleviating malnutrition and related health problems (Peleg et al. 2009; Zhao and Shewry 2011; Bouis and Saltzman 2017). This solution, however, requires a comprehensive exploration of potential genetic resources. Our objective was to evaluate the protein content, carotenoid level, antioxidant activity, and trace mineral contents, as well as performance and processing characteristics of underinvestigated *T. persicum* var. *rubiginozum* grain.

Materials and methods. *T. persicum* var. *rubiginosum* UA0300066 under investigation is a national asset of Ukraine and was kindly granted by The National Centre for Plant Genetic Resources of Ukraine. Plants were grown on typical black soil in the experimental field of the Plant Production Institute nd. a. VYa Yuriev of NAAS. Grain harvested in 2015, 2016, and 2017 (years with various weather conditions) was used in analyses.

Protein content was determined by Kjeldahl digestion (S'aez-Plaza 2013a, 2013b). The carotenoid level was spectrophotometrically assessed in acetone extracts as described in (Luterotti and Kljak 2010). The antiradical activity was investigated in ethanol extracts by DPPH• assay (Sytar et al. 2018; Żmijewski et al. 2015). The content of iron, zinc and copper were determined by atomic absorption spectrometry (Jorhem 2008). The test weight and vitreousness were evaluated in compliance with (State Standard of Ukraine 3768:2010). The grain hardness was determined on a YPD-300 hardness tester (Ltpm, China) (measuring force applied to crush kernels) (Yarosh 2014). The data are presented as the mean ± standard error of the mean.

Results and discussion. The protein content in *T. persicum var. rubiginozum* grain ranged within 15.7±0.8–20.4±1.2% (Table 1). The highest protein content accumulated in 2015, when the precipitation during grain filling was medium (156 mm) throughout the study years. No obvious relationship between protein content and average air temperature during the crop vegetation was observed. These values are rather high as good durum wheat grain contains 15–18% of protein (grade I grain has ≥14.0% of protein (State Standard of Ukraine 3768:2010). Despite the year-to-year variation, high protein content in grain seems to be a consistently expressed trait in *T. persicum var. rubiginozum*. Thus, this species can be considered as a source of high protein content.

Table 1. Biochemical parameters of *Triticum persicum* var. *rubiginozum* grain depending on weather conditions during the vegetation period (Σ_p – precipitation amount, t_{av} – average temperature, CGAE – chlorogenic acid equivalents).

Flowering date	Vegetative period		Grain filling		Protein content (%)	Carotenoid content (mg/kg)	Antiradical activity (CGAE/g of seed)
	Σ_p (mm)	t_{av} (°C)	Σ_p (mm)	t_{av} (°C)			
06/16/2015	13	20.7	156	22.0	20.4±1.2	2.0±0.1	568.8±17.3
06/21/2016	157	17.1	107	23.2	16.8±0.9	3.1±0.2	559.7±13.9
06/17/2017	53	20.5	208	22.9	15.7±0.8	2.5±0.1	636.2±24.1

Staples are not referred as important sources of vitamins, antioxidants, or minerals in human rations. However, they are consumed in abundance and, hence, some believe that a rise in levels of these substances may have significant effects on human nutrition and health (Kumar et al. 2014; Garcia-Oliveira et al. 2018). Being the major staple crop in many countries, wheat made up 179.26 g of food/capita/day, or 15.87 g of protein/capita/day, or 527 kcal/capita/day (food supply quantity), in 2013 (FAOSTAT 2013).

Carotenoid content is a factor determining nutritional value of wheat and the quality of end products, especially pasta. Wheat grain, generally, is not very rich in carotenoids; therefore, new high-carotenoid sources are sought. The carotenoid content in *T. persicum* var. *rubiginozum* grain varied within 2.0 ±0.1–3.1±0.2 mg/kg (Table 1). High-quality, bright-yellow pasta is acceptable when made from grain containing ≥ 5.5 mg/kg of carotenoids (Abdel-Aal and Rabalski 2012). Hence, this species cannot be a source of high carotenoid content. The highest carotenoid content was recorded in 2016, when the average air temperature was the highest (23.2°C) and precipitation was the lowest during grain filling. Such weather conditions may contribute to the accumulation of carotenoids. Similar results were obtained on cereals by Paznocht et al. (2018), who reported that 10 out of 14 tested cultivars had increased carotenoid contents in response to higher temperatures and lower precipitation.

Antioxidant content is another determinant of wheat nutritional value. The antiradical activity (ARA) of ethanol extracts from *T. persicum* var. *rubiginozum* grain amounted to 636.2±24.1 chlorogenic acid equivalents (CGAE)/g of seed in 2017, decreasing in the other years (see Table 1). The peak content of ethanol soluble antioxidants in the year with the minimal precipitation during the wheat green mass development may be due to enhanced nonspecific protection against stress. A positive correlation was observed between seed antioxidants and drought tolerance in other plant species (Lakshmi et al. 2018). One could expect that the carotenoid content and antioxidant activity would change in parallel, depending on weather conditions. However, we observed that an increased carotenoid content was associated with higher temperature and lower precipitation during grain filling, whereas an increased ARA was associated with higher temperature and lower precipitation during green mass development. This dissimilarity may account for the differences in regulation of synthesis and consumption of carotenoids and polyphenols/flavonoids (major compounds extracted by ethanol and contributing to DPPH• scavenging activity). The average (for the study years) ARA in *T. persicum* var. *rubiginozum* grain (588.2± 24.1 CGAE/g of seed) was higher than that in the reference durum wheat grain of cultivar Spadshchyna (525.4± 38.9 CGAE/g of seed). Thus, *T. persicum* var. *rubiginozum* can be tested for use in wheat breeding for high antioxidant content.

Some minerals are essential in metabolism or for the synthesis of essential compounds. Bread and breakfast cereals are sometimes specifically fortified with iron (Food Standards Agency 2012); therefore, breeders seek to develop high-iron wheat cultivars. The iron content in commercial durum wheat varies within 25.7–40.5 mg/kg (Magallanes-López 2017). *T. persicum* var. *rubiginozum* grain contains 30.73±1.63–39.75±1.87 mg/kg of iron (see Table 2), which is comparable to the iron levels in commercial durum wheat cultivars. This variation can be attributed to weather fluctuations during the crucial periods in the plant development. The grain accumulated 39.75±1.87 (maximum) mg/kg of iron, when the precipitation amount was 53 and 208 mm, and 30.73±1.63 (minimum) mg/kg, when the precipitation was 157 and 107 mm, during vegetative development and grain filling, respectively. The plant actively accumulates nutrients from soil during the vegetative development; therefore, a dilution of soil substances due to abundant rainfall may reduce mineral levels. However, a drop in the precipitation amount to 13.1 mm was associated with a decrease in the iron level (to 35.65±1.76 mg/kg). Thus, we assume that too little moisture does not allow plants to absorb minerals from soil. On the other hand, abundant precipitation during grain filling (208 mm) may exert a negligible effect, as the species is tolerant to abundant rainfall during maturation (Dorofeev 1987). We observed no apparent relationship between iron content and temperatures during the crucial phases of the plant development. Despite this variation, high iron content in grain appears to be genetically intrinsic to *T. persicum* var. *rubiginozum*, hence it can serve as a source high iron content.

Table 2. Mineral content in *Triticum persicum* var. *rubiginozum* grain depending on the weather conditions during the vegetation periods (* 2017–2016 and 2017–2015 significant differences, p≤0.05; # 2017–2016 and 2017–2015 significant differences, p≤0.001; • 2015–2016 significant difference, p≤0.001).

Flowering date	Vegetative period		Grain filling		Minerals		
	Σ_p (mm)	t_{av} (°C)	Σ_p (mm)	t_{av} (°C)	Zn	Fe	Cu
06/16/2015	13	20.7	156	22.0	35.6±1.7	35.65±1.76*	3.47±0.13 # •
06/21/2016	157	17.1	107	23.2	31.1±1.5	30.73±1.63*	0.62±0.02 # •
06/17/2017	53	20.5	208	22.9	43.9±1.9	39.75±1.87	1.03±0.04

Zinc also is an essential trace element for humans. Wheat is an excellent source of zinc (Hernández Rodríguez 2011). Cereals were recommended as cheap and stable sources of easily absorbed zinc (Rosado 2003). The zinc content in commercial durum wheat varies within 24.8–48.8 mg/kg (Food Standards Agency 2012). Conti et al. (2000) reported that Italian durum wheat contained 24 mg/kg of zinc. The maximum allowable concentration of zinc in grain is 50.0 mg/kg (Feschenko 2014). *T. persicum* var. *rubiginozum* grain contained 31.13±1.53–43.90±1.91 mg/kg of zinc (Table 2), which is comparable to commercial durum wheat. The zinc content–weather conditions relationship was similar to that for iron, which was expected because the high grain protein content gene (*GPC-B1)* also was shown to confer higher concentrations of both Fe and Zn in grain (Cakmak et al. 2004; Distelfeld et al. 2007). Correlations between Zn and Fe contents were positive for wild and domesticated emmer (Cakmak et al. 2004; Distelfeld et al. 2007; Peleg et al. 2008; Chatzav et al. 2010). Taking the literature into account, we expected that the protein content would change concurrently with the Zn and Fe content. Nevertheless, the protein content reached a peak in 2015 and was at a minimum in 2017, whereas Zn and Fe content were at a maximum in 2017 and the minimum in 2016. We can assume that the protein/iron/zinc relationship may be not a common feature of tetraploid wheats, but a peculiarity of the emmer accessions described in these articles.

Copper also is an essential trace element. Italian durum wheat, for example, contains 3.5 mg/kg of copper (Conti et al. 2000). Variation in this parameter can be wide, 1.8–39.7 mg/kg in durum wheat milling products (Micco et al. 1987). In Russian wheat grain, the copper content ranged within 2.0–12.8 mg/kg, depending on the cultivation site (Pugaev 2013). Feschenko (2014) reported that the copper level in spring wheat grain averaged 5.15±0.40 mg/kg (through 10 years) with the maximum allowable concentration of 10 mg/kg. *T. persicum* var. *rubiginozum* grain contained of 0.62±0.02–3.47±0.13 mg/kg of copper, depending on the year (Table 2). Thus, such levels can satisfy the need of human body for copper, on one hand, and are far below the maximum allowable concentration, on the other. In general, the copper content–weather conditions relationship was similar to those for iron and zinc, although the maximum copper content was recorded in 2015 with the lowest and medium precipitation during the vegetative period and grain filling, respectively, and the highest average air temperature during vegetation.

Concurrently, with biochemical characterization, we measured the performance and processing parameters of *T. persicum* var. *rubiginozum* (Table 3).

Table 3. Technological parameters of *Triticum persicum* var. *rubiginozum* grain 2015–2017.

Year	Grain hardness (N)	Test weight (kg/hL)	Vitreousness (%)	1,000-kernel weight (g)
2015	214±15	75±1.4	52±4	26±2
2016	188±9	76±1.2	44±3	26±1
2017	193±10	77±1.7	47±3	29±2

The 1,000-kernel weight was 26±1–29±2 g, meaning that *T. persicum* var. *rubiginozum* has small grain, which was identified by Vavilov and Yakushkina (1925) for many *T. persicum* races, and needs to be crossed with large-seeded lines to achieve grain of desirable (larger) size. Test weight was within 75±1.4–77±1.7 kg/hL, which is satisfactory, as a grade I grain has ≥75 kg/hL. Vitreousness was not remarkable (44±3–52±4%), therefore, to achieve easy milling this species needs crossing with highly vitreous accessions. Grain hardness is one of the key determinants of milling behavior and has a great influence on flour and dough quality (Hoseney 1987; Pomeranz and Williams 1990). For example, grain hardness was shown to correlate with bread-making quality (Medvedev et al. 2015). The grain hardness of *T. persicum* var. *rubiginozum* was 188±9–214±15 N, depending on the year. Comparing different researchers' data is difficult, because different techniques and devices were used to measure the grain hardness. However, Veha et al. (2011) cross-checked the hardness index produced by Perten SKCS 4100 equipment against maximum breaking force in Newtons produced by Lloyd 1000R Testing Machines. Using their data, we can assume that 188–214 N measured on a YPD-300 hardness tester corresponds approximately a hardness index of 40. Using the data from Szaby et al. (2007), we obtained a similar result, implying that *T. persicum* var. *rubiginozum* is likely to be a soft wheat according to the classification of Haraszi et al. (2013, 2016). Because *T. persicum* var. *rubiginozum* has low grain hardness coupled with a medium carotenoid content, it is unlikely to be used in breeding for pasta qualities. In further studies, it is worth evaluating for gluten quality and bread-making characteristics.

Conclusions.

1. *Triticum persicum* var. *rubiginozum* needs to be crossed with large-seeded and highly vitreous accessions to achieve grain of desirable (larger) size and greater vitreousness.
2. *T. persicum* var. *rubiginozum* can be used in wheat breeding a source of high-protein content, sufficient iron and zinc content, and a balanced copper content.
3. Grain of *T. persicum* var. *rubiginozum* can be a source of ethanol-soluble antioxidants.
4. *T. persicum* var. *rubiginozum* is not a good candidate for breeding for pasta qualities.

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Seed longevity of some wheat species and cultivars based on their antioxidant activity.

N.Yu. Skorokhodov, V.V. Pozdniakov, O.V. Antsiferova, and R.L. Boguslavskiy.

Introduction. Long-term storage of seed in a viable state is a prerequisite for the effective use of the plant gene pool by current and future generations. The main problem is that the longevity of seed is due to a complex set of factors, including the physiological state of the seed, genotype characteristics, and storage conditions, to name a few. Different approaches have been advanced in diagnosing the state of seed and predicting its longevity (Baskin and Baskin 2014). One informative criteria for evaluating the seeds longevity is the antioxidant activity (AA), which is considered an integral indicator of the ability of seed to withstand the oxidative processes that accompany the action of stress factors of different nature, including seed aging during storage (Pinzino et al. 1999; Yu 2008).

Species and intraspecific diversity of crops, in particular wheat, are at risk of loss due to genetic erosion (Van de Wouw et al. 2008) and, therefore, are the subject of special attention from a conservation viewpoint. Genotypic and physiological differences in the mechanisms that determine seed longevity are found. Such mechanisms include, in particular, antioxidant activity, making research in this area relevant.

Antioxidants are concentrated mainly in the aleurone layer of wheat grains (Zhou et al. 2004) and are predominantly carotenoids, in particular lutein (Pinzino et al. 1999). In the oil-rich embryo, the main antioxidants are tocopherols (Capitani et al. 2011).

Many experiments have simulated the natural aging of seeds during storage by creating special 'accelerated aging' regimes, which can accelerate the study of issues related to seed longevity (Hampton and TeKrony 1995; TeKrony 2005; Safina and Filipenko 2013; Smolikova 2014). In particular, under accelerated aging, the content of antioxidants and carotenoids, especially lutein, is reduced in the seed of bread (Calucci et al. 2004) and durum (Galleschi et al. 2002) wheat. The purpose of our study is to determine the role of antioxidant activity in seed longevity in underutilized species and the intraspecific diversity in wheat based on experiments that simulate the natural aging of seed.

Material and methods. Eight diverse wheat accessions from the National Plant Gene Bank of Ukraine belonging to the three ploidy groups and of different geographical origin included *T. aestivum* (2n = 42) subsp. *aestivum*, represented by the standard cultivar (cv) Kharkivska 26 (Ukraine) and two accessions with waxy endosperm, PI619376 and PI619379 (USA), and subsp. *spelta* cv. Frankenkorn (Germany); *T. turgidum* (2n = 28) subsp. *durum* cv. Spadshchyna (Ukraine), and subsp. *dicoccum* cv. Polba 3 (Russia, Udmurtia); *T. monococcum* (2n = 14) subsp. *monococcum* line UA0300439 (Hungary) and *T. sinskajae* line UA0300224 (Russia) (**Authors note:** *T. sinskajae* is an invalid name, because this line was created by an induced mutation. According to van Slageren (1994), it should be considered as a synonym under the cultivated taxa *T. monococcum* subsp. *monococcum*. However, for clarity in this article, we will refer to it as subsp. *sinskajae*). The hulls were manually removed from the grain in subspecies *spelta, dicoccum,* and *monococcum*. In the control and each experiment, 100 seeds were analyzed in three replications. The longevity of the seeds was studied in an 'accelerated aging' experiment, which simulates the process of natural aging of seeds during long storage in unregulated conditions.

Two methods of accelerated aging were used:

1. Hampton & TeKrony (1995) and TeKrony (2005). Seed samples kept in a water desiccator for three days (72 hours) in open glass containers at 43°C±2°C and a relative air humidity 100% and
2. Likhachev (1980). Seed samples dried to humidity levels of 5% and 6% were kept in hermetically sealed containers at 37°C±2°C for 30 days (720 hours).

In addition, as an experimental variant, seed was stored for 30 days (720 hours) in hermetically sealed glass containers in a freezing chamber at –20°C±2°C, which corresponds to the regime for long-term storage in the National Plant Genebank of Ukraine. As a control for all experimental variants, seeds were placed in hermetically sealed glass containers and stored in a chamber at 4°C.

Seeds of the control and all experimental options were tested for germination energy and germination rate according to the international rules for the analysis of seeds (Anonymous 1984) and for the length of the sprout and the primary roots on the seventh day after germination.

Antiradical activity was determined using a stable radical of 2,2-diphenyl-1-picrylhydrazyl according to Arabshahi and Urooj (2007) with minor changes. The alcoholic solution of the radical was prepared by dissolving 22 mg of DPPH in 400 mL of an 80% aqueous ethanol solution and used during the working day. 0.5 mL of seed extract was thoroughly mixed with 3.5 mL of the DPPH solution and, after two hours, the optical density was determined on a SF Shimadzu UV-VIS-1800 at a wavelength of 517 nm. The ability of the samples to neutralize the free radical DPPH (antiradical activity - AA %) was determined by the formula:

$$AA(\%) = (A - B) / A \times 100$$

where A is the extinction of the control sample (instead of 0.5 mL of the sample extract, 0.5 mL of 80% ethanol solution was added to the DPPH solution) and B is the extinction of the experimental sample after a two hour reaction with the DPPH solution.

The determination of the equivalent of chlorogenic acid was carried out using a calibration graph (the concentration range of the standard 0–300 μM).

The influence of the methods of accelerated aging and freezing on the seeds was estimated by index of indicator's change under the influence of stress factor (*I*), which is used to assess the degree of stress resistance of plants (Udovenko 1988):

$$I = (X_1 - X_2) / (X_2) * 100$$

where I is the index of the indicator's change. A positive index value means growth of the index, that is, the positive effect of the investigated factor; a negative value, a decrease in the index, indicates a negative influence of the factor; X_1 is the average indicator in the experimental variant; and X_2 is the average indicator in the control variant.

Results and discussion. The main indicators of seed viability are germination energy and germination rate. In the control in both years of research, both indicators were relatively high (96% and above) in the seed samples of subsp. *monococcum*, subsp. *dicoccum* cv. Holykovskaya, and subsp. *spelta* cv. Frankenkorn, and reduced in subsp. *sinskajae* (<91–93% for germination energy and 95–96% for germination rate) (Table 4, p. 53). In 2014, the lowest rates were in seed of subsp. *durum* cv. Spadshchyna; 82% germination energy and 85% germination rate. Reduced rates also were found in subsp. *sinskajae*, subsp. *dicoccum* cv. Polba 3, subsp. *aestivum* PI619376 waxy (90–92% for germination

Table 4. Seed viability indicators of the wheat accessions in the control option.

Accession	Germination energy (%)	Germination rate (%)	Length (cm) root	Length (cm) sprout	Antiradical activity
2014					
subsp. *monococcum*	98±0.7	100±0.0	11.6±1.9	11.7±3.0	38.5
subsp. *sinskajae*	91±2.8	95±1.4	10.2±3.1	9.0±2.3	35.1
subsp. *dicoccum* cv. Polba 3	92±7.1	96±2.8	16.5±2.1	13.7±1.6	42.9
subsp. *dicoccum* cv. Holikovs'ka	96±2.1	99±2.1	15.7±2.9	10.7±2.7	37.8
subsp. *durum* cv. Spadshchyna	82±8.5	85±3.5	9.8±1.5	6.8±2.7	49.5
subsp. *aestivum* cv. Kharkivska 26	95±1.4	99±0.7	13.0±3.9	8,8±2,6	39.8
subsp. *spelta* cv. Frankenkorn	97±5.7	100±2.8	14.4±2.1	11.4±1.2	43.2
2016					
subsp. *monococcum*	100±0.7	100±0.0	12.8±2.2	12.6±2.8	47.9
subsp. *sinskajae*	93±4.2	96±2.8	13.3±2.7	11.7±1.4	43.7
subsp. *dicoccum* cv. Polba 3	100±0.6	100±0.6	16.4±2.1	12.8±2.3	40.8
subsp. *dicoccum* cv. Holikovs'ka	97±1.4	97±0.7	14.3±2.5	9.2±1.6	37.5
subsp. *durum* Spadshchyna	98±0.0	100±0.7	16.6±2.7	11.3±1.8	31.7
subsp. *aestivum* cv. Kharkivska 26	99±0.6	100±0.0	15.4±3.1	8.8±1.9	40.4
subsp. *spelta* cv. Frankenkorn	98±1.4	100±0.0	15.8±3.0	10.6±3.1	41.1

energy and 94–96% for germination rate). In 2016, slightly reduced germination energy and rate were found in subsp. *spelta* cv. Holikovs'ka.

Additional seed viability characteristics are the length of the primary roots and the coleoptile (hereafter referred to as root length and shoot length, respectively). The largest root length in both years of research was in cultivars Polba 3 and Frankenkorn, which also had a comparatively high shoot length in both years and, as mentioned above, also was distinguished by the germination energy and germination rate. At the same time, these indicators were low in Polba 3 in 2014 and high in 2016. In general, the ranking of the accessions for each of the four indicators in 2014 did not correspond to the 2016 ranking, as evidenced by the lack of correlation between the traits in both years (r = 0.05–0.27).

The AA level of the seed grown in 2014 ranged from 35.1% to 52.0%. Moreover, the diploids were low, subsp. *sinskajae* was 35.1% and subsp. *monococcum* was 38.5%. Relatively high levels were in cultivars Polba 3 (42.9%), Spadshchyna (49.5%), and Frankenkorn (43.2%), and the waxy wheats (52.0%). In seed grown in 2016, the AA of the diploids were the highest, 43.71% for subsp. *sinskajae* and 47.93% for subsp. *monococcum*. The spelt wheat Frankenkorn and the bread wheat Kharkivska 26 approached that of the diploids at 41.08% and 40.41%, respectively. The accessions ranking for AA of the seed grown in 2014 was reciprocal to the more favorable, dry 2016; correlation coefficient was –0.65. In both years, the correlation coefficients between AA and almost all four indicators of seed viability were negative, with the exception of shoot length, which was insignificant in 2016. In 2014, the correlation coefficients of AA with germination energy, germination rate, and shoot length were negative and significant, from –0.56 to –0.60; the root length was negative (–0.38) and insignificant. In 2016, the correlation was negative, significant, and tight (r = –0.86) between AA and root length and negative although not significant for germination rate.

In an overwhelming majority of lines, accelerated aging (Hampton and TeKrony 1995) resulted in a decrease in all four indicators of viability compared with those of the control (Table 5, p. 54). Moreover, in 2014, the degree of this reduction was lower than in 2016. In 2014, the durable to accelerated aging was Polba 3 (the indexes of germination energy and germination rate were respectively 1.1% and 1.0%, the sprout length –8.0%). Somewhat more sensitive but also relatively durable were the *T. monococcum* lines (indices of germination energy and germination rate were –6.1% and –2.1%, respectively), the hexaploid *cultivars* Kharkivska 26 (indices of germination energy, germination rate, and root length from –4.0% to –5.0%, sprout length was even stimulated at 7.8%) and Frankenkorn (indices of –4.1% for germination energy and –5.0% for germination rate). In a number of cases, a rather significant stimulating effect of accelerated aging was observed, which concerned only the root and sprout length but not the germination energy or germination rate; in particular, the sprout length of cultivars Holikovs'ka, Spadshchyna, and Kharkivska 26 in both years

Table 5. Seed viability indicators of the wheat accessions with accelerated aging according to Hampton and TeKrony (1995).

Accession	Germination energy		Germination rate		Length of: root		Length of: sprout		Antiradical activity	
	%	Index	%	Index	cm	Index	cm	Index	%	Index
2014										
subsp. *monococcum*	92±4.2	–6.1	98±2.4	–2.0	7.3±2.4	–37.2	8.9±2.0	–24.1	36.3	–5.7
subsp. *sinskajae*	28±0.0	–69.2	30±4.2	–68.4	6.2±1.7	–39.4	6.9±1.9	–22.8	32.6	–7.1
subsp. *dicoccum* cv. Polba 3	93±6.7	1.1	97±2.6	1.0	13.7±2.9	–17.1	12.6±2.0	–8.0	42.9	0.0
subsp. *dicoccum* cv. Holikovs'ka	27±13.4	–71.9	33±±9.9	–66.7	13.0±2.9	–17.6	16.0±3.1	50.4	34.7	–8.2
subsp. *durum* cv. Spadshchyna	70±4.2	–14.6	80±2.8	–5.9	10.8±2.3	9.1	9.7±2.1	42.6	42.0	–15.2
subsp. *aestivum* cv. Kharkivska 26	93±4.2	–2.1	95±1.4	–4.0	12.9±2.3	–0.5	9.5±0.9	7.8	37.1	–6.8
subsp. *spelta* cv. Frankenkorn	93±2.8	–4.1	95±0.7	–5.0	11.4±1.6	–21.1	8.6±2.1	–24.3	43.2	0.0
2016										
subsp. *monococcum*	39±6.1	–61.0	50±10.0	–50.0	10.9±3.2	–14.5	15.1±2.1	19.8	42.0	–12.3
subsp. *sinskajae*	24±5.7	–74.2	30±10.0	–68.8	6.8±3.4	–48.6	9.4±2.9	–19.9	44.9	2.8
subsp. *dicoccum* cv. Polba 3	42±8.5	–58.0	50±0.0	–50.0	13.1±2.8	–20.6	17.8±3.9	38.7	38.6	–5.5
subsp. *dicoccum* cv. Holikovs'ka	9±5.9	–59.8	45±7.1	–53.6	11.5±4.4	–20.1	12.1±3.1	31.7	35.4	–5.6
subsp. *durum* Spadshchyna	30±5.7	–69.4	45±7.1	–55.0	12.0±3.0	–28.0	13.8±3.2	23.1	31.1	–2.1
subsp. *aestivum* cv. Kharkivska 26	62±5.3	–37.4	81±6.5	–19.0	16.1±3.3	4.5	12.6±3.2	44.0	36.7	–9.1
subsp. *spelta* cv. Frankenkorn	15±5.5	–84.7	60±2.0	–40.0	14.1±5.4	–10.9	13.9±4.2	31.4	39.2	–4.5

(indices 7.8–50.4%); subsp. *monococcum*, Polba 3, and Frankenkorn in 2016 (indices 19.8–38,7%); and the root lengths of Spadshchyna in 2014 (9.1%) and Kharkivska 26 (4.5%).

The degree of reduction of AA under the influence of accelerated aging by the method of Hampton & TeKrony (1995) was the smallest in Polba 3 and Frankenkorn in 2014 (I = 0.0%) and the largest in Spadshchyna (I = –15.2%). In the remaining accessions, the reduction of this indicator ranged from –5.7% to –8.2%. In 2016, accelerated aging caused in a slight increase of AA in subsp. *sinskajae* (I = 2.8%), but decreased in the rest of the accessions with a range of –2.1 to –12.3%. Accelerated aging by the method of Likhachov (1978) mostly cause a small increase in seed of 2014 for all four viability indicators compared with the control, and a decrease in seeds in 2016.

In seed with a moisture content of 5% grown in 2014, a slight decrease in germination energy (–4.1) and germination rate (–3.0%) occurred in Frankenkorn; the root length was substantially reduced in subsps. *monococcum* (–48.3%) and *sinskajae* (–17.2%) and the cultivars Holikovs'ka (–6.9%) and Spadshchyna (–17.5%); the sprout length in subsp. *monococcum* (–17.4%) and Kharkivska 26 (–5.9%) (Table 6, p. 55). Indicators of viability increased in 16 of the 28 cases but remained unchanged in four. Seed with a moisture content of 5% grown in 2016 decreased in 20 of the 28 cases, with an especially significant decrease in root length (–3.5 to –38.3%). An increase occurred only in sprout length for subsp. *monococcum* (11.6%) and cultivars Polba 3 (13.8%), Holikovs'ka (2.2%), Spadshchyna (32.4%), and Kharkivska 26 (48.6%) in five cases; in three the indicator was unchanged.

In seed with a moisture content of 6%, the pattern is similar (Table 7, p. 56). Seed grown in 2014 manifested an increase in 14 cases, a decrease in seven, and remained unchanged in seven of the 28 total. An increase was most significant in the root length of subsps. *monococcum and sinskajae*, cultivars Polba 3, Spadshchyna (indexes from 15.5 to 58.6%), and the sprout length of subsp. *sinskajae* (33.7%) and Spadshchyna (96.8%). Seed grown in 2016 manifested a reduction in indicators in 19 of the 28 cases, an increase in eight, and was nearly unchanged in one.

Table 6. Seed viability indicators at a humidity of 5% of wheat accessions with accelerated aging according to Hampton and TeKrony (1995).

Accession	Germination energy		Germination rate		Length of: root		Length of: sprout		Antiradical activity	
	%	Index	%	Index	cm	Index	cm	Index	%	Index
2014										
subsp. *monococcum*	85±4.2	13.3	91±7.4	–9.0	6.0±2.0	–48.3	9.7±2.0	–17.4	39.1	1.6
subsp. *sinskajae*	97±1.4	6.6	99±1.4	4.2	8.5±4.0	–17.2	9.7±2.4	8.0	33.7	–4.0
subsp. *dicoccum* cv. Polba 3	99±1.4	7.6	100±0.0	4.2	19.3±3.2	16.6	15.2±3.5	10.6	—	—
subsp. *dicoccum* cv. Holikovs'ka	99±0.7	3.1	99±0.71	0.0	14.7±3.1	–6.9	11.2±3.3	5.1	36.7	–2.9
subsp. *durum* cv. Spadshchyna	88±5.7	7.3	97±1.4	14.1	8.2±2.6	–17.5	8.8±2.5	29.5	50.6	2.2
subsp. *aestivum* cv. Kharkivska 26	94±2.8	–1.1	98±2.8	–1.0	13.7±2.8	5.6	8.3±2.2	–5.9	40.1	0.8
subsp. *spelta* cv. Frankenkorn	93±1.4	–4.1	97±1.4	–3.0	14.8±3.8	2.9	11.6±2.4	1.5	43.4	0.5
2016										
subsp. *monococcum*	96±0.0	–4.0	99±0.0	–1.0	12.3±3.0	–3.5	14.1±2.0	11.6	47.5	–0.9
subsp. *sinskajae*	15±0.0	–83.9	40±0.0	–58.3	11.5±4.5	–13.5	10.5±3.3	–10.3	41.2	–5.7
subsp. *dicoccum* cv. Polba 3	95±3.5	–5.0	98±2.1	–2.0	15.1±4.3	–8.1	14.6±3.4	13.8	44.6	9.2
subsp. *dicoccum* cv. Holikovs'ka	85±7.1	–12.4	95±6.4	–2.1	11.5±3.4	–19.4	9.4±2.4	2.2	37.2	–0.8
subsp. *durum* Spadshchyna	92±0.0	–6.1	94±0.0	–6.0	11.6±5.6	–30.1	14.9±3.0	32.4	30.1	–5.3
subsp. *aestivum* cv. Kharkivska 26	93±4.2	–6.1	99±1.4	–1.0	10.8±2.6	–30.2	13.0±3.3	48.6	40.3	–0.4
subsp. *spelta* cv. Frankenkorn	82±11.3	–16.3	98±2.8	–2.0	13.2±3.6	–17.0	9.5±2.4	–10.4	39.2	–4.7

The increase was mainly in sprout length in subsp. *monococcum*, and cultivars Polba 3, Holikovs'ka, and Frankenkorn (8.5 to 35.0%) and also in the root length of Holikovs'ka (4.3%). Less viable for all four traits was subsp. *sinskajae* seed grown in 2016 (–38.0 to –96.8%). By comparing the parameters and their changes under accelerated aging in seeds with humidity of 5% and 6%, we concluded that a humidity of 5% provides for a greater seed longevity than 6%.

After accelerated aging by the method of Lihachev (1980), the level of AA for seed with a 5% moisture content changed compared with the control in seed grown from 2014 in limits of –4.0–2.2% and in seed from 2016 from –5.7–9.3%. For seed with a moisture content of 6%, the AA changes were in the seeds grown in 2014 from –2.28–6.26% and in seed of 2016 from –7.05–2.99%.

Unlike the alternatives to accelerated aging, the relationship between AA in the control and after freezing was insignificant, although positive. The effect of freezing wheat seed at –20°C for 30 days was different in degree but mostly positive (Table 8, p. 57). The most significant was the increase of all four indicators in the cultivar Spadshchyna in 2014 and the sprout length in 2016, the root and sprout length in *subsp. sinskajae* in both years and in subsp. *monococcum* in 2016. Root and sprout length in 2016 and only root length in 2014 in Kharkivska 26 and both indicators in Frankenkorn in 2016. The germination energy and rate of seed of all accessions except Spadshchyna either did not change or changed very little; the absolute value of the index did not exceed 4.4%. However, in some cases, the indices were negative with a small absolute value. In only two cases was the decline significant (approaching –6%); subsp. *monococcum* and cultivar Kharkivska 26 for sprout length in 2014. Overall, freezing had a more significant effect on the length of the roots and sprouts than on the germination energy and rate of the studied accessions.

Freezing caused a change in the AA of the seed within the limits of the indices from –7.7% (Frankenkorn, 2016)

Table 7. Seed viability indicators at a humidity of 6% of wheat accessions with accelerated aging according to Hampton and TeKrony (1995).

Accession	Germination energy		Germination rate		Length of: root		Length of: sprout		Antiradical activity	
	%	Index	%	Index	cm	Index	cm	Index	%	Index
2014										
subsp. *monococcum*	97±1.4	–1.0	99±1.4	–1.0	13.8±2.6	19.0	12.6±2.3	8.0	38.7	0.5
subsp. *sinskajae*	99±1.4	8.8	100±1.4	5.3	13.1±3.5	27.6	12.0±3.1	33.7	34.3	–2.3
subsp. *dicoccum* cv. Polba 3	87±4.2	–5.4	92±2.7	–4.2	19.1±4.1	15.5	14.2±3.8	3.6	—	—
subsp. *dicoccum* cv. Holikovs'ka	98±2.3	2.1	99±0.7	0.0	13.9±3.5	–11.6	11.1±4.2	3.8	37.8	0.1
subsp. *durum* cv. Spadshchyna	88±2.8	7.3	95±1.4	11.8	15.6±3.9	58.6	13.2±2.5	94.8	52.6	6.3
subsp. *aestivum* cv. Kharkivska 26	96±5.7	1.1	96±1.4	–3.0	13.1±2.8	0.5	8.1±2.1	–8.1	41.0	3.0
subsp. *spelta* cv. Frankenkorn	91±3.8	–6.2	96±0.3	–4.0	14.7±3.5	1.7	12.1±2.0	6.2	45.6	5.6
2016										
subsp. *monococcum*	98±0.0	-2.0	99±0.0	–1.0	11.5±1.9	–9.8	14.7±2.5	16.4	49.3	3.0
subsp. *sinskajae*	3±0.0	–96.8	10±0.0	–89.6	8.0±3.7	–39.8	7.3±2.2	–38.0	44.4	1.6
subsp. *dicoccum* cv. Polba 3	94±5.7	–6.0	97±3.5	–3.0	16.1±4.3	–2.3	15.2±3.1	18.5	40.7	–0.3
subsp. *dicoccum* cv. Holikovs'ka	63±10.6	–35.1	83±10.6	–14.4	15.0±3.0	4.3	12.4±2.6	35.0	36.7	–2.0
subsp. *durum* Spadshchyna	93±0.0	–5.1	95±0.0	–5.0	11.8±4.1	–29.2	12.9±3.0	14.7	31.4	–0.9
subsp. *aestivum* cv. Kharkivska 26	12±4.24	–87.9	15±7.1	–85.0	3.0±0.0	–80.5	1.5±0.7	–82.9	37.6	–7.1
subsp. *spelta* cv. Frankenkorn	68±11.3	–30.6	85±7.1	–15.0	14.9±4.2	–6.3	11.5±3.4	8.5	42.3	3.0

to 7.9% (Kharkivska 26, 2016). Moreover, in the seed grown in the less favorable 2014, AA was reduced (negative indices) to a greater extent in subsp. *sinskajae* (I = –7.4) and Holikovs'ka (I = –6.9) and were practically unchanged in subsp. *monococcum* (I = 0.0) and Spadshchyna (I = –0.8). In 2016, AA increased in all accessions, with the exception of the spelt Frankenkorn, where the index is negative, and the emmer Holikovs'ka, where it is nearly zero. A significant increase was observed in the AA in those accessions in which the length of the roots and sprouts significantly increased. The exception is Frankenkorn, where the increase in these indicators is associated with a decrease in AA.

When the seed was frozen in 2014, there was a tendency to positive connection AA with germination energy and germination rate, in 2016 with sprout length. In this option, no significant relationship with the indices of individual viability indicators was observed. Thus, in the case of freezing, AA does not play such a significant protector role for seed viability as in the case of accelerated aging.

The relationship between AA and traits of seed viability in the experimental variants was estimated by the coefficient of pair correlation (Table 9, p. 58). First of all, a close positive correlation with coefficient from 0.80 to 0.97 between AA in the control and AA in accelerated aging by Hampton & TeKrony (1995) and B.S. Lihachov (1978) at grain moisture content of 5% and 6%. This holds true for the seeds grown in the both years and suggests that the ranks of the accessions for AA in these experimental and control variants generally coincide. Consequently, the accessions with high AA levels in the control remained at this level after accelerated aging. Similarly, the accessions with low AA levels in control were characterized by a low level of this indicator after accelerated aging.

In the control for seed grown in the less favorable year 2014, the relationship between AA and all traits of the seed viability is negative;.for germination

Table 8. Seed viability indicators after freezing at –20°C.

Accession	Germination energy		Germination rate		Length of: root		Length of: sprout		Antiradical activity	
	%	Index	%	Index	cm	Index	cm	Index	%	Index
2014										
subsp. *monococcum*	97±4.2	–1.0	100±1.4	0.0	12.0±2.0	3.4	11.0±1.5	–5.8	38.5	0.0
subsp. *sinskajae*	95±0.7	4.4	99±0.0	4.2	14.7±1.7	44.0	11.1±2.1	24.0	32.5	–7.4
subsp. *dicoccum* cv. Polba 3	—	—	—	—	—	—	—	—	—	—
subsp. *dicoccum* cv. Holikovs'ka	99±2.3	3.1	100±1.4	1.0	16.9±2.4	7.1	11.5±2.9	8.0	35.2	–6.9
subsp. *durum* cv. Spadshchyna	99±5.7	20.7	100±1.4	17.6	13.7±2.5	39.1	12.5±2.9	84.4	49.1	–0.8
subsp. *aestivum* cv. Kharkivska 26	97±3.5	2.1	99±1.4	0.0	14.9±2.1	15.1	8.3±1.3	–6.1	38.8	–2.5
subsp. *spelta* cv. Frankenkorn	—	—	—	—	—	—	—	—	—	—
2016										
subsp. *monococcum*	100±0.0	0.0	100±0.0	0.0	16.5±2.9	29.4	16.9±1.7	33.8	51.1	6.6
subsp. *sinskajae*	90±0.0	–3.2	94±0.0	–2.1	16.6±2.2	24.8	16.9±2.1	44.4	45.7	4.5
subsp. *dicoccum* cv. Polba 3	99±0.0	–1.0	100±0.0	0.0	18.9±1.8	15.0	14.4±3.6	12.2	43.1	5.5
subsp. *dicoccum* cv. Holikovs'ka	96±0.0	–1.0	99±0.0	2.1	15.3±1.9	6.8	9.1±2.8	–0.5	37.1	–0.9
subsp. *durum* Spadshchyna	99±2.1	1.0	100±0.0	0.0	16.7±2.9	0.6	14.2±2.1	26.2	33.3	4.8
subsp. *aestivum* cv. Kharkivska 26	97±1.4	–2.0	99±2.1	–1.0	17.8±3.5	15.3	11.5±2.3	30.9	43.6	7.8
subsp. *spelta* cv. Frankenkorn	98±2.1	0.0	99±0.0	–1.0	18.1±3.9	13.9	13.1±2.6	23.6	38.0	–7.6

energy and rate, tightly negative (in both cases r = –0.74). In the 2016, the correlation was significant only for the root length (r = –0.73) and insignificant for the rest of the traits. Consequently, the seed samples with greater viability exhibit lower AA and vice versa. As an explanation, we can assume that less viable seed more actively mobilizes the antioxidant complex as a mechanism of resistance to oxidizing processes reducing viability.

For seed from 2014 in the variant with accelerated aging by Hampton and TeKrony (1995), the correlation between the AA and the germination energy, germination rate, and root length was positive and also tight (from 0.68 to 0.74), testifying to the effectiveness of AA as a mechanism of resistance to oxidative processes reducing seed viability. For seed of 2016, the correlation is insignificantly negative. In variants with accelerated aging using Lichachov's method for seed of 2014, humidity of 5% and 6% showed a negative AA bond with germination energy and rate. At a moisture content of 6%, the correlation coefficient was significant, –0.85 (energy) and –0.73 (rate). In both years, at 5% humidity, a positive average correlation took place between AA and germination energy and rate and sprout length (from 0.55 to 0.58). In seed of 2016, the link was also positive, although not significant. The negative correlation of AA with germination energy and rate in the variants of the experiment with accelerated aging by the Lichachov method for the seed grown in 2014 indicates the activation in seed of mechanisms of resistance to oxidative processes in stressful conditions, and this process is more active in a seed moisture level of 6% than of 5%.

Conclusions. In the control, the antioxidant activity of the seed grown in the 2014, with less favorable maturation conditions, was reciprocal to the more favorable 2016 (correlation coefficient of –0.65). In seed grown in 2014, the indices of the einkorns, subsps. *monococcum* and *sinskajae*, were low and relatively high in cultivars Polba 3, Spadshchyna, and Frankenkorn. For seed grown in 2016, the AA of the

Table 9. Coeffieients of pair correlation between seed antiradical activity (AA) and viability indicators of wheat accessions (2014 / 2016).

AA in experimental options	AA in control	Germination energy	Germination rate	Length of	
				root	sprout
Control	—	–0.74*/0.08	–0.74*/–0.07	–0.03/–0.73	–0.38/0.39
Accelerated aging by the method of Hampton & TeKrony	0.85*/0.85	0.68*/–0.21	0.71*/–0.24	0.74/–0.48	0.03/–0.22
Index of accelerated aging by method of Hampton & TeKrony to control	–0.27/–0.48	0.32/0.04	0.24/0.10	–0.47/–0.22	–0.68/–0.57
Accelerated aging by method of Likhachov at seed humidity of 5%	0.97*/0.80	–0.49/0.01	–0.44/0.00	–0.27/–0.65	–0.47/0.00
Index of accelerated aging by method of Likhachov at seed humidity of 5% to the control	0.08/–0.21	0.55*/0.42	0.58*/0.33	0.33/0.34	0.55*/–0.21
Accelerated aging by the method of Likhachov at seed humidity of 6%	0.94*/0.90	–0.85*/–0.04	–0.73*/0.01	0.89*/0.01	0.14/0.13
Index of accelerated aging by method of Likhachov at seed humidity of 6% to the control	0.08/–0.10	0.00/0.29	0.14/0.27	0.28/0.11	0.32/0.10
Freezing	0.50/0.13	0.61*/–0.16	0.50/–0.26	–0.39/0.17	0.33/0.58
Index of freezing to the control	0.62*/–0.02	0.23/0.14	0.27/0.03	–0.24/-0.02	0.16/–0.04

einkorns was the highest, whereas that of Frankenkorn and bread wheat approached that of Kharkivska 26. At the same time, the ranking of samples for each of the four viability indicators in 2014 did not match the ranking in 2016.

The accelerated aging by the Hampton and TeKrony (1995) method resulted in a decrease, compared with the control, of all four indicators of viability: germination energy, germination rate, root length, and sprout length. Moreover, in 2014, the degree of this decrease was lower than those in 2016. In a number of cases, a rather significant stimulating effect of accelerated aging concerned only in root and sprout length, but not in germination energy and rate. Accelerated aging by the method of Likhachov (1980), the moisture content of seed at 5%, as a whole, provides for greater longevity than at 6%. In the control, the seed samples with greater viability exhibit lower AA and vice versa. Thus, less viable seed is more actively mobilized antioxidant complex as a mechanism of resistance to oxidative processes that reduce viability.

Unlike the alternatives to accelerated aging, the relationship between AA in the control and that in the freezing option was insignificant, although positive. The effect of freezing at –20°C for 30 days on the seed of the accessions was different in degree but mostly positive. Most significant was the increase of all four indicators in the durum cultivar Spadshchyna in 2014 and the sprout length in 2016, root and sprout length in subsp. *sinskajae* in both years and in subsp. *monococcum* in 2016, root length in 2014 and root and sprout length in 2016 in Kharkivska 26, and root and sprout length in 2016 in Frankenkorn. Germination energy and rate of seed of all the accessions except Spadshchyna either did not change or changed very little; the absolute value of the index did not exceed 4.4%. However, in some cases, the indices were negative and small in absolute value. In only two cases was the decline significant (index approached –6%, subsp. *monococcum* and Kharkivska 26 for the sprout length in 2014. Overall, freezing had a more significant effect on the length of the root and sprout than on germination energy and rate of the seed. Freezing caused a decrease in AA in seed grown in 2014 (less favorable), but an increase in seeds of 2016. Under freezing conditions, AA does not play such a significant protector role for seed viability as under accelerated aging.

Antiradical activity in the control, closely and substantially positive (r = 0.80–0.97), correlates with AA in variants with accelerated aging by the methods of Hampton and TeKrony and Lihachov at seed moisture contents of 5% and 6%. This holds true for seed grown in both years and suggests that the ranking of the accessions for AA in the experimental and control variants generally coincide. In the variant with accelerated aging by the method of Hampton and TeKrony, in seed of 2014, the correlations between the AA and germination energy, rate, and root length were positive

and tight (from 0.68 to 0.74), showing the effectiveness of AA as a mechanism for confronting the oxidative processes that reduce seed viability. The negative correlation of AA with germination energy and rate in accelerated aging by the Lichachov method for the seed grown in 2014 indicates the activation of mechanisms of resistance to oxidative processes in stressful conditions, and this process is more active at a seed moisture of 6% than at 5%.

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Breeding value of spelt (Triticum aestivum subsp. spelta L.) accessions in the conditions of the east forest-steppe of Ukraine.

N.I. Kryshtopa, R.L. Boguslavskyi, and V.V. Liubych (Umanskyi National University of Horticulture).

Introduction. Among the underutilized wheat species, spelt is characterized by a combination of high quality for a healthy diet, suitability for organic farming (Osokina et al. 2018; Rustigi et al. 2018), and a relatively high grain yield potential (Winzeler et al. 1994; Poltoretskyi et al. 2018). Three spelt cultivars have been released in Ukraine, of which two are products of Ukrainian breeding, Zoria Ukrainy and Yevropa, and the other, Zollernspelz, was created in Germany (State Register of Plant Varieties 2019). Under the conditions of Ukraine, spelt grain yield can be 2.1–3.5 t/ha, and the protein content varies from 14.2 to 18.5% depending on the genotype and weather conditions (Hospodarenko et al. 2016; Osokina et al. 2018; Poltoretskyi et al. 2018). In addition, spelt plants are resistant or tolerant to leaf disease (Longin and Würschum 2014; Kiseleva et al. 2016). Improving the nutrition of people, especially those requiring a special diet, necessitates an increase in the grain production of this crop, primarily through breeding improvement. The success of spelt breeding is largely determined by the correct selection of source material. For Ukraine, the stability of economic and biological trait manifestation is important, along with the level of their manifestation. Valuable information also is provided by studying the relationship between traits in connection with the problem of combining valuable properties in a single genotype. Our purpose was to evaluate the breeding value of the genetic diversity in spelt accessions from the

collection of the National Plant Genebank of Ukraine in terms of the complex of economic and biological characteristics and select the source material for breeding of this crop.

Materials and methods. The materials for this research were accessions of the NPGU winter spelt collection, which is represented by 90 samples. The accessions were grown in a scientific crop rotation under the conditions of the eastern forest–steppe of Ukraine (Elitne, Kharkiv district, Kharkiv region). The soil is a black earth (chernozem), powerful, and weakly deployed. The spelt accessions were sown by spikelets, i.e., grain in hulls, by means of a hand-held sowing device. The parcel area was 1 m^2 with an inter-row width of 15 cm and a seeding rate of 500 grains/m^2 in four replications. The cultivar Frankenkorn served as the reference accession.

During the growing season, we determined the dates of shoots emergence, spike appearance, waxy grain ripeness, lodging hardiness, and resistance to disease for each accession. For diseases, Septoria, leaf and yellow rust, and powdery mildew, were scored during natural infections according to a 9-point scale (9 = highest resistance, 1 = least resistance) according to Meezhko et al. (1999).

The grain yield was determined in terms of dehulled grains. Protein content in grain was determined according to DSTU 4117: 2007, and the gluten content of and its quality (according to DSTU 21415-1:2005). The stability index SE was determined by the formula:

SE = HE / LE,

where: HE = the greatest manifestation of the trait and LE = the lowest manifestation of the trait.

For data analysis, methods of variation, dispersion, and correlation analysis were according Dospekvov (1985).

The research years differed in the main meteorological indicators during the vegetative period of the winter spelt; creating the proper conditions for an objective assessment of the collection for valuable economic and biological traits. In particular, overwintering conditions were favorable for spelt in both years of research. The vegetative period of 2017 was characterized as cool (the sum of effective temperatures was lower than the long-term average by 5–20°C) and not sufficiently moist (the precipitation amount in May and June was less than the long-term average by 6 and 43 mm, respectively). In 2018, at the beginning of the growing season (March), the amount of precipitation (109 mm) was four times that of the norm, but only twice that later in the season (April–July). As a result, the plants were strongly depressed and the yield of winter crops dropped sharply compared to other years.

Results. The **y**ield of spelt under conditions of Ukraine are generally quite high, on average, 443 g/m^2 in 2017 and 777 g/m^2 in 2018 (Table 10, p. 61). In 2018, the yield of the accessions was more than 1.5 times lower than that in 2017. The degree of this decrease was the highest, 2.1–3.1-times, for accessionsYevropa, Opushena 39/15, Rouquin, Kreuzung Dinkel, Forenza, and UA0300278, due to a long drought in 2018.

In each year of the study, approximately half of the accessions studied showed a significant excess compared with the reference accession Frankenkorn. In both years, the group that exceeded Frankenkorn included the accessions Yevropa, Zoria Ukrainy, Opushena 39/15, L 2018, Schwabenkorn, and Elsenegger Weisskorn. Of these six, four are of Ukrainian origin and the last two are German. A number of samples exceeded the reference in 2017 but not in 2018 (Evrika, NAK 34–1, NAK 18–2, Bregenzer Roter Spelz, Steiners Roter Tiroler, and Holstenkorn), and exceeded the reference in 2018 but not in 2017 (Kreuzung Dinkel, Forenza, Farnsburg 6, Rouquin, Rubiota, and UA0300278).

In terms of productivity elements, the highest 1,000-kernel weight (50.0–57.4 g) was found in lines UA0300431 (AZE), Opushena 39/15, Yevropa Krasnaya, Brauner Spelz (CHE), and Bauländer (DEU). The grain number/ear in Yevropa stood out at 55 grains and equal to that of the control were Opushena 39/15, NAK34-1 (UKR), and IR00500 (TJK). Grain weight/spike exceeded that of Frankenkorn in 2018 in Yevropa Krasnaya and Opushena 39/15.

Notable accessions for spike traits are Yevropa Krasnaya (exceeded the Frankenkorn reference in all productivity elements), Steiners Roter Tiroler (distinguished by spike length, 13 cm; spikelets/spike, 20; and 1,000-kernel weight, 45.1 g), NAK 34-1 (spike length, 15 cm; spikelets/spike, 21, and grain number/spike, 50); and Bauländer (1,000-kernel weigth, 48.1 g).

The grain yield significantly correlated with the number of spikes per unit area (r = 0.56 in 2017 and r= 0.64 in 2018) and grain weight/spike (*r* = 0.45 in 2017 and 0.50 in 2018).

Plant height of most winter spelt accessions of the European subspecies (subsp. *spelta*) is 110–157 cm. Among the tallest are Frankenkorn (DEU), Rothenburg 10 (DEU), Elsenegger Weisskorn (CHE), Forenza (ITA), Rubiota (ITA), and Europe (UKR). At the same time, lodging resistance was estimated at 6–8 points. Asian subspecies (subsp. *kuckuckianum*) UA0300580, UA0300583, although they have a shorter plant height (85–100 cm), are less resistant to lodging (4–5 points).

Table 10. Yield of winter spelt accessions (g/m^2).

Accession name	Country of origin	Years		2017 ± to 2018	SE
		2017	2018		
Frankenkorn (reference)	DEU	700	385	315	1.8
Yevropa	UKR	1,500	490	1,010	3.1
Evrika	UKR	685	607	78	1.1
NAK 18–2	UKR	630	513	117	1.2
NAK 34–1	UKR	650	525	125	1.2
Zoria Ukrainy	UKR	860	443	417	1.9
L 2018	UKR	960	502	458	1.9
Opushena 39/15	UKR	980	443	537	2.2
Bregenzer Roter Spelz	DEU	350	443	-93	1.3
Steiners Roter Tiroler	DEU	500	443	57	1.1
Renval	DEU	650	373	277	1.7
Bauländer	DEU	700	397	303	1.8
Rothenburg 10	DEU	700	408	292	1.7
Holstenkorn	DEU	710	443	267	1.6
Rouquin	DEU	750	350	400	2.1
Schwabenkorn	DEU	850	455	395	1.9
Kreuzung Dinkel	DEU	950	327	623	2.9
Brauner Spelz aus Schefflenz	CHE	700	408	292	1.7
Elsenegger Weisskorn	CHE	770	548	222	1.4
Farnsburg 6	CHE	770	373	397	2.1
UA0300076	GBR	983	607	376	1.6
Rubiota	ITA	750	408	342	1.8
Forenza	ITA	800	385	415	2.1
UA0300278	TJK	750	350	400	2.1
LSD_{05} for the factors	accession (genotype)				40
	year				46
	interaction accession / year				65

For disease resistance, powdery mildew reached an epidemic level in 2018; leaf rust, yellow rust and Septoria in 2018. Among the winter spelts, the highest level of group resistance to yellow and leaf rust (9) and Septoria (8) was observed in the cultivars Rubiota and Forenza (ITA), Frankenkorn and Schwabenkorn (DEU), Brauner Spelz aus Schefflenz (CHE), IR0050 (TJK), and Yevropa (UKR). High resistance to powdery mildew was found in Evrika and Yevropa (UKR), whereas Kreuzung Dinkel and Renval (DEU) were not resistant (5 points). Other collections of the European subspecies were relatively resistant (7 points). As the grain quality indicators, the content of protein and gluten was evaluated, on which the baking, groat, and confectionary properties of spelt grain depend.

Protein content varied widely, from 15.1 to 26.5% (Table 11, p. 62). Favorable weather conditions in 2017 led to a significantly higher protein content than in the less favorable year 2018. Gluten content in spelt grain was 33.2–59.3%, depending on the genotype and year. Cultivars Frankenkorn, Zoria Ukrainy, Rubiota, and UA0300278 are valuable for breeding for high-protein and high-gluten content, 21.2–25.8% (protein) and 47.0–57.6% (gluten). In addition, these cultivars are capable of grain yields up to 750 g/m^2.

The protein and gluten content of spelt accessions was stable; the SE was between 1.0 and 1.1 for all cultivars except Steiners Roter Tiroler (0.9). No correlation was found between yield or grain size and protein and gluten content of spelt accessions ($r < 0.04$). The gluten of most of the spelt samples studied is weak and flowing, making it unsuitable for baking, but more favorable for human absorption.

Conclusions. In the conditions of Ukraine, spelt cultivars with high and stable yield capacity were identified: Yevropa, Zoria Ukrainy, Opushena 39/15, L 2018, Schwabenkorn, and Elsenegger Weisskorn. The grain yield significantly cor-

Table 11. Content of protein and gluten in spelt grain (%).

Accession name	Country of origin	Protein content			Gluten content		
		2017	2018	average	2017	2018	average
Frankenkorn (reference)	DEU	21.8	20.6	21.2	49.0	45.0	47.0
Yevropa	UKR	17.3	16.4	16.9	38.8	36.2	37.5
Evrika	UKR	19.1	19.0	19.1	42.5	41.9	42.2
NAK 18–2	UKR	17.5	16.2	16.9	38.5	34.6	36.6
NAK 34–1	UKR	18.8	16.9	17.9	41.7	37.2	39.5
Zoria Ukrainy	UKR	24.5	24.1	24.3	54.2	53.5	53.9
L2018	UKR	18.0	17.3	17.7	39.1	37.1	38.1
Opushena 39/15	UKR	20.5	19.6	20.1	45.3	43.2	44.3
Bregenzer Roter Spelz	DEU	17.4	17.0	17.2	38.8	37.4	38.1
Steiners Roter Tiroler	DEU	17.0	18.5	17.8	37.7	40.7	39.2
Renval	DEU	15.9	15.3	15.6	35.2	33.7	34.5
Bauländer	DEU	16.5	15.3	15.9	36.3	33.7	35.0
Rothenburg 10	DEU	15.1	14.6	14.9	33.3	32.4	32.9
Holstenkorn	DEU	16.6	16.0	16.3	36.1	35.4	35.8
Rouquin	DEU	18.4	17.0	17.7	40.9	37.3	39.1
Schwabenkorn	DEU	15.5	14.9	15.2	35.1	32.7	33.9
Kreuzung Dinkel	DEU	15.1	14.8	15.0	33.2	32.2	32.7
Brauner Spelz aus Schefflenz	CHE	17.3	16.4	16.9	39.1	35.5	37.3
Elsenegger Weisskorn	CHE	19.9	19.2	19.6	43.8	42.8	43.3
Farnsburg 6	CHE	15.5	14.3	14.9	34.7	31.6	33.2
UA0300076	GBR	18.5	17.4	18.0	40.7	38.3	39.5
Rubiota	ITA	26.5	25.1	25.8	59.3	55.8	57.6
Forenza	ITA	20.2	19.5	19.9	46.4	42.7	44.6
UA0300278	TJK	22.7	22.2	22.5	49.9	48.9	49.4
LSD_{05} for the factors	accession (genotype)	0.6			1.3		
	year	0.3			0.7		
	interaction accession / year	0.9			1.9		

related with the number of spikes per unit area ($r = 0.56$ in 2017 and $r = 0.64$ in 2018) and grain weight/spike ($r = 0.45$ in 2017 and 0.50 in 2018). The largest 1,000-kernel weights (50.0–57.4 g) were in lines UA0300431 (AZE); Opushena 39/15, Yevropa Krasnaya, and Brauner Spelz (CHE); and Bauländer (DEU). Accession Yevropa Krasnaya exceeded the Frankenkorn reference in all productivity elements. The highest level of resistance (8–9) to yellow and leaf rusts and Septoria was observed in the cultivars Rubiota and Forenza (ITA), Frankenkorn and Schwabenkorn (DEU), Brauner Spelz aus Schefflenz (CHE), IR0050 (TJK), and Yevropa (UKR). Valuable for breeding in terms of high-protein and high-gluten content are the cultivars Frankenkorn, Zoria Ukrainy, Rubiota, and UA0300278, 21.2–25.8% (protein) and 47.0–57.6% (gluten). No correlation was found between yield or grain size and protein and gluten content for of any of the spelt accessions ($r < 0.04$). The gluten of most of the spelt samples studied is weak, flowing.

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Brachypodium distachyon identified as potential surrogate model for functional characterization of Hessian fly-responsive defense genes in wheat.

Subhashree Subramanyam.

The Hessian fly (*Mayetiola destructor*) is a destructive pest of wheat causing severe economic damage. Deployment of Hessian fly (Hf) resistance (*H*) genes is the most effective way to manage the dipteran insect pest. However, the use of *H*-gene resistance results in selection pressure on Hf biotypes resulting in breakdown of deployed resistance. Utilization of Hf-responsive defense genes in a transgene approach offers an alternate pathway to complement native or introgressed *H*-gene resistance in wheat. Despite identification of numerous Hf-responsive genes by various expression profiling methods, such as RNA-Seq, Affymetrix, and qRT-PCR in wheat, further functional analyses of these defense genes through supplementation and/or mutational approaches are challenging due to the complexity of the wheat genome (hexaploid), and limited genetic and genomic resources. Physically, *Brachypodium distachyon* (Bd) exhibits nonhost resistance to Hf, and with a small genome size (diploid), short life cycle, vast genetic resources and amenability to transformation, it offers an alternate functional genomic model for deciphering plant–Hf interactions.

Global transcriptome expression profiling was used to reveal thousands of Hf-responsive genes in Bd at 1, 3, and 5 days after egg-hatch (DAH). Bd plants launched an early defense response on multiple fronts through the transcriptional activation of some classes of anti-pathogen transcription factors (TFs), initiation of hypersensitive response by generation of reactive oxygen species, production of insecticidal and antifeedant lectins, secondary metabolites, signaling molecules, and protease inhibitors countering larval extra-oral salivary plant cell-degrading proteases (Fig. 1, p. 64). These defense responses (DR) are similar to the ones observed in resistant host wheat against Hf. At the same time, other molecular mechanisms comparable to those in susceptible host wheat are activated by Hf larval feeding including early

activation of certain TFs known to be associated with susceptibility and a suppression of other TFs that play crucial roles in defense.

In addition, at later time-points, transcripts for genes encoding small heat shock proteins and signal transduction, also associated with susceptibility, were increased along with up-regulation of cytokinins that potentially help establish nutrient centers for the larvae, and the down-regulation of genes involved in cell wall fortification that acts as a barrier to the feeding larvae. An extended expression of DR genes in Bd plants temporally over-lapped responses linked to susceptibility and promoted intermediate physical and metabolic responses between resistant and susceptible phenotypes seen in host wheat. Our data reveal some of the molecular mechanisms that contribute to the ultimate battle for survival of a nonhost against an insect pest. It also confirms the suitability of Bd as a model genome for future work involving functional studies of candidate Hf-responsive genes that will aid in crop improvement strategies to increase resistance against this and other insect pests, and thereby prolong the durability of wheat cultivars in the field, benefitting breeders and farmers.

Publication.

Subramanyam S, Nemacheck JA, Hargarten AM, Sardesai N, Schemerhorn BJ, and Williams CE. 2019. Multiple molecular defense strategies in *Brachypodium distachyon* surmount Hessian fly (*Mayetiola destructor*) larvae-induced susceptibility for plant survival. Sci Rep **9**:2596. [https://www.nature.com/articles/s41598-019-39615-2]

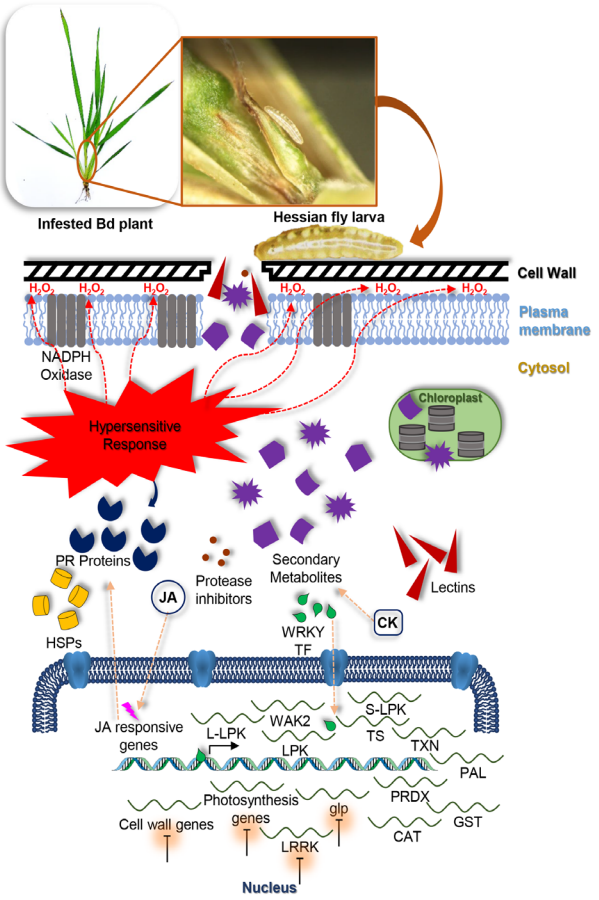

Fig. 1. Model showing the major pathways involved during *Brachypodium*-Hessian fly interactions. Damage to cell wall and membrane by Hessian fly larval feeding triggers the production of a hypersensitive response resulting in the production of ROS such as H_2O_2 through the action of NADPH oxidase. Multiple defense strategies are mounted simultaneously. Jasmonic acid (JA)-responsive genes are induced leading to up-regulation of PR proteins. Various transcription factors (TF) such as WRKY trigger defense response genes such as different kinases, lectins, and protease inhibitors, while a number of photosynthesis and cell wall-associated genes are repressed resulting in delayed or suppressed cell wall fortification. Increased cytokinins (CK) induce secondary metabolite formation that may directly affect the survivability of the larvae. Some defense-responsive heat shock proteins (HSPs) play a role in resistance to the larvae, whereas some small HSPs induce susceptibility. WAK2: wall-associated kinase 2, SRK: s-locus protein kinase, CLK: conA lectin-like kinase, LPK: lectin protein kinase, LRRK: leucine rich repeat kinase, glp: germin-like protein, CAT: catalase, PRDX: peroxiredoxin, TXN: thioredoxin, GST: glutathione-S-transferase, TS: tryptophan synthase, PAL: phenylalanine ammonia lyase.

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

Seed size and cold tolerance.

Reshma Moolakkal Antony and M.B. Kirkham.

The past year involved publishing results of an experiment investigating the cold tolerance of seedlings of two cereals, sorghum (*Sorghum bicolor* (L.) Moench) and maize (*Zea mays* L.) (Antony et al. 2019). Five commercial hybrids of maize and 18 genotypes of sorghum were maintained in growth chambers for 31 days at two temperatures: a control air temperature (25/20°C, day/night) and cold air temperatures (11/8°C for 14 days; 12.5/9.5°C for 14 days; and 14/11°C for 3 days). Plants grew under well-watered conditions in pots with a fertilized horticultural mix. In the control chambers, the control air and soil temperatures were about the same. In the cold chambers, soil temperatures were 0.6°C and 0.4°C warmer than air during the day and night, respectively. No plants emerged at the coldest temperatures. Both maize and sorghum began to emerge when the air temperature was 12.5/9.5°C. Emergence of sorghum under the cold temperatures was low (18%), and average height of the emerged seedlings at the end of the experiment was 1.4 cm compared to 55.5 cm in the control treatment. Under the cold temperatures, all maize hybrids emerged by the end of the experiment. Growth of maize was slowed by the cold temperatures, the average height of the hybrids at the end of the experiment was 4.6 cm compared to 96.1 cm in the control treatment. Mean widths of the maize and sorghum seeds were 7.9 mm and 2.6 mm, respectively. Maize was found to be more cold-temperature tolerant than sorghum, perhaps due, in part, to its larger seed size.

The research has relevance to wheat. For decades, it has been known that the number of ears per plant and yield per plant are much greater from large wheat seeds than from small wheat seeds (Percival 1921, p. 425-427). However, the relationship between seed size of wheat and its cold tolerance is less well known. Studies of wheat seed size and cold tolerance should be carried out.

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Book edited.

The past year also has involved editing a book entitled *Global Soil Proverbs: Cultural Language of the Soil* by Yang JE, Kirkham MB, Lal R, and Huber S, Eds, 2018, Catena-Schweizerbart, Stuttgart, Germany, xv + 275 p. Every country has a vast archive of proverbs that has been transferred orally from generation to generation. The very name 'proverb' indicates that they originated 'before' (Latin, pro) the written 'word' (Latin, verbum). Ever since our ancestors settled down and started to farm the soil, proverbs have been used to communicate knowledge. Many proverbs about soils are available globally, but no effort has been made to compile them into a comprehensive book. The objective of *Global Soil Proverbs: Cultural Language of the Soil* is to collect soil proverbs from around the world, and through them, share insights about philosophy, culture, and life in each country, as they relate to soils and the crops that grow on them. The book has 32 chapters from 29 different countries. Many of the proverbs relate to wheat. The index lists 27 pages on which wheat is mentioned in a proverb.

News.

Reshma M. Antony, graduate student in the Department of Agronomy at Kansas State University, graduated in December, 2018, and now is working as a Laboratory Research Specialist at MSBiotec, 1300 Kaw Valley Road, Wamego, KS 66547.

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

The road to chromosome-wide enhancement of genetic recombination in wheat.

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

Gene transfer from wild wheat relatives to bread wheat cannot be achieved by homologous recombination, because the *Ph1* gene on chromosome arm 5BL allows only homologous chromosomes to pair and recombine. The deletion of the *Ph1* gene in the *ph1b* mutant stock allows homoeologous wheat and distantly related chromosomes to pair and recombine. However, *ph1b*-induced recombination is low and usually restricted to distal regions of chromosomes. We have identified chromosome $5M^g$ from *Aegilops geniculata*, which escapes diploid-pairing control and freely recombines with wheat in the presence of *Ph1*, even in proximal chromosome regions where recombination is usually suppressed. Furthermore, in the absence of *Ph1*, chromosome $5M^g$ led to a vast genome-wide increase in homoeologous recombination, including the proximal regions of chromosomes. Our results demonstrate that chromosome $5M^g$ can be used in wheat crop improvement by increasing homoeologous recombination between wheat and wild wheat relatives.

Extrachromosomal DNA-mediated herbicide resistance.

Dal-Hoe Koo, Mithila Jugulam, Bernd Friebe, and Bikram S. Gill.

Evolution of herbicide resistance in weed species is a major constraint to crop production around the globe. Many agriculturally important weed species throughout the world have naturally evolved resistance to several major herbicides used in our agriculture. The investigation of physiological, genetic, and molecular mechanisms of weed resistance to herbicides have uncovered several novel, and exciting results related to fundamental, evolutionary mechanisms of herbicide resistance in weeds, specifically, regarding the evolution of resistance to glyphosate, one of the important herbicides used in crop production. With the introduction and wide acceptance of Roundup Ready crops in many countries, glyphosate

has been used extensively for weed control, consequently, many weeds have developed resistance to glyphosate. The target site of glyphosate is 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), an important enzyme in shikimate pathway. Several types of mutations including amplification of EPSPS gene can bestow weed resistance to this herbicide. Recently, our molecular cytogenetic research indicated that the EPSPS gene amplification in glyphosate-resistant Palmer amaranth (*Amaranthus palmeri*), one of the top problem weeds of the USA, was driven by extra-chromosomal, circular DNA (eccDNA) molecules. Each eccDNA carried one copy of the target gene EPSPS. However, freed from the rules of mitosis, EPSPS genes can multiply rapidly during the growth of the sporophyte and produce copy number variation in somatic cells. The somatic cells with amplified EPSPS survive in the presence of the herbicide, and this acquired trait is transmitted to the germ cells and the progeny. Importantly, eccDNA replicons appear to be transmitted by an unknown mechanism of tethering to mitotic and meiotic chromosomes and modulate rapid glyphosate resistance response.

Towards a futuristic, elite crop–crop wild relative germplasm enhancement program.

Bikram S Gill, W John Raupp, Duane L Wilson, Hannah Shult, Dal-Hoe Koo, Narinder Singh, Allan K. Fritz, Mary Guttieri (USDA–ARS, Manhattan, KS), Jesse Poland, and Bernd Friebe.

Crop wild relatives (CWRs) will play a major role as we face the challenge of feeding 9 x 10^6 people by 2050 under reduced water and fertilizer inputs, soil degradation, and a warming planet producing episodes of extreme weather. Anecdotal evidence suggests that, in the last few years, breeder's nurseries have suffered a massive loss of breeding material because extreme weather, including cold, heat, and drought, disrupts crop adaptation and phenology or spawns new pest epidemics. Over millennia, CWRs, having been exposed to climate extremes and disease epidemics and evolved adaptive traits, will be one important source of novel traits. However, in the Anthropocene era, we also are witnessing a massive genetic erosion of CWRs in native agroecosystems and, thus, we also must deal with challenge of conserving CWRs in nature as genetic reservoirs for future agriculture (Gill et al. 2014). Here we present a framework for a comprehensive program of CWR management, conservation, and utilization for crop germplasm enhancement for wheat.

CWR diversity analysis, unique and core sets. The first urgent task is a diversity analysis of CWR collections in gene banks for more efficient curation and identification of unique (nonredundant) sets of georeferenced accessions for each CWR species of the primary, secondary, and tertiary gene pools (Amri et al. 2016; Singh et al. 2019a). The second task is to develop core sets of accessions capturing greater than 90% of the diversity of each CWR species. Recently, using genotyping-by-sequencing (GBS), we identified unique and core sets of accessions for *Triticum turgidum* and *timopheevii* and *Aegilops tauschii*, the primary gene pool of *T. aestivum* (Singh et al. 2019a, b; unpublished results). This data also has been used to pinpoint the center of genetic diversity for each species as a guide for future conservation and utilization in prebreeding.

As an example, we analyzed the working collection of 549 *Ae. tauschii* accessions maintained by the Wheat Genetics Resource Center at Kansas State and found 26% duplicates and identified 421 unique accessions. At CIMMYT, 43% of the accessions were duplicated and the collection at Punjab Agricultural University (PAU) had 54% duplication. Because substantial portions of PAU and CIMMYT collections came from the WGRC, we were able to cross reference passport data. Overall, we identified 564 unique accessions among the three gene banks. We were able to impute passport information from genotypic data, including geographic origin for collections of unknown origin. In addition, we were able to evaluate genetic diversity of a set of newly collected *Ae. tauschii*; 36 of 44 new collections were unique, seven were duplicates, and one was identical to a previously collected unique set. This foundation data set and methodology (see Singh et al. 2019a) can be extended to *Ae. tauschii* holdings in other gene banks to identify a truly unique, world collection of *Ae. tauschii* for efficient curation, conservation, and prebreeding.

The GBS data set (Singh et al. 2019b) also confirmed previous reports (Lubbers et al. 1991; Wang et al. 2013) on the incipient speciation of *Ae. tauschii* into lineages L1 (form *tauschii*) and L2 (form *strangulata*). Caspian Iran is the center of diversity and origin of *Ae. tauschii* where both lineages coexist; L2 at lower elevations and L1 at higher elevations. Afghanistan is the center of diversity for L1. GBS data, along with phenotypic data, was used to identify a core set of 40 *Ae. tauschii* accessions, 11 from L2 and 29 from L1, capturing 84% of genetic diversity of the species (Singh et al. 2019b). Because the D genome of *T. aestivum* originated from L2 lineage, the 29 L1 accessions represent new genetic diversity for wheat improvement.

Evaluation of unique CWR sets for phenotypic traits for hot spots of genetic diversity for each trait. Climatic, edaphic, and many other factors have shaped the adaptive evolution of each of the CWR species. The Focused Identification of Germplasm Strategy (FIGS, Bari et al. 2012) and experimental evaluation of CWRs, among others, should be used to identify hot spots of genetic diversity for specific traits. We have good evaluation data for *Ae. tauschii* for disease and insect resistance (our unpublished results). The L2 lineage in Caspian Iran is a hot spot for genetic diversity for seedling resistance to leaf rust, whereas adult-plant resistance to leaf rust is restricted to L1 lines in Afghanistan. Lineage 2 also has resistance to the wheat curl mite. Both lineages include accessions resistant to stripe rust, Septoria, Hessian fly and greenbug.

Germplasm enhancement strategies using primary gene pool CWR species. Genetic transfers from primary gene pool species, *T. turgidum* and *Ae. tauschii,* can be made by direct crosses and backcrosses with *T. aestivum* (McFadden 1927; Gill and Raupp 1987). The most widely used approach is the production of synthetic wheat by crossing *T. turgidum* with *Ae. tauschii* (McFadden and Sears 1946). We are producing 'super-wild' synthetic wheats from hybridization of core set accessions of *T. turgidum* subsp. *dicoccoides* and *Ae. tauschii*. A third approach, using a bridge-cross scheme, is through the production of octoploids (AABBDDDD) by colchicine doubling of *T. aestivum*/*Ae tauschii* (ABDD) F_1 hybrids (discussed in Singh et al. 2019b; see also Zhang et al. 2018). We are using this strategy for genetic transfers from *Ae. tauschii* via octoploid amphiploids, followed by backcrossing with elite wheat recurrent parents (Fritz AK, unpublished results). We are transferring genes from the *T. turgidum* core set by direct crosses with *T. aestivum* cultivars, followed by backcrosses of F_1 hybrids with elite wheat genotypes (Gutteri M, unpublished results).

Germplasm enhancement strategies using secondary gene pool CWR species. The secondary gene pool CWR species of *T. aestivum* include three *Triticum* species: *T. timopheevii* (A^tA^tGG), *T. monococcum* subsp. *aegilopoides* (A^m), and *T. urartu* (A^u). Although the A genome of polyploid *Triticum* species traces to *T. urartu*, certain species-specific translocations (T4A–5A–7B) in *T. turgidum* and *T. aestivum* and others (T6A–1G–4G) in *T. timopheevii* preclude recombination and, hence, genetic transfers involving these chromosomes. In addition, formidable hybridization barriers, including hybrid seed abortion, hybrid embryo lethality, and floral defects of the ovary and stamens in F_1 hybrids preclude genetic transfers from many accessions of *T. monococcum* and *T. urartu* (Cox et al. 1991).

The polyploid, D-genome cluster species of *Aegilops*, such as *Ae. cylindirica* (CCDD), *Ae. crassa* (DDMM and DDMMM), *Ae. juvenalis* (DDMMUU), and *Ae. ventricosa* (DDNN) also constitute the secondary gene pool of wheat as they share the D-genome. The D-genome of *T. aestivum* has no known chromosomal rearrangements, but similar information is not available for the D-genome chromosomes of polyploid *Aegilops* species. However, most chromosomes are accessible for genetic transfers by recombination.

Germplasm enhancement strategies using tertiary gene pool CWR species. Polyploid *Aegilops* species of the secondary gene pool that also contain an additional genome(s) other than A or D; all other diploid and polyploid *Aegilops* species that carry genomes other than A, B, or D, including all other genera; and species of the Triticeae tribe constitute the tertiary gene pool of wheat. The *Ph1* gene does not allow pairing among the homoeologous chromosomes of A, B, or D genomes of polyploid wheats (Riley and Chapman 1958) and also those of the homoeologous chromosomes of the tertiary gene pool species. Broadly, two general methods, one interfering with the homoeologous recombination system (Riley et al. 1968; Sears 1977) and the second using irradiation (Sears 1956) have been used for accessing genes from the tertiary gene pool species (for review see Qi et al. 2007; Lukaszewski 2016).

As a rule, induced homoeologous recombination is the method of choice because genetically compensating wheat/alien segments are exchanged. However, irradiation is a back-up method in those instances where either the alien (CWR) chromosome is structurally rearranged and, hence, is no longer competent for synapsis and homoeologous recombination with a wheat chromosome or if the target gene is located in a proximal (centromeric) region where recombination is highly suppressed.

Recently, we have a discovered a homoeologous pairing promoter factor(s) on chromosome $5M^g$ of *Ae. geniculata* (*Hpp5M*^{g}) that greatly enhanced homoeologous recombination in plants that are lacking *Ph1* (our unpublished results). Moreover, homoeologous recombination is also observed in proximal regions where even homologous recombination is suppressed.

Cryptic alien transfers. Anecdotal reports have suggested transfer of target genes in wheat/alien derivatives although the transfers could not be experimentally verified in earlier experiments. Kuraparthy et al. (2007, 2009) reported cryp-

tic transfers of leaf rust resistance gene *Lr58* from *Ae. triuncialis* and *Lr57*/*Yr40* genes from *Ae. geniculata*. They were not able to verify the transfers by GISH but did detect them using molecular markers at the tip of the chromosomes, which are known to be recombination hot spots. Using a more sensitive GISH technique, we could later visualise the *Ae. geniculata* segment at the telomere of the short arm of chromosome 5D (Zhang et al. 2015). We now know that the *Ph1* gene is leaky, and the *Ph1* effect can be suppressed in specific hybrid combinations (Koo et al. 2017). A second source of cryptic variation may be non-crossover recombination leading to transfer of small interstitial alien segments (our unpublished results). Finally, another source of cryptic variation may be recently discovered eccDNA elements, where genes can escape from chromosomes and exist as autonomously replicating circular or episomal DNA elements, which are inherited in the progeny (Koo et al. 2018).

***In situ* and *ex situ* conservation and germplasm enhancement.** Agriculture began in centers of origins of crop plants from domestication of CWRs in the so-called 'Gardens of Eden' or native agroecosystems. The rich natural CWR genetic diversity broadened the crop genetic base through spontaneous hybridization and selection. An expanding human population and area under agriculture have greatly eroded CWRs. Fortunately, we have done a good job of *ex situ* conservation of CWRs. However, we must address the critical issue of *in situ* conservation of CWRs as future reservoirs of genetic diversity moulded by climate change and global warming. Wilson (2016) has argued that we need half of the earth to conserve nature for a sustainable planet. Hundreds and thousands of CWR species are native to centers of origin of crop plants. The *in situ* conservation of all the CWRs in these centers of origin of crop plants should be considered a number one food security issue of the 21st century. Perhaps native habitat loss is so great that such a project is not even feasible. We must then attempt to tackle the thorny issue of rewilding of CWRs in non-native countries, such as the Great Plains of the USA and other similar regions of the world.

Futuristic germplasm enhancement programs. Advances in genotyping, phenotyping, and sexual biology (crossability/fertilization/meiosis/recombination) open immense possibilities of accessing great genetic diversity of CWRs. The WGRC research in genetics, germplasm enhancement, and graduate education can perhaps serve as a great model; multidisciplinary, multinational in which university, federal, industry, and more importantly wheat growers have ownership. For each CWR, we need to establish across gene banks a set of the world's unique accessions with accurate passport data as demonstrated for *Ae. tauschii*. These unique CWR sets should be focus of *ex situ* and *in situ* conservation, phenotyping, and germplasm enhancement. Core sets should be identified for each CWR species and immortalized as amphiploids. We have accomplished this for *Ae. tauschii* by producing 11 amphiploids involving 8 of the 40 accessions of the core set. For the species of the tertiary gene pool, amphiploids will be used to isolate sets of Robertsonian translocations for evaluation and chromosome engineering (Qi et al. 2007). Bulk populations of the core sets, amphiploids, and Robertsonian translocation (alien translocation lines) may be grown in garden plots across wheat-growing regions as genetic reservoirs for near and future germplasm enhancement.

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Evaluation of A-genome species for pest resistance and agronomic traits in the greenhouse and field.

Duane L. Wilson and W. John Raupp.

We selected 111 lines from the three A-genome species, *Triticum monococcum* subsps. *monococcum* and *aegilopoides* and *T. urartu* from diverse geographical distribution, for evaluation in the greenhouse and field for seedling leaf and stem rust, BYDV, heading date, and staygreen ability (Table 1, pp. 71-74). This project continues our efforts to identify wheat crop wild relatives that may be useful for breeding programs.

Resistance for a single disease or a beneficial trait was identified in about 25% of the accessions tested. Multiple resistance was found in seven accessions, all having leaf and stripe rust resistance (TA2004, TA2702, TA10568, TA10636, TA10651, TA10656, and TA10909). Two accessions had resistance to leaf rust and reduced BYDV infection (TA 307 and TA10587) with one accession resistant to stripe rust and BYDV (TA 10900). *T. monococcum* subsp. *monococcum* line TA10581 is resistant to leaf rust, stripe rust, and BYDV, and stayed green after maturing. Continued field and greenhouse screening in 2019–20 will increase our confidence in having the better information for the wheat breeding community.

Table 1. Ratings of A-genome species, *Triticum monococcum* subsps. *monococcum* and *aegilopoides* and *T. urartu*. Disease severity in the greenhouse (adult-plant leaf (culture LrComp19) and seedling stripe (culture Yr12-9.1) rust) and in the field (leaf rust and barley yellow dwarf virus (BYDV)), Manhattan, KS, during the 2018–19 crop season. Heading date and stay-green ability also were recorded. Leaf rust was evaluated using the Cobb scale, where a number indicating the percent of leaf area affected is followed by a letter designation, R = resistant flecks or very small pustules, MR = moderately resistant, small pustules, M = moderate, small to medium size pustules, MS = moderately susceptible, medium to large pustules, and S = susceptible, with large pustules. Rating of the leaves with BYDV symptoms was 0 = no visible signs of infection, L = low infection with 10% or less of the leaf area with visible symptoms, M = moderate infection with up to 40% of the leaf area with visible symptoms, and H = high infection with over 40% of the leaf area showing symptoms. — = no test. Seedling stripe rust reactions were scored in the greenhouse; the seedling test is a 0–4 scale with ;–2 resistant, 2+–3- intermediate, and 3–4 susceptible. Stay-green ablility was recorded when ~50% of the lines had reached physiological maturity; G = green leaves, I = dry leaves with partially green spikes; and D = plants completely dry.

Line #	Species/ subspecies	Country of origin	Greenhouse		Field			
			Leaf rust	Stem rust	Heading date	BYDV	Leaf rust	Staygreen
TA136	*monococcum*	Sweden	10R–20R	3–3+	5–7 June	L–M	15MR–20MR	G
TA137	*monococcum*	Turkey	20R–30MR	3+–4	16–26 June	M–H	15MR–20MR	G–I
TA139	*monococcum*	Russian Federation	20R–40MR	3+–4	14–28 June	M–H	20MR–20M	G–D
TA142	*monococcum*	Bosnia–Herzegovina	10R–10MR	2+–3	6–19-June	M–H	20MR	G–I
TA176	*aegilopoides*	Iran	40S–50S	3–3+	28 May–3 June	M–H	30MR–30M	D
TA177	*aegilopoides*	Iraq	30MS–50M	3–4	1–14 June	M	20MR	I
TA179	*aegilopoides*	Turkey	20MR–50M	1–1+	20 June	M	10MR	I
TA182	*aegilopoides*	Iran	10R–30M	2- –3	2–4 June	M–H	20MR–20M	D
TA185	*aegilopoides*	Iran	20MR–30MR	2–3-	3–17 June	M–H	20MR–30M	D
TA191	*aegilopoides*	Iran	10R–10MR	2–3+	31 May–2 June	M–H	20MR	D
TA197	*aegilopoides*	Iran	15MR–30MS	3+	28 May–1 June	H	15R–20MR	D
TA198	*aegilopoides*	Lebanon	20MR–40M	3+–4	2–18 June	M	10MR–20M	I
TA199	*aegilopoides*	Azerbaijan	30MS–40MS	2	3–6 June	M	10MR–20M	I
TA200	*aegilopoides*	Iraq	30MR–40M	2+–3	28 May–3 June	M	20MR	I–D
TA204	*aegilopoides*	Turkey	30MS–50MS	3–4	6–19 June	M–H	30MR	I–D
TA211	*aegilopoides*	Iraq	10R	3	28 May–2 June	H	30M	D
TA261	*aegilopoides*	Turkey	15M–20M	3	5–14 June	M–H	15MR–30M	I
TA271	*aegilopoides*	Iraq	10MR–30MR	2–3	30 May–3 June	H	20MR–30MR	D
TA290	*aegilopoides*	Iraq	20MR–40M	4	1–7 June	H	20MR	D
TA307	*aegilopoides*	Iraq	10R–10MR	3–4	1–3 June	L–M	15MR–20MR	I
TA315	*aegilopoides*	Iraq	20R–50M	4	3–5 June	M–H	20MR–20M	I
TA351	*aegilopoides*	Iraq	30MS–60MS	3–4	27–31 May	M–H	20MR–30MR	D
TA366	*aegilopoides*	Iraq	10R–30M	3–4	28 May–1 June	M	20MR	I–D
TA391	*aegilopoides*	Iraq	20M–30M	3–3+	31 May–3 June	M	20MR–20M	I–D
TA520	*aegilopoides*	Turkey	10R–40M	2+–3	3–5 June	M–H	15MR–20M	D
TA570	*aegilopoides*	Azerbaijan	50S–70S	2–2+	5–7 June	M–H	20M–30M	I
TA582	*aegilopoides*	Armenia	60S–80S	2- –3	4–6 June	M–H	30MR–30MS	I
TA664	*aegilopoides*	Turkey	20MR–30M	3- –3	31 May–5 June	H	20MR–20M	I–D
TA704	*urartu*	Turkey	30S–70S	3+–4	29 May	H	30MR	D
TA709	*urartu*	Turkey	50MS–60S	3–3+	29 May–1 June	M–H	15MR–20MR	D
TA711	*urartu*	Turkey	40S–50S	3+–4	1 June	H	20M	D
TA729	*urartu*	Turkey	50MS–50S	2+–3+	27–31 May	M–H	15MR–20MR	D
TA736	*urartu*	Turkey	30M–60S	1+–2-	18 May–2 June	M–H	10MR–20M	D
TA751	*urartu*	Turkey	50S	3+	1–6 June	H	20M–30M	D

Table 1. Ratings of A-genome species, *Triticum monococcum* subsps. *monococcum* and *aegilopoides* and *T. urartu*. Disease severity in the greenhouse (adult-plant leaf (culture LrComp19) and seedling stripe (culture Yr12-9.1) rust) and in the field (leaf rust and barley yellow dwarf virus (BYDV)), Manhattan, KS, during the 2018–19 crop season. Heading date and stay-green ability also were recorded. Leaf rust was evaluated using the Cobb scale, where a number indicating the percent of leaf area affected is followed by a letter designation, R = resistant flecks or very small pustules, MR = moderately resistant, small pustules, M = moderate, small to medium size pustules, MS = moderately susceptible, medium to large pustules, and S = susceptible, with large pustules. Rating of the leaves with BYDV symptoms was 0 = no visible signs of infection, L = low infection with 10% or less of the leaf area with visible symptoms, M = moderate infection with up to 40% of the leaf area with visible symptoms, and H = high infection with over 40% of the leaf area showing symptoms. — = no test. Seedling stripe rust reactions were scored in the greenhouse; the seedling test is a 0–4 scale with ;–2 resistant, 2+–3- intermediate, and 3–4 susceptible. Stay-green ablility was recorded when ~50% of the lines had reached physiological maturity; G = green leaves, I = dry leaves with partially green spikes; and D = plants completely dry.

Line #	Species/ subspecies	Country of origin	Greenhouse		Field			
			Leaf rust	Stem rust	Heading date	BYDV	Leaf rust	Staygreen
TA763	*urartu*	Lebanon	15MR–40M	2–2+	5–7 June	M	15MR–20MR	D
TA771	*urartu*	Lebanon	30M–40M	3+–4	22 June	M–H	10R–20MR	I–D
TA786	*urartu*	Lebanon	20MS–40S	3+–4	5 June	M	20MR	I
TA787	*urartu*	Lebanon	40MS–60M	2+–3+	18 June	M	15R–20M	I–D
TA792	*urartu*	Lebanon	40MR–80MS	4	7–17 June	M	10R–20M	G–I
TA795	*urartu*	Lebanon	20MR–40M	4	5 June	M	15MR	I
TA806	*urartu*	Turkey	50MS–60S	3+	3–17 Jun	M–H	20MR–30MS	I
TA824	*urartu*	Turkey	50MS	3+	28-May–1 June	H	15MR–20M	I–D
TA826	*urartu*	Turkey	30MR–40M	3–3+	31 May–1 June	M	15MR–20MR	I–D
TA829	*urartu*	Armenia	30MS–80MS	3–3+	6–18 June	M–H	20M	G
TA831	*urartu*	Iran	50MS–60MS	3–3+	26 May–2 June	H	20M–30MS	D
TA832	*urartu*	Turkey	30S–50MS	3–3+	28 May–3 June	H	20M–30M	D
TA839	*urartu*	Turkey	30M–60MS	3+–4	26 May–3 June	H	20MR–25M	I–D
TA850	*urartu*	Russian Federation	30MS–50S	3+	4–6 June	M	20MR–20M	G
TA858	*urartu*	Turkey	20MR–40M	3+–4	3–4 June	H	20MR–20M	I–D
TA1284	*urartu*	Lebanon	10R–40MS	2–3-	1–2 June	M	10MR–20M	D
TA1306	*urartu*	Lebanon	40M	3–4	21–26 June	M–H	15MR–20M	G–D
TA1354	*aegilopoides*	Iraq	20MR	3+–4	1–6 June	M–H	20MR	D
TA2004	*aegilopoides*	Turkey	10MR	1–1+	30 May–3 June	M–H	20MR–20M	D
TA2005	*aegilopoides*	Turkey	20MR–40M	3–4	NT	H	20M	D
TA2007	*aegilopoides*	Turkey	70MS	3+–4	4–6 June	M–H	15MR–20M	I–D
TA2013	*urartu*	Turkey	40MS–70MS	2- –3-	27 May–1 June	H	20MR	D
TA2014	*urartu*	Turkey	30MS–50MS	3+	29 May–3 June	M–H	15MR–20MR	D
TA2022	*aegilopoides*	Turkey	30MS–50MS	1+	2–6 June	M–H	20MR–30MR	I–D
TA2024	*monococcum*	Turkey	15R–30MR	2+–3+	6–14 June	M–H	10R–20MR	I
TA2025	*monococcum*	Turkey	10R–20MR	2–2+	15–18 June	M	10MR–20MR	G–I
TA2026	*monococcum*	Turkey	10MR–20MR	2–2+	13–20 June	M–H	10MR–20MR	G–I
TA2032	*monococcum*	Spain	15R–30MR	1+–2	5–19 June	H	15MR–20MR	G–I
TA2033	*monococcum*	Portugal	5R–20MR	2–3-	4–5 June	M	10MR–15MR	G–I
TA2034	*monococcum*	Bosnia–Herzegovina	10R	2+–3	3–22 June	M	10MR–15MR	G–I
TA2038	*monococcum*	Albania	20R	2–2+	7–18 June	M	20MR	G–I
TA2702	*monococcum*	Italy	10R–20MR	1+–2	6–17 June	M	20M	G
TA2704	*monococcum*	United Kingdom	10R–20R	2–2+	7–25 June	L–M	20MR	G–I

Table 1. Ratings of A-genome species, *Triticum monococcum* subsps. *monococcum* and *aegilopoides* and *T. urartu*. Disease severity in the greenhouse (adult-plant leaf (culture LrComp19) and seedling stripe (culture Yr12-9.1) rust) and in the field (leaf rust and barley yellow dwarf virus (BYDV)), Manhattan, KS, during the 2018–19 crop season. Heading date and stay-green ability also were recorded. Leaf rust was evaluated using the Cobb scale, where a number indicating the percent of leaf area affected is followed by a letter designation, R = resistant flecks or very small pustules, MR = moderately resistant, small pustules, M = moderate, small to medium size pustules, MS = moderately susceptible, medium to large pustules, and S = susceptible, with large pustules. Rating of the leaves with BYDV symptoms was 0 = no visible signs of infection, L = low infection with 10% or less of the leaf area with visible symptoms, M = moderate infection with up to 40% of the leaf area with visible symptoms, and H = high infection with over 40% of the leaf area showing symptoms. — = no test. Seedling stripe rust reactions were scored in the greenhouse; the seedling test is a 0–4 scale with ;–2 resistant, 2+–3- intermediate, and 3–4 susceptible. Stay-green ablility was recorded when ~50% of the lines had reached physiological maturity; G = green leaves, I = dry leaves with partially green spikes; and D = plants completely dry.

Line #	Species/ subspecies	Country of origin	Greenhouse		Field			
			Leaf rust	Stem rust	Heading date	BYDV	Leaf rust	Staygreen
TA2711	*monococcum*	Serbia	10R–20R	2+	7 June	M	15MR–20M	I
TA10547	*aegilopoides*	Serbia & Montenegro	5R–20MR	3+–4	26-Jun	M	10MR–15MR	G
TA10555	*monococcum*	Serbia	5R–20R	2–3-	8–15 June	M	20MR–20M	G–I
TA10562	*monococcum*	Romania	10R–30MR	1–2	16–22 June	M	15MR–20M	G–I
TA10568	*monococcum*	Italy	1R–5R	1–1-	14–26 June	M–H	10MR–20MR	G–I
TA10581	*monococcum*	Austria	10R–30MR	;–1-	6–17 June	L–M	15R–20M	G
TA10587	*monococcum*	Montenegro	5R–10R	3–3+	4–7 June	L–M	10MR–15MR	G–I
TA10588	*monococcum*	Turkey	10R–20MR	1+	—	M	10MR–20MR	G–I
TA10591	*monococcum*	Turkey	10MR–30MR	2–2+	8–15 June	M	20MR	G–I
TA10601	*aegilopoides*	Turkey	20MS–30M	2–2+	6–21 June	M–H	10MR–20MR	G–I
TA10604	*monococcum*	Turkey	5R–10R	3+	25 June	M–H	15MR–20MR	G–D
TA10605	*monococcum*	Bulgaria	15R–30MR	1–1+	7–16 June	H	10MR–30M	G–D
TA10612	*monococcum*	Albania	10R–20R	2+–3-	14–17 June	M	15MR–20MR	G–I
TA10617	*monococcum*	Georgia	15R–30MR	1–1+	7–19 June	M–H	20MR–20M	I
TA10621	*monococcum*	Greece	5R–10R	3+–4	6–21 June	H	20MR	I
TA10623	*monococcum*	Albania	5R–15R	2+–3-	6–8 June	M	20MR–20M	G
TA10625	*monococcum*	Albania	10R–20MR	2–2+	6–15 June	M–H	20M–30M	G–I
TA10632	*monococcum*	Romania	20MR–30MR	2–2+	8–15 June	M–H	20MR–30M	G–I
TA10634	*monococcum*	Italy	5R–20R	3–3+	7–20 June	M	20MR–25MR	G
TA10636	*monococcum*	Georgia	5R–20R	1–2	5–14 June	M–H	20MR–20M	G–I
TA10640	*monococcum*	Germany	10R–20R	2–2+	18–28 June	M–H	20M	G
TA10650	*monococcum*	Turkey	15R–20R	3+	7–15 June	M–H	15MR–30MR	G–I
TA10651	*monococcum*	Turkey	1R–10R	1+–2-	7–25 June	M–H	20MR–30M	G–I
TA10656	*monococcum*	Turkey	10R	;–1-	—	M–H	10MR–20MR	G–I
TA10873	*urartu*	Jordan	40MS–50MS	3	—	—	—	—
TA10878	*urartu*	Iran	50MS–60S	3–3+	4–15 June	M–H	40MS–50MS	G–D
TA10879	*urartu*	Iraq	20MS–50MS	;–1	3–4 June	M	10MR–20MR	I–D
TA10880	*urartu*	Iraq	30MS–50MS	3–3+	16–26 May	H	—	D
TA10881	*urartu*	Syria	20MS–80S	2–3+	17 May	H	—	D
TA10882	*urartu*	Syria	30MS–40MS	3+	1–4 June	M	15MR–30M	D
TA10884	*urartu*	Syria	30MS–50MS	2+	1–4 June	M	20MR–30MR	I–D
TA10885	*urartu*	Syria	20MS–40MS	2+	26 May–2 June	M–H	20MR–30MR	D
TA10886	*urartu*	Syria	20MS–40MS	2+	28 May–1 June	H	15MR–20M	D
TA10887	*urartu*	Turkey	50S	3	27 May–5 June	M–H	15MR–20M	I–D
TA10888	*urartu*	Turkey	10MR–15MR	3–3-	1–2 June	H	15MR–20M	I–D

Table 1. Ratings of A-genome species, *Triticum monococcum* subsps. *monococcum* and *aegilopoides* and *T. urartu*. Disease severity in the greenhouse (adult-plant leaf (culture LrComp19) and seedling stripe (culture Yr12-9.1) rust) and in the field (leaf rust and barley yellow dwarf virus (BYDV)), Manhattan, KS, during the 2018–19 crop season. Heading date and stay-green ability also were recorded. Leaf rust was evaluated using the Cobb scale, where a number indicating the percent of leaf area affected is followed by a letter designation, R = resistant flecks or very small pustules, MR = moderately resistant, small pustules, M = moderate, small to medium size pustules, MS = moderately susceptible, medium to large pustules, and S = susceptible, with large pustules. Rating of the leaves with BYDV symptoms was 0 = no visible signs of infection, L = low infection with 10% or less of the leaf area with visible symptoms, M = moderate infection with up to 40% of the leaf area with visible symptoms, and H = high infection with over 40% of the leaf area showing symptoms. — = no test. Seedling stripe rust reactions were scored in the greenhouse; the seedling test is a 0–4 scale with ;–2 resistant, 2+–3- intermediate, and 3–4 susceptible. Stay-green ablility was recorded when ~50% of the lines had reached physiological maturity; G = green leaves, I = dry leaves with partially green spikes; and D = plants completely dry.

Line #	Species/ subspecies	Country of origin	Greenhouse		Field			
			Leaf rust	Stem rust	Heading date	BYDV	Leaf rust	Staygreen
TA10891	*urartu*	Turkey	30MS–40S	1–2+	2–4 June	M	15MR–20MR	G–D
TA10897	*monococcum*	Italy	10R–20MR	3–3+	—	M–H	10MR–20M	G–I
TA10899	*aegilopoides*	Iran	30M–40MS	3+–4	4–5 June	L–M	10MR–30MR	G–I
TA10900	*aegilopoides*	Iran	15MR–30M	1+–2+	3–4 June	L–M	15MR–30M	I–D
TA10902	*aegilopoides*	Iran	40MS–60MS	2–3-	1–3 June	H	30MR–30M	I–D
TA10906	*aegilopoides*	Lebanon	20M–25M	3+	3–4 June	M	20MR–20M	I–D
TA10909	*aegilopoides*	Turkey	10R–20R	1+–2	5 June	M–H	20MR–30M	I–D
TA11012	*aegilopoides*	Azerbaijan	10R–20MR	2+–3+	3–4 June	M–H	10MR–20MR	G–D
TA11016	*monococcum*	Azerbaijan	15R–20MR	3–3+	3–17 June	M–H	15MR–30MR	G–D
TA11038	*aegilopoides*	United States	10R–40MS	3- –3+	5–8 June	M	20MR–25MR	I–D

Evaluation of A-genome species for drought tolerance using automated rain-out plot shelters.

Duane L. Wilson and W. John Raupp.

Using the 111 A-genome accessions plus 10 widely grown winter wheat cultivars for checks these were planted the autumn of 2018. After growth during spring 2019, on 1 May, prior to boot stage, the rain-out shelters were initiated to cover the plot during any rain event, thus preventing rainfall in the plot area. The A-genome accessions that flowered between 18–31 May to coincided with the wheat cultivar checks that were scored on 28 June for the stay-green trait (see Table 1, pp. 71-74). At this time all wheat cultivars but one were completely dry. We identified eight accessions that were green to intermediate; TA142, TA198, TA199, TA787, TA850, TA2007, TA10088, and TA10891 were the best for drought tolerance.

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

Jordan Hildebrand.

Kansas Hard Red Winter Wheat Tour 2019.

More than 75 people from 25 U.S. states and three countries travelled on six routes between Manhattan and Colby, Kansas, 30 April, stopping at wheat fields every 15–20 miles along the routes, as part of the Wheat Quality Council's 2019 Hard Winter Wheat Tour. Many tour participants, including millers, bakers, food processors, and traders who buy the wheat that Kansas farmers grow, had never stepped foot in a wheat field before and had only seen these Kansas plains from the window seat of passing air plane. If these fields make it to harvest, the resulting crop will go into bread, but also a number of other food items, from snack cakes to donuts to seasonings, batters, and coatings for fish, chicken, and appetizers.

Wheat industry professionals from all over the world gathered in America's Breadbasket, including Claire Hutchins, market analyst for U.S. Wheat Associates. Hutchins grew up on an irrigated wheat, soy, and alfalfa farm near Fruita, Colorado. Her employer, U.S. Wheat Associates, is an export market development organization providing information and technical services to American farmers' overseas customers, including some on this trip. U.S. Wheat Associates educates foreign customers about the quality of U.S. wheat. Every tour participant makes yield calculations at every stop based on three different area samplings per field. These individual estimates are averaged with the rest of their car mates, and eventually added to a formula that produces a final yield estimate for the areas along the routes. Although yields tend to be the spotlight of the Wheat Quality Tour, this tour gives Kansas farmers the chance to interact with and influence their customers around the globe and on the tour.

Day 1. On 30 April, 20 cars of wheat tour scouts made 240 stops at wheat fields across north-central, central, and northwest Kansas, and into southern counties in Nebraska. The calculated yield is based on what scouts saw at this point in time. The crop was behind schedule in terms of development, but a lot will happen between now and harvest. The calculated yield from al l cars was 46.9 bushels/acre. Currently, the condition of winter wheat in Kansas is rated at 3% very

poor, 8% poor, 31% fair, 48% good, and 10% excellent. Winter wheat at jointing stage was 64%, ahead of 50% in 2018, but behind the average of 75%. Heading was 4%, near 2% in 2018, but behind the 22% average.

In addition, scouts from Nebraska and Colorado met the group in Colby, Kansas, to give reports from their states. The estimate for the Nebraska wheat crop is 47.4 x 10^6 bushels, down from 49.5 x 10^6 bushels last year. The estimated yield average is 44 bushels/acre. In Colorado, the estimated yield was 46.5 bushels/acre. Production in Colorado is estimated at 97.2 x 10^6 bushels, up from 70.5 x 10^6 bushels last year.

Day 2. On 1 May, 75 people on the Wheat Quality Council's 2019 winter wheat tour in 20 cars made their way from Colby to Wichita, Kansas, stopping in wheat fields along six different routes. One route included a trip to northern Oklahoma, as well.

Scouts reported seeing widely varying wheat conditions (due, in large part, to planting date) along the route. Although there were sightings of rust and other disease in south-central Kansas, many stops saw signs of nitrogen deficiency, a common nutrient deficiency that could be remedied by fertilizer applications. However, many producers are choosing not to apply fertilizers due to decreasing wheat prices and increased input costs. This year the yield bump with fertilizer application may end up costing producers more than they would gain.

Although the wheat that looks good looks really good, there are a large chunk of fields that were not able to be planted in a typical time frame. These fields are not developing normally, there is no root structure and may increase the potential for a lot of abandoned acres. The next few weeks will be critical for the crop. Signs of leaf rust in the lower canopy in Ford and Edwards counties were observed, but both nitrogen and sulphur deficiencies were seen consistently along Highway 50. One report from Hodgeman County showed a substantial difference in growth and development in neighboring fields. Non-typical planting dates have been at the forefront of conversation for the Wheat Tour with the visible variability in field development evident even to the untrained eye. Tour participants now have a hands on experience showcasing the volatility of Mother Nature and the impact it has on our nation's wheat farmers.

The calculated yield from all cars was 47.6 bushels/acre, but at the Wednesday evening wrap-up meeting, tour scouts again talked about the wheat being behind schedule and very small. Oklahoma reports that the state's production is estimated at 119.27 x 10^6 bushels with 37.38 bushels/acre. Approximately 4.2 x 10^6 acres were seeded last autumn.

Day 3. The 2019 Wheat Quality Council's Hard Winter Wheat Tour across Kansas wrapped up on 2 May. During the three days of wheat scouting, tour participants travelled six routes from Manhattan to Colby to Wichita and back to Manhattan. This year's tour hosted 75 participants from three countries and 25 states in 20 vehicles.

The three-day average yield for the fields that were calculated was 47.2 bushels/acre. While an estimated 7 x 10^6 acres of wheat were planted in the autumn, the Kansas wheat crop varies in condition based on planting date. Wheat that was planted prior to October rains looks good, whereas wheat planted when farmers could get back in fields after the rains is not faring as well. What Mother Nature has in store for the wheat crop still remains unseen, but the tour captures a moment in time for the yield potential for fields across the state. Tour participants saw wheat that was significantly behind schedule, with most areas a week to 10 days behind normal development.

The official tour projection for total production of wheat to be harvested in Kansas is 306.5 x 10^6 bushels. This number is calculated based on the average of estimated predictions from tour participants who gathered information from 469 fields across the state. Scouts reported seeing widely varying wheat conditions (due, in large part, to planting date) along the route. Many stops saw sightings of rust and other disease in south-central Kansas nitrogen deficiency also was observed.

MINNESOTA

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

J.A. Kolmer and Y. Jin.

Wheat Leaf rust in the USA in 2018 – Summary.

Leaf rust caused by *Puccinia triticina* was present at low severity and incidence throughout the eastern soft red winter wheat region and hard red wheat region of the Great Plains in 2018. From February to March, temperatures were

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2018 identified by virulence to 20 lines of wheat with single genes for leaf rust resistance. Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, *Lr39*, and *Lr42*.

Race	Virulence combination (ineffective *Lr* genes)	Southeast		New York		Wisconsin		OK–TX		KS–NE		MN–ND–SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
LBDSG	*1,17,B,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	50.0	1	0.4
LNBJJ	*1,9,24,10,14a,28,39*	1	2.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
LNPSD	*1,9,24,3ka,17,30,B,10,14a,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	2.1	0	0.0	0	00	1	0.4
MBDSD	*1,3,17,B,10,14a,39*	0	0.0	0	0.0	0	0.0	6	10.0	1	2.1	15	18.1	0	0.0	22	9.2
MBDSG	*1,3,17,B,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	50.0	1	0.4
MBNSD	*1,3,3ka,17,B,10,14a,39*	0	0.0	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	0	0.0	1	0.4
MBTNB	*1,3,3ka,11,17,30,B,14a*	17	47.2	0	0.0	4	66.7	1	1.7	1	2.1	0	0.0	0	0.0	23	9.7
MBTSB	*1,3,3ka,11,17,30,B,10,14a*	0	0.0	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	0	0.0	1	0.4
MCTNB	*1,3,26,3ka,11,17,30,B,14a*	5	13.9	0	0.0	0	0.0	2	3.3	0	0.0	0	0.0	0	0.0	7	2.9
MFPSB	*1,3,24,26,3ka,17,30,B,10,14a*	0	0.0	0	0.0	0	0.0	2	3.3	0	0.0	1	0.8	0	0.0	2	0.8
MFPSD	*1,3,24,26,3ka,17,30,B,10,14a,39*	0	0.0	0	0.0	0	0.0	1	1.7	1	2.1	0	0.0	0	0.0	2	0.8
MFSSB	*1,3,24,26,3ka,11,17,B,10,14a*	1	2.8	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
MGPJB	*1,3,16,3ka,17,30,10,14a*	0	0.0	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	0	0.0	1	0.4
MGPSB	*1,3,16,3ka,17,30,B,10,14a*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.2	0	0.0	1	0.4
MJBJB	*1,3,16,24,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	2.4	0	0.0	2	0.8
MJDSD	*1,3,16,24,17,B,10,14a,39*	0	0.0	0	00	0	00	0	00	1	2.1	0	0.0	0	0.0	1	0.4
MLPSD	*1,3,9,3ka,17,30,B,10,14a,39*	0	0.0	0	0.0	0	0.0	5	8.3	1	2.1	5	6.0	0	0.0	11	4.6
MMPSD	*1,3,9,26,3ka,17,30,B,10,14a,39*	0	0.0	0	0.0	0	0.0	6	10.0	1	2.1	0	0.0	0	0.0	7	2.9
MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	4	11.1	0	0.0	1	16.7	19	31.7	27	57.4	33	39.8	0	0.0	84	35.3
MPDSD	*1,3,9,24,26,17,B,10,14a,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	2.1	0	0.0	0	0.0	1	0.4
MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	6	16.7	0	0.0	1	16.7	10	16.7	11	23.4	10	12.0	0	0.0	38	16.0
PBDGJ	*1,2c,3,17,10,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.2	0	0.0	1	0.4
PBDQJ	*1,2c,3,17,8,10,28,39*	0	0.0	0	0.0	0	0.0	3	5.0	0	0.0	1	1.2	0	0.0	4	1.7
TBBGS	*1,2a,2c,3,10,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	9	10.8	0	0.0	9	3.8
TBRKG	*1,2a,2c,3,3ka,11,30,10,14a,18,28*	0	0.0	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	0	0.0	1	0.4
TBTNB	*1,2a,2c,3,3ka,11,17,30,B,14a*	2	5.6	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.8
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	0	0.0	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	0	0.0	1	0.4
TCTBB	*1,2a,2c,3,26,3ka,11,17,30*	0	0.0	3	7.5	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	1.3
TFBJQ	*1,2a,2c,3,24,26,10,14a,21,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	3.6	0	0.0	3	1.3
TFBJS	*1,2a,2c,3,24,26,10,14a,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.2	0	0.0	1	0.4
TFTSB	1,2a,2c,3,24,26,3ka,11,17,30,B, 10,14a	0	0.0	1	2.5	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TNBJJ	1,2a,2c,3,9,24,10,14a,28,39	0	0.0	0	0.0	0	0.0	0	0.0	1	2.1	2	2.4	0	0.0	3	1.3
Total		36		1		6		60		47		83		2		238	

10–15°F higher than average in south Texas and along the Gulf coast area, and leaf rust was present at normal severity and incidence levels. This was followed by a cold April, with temperatures 5–11°F below average throughout most of the USA. May temperatures were 5–11°F above average throughout most of the USA, with lower than normal levels of precipitation in the southern Great Plains. The combination of prolonged and widespread cold temperatures followed by the hot and dry weather drastically slowed the increase and spread of leaf rust in the southern Great Plains and southeastern states. There was very little leaf rust on wheat in the winter wheat and spring wheat regions further north, due to the lack of wind borne urediniospores arriving from the southern Great Plains region, and southeastern states.

Among 238 isolates that were tested for virulence in 2018, 32 races were found (Table 1, p. 77). Overall across the entire USA, race MNPSD with virulence to wheat lines with genes *Lr1*, *Lr3*, *Lr9*, *Lr24*, *Lr3ka*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14*, and *Lr39* at 35%; race MPPSD with virulence to wheat lines with genes *Lr1*, *Lr3*, *Lr9*, *Lr24*, *Lr26*, *Lr3ka*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, and *Lr39* at 16%; and race MBTNB with virulence to wheat lines with genes *Lr1*, *Lr3*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, and *Lr10* at 9.7%, were the most frequent races.

Races MBTNB, MPPSD, MNSPD, and MCTNB with virulence to *Lr11* were the most common races in the southeastern states. Soft red winter wheat cultivars with *Lr11* are grown in this region. Races MNPSD, and MPPSD, were the most common races in the hard red winter wheat area from Texas to Nebraska. Both races are virulent to *Lr39*, which is present in many wheat cultivars grown in this region. In the spring wheat area of North Dakota, South Dakota, and Minnesota, races MNPSD, MBDSD, and TBBGS were the most common. All three races are virulent to *Lr39*, and TBBGS is virulent to *Lr21*, which is present in many spring wheat cultivars in this region.

Table 2 lists the frequency of virulence to leaf rust resistance genes in the different regions and across the overall USA. Table 3 (p.79) lists the hard red winter wheat cultivars grown in Texas, Oklahoma, and Kansas in 2018 and the postulated *Lr* genes. Table 4 (p. 79) lists the hard red spring wheat cultivars grown in Minnesota and North Dakota in 2018 and the postulated *Lr* genes.

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

	Southeast		New York		Wisconsin		OK–TX		KS–NE		MN–ND–SD		Washington		Total	
Resistance gene	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	36	100.0	4	100.0	6	100.0	60	100.0	47	100.0	83	100.0	2	100.0	238	100.0
Lr2a	2	5.6	4	100.0	0	0.0	2	3.3	1	2.1	15	18.1	0	0.0	24	10.1
Lr2c	2	5.6	4	100.0	0	0.0	5	8.3	1	2.1	17	20.5	0	0.0	29	12.2
Lr3	35	97.2	4	100.0	6	100.0	60	100.0	46	97.9	83	100.0	1	50.0	235	98.7
Lr9	11	30.6	0	0.0	2	33.3	40	66.7	43	91.5	50	60.2	0	0.0	146	61.3
Lr16	0	0.0	0	0.0	0	0.0	1	1.7	1	2.1	3	3.6	0	0.0	5	2.1
Lr24	12	33.3	1	25.0	2	33.3	32	53.3	43	91.5	51	61.4	0	0.0	141	59.2
Lr26	12	33.3	4	100.0	1	16.7	22	36.7	14	29.8	14	16.9	0	0.0	67	28.2
Lr3ka	35	97.2	4	100.0	6	100.0	51	85.0	43	91.5	49	59.0	0	0.0	198	79.0
Lr11	25	69.4	4	100.0	4	66.7	6	10.0	1	2.1	0	0.0	0	0.0	40	16.8
Lr17	35	97.2	4	100.0	6	100.0	58	96.7	46	97.9	66	79.5	2	100.0	217	91.2
Lr30	34	94.4	4	100.0	6	100.0	50	83.3	43	91.5	49	59.0	0	0.0	186	78.2
LrB	35	97.2	1	25.0	6	100.0	57	95.0	46	97.9	65	78.3	2	100.0	212	89.1
Lr10	12	33.3	1	25.0	2	33.3	57	95.0	46	97.9	83	100.0	2	100.0	203	85.3
Lr14a	36	100.0	1	25.0	6	100.0	57	95.0	47	100.0	72	86.7	2	100.0	221	92.9
Lr18	0	0.0	0	0.0	0	0.0	2	3.3	0	0.0	0	0.0	0	0.0	2	0.8
Lr21	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	13	15.7	0	0.0	13	5.5
Lr28	1	2.8	0	0.0	0	0.0	5	8.3	1	2.1	19	22.9	2	100.0	28	11.8
Lr39	11	30.6	0	0.0	2	33.3	51	85.0	46	97.9	77	92.8	0	0.0	187	78.6
Lr42	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0

Table 3. Hard Red Winter Wheat Cultivars grown in 2018

Texas	%	Oklahoma	%	Kansas	%
TAM 111–*Lr37,Lr39*	8.9	Gallagher–*Lr26*	18.4	Everest–*Lr1 Lr14a*	9.3
Gallagher–*Lr26*	5.8	Doublestop CL (none)	4.4	T158–*Lr37*	6.6
TAM 114–*Lr18*	3.9	Bentley–*Lr21*	4.4	SY Monument–*?*	6.1
TAM 112–*Lr39*	3.4	Iba–*Lr37*	4.0	WB Grainfield–*Lr39*	5.5
TAM 105	2.7	Duster–*Lr11 Lr34 Lr46 Lr77*	3.0	WinterHawk–*Lr39*	4.2
TAM 113	2.4	Endurance–*Lr1 Lr26*	3.0	Gallagher–*Lr26*	4.0
WinterHawk–*Lr39*	2.4	WinterHawk–*Lr39*	2.5	LCS Mint–*Lr37*	3.5
WB Cedar–*Lr10*	1.7	Ruby Lee–*Lr39*	2.4	Byrd–*Lr14a*	2.8
TAM 204 +	1.6	Jagger–*Lr37*	2.0	TAM 112–*Lr39*	2.4

Table 4. Hard Red Spring Wheat Cultivars grown in 2018

Minnesota	%	North Dakota	%
Linkert +	27.28	SY Ingmar +	20.30
Bolles +	10.45	SY Valda +	8.70
WB–Mayville–*Lr1 Lr10*	9.63	SY Soren +	7.70
SY Valda +	8.91	Barlow–*Lr21*	6.40
Shelly–*Lr21*	8.18	Bp;;es +	6.10
Lang-MN–*Lr21*	4.38	Faller–*Lr21*	6.00
SY Ingmar +	3.73	Linkert +	5.80
WB 9479–*Lr21*	3.45	Elgin-ND–*Lr21* +	4.60
TCG-Spitfire–*Lr21*	3.13	Rollag +	2.60
WB 9590–*?*	2.48	Prosper–*Lr21*	2.50

SOUTH CAROLINA

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

A creative solution to gluten-induced disorders using a unique combination of multigene editing and nanoparticle-based gene delivery.

S. Rustgi, S. Kashyap, N. Gandhi, S. Naveed, and J. Windham; M. Yang (State Key Laboratory of Crop Stress Biology for Arid Areas, College of Agronomy, Northwest A&F University, Yangling, PR China); R. Gemini: and P. Reisenauer (Department of Crop and Soil Sciences, Washington State University, Pullman, WA).

Wheat is the primary staple to 20% of the world population, and the major cash crop in the most resource-deprived and populated parts of the world. Because wheat is affordable and a good source of proteins, carbohydrates, and other food essentials, it is grown widely across the globe (Rustgi et al. 2019a). Contrary to its beneficial attributes, wheat grain proteins, specifically gluten, suffer a major flaw, as parts of this protein complex are indigestible to humans, due to the iterative tracts of proline and glutamine residues. These indigestible gluten peptides are recognized by the human immune system as foreign invaders and were reacted upon in various ways in different body parts leading to a variety of manifestation such as celiac disease (CD), dermatitis herpetiformis, wheat allergy, wheat sensitivity, and gluten ataxia (Brouns et

al. 2019). These disorders together affect about 7–10% of the world's population. Among these disorders, the CD is most notorious as it takes an autoimmune form if left untreated. At present, the only treatment for these disorders is avoiding wheat. However, this solution is not without consequences, as it is difficult to follow, and also deprives the consumer of many essential nutrients, which increase their vulnerability to other disorders.

The way to address this problem is not as straightforward, because i) the common wheat genome consists of three highly related sub-genomes; ii) gluten is not a single protein; instead, it is a mixture of about 100 related proteins; and iii) gluten proteins are coded by a large number of tandemly duplicated genes present on 12 major loci in the wheat genome (Fig. 1). Moreover, we know through our research that none of the natural wheat genotypes are gluten-free (Osorio et al. 2012; Brouns et al. 2019; Rustgi et al. 2019a, b), and the developed transgenics (Wen et al. 2012; Rustgi et al. 2014; Osorio et al. 2019) are unavailable to consumers due to lack of general acceptance for genetically modified crops. Therefore, with the invention of novel genome-editing strategies and the gene-delivery methods, we propose a creative solution to this problem via inducing site-specific mutations in the genes encoding immuno-reactive gluten proteins via CRISPR/Cpf1 mediated multigene editing. The progress made in this direction is elaborated in the following paragraphs.

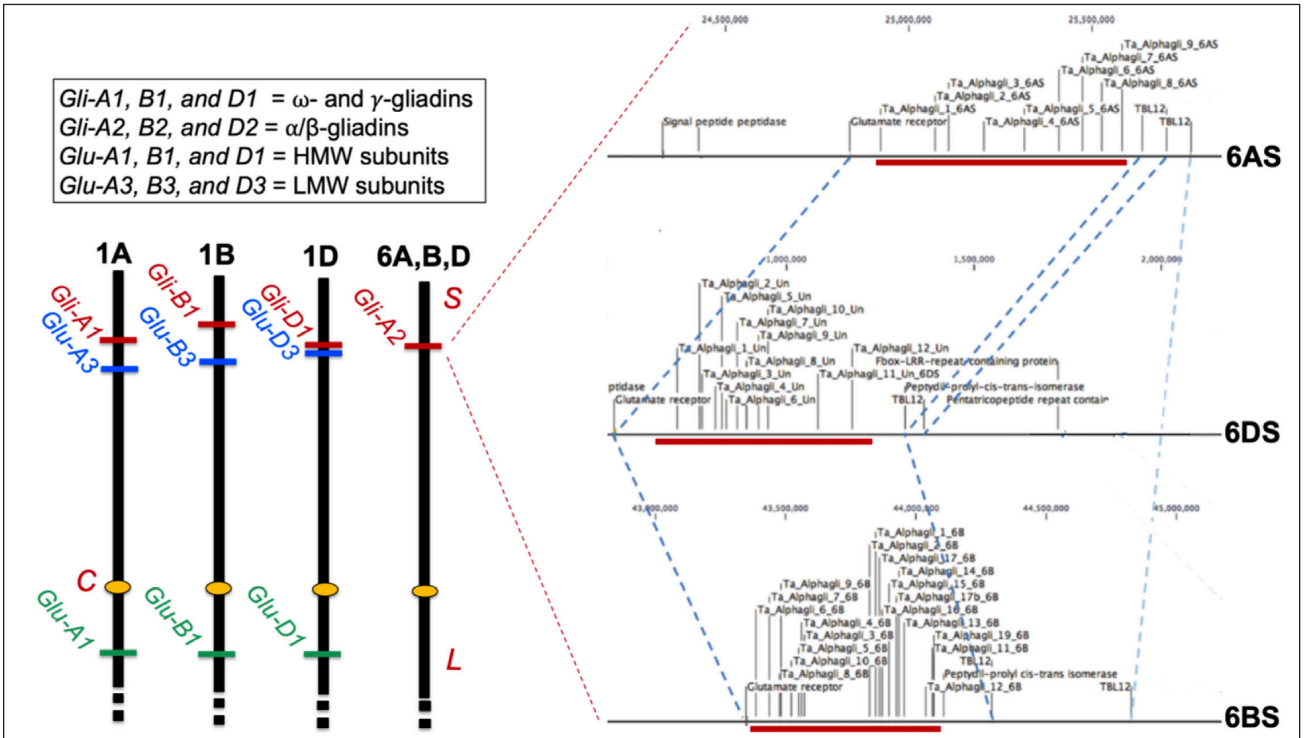

Fig. 1. The complex organization of the prolamin gene in the common wheat genome.

Tailoring of reduced immunogenicity-wheat genotypes. With the advancement in the technology now it is possible to target and silence multiple genes or members of a gene family using a single CRISPR-based construct (Wang M et al. 2017, 2018; Miao et al. 2018; Wang W et al. 2018). Taking the lead from these earlier studies, we have also changed our strategy to develop reduce-gluten wheat genotypes from targeting of the wheat *DEMETER* and *Dre2* genes to inducing targeted-mutations in the wheat gliadin and glutenin genes (Rustgi et al. 2014; 2019a). The proteins of gluten complex are coded by a multigene family distributed on six wheat chromosomes of two homoeologous chromosome groups. At each locus, the genes are duplicated in tandem, making it a complex of homoeologous and paralogous genes (Fig. 1). But, owing to their unique composition, most of the 190 epitopes identified so far map either to gliadins (94 to α-gliadins, 74 to γ-gliadins, and 12 to ω-gliadins) or LMW subunits of glutenins (eight), except for two epitopes that map to HMW subunits. Therefore, we pulled out sequences of the gliadin and LMW subunit genes from the public domain, clustered them, and used for online identification of a target site conserved across each gene family. The target sites were identified keeping the sequence specificity requirements (TTTV, protospacer adjacent motif requirement) of *Lachnospiraceae bacterium* Cpf1 in mind. Subsequently, the gRNAs were tested for targeting efficiency under in vitro assays using PCR product amplified from the wheat genome as targets, in vitro transcribed gRNA (MEGAscript T7 Kit,

Thermo) and LbCpf1 (New England Biolabs, cat. # M0653S). The gRNAs producing desired digestion products in the *in vitro* assays were assembled in the guide RNA module where 23nt protospacers were arranged alternatively with 21nt direct repeat, and the module is flanked on either side by ribozymes. This gRNA module was synthesized and cloned in the gateway vectors developed by Tang et al. (2017) and assembled with the LbCpf1 expression vector using the LR reaction (Fig. 2). Later the triple expression cassette [pZmUbq1::TaCpf1::NosT; pZmUbq1::gRNA mod::NosT, and p35S::HygR::CaMV poly(A)] construct dubbed pSK003 was used to transform wheat via two genetic transformation methods - the conventional biolistic method using the calli derived from the mature grains and pollen magnetofection. The details of the gene-delivery methods used are elaborated in the following paragraphs.

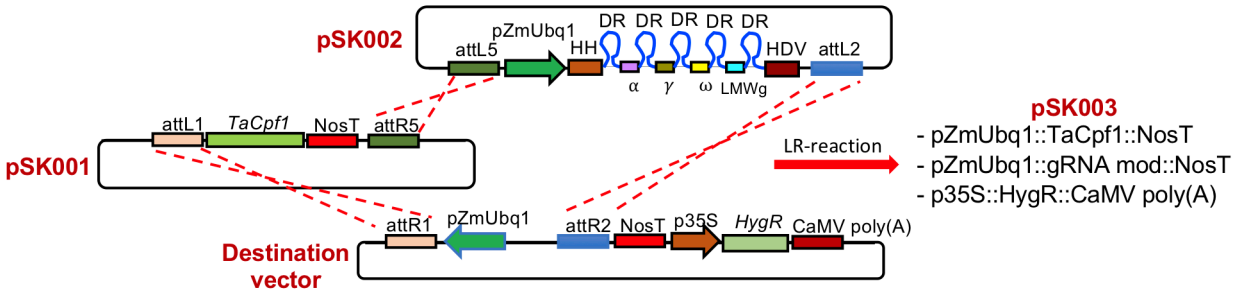

Fig. 2. Assembly of the triple expression cassette [pZmUbq1::TaCpf1::NosT; pZmUbq1::gRNA mod::NosT, and p35S::HygR::CaMV poly(A)] construct, pSK003 via the LR cloning reaction.

Mature seeds as explants for micropropagation. A large number of explants such as immature embryo (scutellum), microspores, inflorescence, shoot meristem, leaf base, coleoptiles, and embryo (from mature seeds) were used so far in wheat for *in vitro* regeneration. Among these explants, immature embryos are most commonly used explants due to their better regeneration efficiency. However, obtaining immature embryos is resource inefficient and constraining due to the requirement of a large number of axenically grown donor plants at all times and skilled personal who could recognize the correct developmental stage for embryo excision. Therefore, to avoid these limitations, we adapted a callus generation approach from mature grains and their use for the delivery of genome-editing reagents using the biolistic approach. For callus generation from mature wheat grains, we used the seeds of spring wheat cultivars WB926 and Fielder and adopted the method by Aadel et al. (2016) with minor modification elaborated below.

For callus generation, we used the basal MS media and supplemented it individually with 2,4-D and Dicamba, and studied the efficiency of the two phytohormones in callus induction (Filippov et al. 2006; Malik et al. 2017). We observed that MS media supplemented with Dicamba produced more calli than the one adulterated with 2,4-D. Regeneration media consisted of basal MS media with a mixture of plant growth supporting vitamins added at the rate of 1 g/L and sucrose at the rate of 20 g/L (Aadel et al. 2016). The media was solidified using 2.5 g/L Phytagel and was supplemented with 0.5 mL of PPM™ (Plant Preservative Mixture) in a liter (Table 1). Before embryo extraction, mature seeds were surface sterilized with 70% ethanol (v/v) for 3 min, 2.4% sodium hypochlorite (v/v) with a drop of Tween 20 for 30 min (under constant shaking), followed by three rinses with sterile distilled water. Subsequently, seeds were imbibed in sterile distilled water overnight at room temperature to facilitate the embryos excision. The embryos were later aseptically dissected from the caryopses, and the remaining endosperm as well as radical were carefully removed to prevent precocious embryo germination. The dissected embryos were placed in Petri dishes containing the induction medium and inducted for seven days at room temperature in the dark before particle bombardment (for details, see Rustgi et al. 2017). Following bombardment callus cultures were sub-cultured in new plates on induction media for three more weeks and subsequently transferred to regeneration media and were sub-cultured to new dishes each month until transferred to soil (Fig. 3, p. 82).

Table 1. List of ingredients used in the callus induction medium.

Components	Concentration
Basal MS medium	1g/L
2,4-D or DICAMBA	2g/L or 12g/L
Myo-inositol	100 mg/L
L-asparagine	150 mg/L
Sucrose	20 g/L
Phytagel	2.5 g/L
PPM™	0.5 mL/L
pH = 5.7–5.8	

Pollen magnetofection as a gene-delivery method. Pollen magnetofection is a nanoparticles-based, gene delivery method, where 200 nm iron oxide magnetic nanoparticles (MNPs) are coated with plasmid DNA and delivered to pollen

grains under the influence of the magnetic field (Zhao et al. 2017; Zhang et al. 2019). The DNA-loaded MNPs deliver DNA to the egg cell upon fertilization, where it transcribes and translates and induce mutations in the F_1 plants. The workflow that we optimized for wheat (Fig. 4), starts with the harvest of wheat spikes at the Feke's developmental stage 10 or 10.2. The florets were trimmed and exposure to sun/artificial light, which makes anther protrude out of florets. At this time point, anthers are harvested, and pollen extracted in the pollen media (for media composition, cf. Rustgi et al. 2017). The pollen was subjected to pollen magnetofection, dried on filter paper and used for artificial pollination. Dried pollen also was subjected to Alexender staining, counting via hemocytometer, and pollen germination test to check pollen viability. Later, the F_1 seedlings obtained from the crossed seeds were tested for the presence of transgene and mutation at the target site.

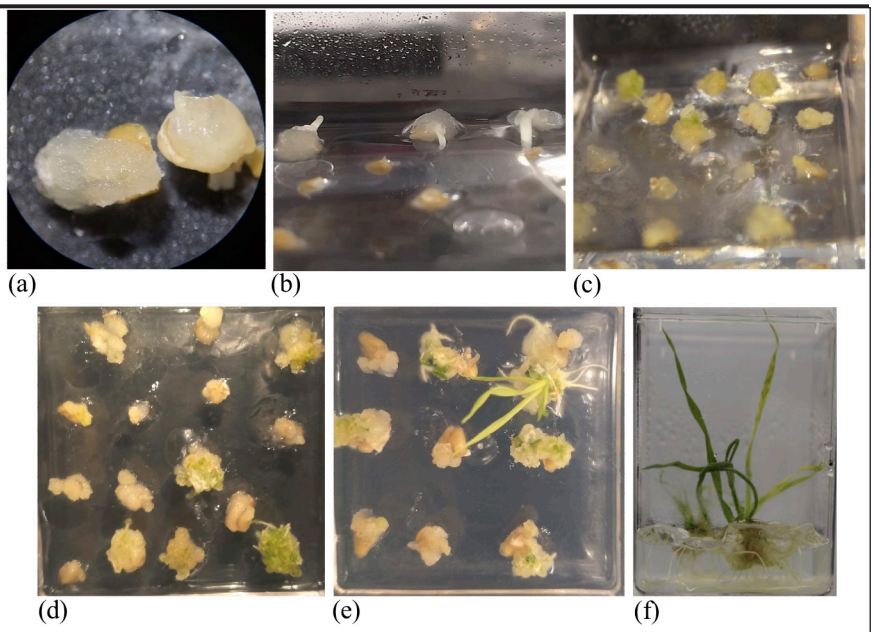

Fig. 3. Steps involved in the procedure of calli from the embryos dissected from the mature seeds: (a) callus culture stage I – 7 days after culture (DAC), (b) callus culture stage II – 21 DAC, (c) callus culture stage III – 35 DAC, (d) callus culture stage IV – ~50 DAC, (e) callus culture stage V – 70 DAC, and (f) Callus culture stage VI – ~90 DAC.

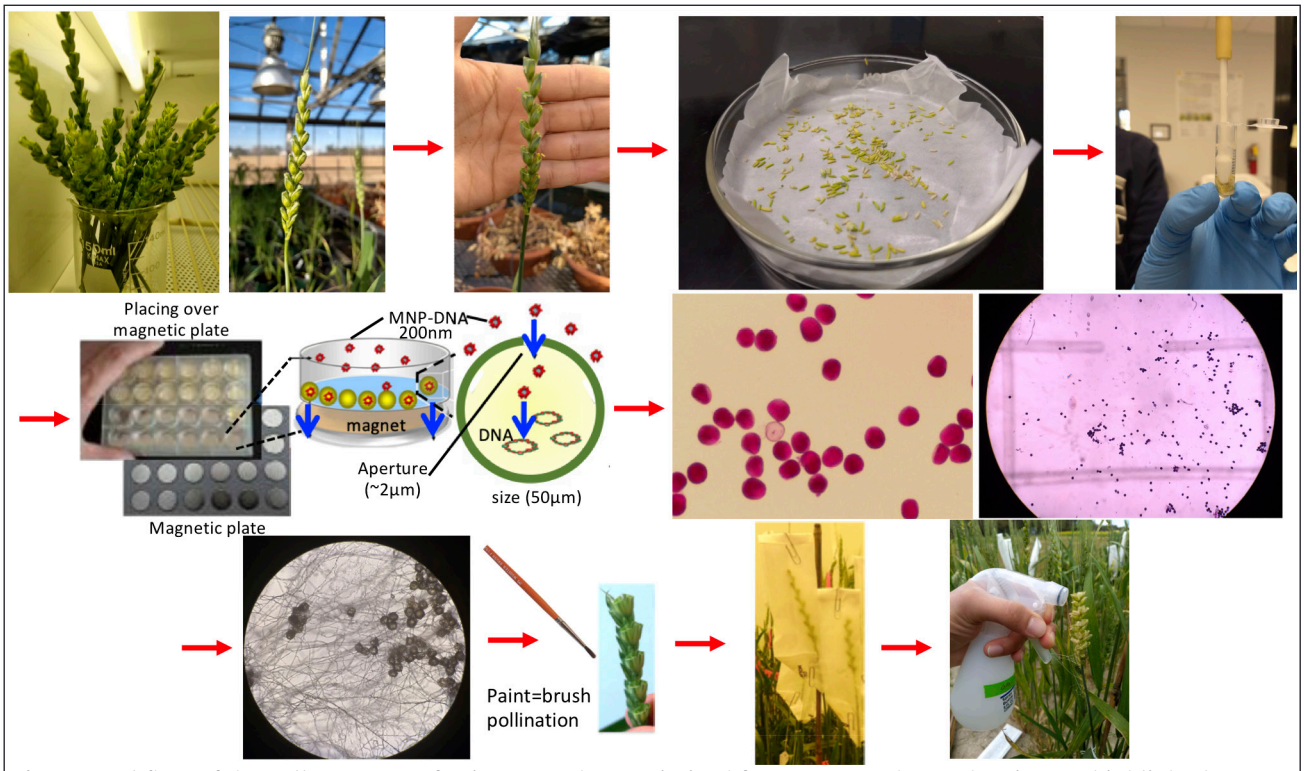

Fig. 4. Workflow of the pollen magnetofection procedure optimized for common wheat. The pictures highlight the steps from the collection of pollen grains, their magnetofection, pollen viability tests to use of transfected pollens for artificial pollination and the mechanism of pollen magnetofection.

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VIRGINIA

VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY
School of Plant and Environmental Sciences, Blacksburg, VA 24061, USA.

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

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

C. Griffey, W. Thomason, J. Seago, K. Brasier, N. Meier, L. Liu, E. Rucker, D. Schmale III, N. McMaster, and M. Flessner (Virginia Polytechnic Institute and State University); J. Fitzgerald and J. Oakes(Eastern Virginia Agricultural Research and Extension Center); and M. Balota and H. Mehl.

2018 Wheat Production in the Commonwealth of Virginia.

Growing season. Statewide temperatures and rainfall in autumn 2017 were generally favorable for wheat seeding. By mid-October, wheat planting reached 20% of intentions, compared with a five year average of 25% by this date. Continued favorable weather allowed 41% wheat to be planted by 3 October. By mid-November, planting progress was near the five year average for all small grains reported with 60% of wheat acres reported as good or excellent. Dry conditions persisted through late November results in a decline in the number of wheat acres rated excellent, though this did allow successful late seeding in some areas. Rainfall in early December returned the total season precipitation to near normal, followed by mild and wet conditions through much of January. February was unseasonably warm with limited rainfall, resulting in soil moisture depletion. Wheat was rated good or excellent on 68% of the acres. March brought mostly mild temperatures with a freeze mid-month. Seventy-five percent of the winter wheat crop was rated good or excellent for the week ending 26 March. Statewide rains were received in mid-March, but season total rainfall continued below normal. By the end of the third week of March, 33% of the wheat crop was reported as headed, up 14% from last year and 23% from the five-year average. Dry soil conditions continued through mid-April with temperature above average through the last half of the month. At the end of April, 75% of the winter wheat crop was still rated good or excellent. Precipitation varied statewide in the first two weeks of May, with 74% of the wheat crop headed, compared with 85% in 2017, but exactly the same as the five-year average for this date. Most areas received significant rainfall in the last half of May resulting in a decline in small grain crop quality and increased risk of Fusarium head blight. By 17 June, 30% of winter wheat had been harvested. Heavy rains continued in many areas in mid-late June. Fifty-three percent of wheat was harvested by 24 June, 10% behind 2017 but 7% ahead of the five-year average for this date. On 1 July, 73% of the wheat crop was harvested with many producers reporting slightly lower yields and poor test weights.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service, Virginia farmers planted 230,000 acres (93,150 hectares) of wheat in 2018 of which 155,000 acres (62,775hectares) were harvested for grain. Wheat yields averaged around 60 bushels/acre (4,031 kilograms per hectare). In total 9.3 x 10^6 bushels (201,810 metric tons) of wheat were produced in Virginia in 2018.

Disease incidence and severity. Many wheat diseases were prevalent and widespread throughout the Commonwealth in 2018. Trace amounts of stripe rust (*Puccinia striiformis*) were found on susceptible varieties in research trials conducted in eastern Virginia (Accomack, Richmond, and Westmoreland Counties). Stripe rust samples from these three locations were sent to Dr. Xianming Chen at USDA–ARS in Pullman, WA, and race PSTv-37 (virulence for genes *Yr6*, *7*, *8*, *9*, *17*, *27*, *43*, *44*, *Tr1*, and *Exp2*) was identified at all three locations. Only trace amounts of leaf rust (*Puccinia triticina*) were noted in wheat trials in eastern Virginia, whereas moderate levels of leaf rust developed late in the crop season in the Official Variety Trial conducted in southwestern Virginia. Leaf rust samples from wheat trials conducted in five counties were sent to Dr. James Kolmer at the USDA–ARS Cereal Disease Lab for race identification. Race TCTBB (virulence

for genes *Lr1, 2a, 2c, 3, 26, 3ka, 11, 17,* and *30*) was identified in Nottoway County. Race TFTSB (virulence for genes (*Lr1, 2a, 2c, 3, 24, 26, 3ka, 11, 17, 30, B, 10,* and *14a*) was identified in Richmond County. Races TBTNB (virulence for genes *Lr1, 2a, 2c, 3, 3ka, 11, 17, 30, B,* and *14a*) and race MBTNB (virulence for genes *Lr1, 3, 3ka, 11, 17, 30, B,* and *14a*) were identified in Montgomery County. Powdery mildew (*Blumeria graminis*) was the most prevalent and widespread disease in 2018, and disease ratings (0 = no infection to 9 = severe infection) varied from 0 to 8 at four test sites. Mean powdery mildew ratings of the 142 entries in the 2018 Official Variety Trial were 2.6 on the Eastern Shore (Accomack County), 1.1 in the northeastern region (Richmond County), 1.6 in the southern Piedmont region (Nottoway County), and 3.7 in a mist-irrigated, disease nursery in Westmoreland County.

State cultivar tests. The 2017–18 soft red winter wheat Official Variety Trial included 142 entries that were planted no-till at the Tidewater test site at 48 seeds per square foot. Tests in the southwestern and northeastern regions, Eastern Shore, and southern and northern Piedmont regions were planted conventional-till at 44 seeds per square foot. Although the growing season was generally favorable, frequent rain showers following physiological maturity delayed harvest throughout the Commonwealth and resulted in significant reductions in grain volume weight and quality. Mean grain yields over five test sites varied from 62.6 bu/acre (4,207 kg/ha) in the southeastern Tidewater region to 80.6 bu/acre (5,416 kg/ha) on the Eastern Shore. For the trial in the southwestern region where deer feeding was a problem, the mean yield for awned entries was 88.0 bu/acre (5,914 kg/ha). Over the five test sites, 27 entries produced mean grain yields that were significantly ($P < 0.05$) higher than the overall trial average of 70.9 bu/acre (4,768 kg/ha). The highest yielding entry (13VTK59-148) had an overall mean yield of 80.3 bu/acre (5,393 kg/ha). Four other entries, including 13VTK429-3, L11719, and USG 3895, had overall mean grain yields that did not differ significantly from the top yielding line. Mean test weights of the 142 entries varied from 56.6 lb/bu (74.5 kg/hl) at the northeastern and Eastern Shore test locations to 50.4 lb/bu (66.5 kg/hl) at the northern Piedmont site with an over location mean test weight of 54.5 lb/bu (71.8 kg/hl). The entry having the highest overall test weight (59.5 lb/bu, 78.3 kg/hl) was DH13SRW023-201.

Newly released cultivars. Two soft red winter wheat varieties including VA12W-31 (Featherstone 31) and VA12W-68 (SR8483) were released by the Virginia Agricultural Experiment Station in May 2018.

Table 1. Virginia Wheat Yield Contest Results (http://www.virginiagrains.com/yield/yieldcontests/).

Place	Grower	Farm	County	Yield (bu/acre)
1	Alan Welch	Welch Farms, Inc.	Northumberland	108.6
2	Justin Welch	Welch Farms, Inc.	Northumberland	105.5
3	Paul Davis	Davis Produce	New Kent	89.6

Using unmanned aerial vehicles (UAVs) to improve nitrogen management of winter wheat.

Joseph Oakes (Eastern Virginia Agricultural Research and Extension Center); and Maria Balota, Wade Thomason, Brice Cazenave, and Sayantan Sarkar (School of Plant and Environmental Sciences).

Optimum wheat yields require high tiller density and adequate nitrogen (N) throughout the growing season. Often the decision of whether to apply N at Zadoks GS 25 is based on the number of tillers present at a particular growth stage. However, applying N based on tiller density is often not utilized by growers due to the time involved and field variability. UAVs give us the ability to fly a field with a sensor and determine the crop's nutrition status. The objectives of this study are to 1) identify aerial indices that are best correlated with tiller density and 2) determine a threshold for whether or not to apply N at GS 25 with aerial indices examined. Small-plot and strip trials with differing N rates were grown throughout Virginia in 2018. Tiller density was collected every 2–3 weeks from GS 20 through jointing. Ground normalized differential vegetative index (NDVI) and aerial images were collected at the same time as tiller density. Aerial images consisted of red–green–blue (RGB), near-infrared, and red-edge images, and were used to extract NDVI and normalized differential red-edge (NDRE) RGB images were used to derive Green Area (GA; hue angle from 60˚ to 120˚) and Greener Area (GGA; hue angle from 80˚ to 120˚). Images were processed in Pix4D and ImageJ, and data was compared to tiller density to determine the relationship between aerial data and tiller density. Data from 2019 in Warsaw, VA, showed aerial NDRE significantly correlated with tiller density at GS 25 ($r^2 = 0.71$, Fig. 1, p. 87) and GS 30 ($r^2 = 0.75$, Fig. 2, p. 87). Future work will develop experiments to evaluate thresholds from aerial indices to compare with established protocols to see how yields between the two methods compare.

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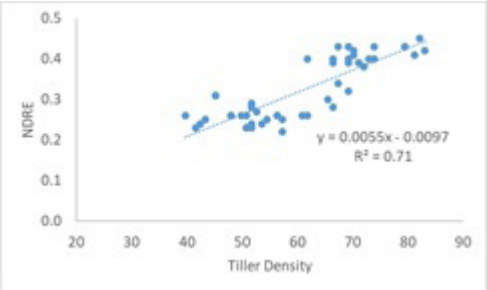

Fig. 1. Relationship between winter wheat tiller density and normalized differential red-edge (NDRE) measurements collected with a MicaSense RedEdge multispectral sensor at GS 25 in Warsaw, VA.

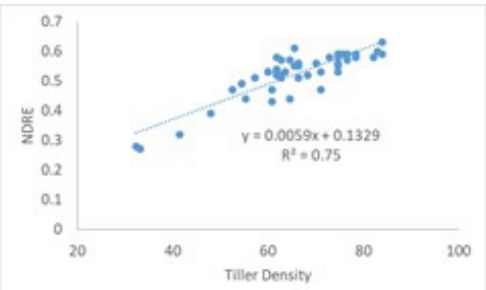

Fig. 2. Relationship between winter wheat tiller density and normalized differential red-edge (NDRE) measurements collected with a MicaSense RedEdge multispectral sensor at GS 30 in Warsaw, VA.

Assessment of Fusarium head blight in small grains using aerial methods.

Joseph Oakes and Josh Fitzgerald (Eastern Virginia Agricultural Research and Extension Center), and Carl Griffey (School of Plant and Environmental Sciences).

Fusarium head blight (FHB or scab) is a disease of small grains that lowers yield and produces a human health risk. However, current field assessment methodologies for evaluating FHB in small grains are time and resource intensive. As such, breeders are often limited to only a single date to assess the incidence and severity of the disease. The advent of UAV technology with multispectral sensors gives us the ability to collect more precise data in a timelier fashion. The objectives of this study are to 1) explore the ability to optically assess FHB index in comparison to currently adopted methods of visual assessment and 2) determine the practicality of using aerial imagery to quantify disease progress throughout the growing season. Six lines with varying maturity and FHB resistance were used in this pilot study. Scab epidemics were established in plots by scattering scabby corn (*Zea mays*) inoculum just prior to boot stage. Plots then received overhead fine-mist irrigation for approximately one month. Starting at heading and continuing twice weekly until maturity, visual FHB index and aerial images were collected. Aerial multispectral images were used to obtain normalized differential vegetative index (NDVI) and normalized differential red edge (NDRE). As expected, an increase in FHB resulted in a decrease in NDRE and NDVI. However, early maturing lines began to turn and dry down, thus causing them to have lower NDVI and NDRE values even though there was no FHB present. Therefore, data from each line was isolated to 21 days after flowering in order to remove the maturity factor. Once this was done, cultivars were ranked according to FHB index and compared with NDVI and NDRE (Table 2). NDVI ranked the cultivars the same as FHB index, with the exception of two. The cultivar Pioneer Brand 26R46, with the highest FHB index, had the lowest NDVI, and the cultivar Jamestown, with the lowest FHB index, had the lowest NDVI. Future work will look at using Convolutional Neural Networks to identify just the spikes and not be influenced by the leaves and stems.

Table 2. A ranking of the cultivars according to Fusarium head blight (FHB) index 21 days after flowering; with normalized differential vegetative index (NDVI) and normalized differential red edge (NDRE) comparisons.

Line	NDVI	NDRE	FHB index	Increase (%)
P26R46	0.73	0.42	84	89
Coker9835	0.81	0.52	40	61
L11541	0.80	0.45	16	36
Shirley	0.82	0.55	13	33
Tribute	0.85	0.55	16	27
Jamestown	0.87	0.56	3	14

Development of genetic markers to enhance breeding for nitrogen-use efficiency.

Kyle Brasier, Maria Balota, John Seago, Wade Thomason, and Carl Griffey (School of Plant and Environmental Sciences); Brian Ward, Myron Fountain, and Gina Brown-Guedira (USDA–ARS, North Carolina State University, Raleigh, NC 27695); Joseph Oakes (Eastern Virginia Agricultural Research and Extension Center); Paul Davis (Davis Produce, New

Table 3. Single genetic markers and combinations of genetic markers effect on nitrogen-use efficiency (kg/grain/kg applied nitrogen (N)) over four testing environments. † Percent increase (PI) conferred from the high nitrogen-use efficiency wheat parent (a; 5187J) and low nitrogen-use efficiency wheat parent (b; Yorktown); ‡ the LSD at $P \leq 0.05$ is used to compare allele groupings within N rates over four testing environments, means within a single or combination of QTL followed by the same letter are not significantly different.

Single marker	Low N kg/kg N		PI† %	High N kg/kg N		PI %	Combination of markers	Low N kg/kg N		PI %	High N kg/kg N		PI %
QNue.151-1D							1D + 6A						
a	64.8	a‡	2.9	36.5	a	2.2	aa	65.5	a	4.1	36.5	a	2.5
b	63.0	b		35.7	a		bb	62.9	b		35.6	a	
QNue.151-4A							1D + 7D						
a	63.5	b	–3.3	35.7	b	–4.2	aa	65.7	a	5.9	37.1	a	5.7
b	65.6	a		37.2	a		bb	62.0	b		35.1	b	
QNue.151-6A							6A + 7D						
a	64.7	a	2.7	36.2	a	0.8	aa	66.2	a	5.6	36.7	a	4.6
b	63.0	b		35.9	a		bb	62.7	b		35.1	b	
QNue.151-7D							1D + 6A + 7D						
a	65.1	a	2.8	36.8	a	3.3	aaa	66.6	a	5.0	36.9	a	4.2
b	63.3	b		35.6	b		bbb	63.4	b		35.4	b	

Kent, VA 22572); and Clay Sneller (Department of Horticulture and Crop Science, The Ohio State University, Wooster, OH 44691).

Maintaining winter wheat productivity with fewer or more efficient nitrogen (N) inputs will enable growers to increase profitability and reduce the negative environmental impacts associated with intensive agriculture. However, yield trials conducted under multiple N conditions are expensive and often not feasible for wheat breeders, who would benefit greatly from the identification and application of genetic markers associated with increased nitrogen-use efficiency. To investigate the genetic regulation of N response, two genetic mapping populations were developed and grown in four site-seasons under low (67 kg N/ha) and normal (134 kg N/ha) nitrogen rates. Both populations utilized a parent with high nitrogen-use efficiency (VA05W-151 (5187J, PI 665039) and VA09W-52) and shared a common low nitrogen-use efficiency parent, Yorktown (PI 667643). A total of 130 significant genetic markers were detected in the two populations; six of which were associated with nitrogen-use efficiency traits in multiple testing environments and, therefore, were deemed reliable. Three of the six genetic markers linked with nitrogen-use efficiency were associated with known day length response and disease resistance genes, two did not co-localize with known disease or morphological genes and had been previously reported, and a genetic marker on wheat chromosome 1D appeared novel. The genetic markers identified (Table 3) have potential implications for the marker-assisted breeding efforts at Virginia Tech and may lead to the eventual development of wheat cultivars with increased capacity to take up and utilize applied N fertilizer.

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WASHINGTON

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

Craig F. Morris, Douglas A. Engle, Mary L. Baldridge, Gail L. Peden, William J. Kelley, Shelle Lenssen, Eric Wegner, Alecia Kiszonas, Shawna Vogl, Janet Luna, Stacey Sykes, Robin Saam, Eden Stout, and Deidrea Power.

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

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

Publications.

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USDA–ARS NATIONAL SMALL GRAINS GERMPLASM RESEARCH FACILITY
1691 S. 2700 W., Aberdeen, ID 83210, USA.
www.ars-grin.gov/npgs

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

H.E. Bockelman, Agronomist and Curator.

Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN–Global): https://npgsweb.ars-grin.gov/gringlobal/search.aspx?. Certain accessions may not be available from the National Small Grains Collection due to intellectual property rights (PVP) or insufficient inventories. Accessions registered in the *Journal of Plant Registrations* (JPR) are available by contacting the developers. Some accessions require agreement with the Standard Material Transfer Agreement of the IT PGRFA in order to receive seed.

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
688251 JPR	*Triticum aestivum* subsp. *aestivum*	KS18WGRC65	United States	Kansas
688260	*Triticum turgidum* subsp. *durum*	Kandur 1171	United States	Kansas
688261	*Triticum turgidum* subsp. *durum*	Kandur 2074	United States	Kansas
688262	*Triticum turgidum* subsp. *durum*	Kandur 2258	United States	Kansas
688263	*Triticum turgidum* subsp. *durum*	Kandur 2291	United States	Kansas
688264	*Triticum turgidum* subsp. *durum*	Kandur 2363	United States	Kansas
688265	*Triticum turgidum* subsp. *durum*	Kandur 2371	United States	Kansas
688266	*Triticum turgidum* subsp. *durum*	Kandur 2380	United States	Kansas
688267	*Triticum turgidum* subsp. *durum*	Parental Line 19	United States	Kansas
688418 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Fusion AX	United States	Colorado
688419 PVP	*Triticum aestivum* subsp. *aestivum*	Incline AX	United States	Colorado
688420 PVP	*Triticum aestivum* subsp. *aestivum*	Breck	United States	Colorado
688423 PVP	*Secale cereale*	KWS Propower	United States	Illinois
688424 PVP	*Secale cereale*	LSR126	United States	Illinois
688425 PVP	*Secale cereale*	Lo1018-PxLo1017-N	United States	Illinois
689006 PVP	*Triticum aestivum* subsp. *aestivum*	AM Eastwood	United States	Colorado
689007 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Avenger	United States	Colorado
689008 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Yeti	United States	Colorado
689009 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Revere	United States	Colorado
689016 PVP	*Triticum aestivum* subsp. *aestivum*	WB9350	United States	Minnesota
689017 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Hulk	United States	Colorado
689018 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Shark	United States	Colorado
689019 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Sonic	United States	Colorado
689020 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Rocket	United States	Colorado
689021 PVP	*Triticum aestivum* subsp. *aestivum*	Thompson	United States	South Dakota
689043 PVP	*Triticum aestivum* subsp. *aestivum*	SY Legend CL2	United States	Iowa
689044 PVP	*Triticum aestivum* subsp. *aestivum*	SY Sienna	United States	Iowa
689045 PVP	*Triticum aestivum* subsp. *aestivum*	SY Candor	United States	Iowa
689046 PVP	*Triticum aestivum* subsp. *aestivum*	122009W	United States	Iowa
689047 PVP	*Triticum aestivum* subsp. *aestivum*	SY Collins	United States	Iowa
689115	*Triticum aestivum* subsp. *aestivum*	KS14U6380R5	United States	Kansas
689116	*Triticum aestivum* subsp. *aestivum*	KS16U6380R10	United States	Kansas

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
689117	*Triticum aestivum* subsp. *aestivum*	KS16U6380R11	United States	Kansas
689120 PVP	*Triticum aestivum* subsp. *aestivum*	UC-Central Red	United States	California
689121 PVP	*Triticum turgidum* subsp. *durum*	UC-Desert Gold	United States	California
689207	*Triticum aestivum* subsp. *aestivum*	NEG2015-9101	United States	Nebraska
689208	*Triticum aestivum* subsp. *aestivum*	NEG2015-9102	United States	Nebraska
689209	*Triticum aestivum* subsp. *aestivum*	NEG2015-9103	United States	Nebraska
689210	*Triticum aestivum* subsp. *aestivum*	NEG2015-9104	United States	Nebraska
689211	*Triticum aestivum* subsp. *aestivum*	NEG2015-9106	United States	Nebraska
689212	*Triticum aestivum* subsp. *aestivum*	NEG2015-9107	United States	Nebraska
689213	*Triticum aestivum* subsp. *aestivum*	NEG2015-9108	United States	Nebraska
689214	*Triticum aestivum* subsp. *aestivum*	NEG2015-9109	United States	Nebraska
689215	*Triticum aestivum* subsp. *aestivum*	NEG2015-9110	United States	Nebraska
689216	*Triticum aestivum* subsp. *aestivum*	NEG2015-9112	United States	Nebraska
689217	*Triticum aestivum* subsp. *aestivum*	NEG2015-9113	United States	Nebraska
689218	*Triticum aestivum* subsp. *aestivum*	NEG2015-9114	United States	Nebraska
689219	*Triticum aestivum* subsp. *aestivum*	NEG2015-9116	United States	Nebraska
689220	*Triticum aestivum* subsp. *aestivum*	NEG2015-9117	United States	Nebraska
689221	*Triticum aestivum* subsp. *aestivum*	NEG2015-9118	United States	Nebraska
689222	*Triticum aestivum* subsp. *aestivum*	NEG2015-9120	United States	Nebraska
689223	*Triticum aestivum* subsp. *aestivum*	NEG2015-9121	United States	Nebraska
689224	*Triticum aestivum* subsp. *aestivum*	NEG2015-9122	United States	Nebraska
689225	*Triticum aestivum* subsp. *aestivum*	NEG2015-9123	United States	Nebraska
689226	*Triticum aestivum* subsp. *aestivum*	NEG2015-9124	United States	Nebraska
689227	*Triticum aestivum* subsp. *aestivum*	NEG2015-9125	United States	Nebraska
689228	*Triticum aestivum* subsp. *aestivum*	NEG2015-9128	United States	Nebraska
689229	*Triticum aestivum* subsp. *aestivum*	NEG2015-9129	United States	Nebraska
689230	*Triticum aestivum* subsp. *aestivum*	NEG2015-9130	United States	Nebraska
689231	*Triticum aestivum* subsp. *aestivum*	NEG2015-9131	United States	Nebraska
689232	*Triticum aestivum* subsp. *aestivum*	NEG2015-9135	United States	Nebraska
689233	*Triticum aestivum* subsp. *aestivum*	NEG2015-9136	United States	Nebraska
689234	*Triticum aestivum* subsp. *aestivum*	NEG2015-9142	United States	Nebraska
689235	*Triticum aestivum* subsp. *aestivum*	NEG2015-9144	United States	Nebraska
689236	*Triticum aestivum* subsp. *aestivum*	NEG2015-9145	United States	Nebraska
689237	*Triticum aestivum* subsp. *aestivum*	NEG2015-9147	United States	Nebraska
689238	*Triticum aestivum* subsp. *aestivum*	NEG2015-9152	United States	Nebraska
689239	*Triticum aestivum* subsp. *aestivum*	NEG2015-9115	United States	Nebraska
689240	*Triticum aestivum* subsp. *aestivum*	NEG2015-9119	United States	Nebraska
689241	*Triticum aestivum* subsp. *aestivum*	N17GH9008-1	United States	Nebraska
689242	*Triticum aestivum* subsp. *aestivum*	N17GH9008-2	United States	Nebraska
689243	*Triticum aestivum* subsp. *aestivum*	N17GH9010-1	United States	Nebraska
689244	*Triticum aestivum* subsp. *aestivum*	N17GH9010-2	United States	Nebraska
689245	*Triticum aestivum* subsp. *aestivum*	N17GH9012-1	United States	Nebraska
689246	*Triticum aestivum* subsp. *aestivum*	N17GH9012-2	United States	Nebraska
689247	*Triticum aestivum* subsp. *aestivum*	N17GH9014-1	United States	Nebraska
689248	*Triticum aestivum* subsp. *aestivum*	N17GH9014-2	United States	Nebraska
689249	*Triticum aestivum* subsp. *aestivum*	N17GH9018-1	United States	Nebraska
689250	*Triticum aestivum* subsp. *aestivum*	N17GH9018-2	United States	Nebraska
689251	*Triticum aestivum* subsp. *aestivum*	N17GH9019-1	United States	Nebraska
689252	*Triticum aestivum* subsp. *aestivum*	N17GH9019-2	United States	Nebraska
689253	*Triticum aestivum* subsp. *aestivum*	N17GH9022-1	United States	Nebraska
689254	*Triticum aestivum* subsp. *aestivum*	N17GH9022-2	United States	Nebraska
689255	*Triticum aestivum* subsp. *aestivum*	N17GH9023-1	United States	Nebraska

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
689256	*Triticum aestivum* subsp. *aestivum*	N17GH9023-2	United States	Nebraska
689257	*Triticum aestivum* subsp. *aestivum*	N17GH9024-1	United States	Nebraska
689258	*Triticum aestivum* subsp. *aestivum*	N17GH9024-2	United States	Nebraska
689259	*Triticum aestivum* subsp. *aestivum*	N17GH9026-1	United States	Nebraska
689260	*Triticum aestivum* subsp. *aestivum*	N17GH9028-1	United States	Nebraska
689261	*Triticum aestivum* subsp. *aestivum*	N17GH9028-2	United States	Nebraska
689262	*Triticum aestivum* subsp. *aestivum*	N17GH9029-1	United States	Nebraska
689263	*Triticum aestivum* subsp. *aestivum*	N17GH9029-2	United States	Nebraska
689264	*Triticum aestivum* subsp. *aestivum*	N17GH9033-1	United States	Nebraska
689265	*Triticum aestivum* subsp. *aestivum*	N17GH9033-2	United States	Nebraska
689266	*Triticum aestivum* subsp. *aestivum*	N17GH9035-1	United States	Nebraska
689267	*Triticum aestivum* subsp. *aestivum*	N17GH9035-2	United States	Nebraska
689268	*Triticum aestivum* subsp. *aestivum*	N17GH9048-1	United States	Nebraska
689269	*Triticum aestivum* subsp. *aestivum*	N17GH9048-2	United States	Nebraska
689270	*Triticum aestivum* subsp. *aestivum*	N17GH9054-1	United States	Nebraska
689271	*Triticum aestivum* subsp. *aestivum*	N17GH9054-2	United States	Nebraska
689272	*Triticum aestivum* subsp. *aestivum*	N17GH9059-1	United States	Nebraska
689273	*Triticum aestivum* subsp. *aestivum*	N17GH9060-1	United States	Nebraska
689274	*Triticum aestivum* subsp. *aestivum*	N17GH9060-2	United States	Nebraska
689275	*Triticum aestivum* subsp. *aestivum*	N17GH9070-1	United States	Nebraska
689276	*Triticum aestivum* subsp. *aestivum*	N17GH9070-2	United States	Nebraska
689277	*Triticum aestivum* subsp. *aestivum*	N17GH9073-1	United States	Nebraska
689278	*Triticum aestivum* subsp. *aestivum*	N17GH9073-2	United States	Nebraska
689279	*Triticum aestivum* subsp. *aestivum*	N17GH9076-1	United States	Nebraska
689280	*Triticum aestivum* subsp. *aestivum*	N17GH9076-2	United States	Nebraska
689281	*Triticum aestivum* subsp. *aestivum*	N17GH9078-1	United States	Nebraska
689282	*Triticum aestivum* subsp. *aestivum*	N17GH9078-2	United States	Nebraska
689283	*Triticum aestivum* subsp. *aestivum*	N17GH9081-1	United States	Nebraska
689284	*Triticum aestivum* subsp. *aestivum*	N17GH9081-2	United States	Nebraska
689285	*Triticum aestivum* subsp. *aestivum*	N17GH9090-1	United States	Nebraska
689286	*Triticum aestivum* subsp. *aestivum*	N17GH9090-2	United States	Nebraska
689287	*Triticum aestivum* subsp. *aestivum*	N17GH9093-1	United States	Nebraska
689288	*Triticum aestivum* subsp. *aestivum*	N17GH9093-2	United States	Nebraska
689289	*Triticum aestivum* subsp. *aestivum*	N17GH9095-1	United States	Nebraska
689290	*Triticum aestivum* subsp. *aestivum*	N17GH9095-2	United States	Nebraska
689291	*Triticum aestivum* subsp. *aestivum*	N17GH9003-1	United States	Nebraska
689292	*Triticum aestivum* subsp. *aestivum*	N17GH9003-2	United States	Nebraska
689293	*Triticum aestivum* subsp. *aestivum*	N17GH9017-1	United States	Nebraska
689294	*Triticum aestivum* subsp. *aestivum*	N17GH9017-2	United States	Nebraska
689295	*Triticum aestivum* subsp. *aestivum*	N17GH9020-1	United States	Nebraska
689296	*Triticum aestivum* subsp. *aestivum*	N17GH9020-2	United States	Nebraska
689297	*Triticum aestivum* subsp. *aestivum*	N17GH9027-1	United States	Nebraska
689298	*Triticum aestivum* subsp. *aestivum*	N17GH9027-2	United States	Nebraska
689299	*Triticum aestivum* subsp. *aestivum*	N17GH9031-1	United States	Nebraska
689300	*Triticum aestivum* subsp. *aestivum*	N17GH9031-2	United States	Nebraska
689301	*Triticum aestivum* subsp. *aestivum*	N17GH9037-1	United States	Nebraska
689302	*Triticum aestivum* subsp. *aestivum*	N17GH9037-2	United States	Nebraska
689303	*Triticum aestivum* subsp. *aestivum*	N17GH9039-1	United States	Nebraska
689304	*Triticum aestivum* subsp. *aestivum*	N17GH9039-2	United States	Nebraska
689305	*Triticum aestivum* subsp. *aestivum*	N17GH9040-1	United States	Nebraska
689306	*Triticum aestivum* subsp. *aestivum*	N17GH9040-2	United States	Nebraska
689307	*Triticum aestivum* subsp. *aestivum*	N17GH9041-1	United States	Nebraska

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
689308	*Triticum aestivum* subsp. *aestivum*	N17GH9041-2	United States	Nebraska
689309	*Triticum aestivum* subsp. *aestivum*	N17GH9043-1	United States	Nebraska
689310	*Triticum aestivum* subsp. *aestivum*	N17GH9043-2	United States	Nebraska
689311	*Triticum aestivum* subsp. *aestivum*	N17GH9044-1	United States	Nebraska
689312	*Triticum aestivum* subsp. *aestivum*	N17GH9044-2	United States	Nebraska
689313	*Triticum aestivum* subsp. *aestivum*	N17GH9049-1	United States	Nebraska
689314	*Triticum aestivum* subsp. *aestivum*	N17GH9050-1	United States	Nebraska
689315	*Triticum aestivum* subsp. *aestivum*	N17GH9050-2	United States	Nebraska
689316	*Triticum aestivum* subsp. *aestivum*	N17GH9052-1	United States	Nebraska
689317	*Triticum aestivum* subsp. *aestivum*	N17GH9052-2	United States	Nebraska
689318	*Triticum aestivum* subsp. *aestivum*	N17GH9058-1	United States	Nebraska
689319	*Triticum aestivum* subsp. *aestivum*	N17GH9058-2	United States	Nebraska
689320	*Triticum aestivum* subsp. *aestivum*	N17GH9061-1	United States	Nebraska
689321	*Triticum aestivum* subsp. *aestivum*	N17GH9061-2	United States	Nebraska
689322	*Triticum aestivum* subsp. *aestivum*	N17GH9066-1	United States	Nebraska
689323	*Triticum aestivum* subsp. *aestivum*	N17GH9066-2	United States	Nebraska
689324	*Triticum aestivum* subsp. *aestivum*	N17GH9067-1	United States	Nebraska
689325	*Triticum aestivum* subsp. *aestivum*	N17GH9067-2	United States	Nebraska
689326	*Triticum aestivum* subsp. *aestivum*	N17GH9072-1	United States	Nebraska
689327	*Triticum aestivum* subsp. *aestivum*	N17GH9072-2	United States	Nebraska
689328	*Triticum aestivum* subsp. *aestivum*	N17GH9077-1	United States	Nebraska
689329	*Triticum aestivum* subsp. *aestivum*	N17GH9077-2	United States	Nebraska
689330	*Triticum aestivum* subsp. *aestivum*	N17GH9084-1	United States	Nebraska
689331	*Triticum aestivum* subsp. *aestivum*	N17GH9084-2	United States	Nebraska
689332	*Triticum aestivum* subsp. *aestivum*	N17GH9085-1	United States	Nebraska
689333	*Triticum aestivum* subsp. *aestivum*	N17GH9088-1	United States	Nebraska
689334	*Triticum aestivum* subsp. *aestivum*	N17GH9088-2	United States	Nebraska
689335	*Triticum aestivum* subsp. *aestivum*	N17GH9098-1	United States	Nebraska
689336	*Triticum aestivum* subsp. *aestivum*	N17GH9098-2	United States	Nebraska
689337	*Triticum aestivum* subsp. *aestivum*	MD1535171	United States	Nebraska
689338	*Triticum aestivum* subsp. *aestivum*	MD1535181	United States	Nebraska
689339	*Triticum aestivum* subsp. *aestivum*	MD1534202	United States	Nebraska
689340	*Triticum aestivum* subsp. *aestivum*	DH15GH8241	United States	Nebraska
689341	*Triticum aestivum* subsp. *aestivum*	DH15GH8248	United States	Nebraska
689342	*Triticum aestivum* subsp. *aestivum*	DH15GH8253	United States	Nebraska
689343	*Triticum aestivum* subsp. *aestivum*	DH15GH8255	United States	Nebraska
689344	*Triticum aestivum* subsp. *aestivum*	DH15GH8261	United States	Nebraska
689345	*Triticum aestivum* subsp. *aestivum*	DH15GH8268	United States	Nebraska
689346	*Triticum aestivum* subsp. *aestivum*	DH15GH8270	United States	Nebraska
689347	*Triticum aestivum* subsp. *aestivum*	DH15GH8272	United States	Nebraska
689348	*Triticum aestivum* subsp. *aestivum*	DH15GH8280	United States	Nebraska
689349	*Triticum aestivum* subsp. *aestivum*	DH15GH8281	United States	Nebraska
689350	*Triticum aestivum* subsp. *aestivum*	DH15GH8017	United States	Nebraska
689351	*Triticum aestivum* subsp. *aestivum*	DH15GH8022	United States	Nebraska
689352	*Triticum aestivum* subsp. *aestivum*	DH2014240-4	United States	Nebraska
689353	*Triticum aestivum* subsp. *aestivum*	DH2014240-8	United States	Nebraska
689354	*Triticum aestivum* subsp. *aestivum*	DH16GH7212	United States	Nebraska
689355	*Triticum aestivum* subsp. *aestivum*	DH16GH7214	United States	Nebraska
689356	*Triticum aestivum* subsp. *aestivum*	DH16GH7233	United States	Nebraska
689357	*Triticum aestivum* subsp. *aestivum*	DH16GH7251	United States	Nebraska
689358	*Triticum aestivum* subsp. *aestivum*	DH16GH7283	United States	Nebraska
689359	*Triticum aestivum* subsp. *aestivum*	DH16GH7296	United States	Nebraska

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
689360	*Triticum aestivum* subsp. *aestivum*	DH16GH8015	United States	Nebraska
689361	*Triticum aestivum* subsp. *aestivum*	DH16GH8031	United States	Nebraska
689362	*Triticum aestivum* subsp. *aestivum*	DH16GH8056	United States	Nebraska
689363	*Triticum aestivum* subsp. *aestivum*	DH2014110-9	United States	Nebraska
689364	*Triticum aestivum* subsp. *aestivum*	DH2014324-6	United States	Nebraska
689365	*Triticum aestivum* subsp. *aestivum*	DH15GH8070	United States	Nebraska
689366	*Triticum aestivum* subsp. *aestivum*	DH15GH8211	United States	Nebraska
689367	*Triticum aestivum* subsp. *aestivum*	DH15GH8214	United States	Nebraska
689368	*Triticum aestivum* subsp. *aestivum*	NX15GH8036	United States	Nebraska
689369	*Triticum aestivum* subsp. *aestivum*	NX15GH8024	United States	Nebraska
689370	*Triticum aestivum* subsp. *aestivum*	N14MD7124-108	United States	Nebraska
689371	*Triticum aestivum* subsp. *aestivum*	MD1534103	United States	Nebraska
689372	*Triticum aestivum* subsp. *aestivum*	N14MD7105-53	United States	Nebraska
689373	*Triticum aestivum* subsp. *aestivum*	N14MD7115-48	United States	Nebraska
689374	*Triticum aestivum* subsp. *aestivum*	MD1535232	United States	Nebraska
689375	*Triticum aestivum* subsp. *aestivum*	MD153583	United States	Nebraska
689376	*Triticum aestivum* subsp. *aestivum*	NX15MD9003-15	United States	Nebraska
689377	*Triticum aestivum* subsp. *aestivum*	N15MD6219	United States	Nebraska
689378	*Triticum aestivum* subsp. *aestivum*	N15MD6250	United States	Nebraska
689379	*Triticum aestivum* subsp. *aestivum*	MD1535212	United States	Nebraska
689380	*Triticum aestivum* subsp. *aestivum*	MD1535223	United States	Nebraska
689381	*Triticum aestivum* subsp. *aestivum*	N14MD7119-27	United States	Nebraska
689382	*Triticum aestivum* subsp. *aestivum*	NW13MD108-3	United States	Nebraska
689383	*Triticum aestivum* subsp. *aestivum*	NW13MD109-1	United States	Nebraska
689432 JPR	*Triticum aestivum* subsp. *aestivum*	PGMB-15-30	Pakistan	
689449 JPR	*Triticum aestivum* subsp. *aestivum*	MT363-4	United States	Montana
689450 JPR	*Triticum aestivum* subsp. *aestivum*	MT421-27	United States	Montana
689451 JPR	*Triticum aestivum* subsp. *aestivum*	MT777-14	United States	Montana
689452 JPR	*Triticum aestivum* subsp. *aestivum*	MT1306-19	United States	Montana
689453 JPR	*Triticum aestivum* subsp. *aestivum*	MT1899-9	United States	Montana
689454 JPR	*Triticum aestivum* subsp. *aestivum*	MT2092-42	United States	Montana
689455 JPR	*Triticum aestivum* subsp. *aestivum*	MT2252-14	United States	Montana
689518 PVP	*Triticum aestivum* subsp. *aestivum*	GA14E53	United States	Georgia
689519 PVP	*Triticum aestivum* subsp. *aestivum*	GA14E45	United States	Georgia
689520 PVP	*Triticum aestivum* subsp. *aestivum*	GA14E19	United States	Georgia
689521 JPR	*Triticum aestivum* subsp. *aestivum*	MNR527	United States	Montana
689522 JPR	*Triticum aestivum* subsp. *aestivum*	MNR434	United States	Montana
689523 PVP	*Triticum aestivum* subsp. *aestivum*	WB4418	United States	Minnesota
689524 PVP	*Triticum aestivum* subsp. *aestivum*	WB7202CLP	United States	Minnesota
689525 PVP	*Triticum aestivum* subsp. *aestivum*	WB9717	United States	Minnesota
689526 PVP	*Triticum aestivum* subsp. *aestivum*	WB9433	United States	Minnesota
689527 PVP	*Triticum aestivum* subsp. *aestivum*	WB1532	United States	Minnesota
689532 PVP	*Triticum aestivum* subsp. *aestivum*	SY Longmire	United States	Iowa
689533 PVP	*Triticum aestivum* subsp. *aestivum*	SY 611 CL2	United States	Iowa
689534 PVP	*Triticum aestivum* subsp. *aestivum*	122010W	United States	Iowa
689535 PVP	*Triticum aestivum* subsp. *aestivum*	SY McCloud	United States	Iowa
689536 PVP	*Triticum aestivum* subsp. *aestivum*	SY Renegade	United States	Iowa
689563	*Triticum aestivum* subsp. *aestivum*	Sr60 Introgression …	United States	California
689609 PVP	*Triticum aestivum* subsp. *aestivum*	Featherstone 31	United States	Virginia
689753 PVP	*Triticum aestivum* subsp. *aestivum*	FourOsix	United States	Montana
689754 PVP	*Triticum aestivum* subsp. *aestivum*	Ray	United States	Montana
689763 PVP	*Triticum aestivum* subsp. *aestivum*	Cannon	United States	Colorado

Table 1. Recent PI assignments in *Triticum, X Triticosecale, Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
689764 PVP	*Triticum aestivum* subsp. *aestivum*	MS Barracuda	United States	Colorado
689766 PVP	*Triticum aestivum* subsp. *aestivum*	SR8483	United States	Virginia
689773 PVP	*Triticum aestivum* subsp. *aestivum*	MTF1435	United States	Montana
689883	*Triticum aestivum* subsp. *spelta*	Diamond	United States	Indiana
689884	*Triticum aestivum* subsp. *spelta*	Moses	United States	Indiana
689885	*Triticum aestivum* subsp. *spelta*	Explorer	United States	Indiana
689886	*Triticum aestivum* subsp. *spelta*	Legacy	United States	Indiana
689887	*Triticum aestivum* subsp. *spelta*	SE 10112-0151170-13	United States	Indiana
689888	*Triticum aestivum* subsp. *spelta*	SE 27790R-18	United States	Indiana
689889	*Triticum aestivum* subsp. *spelta*	26090A-B-R-16	United States	Indiana
689890	*Triticum aestivum* subsp. *spelta*	SE26290A-RA-RB-39	United States	Indiana
689891	*Triticum aestivum* subsp. *spelta*	SE27390RA-RB-18	United States	Indiana
689892	*Triticum aestivum* subsp. *spelta*	Spelt-outcross-2	United States	Indiana
689893	*Triticum aestivum* subsp. *spelta*	WK91009	United States	Indiana
689894	*Triticum aestivum* subsp. *spelta*	WK91037	United States	Indiana
689895	*Triticum aestivum* subsp. *spelta*	WK91079	United States	Indiana
689896	*Triticum aestivum* subsp. *spelta*	WK91115	United States	Indiana
689897	*Triticum aestivum* subsp. *spelta*	WK91175	United States	Indiana
689898	*Triticum aestivum* subsp. *spelta*	WK946153	United States	Indiana
689899	*Triticum aestivum* subsp. *spelta*	SE2609012B-R-23	United States	Indiana
689900	*Triticum aestivum* subsp. *spelta*	ZS27290RA-RB-3	United States	Indiana
689901	*Triticum aestivum* subsp. *spelta*	SE27980A-RA-RB-2	United States	Indiana
689902	*Triticum aestivum* subsp. *spelta*	SE28090RA-RC-20	United States	Indiana
689903	*Triticum aestivum* subsp. *spelta*	WK87066-5	United States	Indiana
689904	*Triticum aestivum* subsp. *spelta*	WK86025-6	United States	Indiana
689905	*Triticum aestivum* subsp. *spelta*	SE500391-12	United States	Indiana
689906	*Triticum aestivum* subsp. *spelta*	224-405	United States	Indiana
689907	*Triticum aestivum* subsp. *spelta*	226-605	United States	Indiana
689908	*Triticum aestivum* subsp. *spelta*	228-905	United States	Indiana
689909	*Triticum aestivum* subsp. *spelta*	229-1005	United States	Indiana
689910	*Triticum aestivum* subsp. *spelta*	230-1105	United States	Indiana
689911	*Triticum aestivum* subsp. *spelta*	235-1605	United States	Indiana
689912	*Triticum aestivum* subsp. *spelta*	239-2105	United States	Indiana
689913	*Triticum aestivum* subsp. *spelta*	240-2205	United States	Indiana
689914	*Triticum aestivum* subsp. *spelta*	245-406	United States	Indiana
689915	*Triticum aestivum* subsp. *spelta*	248-706	United States	Indiana
689916	*Triticum aestivum* subsp. *spelta*	252-1106	United States	Indiana
689917	*Triticum aestivum* subsp. *spelta*	259-1806	United States	Indiana
689918	*Triticum aestivum* subsp. *spelta*	261-2006	United States	Indiana
689919	*Triticum aestivum* subsp. *spelta*	267-2606	United States	Indiana
689920	*Triticum aestivum* subsp. *spelta*	270-2906	United States	Indiana
689921	*Triticum aestivum* subsp. *spelta*	273-3206	United States	Indiana
689922	*Triticum aestivum* subsp. *spelta*	274-3306	United States	Indiana
689923	*Triticum aestivum* subsp. *spelta*	275-3406	United States	Indiana
689924	*Triticum aestivum* subsp. *spelta*	276-3506	United States	Indiana
689925	*Triticum aestivum* subsp. *spelta*	278-3706	United States	Indiana
689994 PVP	*Triticum aestivum* subsp. *aestivum*	112380W	United States	Iowa
689995 PVP	*Triticum aestivum* subsp. *aestivum*	16162669	United States	Iowa
689996 PVP	*Triticum aestivum* subsp. *aestivum*	16162674	United States	Iowa
689997 PVP	*Triticum aestivum* subsp. *aestivum*	16162681	United States	Iowa
690085 PVP	*Triticum aestivum* subsp. *aestivum*	Showdown	United States	Oklahoma
690086 PVP	*Triticum aestivum* subsp. *aestivum*	Green Hammer	United States	Oklahoma

Table 1. Recent PI assignments in *Triticum*, *X Triticosecale*, *Aegilops*, and *Secale* (Note: there were no PI assignments in *Aegilops* during this period).

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
690087 PVP	*Triticum aestivum* subsp. *aestivum*	Baker's Ann	United States	Oklahoma
690088 PVP	*Triticum aestivum* subsp. *aestivum*	Skydance	United States	Oklahoma
690434 PVP	*Triticum aestivum* subsp. *aestivum*	Ag Icon	United States	Kansas
690435 PVP	*Triticum aestivum* subsp. *aestivum*	Bob Dole	United States	Kansas
690467 PVP	*Triticum aestivum* subsp. *aestivum*	KS Venada	United States	Kansas

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2019 SUPPLEMENT

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

[1]The University of Sydney, Plant Breeding Institute Cobbitty, PMB 4011, Narellen, NSW 2570, Australia. robert.mcintosh@sydney.edu.au.
[2]Department of Plant Sciences, University of California, Davis, CA 95616, USA. jdubcovsky@ucdavis.edu.
[3]Catedra de Genetica y Fitotecnia, DCBA y B, Facultad de Agronomia, CIISAS, CIC–BIOLAB AZUL, Universidad Nacional del Centro de la Provincia de Buenos Aires, Argentina; Av. Rep. Italia 780, CC47 73 Azul, Provincia de Buenos Aires, Argentina. CONICET–INBA–CEBB–MdP. rogers@faa.unicen.edu.ar.
[4]Institute of Crop Science, National Wheat Improvement Centre, Chinese Academy of Agricultural Sciences, 12 Zhongguancun South St, Beijing 100081, China. xiaxianchun@caas.cn.
[5]Department of Plant Pathology, Wheat Genetics Resource Center, Kansas State University, Manhattan, Kansas 66506, U.S.A. jraupp@k-state.edu.

The most recent version of the Catalogue, compiled for the 13Th International Wheat Genetics Symposium held in Yokohama, Japan, is available on the Komugi (http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp) and GrainGenes (http://wheat.pw.usda.gov/GG2/*Triticum*/wgc/2008/) websites. Supplements 2014, 2015, 2016, 2017, and 2018 also are available at those sites.

Suggestions of information, preferably in suitable format, for listing in the Wheat Gene Catalogue can be submitted to the curators. Publication details on papers listed as 'Draft Manuscript' or 'In press' also would be helpful.

Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1. Squarehead/spelt

Q. Add synonym '*Ap2-5A*'.
c: Move the last sentence under **ma:** to a new section **c:** and Add: GenBank AY02956.1.

Add note: The pleiotropic features of the *Q* locus include effects on glume toughness, threshability, rachis fragility, spike length, flowering time, and plant height {11342}.

At the end of section: add two references, i.e., '{11192, 11344}. Final spike and reproductive morphology is affected by the *Q*/*q* sequence and its regulation by miR172 {11344} along with direct or indirect interaction with the homoeologues {11344}.

Homoeologues of *Q* were described in {11192}. Both have miRNA172 target sites close to the 3' ends of the coding region. These genes were referred to as *Ap2-5B*, a transcriptionally active pseudogene, and *Ap2-5D*, that encodes a functional protein that contributes to suppression of the speltoid phenotype {11342}. Reduced height gene *Rht23*, a mutationally derived allele in NAUH164, was caused by a SNP (G3147A, Ala416Thr) within the miR172 target site in 5Dq that permitted up-regulation of *Ap2-5D* due to down-regulation of miR172 in leaves, stems and spikes {11345}.

17. Crossability with Rye and *Hordeum* and *Aegilops* spp.

kr5 [{11387}]. *skr* {11352}, {11352}. 5BS {11352}.
su: Courtot (Fukuhokomugi 5B) {11352}.
v: Balthazar-crossable {11352}; Deucendeu {11352}; Ornicar-crossable {11352}.
Balthazar-crossable and Ornicar-crossable probably also carry *kr1* {11352}.

44. Height

44.2. Reduced Height: GA-sensitive

***Rht-B1c*.** **c:** *Rht-B1c* carries a 2,026-bp insertion of a *terminal repeat transposons in miniature* (TRIM) insertion at position 147 bp relative to *Rht-B1a*; this leads to an additional 30 amino acids in the DEELLA domain affecting affinity between GID1 and Della {11390}. Genbank JN857970 (gDNA), JN859791 (cDNA) {11390}.

***Rht14*.** **ma:** Add: Mapped to genomic region 383–422 Mb flanked by *GA20xA9* and *Xwmc753-6A* {11372}.

***Rht25*.** Add synonym: *5Dq* {11345}.

c: NAUH164 has a G3147A (Ala416Thr) SNP mutation relative to its Sumai 3 parent, AP2-D is the likely candidate for *Rht23* {11345}.

46. Hybrid Weakness

46.1. Hybrid necrosis

***Ne1*.** **ma:** *Ne1* – 11 cM – *Xgwm639-5B* {11343}.

***Ne2*.** **ma:** *Xbarc7-2B* – 3 cM – *Ne2* – 6 cM – *Xwmc344-2B* {11343}.

49. Leaf Characteristics

Re-organization

49.1. Leaf erectness Currently: 49. Leaf Erectness

49.2. Leaf tip necrosis Currently: 50. Leaf Tip Necrosis

49.3. Seedling leaf chlorosis Currently: 64. Seedling leaf chlorosis

NEW:

49.4. Early leaf senescence

els1 {11326}. 2BS {11326}.

v: ZK331 / Xiangmai 99171 // 2*Lumai 30 Line 114 {11326}.

ma: *WGGB305* – 0.3 cM – *els1*/*WGGB302* – 1.2 cM – *WGGB303*/*WGGB304*/*WGGB306* – 0.6 cM – *Xbarc92-2B* {11326}.

The *els1* 'mutant' was detected in an F_4 population. Because the parents had a normal phenotype, complementary genes were likely involved. The similar location of *ELS1* to the *NE1* locus in chromosome 2BS and similar phenotype suggests that this gene may be *Ne2*. See 49. Hybrid Weakness; 49.1. Hybrid necrosis

53. Male Sterility

53.1. Chromosomal

***ms2*.** **ma:** Mapped to a 0.05-cM region flanked by *Xsauw27-4D* and *Xsdauw29-4D* {11388}.

c: *Ms2* has a long terminal-repeat in miniature (TRIM) transposon at position –314 to –310 {11388}. Genbank KX585234 {11388}.

The TRIM element acts as an enhancer that activates anther-specific transcription of the *Ms2* allele {11388, 11389}. *Ms2* induced male sterility in barley and *Brachypodium* {11388} as well as triticale {597, 11388}.

57. Meiotic Characters

57.2 Pairing homoeologous

***Ph1b*.** **ma:** Dualplex marker *Xwgc2111* + *Xwgc2049* behaves like a co-dominant marker {11359}.

Add note: The *Ph1b* deletion involves a region of at least 60,014,523 bp {11359}.

57.4 Asynapsis/desynapsis

A putative gene for desynapsis designated *Ddes2* was placed between *Xwmc325-3B* and *wPt-8983* in deletion bin 3BL7-0.63-1.00 by mapping of deletion hybrids {11339}. There is no mutant stock to represent this gene first reported in CS nullisomic 3B by Sears {1293}.

70. Response to Vernalization

Insert above *Vrn-B3*:

Vrn-A3. 7AS.

An earlier variant of *T. turgidum* subps. *dicoccum* line TN28 was caused by a novel allele. Line TN26 lacked a 7-bp insertion, including a cis-element GATA box, in the *Vrn-A3* promoter region {11370}.

80. Yield and Yield Components

80.7. Spikelet number/ear

WAPO1 {11383}. *Wheat Ortholog of APO1.*

WAPO-A1 {11383}. *TraesCS7A02G481600.* 7AL {11383}

ma: IWGSC RefSeq v1.0 coordinates 674,081,462 – 674,082,918.

Wapo-A1a {11383}. Low number of spikelets per spike (115-bp deletion in promoter and D384N amino acid change) {11383}.

v: RAC875 {11383}.

tv: Kronos {11383}.

Wapo-A1b {11383}. High number of spikelets per spike (C47F amino acid change) {11383}.

v: Berkut {11383}; Chinese Spring {11383}.

Wapo-A1c {11383}. Low number of spikelets per spike (115-bp deletion in promoter and D384N amino acid change) {11383}.

v: AGS2000 {11383}; LA95135 {11383}.

tv: PI 519639 {11383}.

Wapo-A1d {11383}. Low number of spikelets per spike {11383}.

tv: Langdon {11383}; Rusty {11383}.

Ful2 {11384}.

Loss of function mutation in gene *FUL-A2* (Kronos mutant T4-837) and *FUL-B2* (Kronos mutant T4-2911) resulted in significant increases in spikelet number {11384}.

Vrn1 {11384}. Loss of function mutation in gene *VRN-A1* (Kronos mutant T4-2268) and *VRN-B2* (Kronos mutant T4-2619) resulted in significant increases in spikelet number {11384}.

Pathogenic Disease/Pest Reaction

89. Reaction to *Bipolaris sorokiniana*

Add note at the beginning of section: This pathogen likely harbours Tox A in common with *Parastagonospora nodurum*, *Parastagonospora avenaria tritici,* and *Pyrenophora tritici-repentis* {11375}.

Sb2 {11375}. *QSb.bhu-5B* {11375} 5BL {11375}.

bin: 5BL1-0.55-0.75.

v: Ning 8201 {11375}; Yangmai 6 {11375}; YS116 {11375}.

ma: *Xgwm639-5B* – 1.4 cM – *Sb2* – 0.06 cM – *Xgwm1043-5B* {11375}.

sb2. *Tsn1* {11376}. **v:** Duster {11376}; Sonalika {11375}. Presumably all genotypes with *Snb1*.

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

Pm4e. **ma:** Add: *Xwgrc763-2A* – 0.13 cM – *Pm4e/Xwgrc872-2A/Xwgrc869-2A* – 0.58 cM – *Xwgrc982-2A*, a region of about 6.1 Mb {11335}.

Pm8. **ma:** An STS marker distinguished *Pm8* from *Pm17* {0186}. *Pm8* is located between *Gli/Glu3* and rust resistance genes *Sr31, Lr26* and *Yr9* {11354}.

c: *Pm8* is an orthologue of *Pm3* and an allele of *Pm8* in the rye genome {11354}. GenBank KF572030.

Delete the final sentence of comments: 'A STS marker…'.

Pm17. **v:** Add: Embrapa 16 {11355}; Hugenoot {11355}; TXGH13622 {11355}.

c: *Pm17* shares 96% nucleotide identity with *Pm8* (83% at the protein level) and low but significant identity with *Pm3CS* {11355}. GenBank MH0779.

Pm21. **v:** Yangmai 18 {11352}.
ma: Genetic mapping in a 'resistant × susceptible' *D. villosum* cross identified two RGA candidate loci (markers 6VS-09.4 and 6VS.09.4b) co-segregating with *Pm21* and overlapped by an EMS-induced, susceptible mutation {11352}.
c: Add: Marker 6VS-09.4 but not marker 6VS-09.4b was deleted in a susceptible mutant indicating that the former was *Pm21* – the protein product had a CC–NBS –LRR structure – GenBank MF370199 {11353}. This gene was different from *Stpk-V* {11275} but was quite similar to *NLR-V1* {11353}.

Pm57. Correction: '…..2BL (T2BS·2BL-2S^{S}#1)…'.
ad: Add: BCS+2S^{S}#1 TA3581 {11159}.

Pm62 {11321}. Adult-plant reaction. *Pm2VL* {11321}. T2BS·2VL#5 {11321}.
v: NAU1823 {11321}.
ma: *X2L4g9P4/Hae111* {11159}.

Pm63 {11331}. *Pm628024* {11331}. 2BL {11331}.
bin: 2BL6-0.89-1.00.
v: PI 628024 {11331}.
ma: *Xwmc175-2B* – 1.7 cM – *Xstars419-2B* – 0.6 cM – *Pm63* – 1.1 cM – *Xbcd135.2 – 2B*; 7103 – 7234 in the CS Reference Assembly {11331}.

Pm64 {11346}. *PmWE35* {11346}. 2BL {11346}.
bin: 2BL4-0.5-0.89.
v: WE35 {11346}.
tv: *T. turgidum* subps. *dicoccoides* G-573-1 {11346}.
ma: *Xwmc175-2B* – 1.12 cM – *Pm64/Xgwm47-2B* – 2.18 cM – *Xwmc332-2B* {11346}. Complete repulsion linkage with *Yr5* in 644 F_3 lines {11346}.

Pm65 {11356}. *PmXM208* {11356}. 2AL {11356}.
v: Xinmai 208 {11356}.
ma: *Xhbg327-2A* – 4.4 cM – *XresPm4/XTaAetPR5* – 0.6 cM – *PmXM208* – 1.6 cM – *Xbarc122-2A* {11356}. An allelism test of *Pm65* and *Pm4a* showed a recombination value of 10.3 cM based on the frequency of susceptible F_2 plants {11356}.

Pm66 {11364}. 4BS (T4BL·4S^{l}#7S) {11364}.
v: TA3465 {11364}.
al: *Ae. longissima* (unknown accession).
ma: 4S^{l}S markers developed in {11364}.

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

Insert at the beginning of the *Pm* series:

Pm10V-2 {11380}. 5DS {11380}.
bin: 5DS-0-0.63.
v: 10V-2 {11380}.
ma: *Xbwm25-5D/Xswgi066-5D* – 1.2 cM – *Pm10V-2/*several markers – 1.2 cM – *Xcfd-5D* {11380}.

The complex nature of temporarily named powdery mildew resistance genes in the *Pm2* region is discussed in {11380}.

Insert alphabetically:

PmTx45 {11374}. Recessive. 4BL {11374}.
bin: 4BL5-0.85-1.00. **v:** Tian Xuan 45 {11374}
ma: *Ax-110673642* – 3.0 cM – *PmTx45* – 2.6 cM – *ILP4B01G266900* {11374}.

95. Reaction to *Diuraphis noxia*

Dn1. Add note at end of section:
'VIGS silencing of *5AL-B4* on chromosome 5A compromised resistance conferred by *Dn1* suggesting a decoy role {11333}.'

96. Reaction to *Fusarium* spp.

96.1. Disease: Add: **Fusarium head scab, scab**

***QFhs.ndsu-3A*.** Add: This gene was transferred to durum cultivars using the closely linked marker *Xgwm2-3A* {11367}.

Luke (S) / AQ24788-83 (R): RIL population: *QFhb.cau-7DL* near marker *Xgwm428-7DL* was equally effective as *Fhb1* {11358}.

Under the heading 'Tetraploid wheat' add:
Ben*2 / Tunisian 108 BIL population: nine QTL for FHB resistance of which new QTL *Qfhb.ndsu-2B* and *Qfhb.ndsu-3BL* and *Qfhb.ndsu-5A* and *Qfhb.ndsu-7BL* were the most important {11382}.

99. Reaction to *Mayetiola destructor*

Add at end of section:
Jagger (S) / 2174 9 (R): RIL population: *QHf.osu-1A* (Syn. *Qhf.osu*^{74} ($R^2 = 0.70$) and *QHf.osu-2A* ($R^2 = 0.18$) {11325}. The QTL in chromosome 1A appeared to be co-linear with several previously named *H* genes in tetraploid wheat; the gene in 2A was in repulsion with the 2N segment present in Jagger {11325}.

Duster (R) / Billings: DH population: *QHf.osu.1A.2* (Syn. *QHf.osu-1A*^{d}), $R^2 = 0.88$, delimited to a 2.7 cM region flanked by *GBS07851* and *GBS10205* {11324}. This was a distinct locus 11.2 cM proximal to *QHf.osu.1A*.

Mayetiola-destructor susceptibility gene-1

Mds-1A [*Mds-1*] {11327}. 3AS {11327}.

v: No allelic variation demonstrated.

c: EST CD453475, GenBank JN162442; *Mds-1A* encodes a 151 amino-acid protein with 96% identity with HSP16.9 {11327}. Homoeologues are present in chromosomes 3B and 3D. Silencing of *Mds-1* expression caused immunity in otherwise FHB-susceptible genotypes {11327}.

101. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter, *Zymoseptoria tritici*

Stb19 {11360}. 1DS {11360}. **v:** Lorikeet {11360}.

ma: KASP markers snp_4909967 and snp_1218021 {11360}.

The source of *Stb19* was a synthetic wheat {11360}.
Add at end of section:
'See {11332, 11361} for reviews.'.

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

102.2 Sensitivity to SNB toxins (necrotrophic effectors)

***Snn1*.** Synonym: *TaWAK* {11341}.

c: *Snn1* encodes a wall-associated kinase (WAK) {11341}. GenBank: KP091701.

Snn1 was present in some *T. turgidum* subsp. *dicoccum* accessions, 73% of durum accessions and 16% of common wheat accessions {11341}.

***snn1*.** **s:** CS/Hope 1B {11341}.

105. Reaction to *Puccinia graminis* Pers.

***Sr26*.** **ma:** Add: Four KASP markers were developed for the original translocation (FL 0.85). WA-1 (AUS91435) a derivative with a shortened 6Ae#1 segment (FL 0.32), amplified only *sunKASP_224* and *sunKASP_225* {11336}. The latter was diagnostic for accession AGG91586WHEA *SrB*, a derivative of line WA-5 (AUS91436) {11338}. PCR markers based on NLR genes in homoeologous group 6 chromosomes were used to confirm that WA-2 Type 1 was the smallest secondary translocation carrying *Sr26* {11357}.

***Sr60*.** **c:** Cloning of *Sr60* from *T. monococcum* PI 306540 revealed a protein with two putative kinase domains designated Wheat Tandem Kinase 2 (WTK2) {11386}.

SrB {11337}. 6A = T6AS.6AL-6Ae#1-6Ae#3 {19018}.

v: AGG91586WHEA Sr26 {19018}.

ma: *SrB* was recombined with a 6Ae#1 segment possessing *Sr26*. Marker *sunKASP_225* {11336} was diagnostic for the recombined line AGG91586WHEA {11338}.

6Ae#3 {11338}. **su:** W3757 {11337}, a (6Ae#3(6D) line {11338}.

Complex genotypes:

Add:

PI 362698: *Sr5*, *Sr8a*, *Sr12*, *Sr15*?, *Sr16* {11347}.

106. Reaction to *Puccinia striiformis* Westend.

106.1. Designated genes for resistance to stripe rust

***YR5*.** Add to introductory sentence: ', but cloning indicated that *Yr7* is not allelic with *Yr5* and *YrSP* {11351}.

Yr5a [{11397}]. *Yr5*.

c: *Yr5* (GenBank MN275771) along with *Yr7* and *YrSP* has a BED–LRR structure lacking a CC-domain {11351}.

Yr5b [{11397}]. See *YrSP*, *YrSp*

c: (GenBank MN273772) along with *Yr5* and *Yr7* has a BED–LRR structure lacking a CC-domain {11351}. *YrSp* is a truncated form of *Yr5* but confers a different specificity {11351}.

***Yr7*.** Add to the introductory sentence: ', but cloning indicated that *Yr7* is not allelic with *Yr5* and *YrSP* {11351}.

v: Paragon {11351}.

c: *Yr7* (GenBank MN273773) along with *Yr5* and *YrSP* has a BED–LRR structure lacking a CC-domain {11351}.

Yr15. **v:** Add: Clearwhite 515 {11392} Expresso {11392}; Patwin 515 {11392}; Seahawk {11392}.

ma: *Xbarc-8-1B* – 4.2 cM – *Yr15* – 3.5 cM – *Xgwm413-1B* {11348}; *Xbarc8-1B* – 4.1 cM – *Yr15* – 2.5 cM – *Xuhw-1B* – 0.5 cM – *Xgwm413-1B* {11348}. *Yr15* is proximal to *Yr64*; recombinant lines are reported in {11349}; *Xwhu300-1B* – 0.013 cM – *Xwhu273-1B* {11392}.

c: Encodes a putative kinase-pseudokinase protein designated as wheat tandom kinase 1 (TPK1), g-DNA 4,655 bp, 665 amino acids. GenBank MG649384, MG674157 {11392}.

***Yr17*.** **v:** Add a reference following Jagger, i.e. 'Jagger {10973, 19008}'.

Add note at end of *Yr17* section: 'Mundt {11340} noted that many genotypes containing *Yr17* continued to have adult-plant resistance to races virulent on the seedlings. These cultivars included Renan, Apache, Jagger, Bobtail, and Madsen. However, it was unclear as to whether this represented additional resistance gene(s) in the introduced segment or APR genes at other loci.'.

***Yr24*.** Replace the final reference 939 in '{10339, 939}' with '{10339, 11391}'.

***Yr26*.** **ma:** Add: *Xgwm11-1B* – 0.9 cM – *Yr26* – 6.3 cM – *Xbarc181* {11350}. Located between KASP markers *WRS435* and *WRS312* in an interval of 0.4 cM {11350}.

Replace the final references '{10339, 939}' with '{10339,11391}'.

***Yr29*.** **ma:** *QYr.ucw-1BL* was mapped to a 0.24 cM region (332 kb IWGSC RefSeq v1.0 between *ucw.k31* and *csLV46G22* {11386}.

***Yr64*.** **ma:** *Yr64* is distal to *Yr15*; recombinant lines are reported in {11349}.

Yr82 {11322}. **bin:** 3BL7-0.63-1.00.

v2: AUS27969 = JI 1190592 *Yr29* {11322}.

ma: *KASP_13376/sunKASP_301* – 0.4 cM – *sunKASP_300* – 2.0 cM – *Yr82* – 2.0 cM – *KASP_8775* {11322}.

106.2. Temporarily designated genes for resistance to stripe rust

YrM866-4 {11381}. 4AL {11381}. **bin:** 4AL13-0.59-0.66.

v: M8664-3 {11381}.

ma: *Xgpw2331-4A* – 2.8 cM – *Yr8664-3* – 8.1 cM – *Xgpw3224-4A* {11381}.

106.3. Stripe rust QTL

Avocet S / PI182103 RIL population: QTL detected on chromosomes 2AS and 3AL for seedling resistance and 4DL, 5BS, and 7BL for APR; *QyrPI182103.wgp-4DL* was designated as *Yr79* {11222}.

Avocet S (S) / Qinnong 142 (R): RIL population: Adult-plant resistance: *QYrqin.nwafu-1BL – AX-95133868 – AX-94522424*, R^2 = 0.16–0.20, likely *Yr29*; *QYrqin.nwafu-2AL*, *AX-94655393 – AX-9489521*, R^2 = 0.08–0.20; *QYrqin.nwafu-2BL*, *AX-94507002 – AX-94562871*, R^2 = 0.18–0.39; *QYrqin.nwafu-6BS* R^2 = 0.14–0.31 {11377}.
Seedling resistance in Qinnong 142 to race CYR23 was attributed to genes on chromosomes 1DS and 4AL {11377}.

Jagger (MR) / 2174 (MS): After {10973}. Add: According to {11356} *Qyr.osu-5A* is an orthologue of *OsXA21* and confers resistance to multiple pathogens/pests.

Luke (MR) / AQ24788-83 (APR): RIL population: *QYr.cau-2AL* near *IWB4475* (R^2 = 23–40%) from AQ24788-83 and *Yr18* (R^2 = 11.0–14.7%) from Luke (11366).

Mingxian 169 (S) / Chakwal 86 (R): RIL population: QTL on chromosomes 1BL (*Yr29*), 3BS (not *Yr30*), and 6BS (*QYrcw.nwafu-6BS*) contributed to the high level of APR in Chakwal 86 {11371}.

Mingxian (S) / P9936 (R): RIL population: *QYr.nwafu-3BS* (probably *Yr30*) and *QYr.nwafu-7BL* flanked by *AX-108819274* and *AX*-11040708 (R^2 = 36.0–38.9%; a KASP marker was developed for the latter {11373}.

Mingxian 169 (S) / Qing Shumai (R): RIL population: APR QTL *QYr.cau.6DL*, *Xbarc1121-6D – Xgpw4005-6D* region: positive interaction with *Yr18* {11323}.

Mingxian 169 (S) / Centrum (R): RIL population: QTL detected on chromosomes 7BL (*QYrcen.nwafu-7BL*, R^2 = 23.4%, *AX-94556751 – AX-110366788*), 1AL (*QYrcen.nwafu-1AL* (R^2 = 11.2%, *AX-94488258 – AX-94458040*), and 4AL (*QYrcen.nwafu-4BL*, R^2 = 12.6%, *AX-94695204 – AX94996273* {11365}.

Mingxian 169 (S) / Toni (R): RIL population: *QYrto.swust-3AS*, *AX-95240 – AX-9482889091*, R^2 = 0.22–0.56: *QYrto.swust-3BS*, *AX-994509749 – AX-94998050*, R^2 = 0.23–0.55 {11379}.

Soru#1 (R) / Naxos (MR): RIL population: Seedling and field tests detected two moderately effective QTL that were likely *Yr24* and *Yr28* derived from Soru#1 {11368}. A KASP marker was developed for *Yr28*.

Thatcher (S) / Hong Qimai (APR) RIL population: *QYr.cau-2AL* near *Xgwm311-2A* and *IWB4475* (R^2 = 47–52%), *Qyr.cau-4AL* (R^2 = 5–7%) and *Qyr.cau-7AL* (R^2 = 9–10%) derived from Hong Mai {11366}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

Lr17.

Lr17a. **v2:** Jagger *Lr37* {11328}.

At the end of section add the following to the list of complex genotypes:
Duster: *Lr34 Lr46 Lr77* {11369}.

LrSV2. Add note:
'According to {11334} *LrSV2* acted in a complementary way with *Lrc*-SV2 on chromosome 4BL. These complementary genes were closely linked to the locations of *Lr27* and *Lr31* but were considered to be different genes.'.

109. Reaction to *Pyrenophora tritici-repentis*

109.1. Resistance to tan spot

Tsr7 {11363}. Dominant. *QTs.zhl-3B* {11362}.
3BL {11362, 11363}. **v:** *Br34* {11363}; Penawawa {11363}.
sutv: LDN (*T. dic*. IsraelA 3B} {11363}.
ma: Linked STARP markers were developed {11363}.

Tsr7 conferred resistance to race 1 (isolate Pti2), race 2 (isolate 86-124), race 3 (isolate 331-9), and race 5 (isolate DW5) {11362}.

QTL
Louise / Penawawa RIL population: *QTs.zhl-1A*, located at interval 0–6.0 cM and likely *Tsc1*; *QTs.zhl-2D*, located at 144.0–152.0 cM; *QTs.zhl-3B*, located at 72.0–78.0; and *QTs.zhl-5A* located at 154–160 cM {11362}.

112. Reaction to *Schizaphis graminum*

Gb8 {11378}. *Gb595379-1* {11378}. 7DL {11378}.

bin: 7DL3-0.81-1.00. **v:** PI 595379-1 {11378}.

ma: *Xbarc11-7D* – 10.41 cM – *Gb8* – 7.4 cM – *Xwmc824-7D* – 4.8 cM – *Xgwm428-7D* {11378}. *Gb3* – *Gb8* 15 cM {11378}.

119. Reaction to Wheat Streak Mosaic Virus

Wsm2.

v: Add: Clara CL PI 1665948 {11329}; Oakley CL PI 670190 {11329}.

ma: Eight SNP markers were mapped within 1 cM of *Wsm2* {11329}. KASP markers were developed from some of these SNP {11330}.

122. Reaction to Wheat Yellow Mosaic Virus

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Updates

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VI. ABBREVIATIONS AND SYNONYMS USED IN THIS VOLUME.

PLANT DISEASES, PESTS, AND PATHOGENS:

BYDV = barley yellow dwarf virus
BMV = barley mosaic virus
CCN = cereal cyst nematode, *Heterodera avenae*
FHB = Fusarium head blight
RWA = Russian wheat aphid
SBMV = soilborne mosaic virus
SLB = Septoria leaf blotch
TMV = *Triticum* mosaic virus
WDF = wheat dwarf mosaic
WSBMV = wheat soilborne mosaic virus
WSMV = wheat streak mosaic virus
WSSMV = wheat spindle streak 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*
Front Plant Sci = *Frontiers in Plant Science*
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*
J Plant Registr = *Journal of Plant Registrations*
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

VII. ADDRESSES OF CONTRIBUTORS.

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

BRAZIL

BRAZILIAN AGRICULTURAL RESEARCH CORPORATION — EMBRAPA TRIGO Centro Nacional de Pesquisa de Trigo, Rodovia BR 285, Km 174, Caixa Postal 451, 99001-970, Passo Fundo, Rio Grande do Sul, Brazil. 54 3316.5817 or 54 99915.9163 (TEL); 54 3316.5801 (FAX). Pedro Luiz Scheeren, Eduardo Caierão*, Márcio Só e Silva, Luiz Eichelberger, Martha Zavariz de Miranda, Alfredo do Nascimento Junior, Douglas Lau, Flávio Martins Santana, Leila Maria Costamilan, Márcia Soares Chaves, Maria Imaculada Pontes Moreira Lima, Paulo Roberto Valle da Silva Pereira, José Pereira da Silva Júnior, Leandro Vargas, Eliana Maria Guarienti, João Leonardo Fernandes Pires, Gilberto Rocca da Cunha, Ricardo Lima de Castro, Sirio Wiethölter, Aldemir Pasinato.

DDPA/SEAPDR C.P. 20, 95.200-970, Vacaria, Rio Grande do Sul, Brazil. Marcelo de Carli Toigo, Rogérui Ferreura Aires.

EMBRAPA CLIMA TEMPORADO C.P. 403, 96010-971 Pelotas, Rio Grande do Sul, Brazil. Vanderlei da Rosa Caetano.

CHINA, PEOPLES REPUBLIC OF

NORTHWEST A&F UNIVERSITY State Key Laboratory of Crop Stress Biology for Arid Areas, College of Agronomy, Yangling, PR China. M. Yang.

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

GERMANY

INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG (IPK) Corrensstraße 3, 06466 OT Gatersleben, Germany. (049) 39482 5229 (TEL); (049) 39482 280/5139 (FAX). http://www.ipk-gatersleben.de. A. Börner*, A. Börner, A.M. Alqudah, D.Z. Alomari, W. Berrueta, M. Cardelli, A.C. Castro, A.M. Castro, Yu.V. Chesnokov, J. del Río, K. Eggert, D. Giménez, M. Jayakodi, T. Kartseva, U. Lohwasser, G. Lori, I. Malbrán, S. Misheva, Q.H. Muqaddasi, M. Nagel, M.S. Röder, L. Saldúa, M. Schierenbeck, V.P. Shamanin, M.R. Simón, R. Tarawneh, J.P. Uranga, N. von Wirén, M. Yanniccari, K. Zaynali Nezhad.

INDIA

BHABHA ATOMIC RESEARCH CENTRE Mumbai-400085, India.
Nuclear Agriculture & Biotechnology Division. G. Vishwakarma, Bikram K. Das*.
Molecular Biology Division. A. Saini.

CH. CHARAN SINGH UNIVERSITY, MEERUT Molecular Biology Laboratory, Department of Genetics and Plant Breeding, CCS University, Meerut 250004, India. http://molbiolabccsumrt.webs.com/founder.htm; http://ccsubiflaboratory-com.webs.com/. P.K. Gupta*, H.S. Balyan, P.K. Sharma, Shailendra Sharma, Sachin Kumar, Kalpana Singh, Ritu Batra, Supriya Kumar, Jitendra Kumar, Gautam Saripalli, Tinku Gautam, Rakhi, Sunita Pal, Anuj Kumar, Irfat Jan, Kuldeep Kumar, Manoj Kumar, Divya Malik, Sourabh Kumar, Vivudh P Singh, Hemant Sharma, Deepti Chaturvedi, Parveen Malik

ICAR — INIDAN INSTITUTE OF WHEAT & BARLEY RESEARCH Karnal – 132001, Haryana. India. 91-184-2209191 (TEL); 91-184-2267390 (FAX). R. Sendhil*, Anuj Kumar, Satyavir Singh, Mangal Singh, J.K. Pandey, G.P. Singh, Satish Kumar, M.S. Saharan, C.N. Mishra.

MPKV–AGRICULTURE RESEARCH STATION Niphad, Nashik, India. D.A. Gadekar.

MEXICO

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

JUNTA LOCAL DE SANIDAD VEGETAL DE NAVOJOA Rafael Almada 2403, Col. Brisas del Valle, Navojoa, Sonora, México 85864. Benjamín Valdenebro-Esquer.

JUNTA LOCAL DE SANIDAD VEGETAL DEL VALLE DEL YAQUI Blvd. Rodolfo Elías Calles 711 Poniente, Sochiloa, 85150 Cd Obregón, Sonora, México 85150. Germán Castelo-Muñoz.

NATIONAL INSTITUTE FOR FORESTRY, AGRICULTURE, AND LIVESTOCK RESEARCH (INIFAP–CIRNO) Campo Experimetal Norman E. Borlaug Apdo. Postal 155, km 12 Norman E. Borlaug, entre 800 y 900, Valle del Yaqui, Cd. Obregón, Sonora, México CP 85000. Guillermo Fuentes-Dávila*, José Luis Félix-Fuentes*, Ivón Alejandra Rosas-Jáuregui, Carlos Antonio Ayón-Ibarra, María Monserrat Torres-Cruz, Pedro Félix-Valencia, José Luis

Félix-Fuentes, Gabriela Chávez-Villalba.

RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE FOR SOUTH-EAST REGIONS – ARISER Department of Genetics, Toulaikov Str., 7, Saratov, 410020, Russian Federation. 8452-64-76-88 (FAX).

Laboratory of Genetics and Cytology S.N. Sibikeev*, A.E. Druzhin*, L.T. Vlasovets, T.D. Golubeva, T.V. Kalintseva.

Laboratory of Plant Immunity to Diseases. E.A. Konkova.

UKRAINE

PLANT PRODUCTION INSTITUTE ND. A. V.YA. YURIEV National Academy of Agrarian Sciences of Ukraine, Laboratory of Genetics, Biotechnology and Quality, Moskovski avenue, 142, 61060, Kharkiv, Ukraine. L.I. Relina, L.A. Vecherska*, R.L. Boguslavskyi*, N.Yu. Skorokhodov, V.V. Pozdniakov, O.V. Antsiferova, N.I. Kryshtopa*.

UMANS'KYI NATIONAL UNIVERSITY OF HORTICULTURE V.V. Liubych*.

THE UNITED STATES OF AMERICA

INDIANA

USDA–ARD CROP PRODUCTION & PEST CONTROL RESEARCH UNIT Purdue University, 915 W. State Street, West Lafayette, IN 47907-2054, USA. https://www.ars.usda.gov/midwest-area/west-lafayette-in/crop-production-and-pest-control-research/. Subhashree Subramanyam*.

IDAHO

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

KANSAS

KANSAS STATE UNIVERSITY

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

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

KANSAS WHEAT 1990 Kimball Avenue, Manhattan, KS 66506, USA. Jordan Hildebrand.

MINNESOTA

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

NORTH CAROLINA

USDA–ARS North Carolina State University, Raleigh, NC 27695, USA. Brian Ward, Myron Fountain, Gina Brown-Guedira.

OHIO

THE OHIO STATE UNIVERSITY Department of Horticulture and Crop Science, Wooster, OH 44691, USA. Clay Sneller.

SOUTH CAROLINA

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

VIRGINIA

DAVIS PRODUCE New Kent, VA 22572, USA. Paul Davis.

EASTERN VIRGINIA AGRICULTURAL RESEARCH & EXTENSION CENTER Warsaw, VA 22572, USA. Josh Fitzgerald, Joseph Oakes.

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

VIRGINIA POLYTECHNIC AND STATE UNIVERSITY

School of Plant and Environmental Sciences, Blacksburg, VA 24061, USA. Carl A. Griffey,* Wade E. Thomason, John E. Seago*, Kyle Brasier, Nick Meier, L. Liu, E. Rucker, D. Schmale III, N. McMaster, M.

Flessner, Josh Fitzgerald, Brice Cazenave, Sayantan Sarkar.

WASHINGTON

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

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

VIII. E-MAIL DIRECTORY OF SMALL GRAINS WORKERS.

These E-mail addresses are updated each year only for contributors to the current *Newsletter*, therefore, some addresses may be out of date. Names followed by [19] were verified with this issue of the *Newsletter,* other numbers indicate the last year that the E-mail address was verified.

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

Name (year updated)	E-mail address	Affiliation
Bhatta, MR	rwp@nwrp.mos.com.np	Natl Wheat Research Program, Nepal
Bykovskaya, Irina [17]	bykovskaya_irina@bk.ru	All-Rus Sci Res Inst Agric Chem, Moscow
Bivilienė, Aušra [15]	agb@agb.lt	Plant Gene Bank, Dotnuva, Lithuania
Blake, Nancy [15]	nblake@montana.edu	Montana State University, Bozeman
Blake, Tom	isstb@montana.edu	Montana State University, Bozeman
Blanco, Antonia	blanco@afr.uniba.it	Institue of Plant Breeding, Bari, Italy
Blum, Abraham	vcablm@volcani.agri.gov.il	Volcani Center, Israel
Bockelman, Harold E [18]	Harold.Bockelman@ARS.USDA.GOV	USDA–ARS, Aberdeen, ID
Bockus, William W [13]	bockus@k-state.edu	KS State University, Manhattan
Boggini, Gaetano	cerealicoltura@iscsal.it	Exp Inst Cereal Research, Italy
Boguslavskiy, Roman L [19]	boguslavr@meta.ua	Plant Prod Inst VY Yuryev, Ukraine
Bonman, J. Michael [17]	Mike.Bonman@ARS.USDA.GOV	USDA–ARS, Aberdeen, ID
Börner, Andreas [19]	boerner@ipk-gatersleben.de	IPK, Gatersleben, Germany
Borovskii, Genadii	borovskii@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Boswell, Marsha [18]	mboswell@kswheat.com	Kansas Wheat, Manhattan
Botha-Oberholster, Anna-Marie	ambothao@postino.up.ac.za	University of Pretoria, South Africa
Bowden, Robert L [18]	Robert.Bowden@ARS.USDA.GOV	USDA–ARS, Manhattan, KS
Boyd, Lesley A [10]	lesley.boyd@bbsrc.ac.uk	John Innes Centre, Norwich, UK
Brahma, RN	amaljoe@rediffmail.com	Indian Agric Res Inst, Wellington
Brantestam, Agnese Kolodinska	agnese.kolodinska@nordgen.org	Nordic Gene Bank, Alnarp, Sweden
Brendel, Volker	vbrendel@iastate.edu	Iowa State University, Ames
Brown, John S	john.brown@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Brammer, Sandra P	sandra@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Bradová, Jane	bradova@hb.vurv.cz	RICP, Prague, Czech Republic
Braun, Hans J [08]	H.J.Braun@cgiar.org	CIMMYT, México
Brennan, Paul	paulb@qdpit.sth.dpi.qld.gov.au	Queensland Wheat Res Inst, Australia
Brooks, Steven A [08]	steven.brooks@ars.usda.gov	USDA–ARS, Stuttgart, Arkansas
Brown, Douglas	dbrown@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Brown, James	jbrown@bbsrc.ac.uk	JI Centre, Norwich, UK
Brown-Guedira, Gina [08]	Gina.Brown-Guedira@ars.usda.gov	USDA–ARS, Raliegh, NC
Bruckner, Phil [15]	bruckner@montana.edu	Montana State University, Bozeman
Bruns, Rob	rbruns@frii.com	AgriPro Wheat, Berthoud, CO
Buerstmayr, Hermann	buerst@ifa-tulln.ac.at	IFA, Tulln, Austria
Burd, John D	jdburd@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Burns, John	burnsjw@wsu.edu	Washington State University, Pullman
Busch, Robert	Robert.H.Busch-1@umn.edu	USDA–ARS, St. Paul, MN
Bux, Hadi [12]	hadiqau@gmail.com	University of Sindh, Jamshoro, Pakistan
Byrne, Pat	pbyrne@lamar.colostate.edu	Colorado State University, Ft. Collins
Caccamo, Mario [10]	Mario.Caccamo@bbsrc.ac.jk	John Innes Centre, Norwich, UK
Cai, Xiwen [17]	xiwen.cai@ndsu.edu	North Dakota State University, Fargo
Caierão, Eduardo [19]	eduardo.caierao@embrapa.br	EMBRAPA–Trigo, Passo Fundo, Brazil
Caley, MS	margo@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Cambron, Sue [10]	cambron@purdue.edu	Purdue University, W. Lafayette, IN
Camerini, Massimiliano	massimiliano.camerini@unimol.it	University of Molise, Italy
Campbell, Kimberly G [09]	kim.garland-campbell@ars.usda.gov	USDA–ARS, Pullman, WA
Carillo, Jose M [08]	josem.carrillo@upm.es	Univ Politécnica de Madrid, Spain
Carmona, M	mcarmona@sion.com.ar	University of Buenos Aires, Argentina
Carson, Marty [10]	marty.carson@ars.usda.gov	USDA–ARS, St. Paul, MN
Carver, Brett F [09]	brett.carver@okstate.edu	Oklahoma State University, Stillwater

Name (year updated)	E-mail address	Affiliation
Casada, ME	casada@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Casanova, Nicholás [08]	nicocasanova@hotmail.com	University of Córdoba, Argentina
Cattonaro, Federica [10]	cattonaro@appliedgenomics.org	IGA, Italy
Cerana, María M	macerana@agro.uncor.edu	Córdoba National University, Argentina
Chalhoub, Boulous	chalhoub@evry.inra.fr	INRA, Evry, France
Chapin, Jay	jchapin@clust1.clemson.edu	Clemson University
Chapon, Michel [08]	michel-chapon@wanadoo.fr	Bourges, France
Chao, Shioman [08]	chaos@fargo.ars.usda.gov	USDA–ARS, Fargo, ND
Chen, Peidu [09]	pdchen@njau.edu.cn	Nanjing Agricultural University, PR China
Chen, Xianming	xianming@mail.wsu.edu	USDA–ARS, Pullman, WA
Chhuneja, Parveen	pchhuneja@rediffmail.com	Punjab Agric Univ, Ludhiana, India
Christiansen, Merethe	mjc@sejet.com	Sojet Plantbreeding, Denmark
Christopher, Mandy	Mandy.Christopher@dpi.qld.gov.au	Leslie Res Centre, Toowomba, Australia
Chung, OK	okchung@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Cisar, Gordon L [08]	rsi.gordon@comcast.net	
Clark, Dale R [08]	dclark@westbred.com	Western Plant Breeders, Bozeman, MT
Comeau, André	comeaua@agr.gc.ca	AAFC–Ste-Foy, Quebec, Canada
Condon, Tony	Tony.Condon@csiro.au	CSIRO, Canberra, Australia
Contento, Alessandra	ac153@mail.cfs.le.ac.uk	University of Leicester, UK
Cortés-Jiménez, Juan M [11]	cortes.juanmanuel@inifap.gob.mx	INIFAP, Obregon, Mexico
Costa, Jose M [08]	costaj@umd.edu	University of Maryland, College Park
Couture, Luc	couturel.stfoyres.stfoy@agr.gc.ca	AAFC–Ste-Foy, Quebec, Canada
Cowger, Cristina [08]	christina_cowger@ncsu.edu	North Carolina State University, Raleigh
Czarnecki, E	eczarnecki@mbrswi.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Daggard, Grant	creb@usq.edu.au	Univ of Southern Queensland, Australia
Datta, Dibendu [08]	dd221004@hotmail.com	Directorate of Wheat Research, India
Danilova, Tatiana [18]	tatianad@k-state.edu	Kansas State University, Manhattan
Davydov, VA	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Das, Bikram K [18]	bikram_das2001@yahoo.com	Bhaba Atomic Res Cen, Mumbai, India
D'Antuono, Mario [18]	Mario.Dantuono@dpird.wa.gov.au	West Australia Grains Res & Innovation
Debes, Julia [15]	jdebes@kswheat.com	Kansas Wheat, Manhattan
Del Duca, Fabio	f.dd@ibestvip.com.br	EMBRAPA, Brazil
Del Duca, Leo JA	leodelduca@gmail.com	EMBRAPA, Brazil
Delibes, A	adelibes@bit.etsia.upm.es	Univ Politécnica de Madrid, Spain
del Moral, J.	moral@inia.es	Junta de Extramadura Servicio, Spain
Dempster, RE	rdempster@aibonline.org	Amer Inst Baking, Manhattan, KS
de Sousa, Cantído NA	cantidio@cnpt.embrapa.br	EMBRAPA, Brazil
DePauw, Ron	depauw@em.agr.ca	AAFC–Swift Current
Devos, Katrien	kdevos@uga.edu	University of Georgia, Athens
Dion, Yves	yves.dion@cerom.qc.ca	CEROM, Quebec, Canada
Dill-Macky, Ruth	ruthdm@puccini.crl.umn.edu	University Of Minnesota, St. Paul
Dotlacil, Ladislav	dotlacil@hb.vurv.cz	RICP, Prague, Czech Republic
Dolezel, Jaroslav [10]	dolezel@ueb.cas.cz	Inst Exp Bo, Olomouc, Czech Republic
Dorlencourt, Guy	dorlencourt@phibred.com	Pioneer Hi-bred–Frouville France
Dowell, Floyd E	floyd.dowell@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Drake, David R [10]	drdrake@ag.tamu.edu	TX AgriLife Extension, San Angelo
Dreccer, F	fernanda.dreccer@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Druzhin, Alex E [19]	alex_druzhin@mail.ru	Agric Res Inst SE Reg, Saratov, Russia
du Toit, Andre [08]	andre.dutoit@pannar.co.za	PANNAR Res, South Africa
Dubcovsky, Jorge [18]	jdubcovsky@ucdavis.edu	Univesity of California, Davis

Name (year updated)	E-mail address	Affiliation
Dubin, Jesse	JDubin@cimmyt.mx	CIMMYT, Mexico
Dubois, María E	mdubois@agro.uncor.edu	Córdoba National University, Argentina
Dubuc, Jean-Pierre	jeanpierredubuc45@hotmail.com	Cap-Rouge, Quebec, Canada
Duncan, Robert W [10]	rduncan@tamu.edu	TX AgriLife Extension, College Station
Dundas, Ian	idundas@waite.adelaide.edu.au	University of Adelaide, Australia
Dunphy, Dennis	dennis.j.dunphy@monsanto.com	Monsanto Corp., Lafayette, IN
Dvorak, Jan	jdvorak@ucdavis.edu	Univesity of California, Davis
Eastwood, Russell	russell.eastwood@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Edge, Benjamin [08]	bedge@clemson.edu	Clemson University, SC
Edwards, Dave [10]	dave.edwards@uq.edu.au	University of Queensland, Australia
Edwards, Ian	edstar@iinet.net.au	Edstar Genetics Pty Ltd, Australia
Egorov, Tsezi [10]	ego@ibch.ru	Shemyakin Ovchinnikov Inst, Moscow
Elias, Elias [08]	Elias.Elias@ndsu.nodak.edu	North Dakota State University, Fargo
Elliott, Norman C	nelliott@ag.gov	USDA–ARS, Stillwater, OK
Endo, Takashi R	endo@kais.kyoto-u.ac.jp	Kyoto University, Japan
Eversole, Kellye [10]	eversole@eversoleassociates.com	Eversole Associates, Rockville, MD
Evseeva, Nina V [13]	evseeva@ibppm.sgu.ru	Inst Biochem Physiol Plants, Saratov, Russian Federatioin
Faberova, Iva	faberova@genbank.vurv.cz	RICP, Prague, Czech Republic
Fahima, Tzion	rabi310@haifauvm.bitnet	University of Haifa, Israel
Faris, Justin D [17]	Justin.Faris@ARS.USDA.GOV	UDSA–ARS–CCRU, Fargo, ND
Fazekas, Miklós	forizsne@dateki.hu	Karcag Research Institute, Hungary
Fedak, George	fedakga@em.agr.ca	AAFC, Ottawa, Ontario
Federov, AK	meraserv@mega.ru	Russian Univ People Friend, Moscow
Feldman, Moshe	lpfeld@weizmann.weizmann.ac.il	Weizmann Institute, Rehovot, Israel
Feliz Fuentes José Luis	j_luis_ff@yahoo.com.mex	INIFAP, Obregon, Mexico
Fellers, John P [08]	jpf@pseru.ksu.edu	USDA–ARS, Manhattan, KS
Feuillet, Catherine [10]	catherine.feuillet@clermont.inra.fr	INRA–Clermont-Ferrand, France
Fox, Paul	pfox@alphac.cimmyt.mx	CIMMYT–Mexico
Fogelman Jr, J Barton	jbarton@ipa.net	AgriPro Seeds, Inc., Jonesboro, AK
Frank, Robert W	frankr@idea.ag.uiuc.edu	University of Illinois, Urbana
Fritz, Alan K [19]	akf@k-state.edu	Kansas State University, Manhattan
Friebe, Bernd [19]	friebe@k-state.edu	Kansas State University, Manhattan
Fuentes-Davila, Guillermo [19]	fuentes.davila@gmail.com	INIFAP, Obregon, Mexico
Gaido, Zulema	zulgaido@agro.uncor.edu	University of Córdoba, Argentina
Gailite, Agnese [15]	agnese.gailite@silava.lv	Genetic Res Cent, Rigas, Latvia
Gale, Sam [15]	Sam.Gale@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Garvin, David [08]	Garvi007@umn.edu	USDA–ARS, St. Paul, MN
Giese, Henriette	h.giese@risoe.dk	Risoe National Lab, DK
Gil, S Patricia	patrigil@agro.uncor.edu	University of Córdoba, Argentina
Gilbert, Jeannie	jgilbert.winres.winnipeg2@agr.gc.ca	AAFC, Winnipeg, Canada
Gill, Bikram S [19]	bsgill@k-state.edu	Kansas State University, Manhattan
Giroux, Mike [15]	mgiroux@montana.edu	Montana State University, Bozeman
Gitt, Michael	mgitt@pw.usda.gov	USDA–ARS–WRRC, Albany, CA
Glyanko, AK	ustaft@sifibr.irk.ru	Siberian Inst Pl Physio Biochem, Russia
Gonzalez-de-Leon, Diego	dgdeleon@alphac.cimmyt.mx	CIMMYT–Mexico
Gooding, Rob	rgooding@magnus.acs.ohio-state.edu	Ohio State University, Wooster
Goodwin, Steve [10]	goodwin@purdue.edu	Purdue University, W. Lafayette, IN
Gothandam, KM	gothandam@yahoo.com	Bharathiar University, Coimbatore, India
Grabelnych, Olga I [11]	grolga@sifibr.irk.ru	Siber Inst Plant Physiol, Irkutsk, Russia

Name (year updated)	E-mail address	Affiliation
Grausgruber, Heinrich	grausgruber@ipp.boku.ac.at	Univ of Agriculture Sciences, Vienna
Graham, W Doyce	dgraham@clust1.clemson.edu	Clemson University, SC
Graybosch, Bob [16]	Bob.Graybosch@ARS.USDA.GOV	USDA–ARS, Lincoln, NE
Greenstone, Matthew H	mgreenstone@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Grienenberger, Jean M	grienen@medoc.u-strasbg.fr	University of Strasberg, France
Griffey, Carl [19]	CGriffey@vt.edu	Virginia Tech, Blacksburg
Griffin, Bill	griffinw@lincoln.cri.nz	DSIR, New Zealand
Groeger, Sabine	probstdorfer.saatzucht@netway.at	Probstdorfer Saatzucht, Austria
Guenzi, Arron	acg@mail.pss.okstate.edu	Oklahoma State University, Stillwater
Guidobaldi, Héctor A	guidobaldi@uol.com.ar	Univrsity of Córdoba, Argentina
Guilhot, Nicolas [10]	nicolas.guilhot@clermont.inra.fr	INRA, Clermont-Ferrand, France
Guttieri, Mary [19]	mary.guttieri@ars.usda.gov	USDA–ARS, Manhattan, KS
Gul-Kazi, Alvina [15]	alvina_gul@yahoo.com	Natl Agric Res Cent, Islamabad, Pakistan
Gupta, Pushpendra K [19]	pkgupta36@gmail.com	Ch. Charan Singh Univ, Meerut, India
Gustafson, Perry [08]	gustafsonp@missouri.edu	USDA–ARS, Columbia, MO
Gutin, Alexander	agutin@myriad.com	Myriad Genetics, Salt Lake City, UT
Guttieri, Mary J [16]	Mary.Guttieri@ARS.USDA.GOV	USDA–ARS, Manhattan, KS
Haber, Steve	shaber.winres.winnipeg2@agr.gc.ca	AAFC, Winnipeg, Manitoba, Canada
Haghparast, Reza	rezahaghparast@yahoo.com	IARI, New Delhi, India
Haley, Scott D [17]	Scott.Haley@colostate.edu	Colorado State University, Ft. Collins
Hancock, June	june.hancock@seeds.Novartis.com	Novartis Seeds Inc., Bay, AR
Harrison, Steve	sharris@lsuvm.sncc.lsu.edu	Louisiana State University, Baton Rouge
Harder, Don	dharder@mbrswi.agr.ca	Winnipeg, Manitoba, Canada
Hart, Gary E	ghart@acs.tamu.edu	Texas A & M Univ, College Station
Hassan, Amjad [08]	amjadhassan@mx1.cc.ksu.edu	COMSATS Inst Inf Tech, Pakistan
Hays, Dirk B	dhays@ag.gov	USDA–ARS, Stillwater, OK
Hayes, Pat	hayesp@css.orst.edu	Oregon State University, Corvallis
He, Zhonghu [08]	z.he@CGIAR.ORG	Chinese Acad Agric Sciences, Beijing
Heo, Hwa-Young [15]	hwayoung@montana.edu	Montana State University, Bozeman
Hearnden, PR	phillippa.hearden@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Hede, Arne R	a.hede@cgiar.org	CIMMYT–Turkey, Ankara
Henzell, Bob	bobh@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland, AU
Hershman, Don	dhershman@ca.uky.edu	University of Kentucky, Lexington
Heslop-Harrison, JS (Pat)	phh4@mail.cfs.le.ac.uk	University of Leicester, UK
Hoffman, David	A03dhoffman@attmail.com	USDA–ARS, Aberdeen, ID
Hohmann, Uwe	uhemail@botanik.biologie.unim-uenchen.de	Botanical Institute, Munich, Germany
Hoisington, David [08]	D.Hoisington@cgiar.org	CIMMYT–Mexico
Hole, David	dhole@mendel.usu.edu	Utah State University, Logan
Holubec, Vojtech [15]	holubec@vurv.cz	Crop Res Inst, Prague, Czech Republic
Howell, Kimberly D [15]	Kim.Howell@ARS.USDA.GOV	USDA–ARS, Raleigh, NC
Howes, Neil	nhowes@mbrswi.agr.ca	Winnipeg, Manitoba, Canada
Hubbard, JD	john@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Huber, Don M	huber@btny.purdue.edu	Purdue University, W. Lafayette, IN
Hucl, Pierre	hucl@sask.usask.ca	University of Saskatchewan, Canada
Huerta, Julio [08]	J.HUERTA@CGIAR.ORG	CIMMYT, México
Hughes, Mark E [16]	Mark.Hughes@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Hulbert, Scot [08]	scot_hulbert@wsu.edu	Washington State University, Pullman
Hunger, Robert [09]	bob.hunger@okstate.edu	Oklahoma State University, Stillwater
Ibrahim, Amir	amir_ibrahim@sdstate.edu	South Dakota State Univ, Brookings

Name (year updated)	E-mail address	Affiliation
Imtiaz, Muhammad [17]	m.imtiaz@cgiar.org	CIMMYT, Pakistan
Ionova, Helen [10]	ionova-ev@yandex.ru	All-Russian Sci Res Inst, Zernograd
Iori, Angela [11]	angela.iori@entecra.it	CRA–QCE, Roma, Italy
Isaac, Peter G	mbnis@seqnet.dl.ac.uk	Nickerson Biocem, UK
Isaía, Juan A [08]	juanandresisaia@hotmail.com	University of Córdoba, Argentina
Ivanušić, Tomislav [10]	tomislav.ivanusic@bc-institut.hr	BC Insitute, Zagreb, Croatia
Jacquemin, Jean	stamel@fsagx.ac.be	Cra-Gembloux, Belgium
Jamali, Karim Dino [13]	karimdino2001@yahoo.com.in	Nuclear Institute Agriculture, Pakistan
Jaiswal, Jai P [10]	jpj.gbpu@gmail.com	GB Pant University, Pantnagar, India
Jayaprakash, P [13]	jpsarit@gmail.com	IARI, Wellington, India
Jelic, Miodrag	miodrag@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Jia, Jizeng	jzjia@mail.caas.net.cn	Chinese Academy of Sciences, Beijing
Jiang, Guo-Liang	dzx@njau.edu.cn	Nanjing Agricultural University, China
Jin, Yue [17]	Yue.Jin@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Johnson, Doug	djohnson@ca.uky.edu	University of Kentucky, Lexington
Johnson, Jerry [09]	jjohnson@griffin.uga.edu	University of Georgia, Griffin
Johnston, Paul	paulj@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland, AU
Jones, Steven S	joness@wsuvm1.csc.wsu.edu	Washington State University, Pullman
Jordan, Mark	mcjordan@agr.gc.ca	AAFC, Winnipeg, Manitoba, Canada
Joshi, Anupama	anupama@k-state.edu	Kansas State University, Manhattan
Kalaiselvi, G	kalaipugal@rediffmail.com	Bharathiar Univ, Coimbatore, India
Kalia, Bhanu [15]	bkalia@k-state.edu	Kansas State University, Manhattan
Kalous, Jay [15]	jay.kalous@msu.montana.edu	Montana State University, Bozeman
Karabayev, Muratbek	mkarabayev@astel.kz	CIMMYT, Kazakhstan
Karow, Russell S [08]	russell.s.karow@oregonstate.edu	Oregon State University, Corvallis
Karsai, Ildiko	karsai@buza.mgki.hu	ARI, Martonvasar, Hungary
Kasha, Ken	kkasha@crop.uoguelph.ca	University of Guelph, Canada
Keefer, Peg	peg_keefer@entm.purdue.edu	Purdue University, West Lafayette, IN
Keller, Beat	bkeller@botinst.unizh.ch	University of Zurich, Switzerland
Khusnidinov, ShK	ustaft@sifibr.irk.ru	Irkutsk State Agric Univ, Irkutsk, Russia
Kianian, Sharyiar [08]	s.kianian@ndsu.nodak.edu	North Dakota State University, Fargo
Kidwell, Kim [08]	kidwell@wsu.edu	Washington State University, Pullman
Kindler, S Dean	sdkindler@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Kirkham, MB [19]	mbk@k-state.edu	Kansas State University, Manhattan
Kisha, Theodore	tkisha@dept.agry.purdue.edu	Purdue University, W. Lafayette, IN
Kishii, Masahiro [08]	m.kishii@CGIAR.ORG	CIMMYT, Mexico
Klatt, Art [08]	aklatt@okstate.edu	Oklahoma State University, Stillwater
Kleinhofs, Andy	coleco@bobcat.csc.wsu.edu	Washington State University, Pullman
Knezevic, Desimir	deskok@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Koebner, Robert	mockbeggars@gmail.com	Norwich, UK
Koemel, John Butch	jbk@soilwater.agr.okstate.edu	Oklahoma State University, Stillwater
Koenig, Jean [08]	koenig@clermont.inra.fr	INRA, Clermont-Ferrand, France
Kokhmetova, Alma	kalma@ippgb.academ.alma-ata.su	Kazakh Research Institute of Agriculture
Kolb, Fred [08]	f-kolb@uiuc.edu	University Of Illinois, Urbana
Kolesnichenko, AV	akol@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Kolmer, Jim [19]	Jim.Kolmer@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Koppel, R	Reine.Koppel@jpbi.ee	Jõgeva Plant Breeding Institute, Estonia
Koo, Dal-Hoe [18]	dkoo@k-state.edu	Kansas State Unviersity, Manhattan
Korol, Abraham	rabi309@haifauvm.bitnet	University of Haifa, Israel
Kosina, Romuald [18]	romuald.kosina@uni.wroc.pl	University of Wroclaw, Poland

Name (year updated)	E-mail address	Affiliation
Kovalenko, ED	kovalenko@vniif.rosmail.com	Russian Res Inst Phytopath, Moscow
Krasilovets, Yuri G [09]	ppi@kharkov.ukrtel.net	Inst Plant Production, Karkiv, Ukraine
Krenzer, Gene	egk@agr.okstate.edu	Oklahoma State University, Stillwater
Kronstad, Warren E	kronstaw@css.orst.edu	Oregon State University, Corvallis
Krupnov, VA	alex_dr@renet.com.ru	Agric Res Inst SE Reg, Saratov, Russia
Kryshtopa, Natalia [19]	nikanei@meta.ua	Plant Prod Inst VY Yuryev, Ukraine
Kudirka, Dalia	KUDIRKAD@agr.gc.ca	AAFC, Ottawa, Ontario, Canada
Kudryavtseva, TG	ustaft@sifibr.irk.ru	Irkutsk State Agric Univ, Irkutsk, Russia
Kuhr, Steven L	slkuhr@ccmail.monsanto.com	Hybritech–Mt. Hope, KS
Kumar, Jagdish [16]	moola01@yahoo.com	Indian Agric Res Inst, Wellington
Kumar, Sarvan [11]	sarvandwr@yahoo.co.in	Directorate of Wheat Research, India
Kuraparthy, Vasu [10]	vasu_kuraparthy@ncsu.edu	North Carolina State University, Raleigh
Kurmanbaeva, A.S. [11]	safronat@rambler.ru	Kokshetau State Univ, Kazakhstan
Kuzmina, Natalia	natakuzmina@yandex.ru	Omsk State Pedagogical Univ, Russia
Kuzmenko, Natalia V [17]	ogurtsow@mail.ru	Plant Production Institute, Ukraine
Kyzlasov, VG [11]	norma-tm@rambler.ru	Moscow Agric Res Inst, Russia
Lafferty, Julia	lafferty@edv1.boku.ac.at	Saatzucht Donau, Austria
Lagudah, Evans	e.lagudah@pi.csiro.au	CSIRO, Australia
Lankevich, SV	laser@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Láng, László [13]	lang.laszlo@agrar.mta.hu	Agricultural Inst, Martonvásár, Hungary
Langridge, Peter	plangridge@waite.adelaide.edu.au	University of Adelaide, Australia
Lapitan, Nora LV [08]	nlapitan@lamar.colostate.edu	Colorado State University, Ft. Collins
Lapochkina, Inna F	lapochkina@chat.ru	Research Inst of Agric, Moscow, Russia
Laskar, Bill	laskarb@phibred.com	Pioneer Hi-Bred–Windfall, IN
Leath, Steve	steven_leath@ncsu.edu	USDA–ARS, Raleigh, NC
Leonard, Kurt J	kurtl@puccini.crl.umn.edu	USDA–ARS, St. Paul, MN
Leroy, Philippe	leroy@valmont.clermont.inra.fr	INRA, Clermont
Lekomtseva, Svetlana N [09]	lekom37@mail.ru	Moscow State University, Russia
Leske, Brenton [18]	brenton.leske@research.uwa.edu.au	University of Western Australia, Perth
Lewis, Hal A	halewi@ccmail.monsanto.com	Hybritech–Corvallis OR
Lewis, Silvina	slewis@cirn.inta.gov.ar	CNIA–INTA, Buenos Aires, Argentina
Li, Wanlong [17]	Wanlong.Li@sdstate.edu	South Dakota State University, Brookings
Linc, Gabriella [15]	linc.gabriella@agrar.mta.hu	Agricultural Inst, Martonvásár, Hungary
Line, RF	rline@wsu.edu	USDA–ARS, Pullman, WA
Liu, Dajun	djliu@public1.ptt.js.cn	Nanjing Agricultural University, China
Liubych, Vitaly [19]	lyubichv@gmail.com	Umans'kyi Natl Univ of Horticulture
Lively, Kyle	livelyk@phibred.com	Pioneer Hi-Bred–Windfall, IN
Lobachev, Yuri V [11]	lobachyovyuv@sgau.ru	Saratov State Agr Univ, Saratov, Russia
Long, David [10]	david.long@ars.usda.gov	USDA–ARS, St. Paul, MN
Lookhart, George	george@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Liubych, Vitaly [19]	lyubichv@gmail.com	Umans'kyi Nat Univ Hort, Ukraine
Luckow, Odean	alvkow@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Lukaszewski, Adam	ajoel@ucrac1.ucr.edu	University of California–Riverside
Luo, Ming Cheng [10]	mcluo@plantsciences.ucdavis.edu	University of CA, Davis
Maas, Fred	fred_maas@entm.purdue.edu	Purdue University, West Lafayette, IN
Mackay, Michael	mackaym@quord.agric.nsw.gov.au	AWEE, Tamworth, NSW, Australia
Maggio, Albino	maggio@trisaia.enea.it	ENEA–Trisaia Research Center, Italy
Maich, Ricardo H [11]	rimaich@agro.unc.edu.ar	University of Córdoba, Argentina
Malik, BS [08]	bsmalik2000@yahoo.com	IARI, New Delhi, India
Manera, Gabriel	gamanera@agro.uncor.edu	University of Córdoba, Argentina

Name (year updated)	E-mail address	Affiliation
Manifesto, María M	mmanifes@cicv.intgov.ar	INTA Castelar, Argentina
Marais, G Frans [08]	gfm@sun.ac.za	University of Stellenbosch, R.S.A.
Mares, Daryl J [08]	daryl.mares@adelaide.edu.au	University of Adelaide, Australia
Mardi, Mohsen	mardi@abrii.ac.ir	Ag Biotech Res Inst of Iran, Karaj
Marshall, David [08]	David.Marshall@ARS.USDA.GOV	USDA–ARS, Raleigh, NC
Marshall, Gregory C	marshallg@phibred.com	Pioneer Hi-Bred–Windfall, IN
Martin, Erica	erica.martin@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Martín-Sánchez, JA [10]	JuanAntonio.Martin@irta.cat	IRTA, Lleida, Spain
Martynov, Sergei [08]	sergej_martynov@mail.ru	Vavilov Inst Plant Prod, St. Petersburg
Mather, Diane	indm@musicb.mcgill.ca	McGill University, Canada
Matthews, Dave [10]	matthews@greengenes.cit.cornell.edu	Cornell University, Ithaca, NY
McCallum, John	mccallumj@lan.lincoln.cri.nz	Crop & Food Res. Ltd, NZ
McGuire, Pat	pemcguire@ucdavis.edu	University of California, Davis
McIntosh, Robert A [17]	robert.mcintosh@sydney.edu.au	PBI Cobbitty, Australia
McKendry, Anne L	mckendrya@missouri.edu	University of Missouri, Columbia
McKenzie, RIH	rmckenzie@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
McVey, Donald	donm@puccini.crl.umn.edu	USDA–ARS, St. Paul, MN
Meena, Raj Pal	adityarajjaipur@gmail.com	Directorate Wheat Research, Karnal, India
Messing, Joachim	messing@waksman.rutgers.edu	Rutgers University, Piscataway, NJ
Mi, Q.L.	qlm@ksu.edu	Kansas State University, Manhattan
Milach, Sandra	mila0001@student.tc.umn.edu	University of Minnesota, St. Paul
Miller, James	millerid@fargo.ars.usda.gov	USDA–ARS, Fargo, ND
Milovanovic, Milivoje	mikim@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Milus, Gene [08]	gmilus@uark.edu	University of Arkansas, Fayetteville
Mishra, Chandra Nath [13]	mishracn1980@gmail.com	Directorate of Wheat Research, Karnal
Miskin, Koy E	miskin@dcwi.com	AgriPro Wheat, Berthoud, CO
Miyan, Shahajahan	Shahajahan.Miyan@dpird.wa.gov.au	West Australia Grains Res & Innovation
Mlinar, Rade	bc-botinec@bc-institut.hr	Bc Institute, Zagreb, Croatia
Mochini, RC	rmoschini@inta.gov.ar	INTA, Castelar, Argentina
Moffat, John	apwheat@frii.com	AgriPro Wheat, Berthoud, CO
Moldovan, Vasile [16]	ameliorareagraului@scdaturda.ro	Agric Research Station, Turda, Romania
Molnár-Láng, Marta	molnarm@fsnew.mgki.hu	Agricultural Inst, Martonvásár, Hungary
Moore, Paul	ejh@uhccvx.uhcc.hawaii.edu	University of Hawaii, Honolulu
Moreira, João C.S.	moreira@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Morgounov, Alexei [08]	a.morgounov@cgiar.org	CIMMYT, Kazakhstan
Morino-Sevilla, Ben	bmoreno-sevilla@westbred.com	Western Plant Breeders, Lafayette, IN
Mornhinweg, Dolores W	dmornhin@ag.gov	USDA–ARS, Stillwater, OK
Morris, Craig F [18]	craig.morris@ars.usda.gov	USDA–ARS–WWQL, Pullman, WA
Morrison, Laura	alura@peak.org	Oregon State University, Corvallis
Moser, Hal	hsmoser@iastate.edu	Iowa State University, Ames
Mostafa, Ayman	insectarus@yahoo.com	University of Manitoba, Canada
Mujeeb-Kazi, A [15]	kayshtr@gmail.com	Natl Agric Res Cent, Islamabad, Pakistan
Mukai, Yasuhiko	ymukai@cc.osaka-kyoiku.ac.jp	Osaka Kyoiku University, Japan
Murphy, Paul [08]	Paul_Murphy@ncsu.edu	North Carolina State University
Murray, Tim	tim_murray@wsu.edu	Washington State University, Pullman
Muthukrishnan, S [10]	smk@k-state.edu	Kansas State University, Manhattan
Nakamura, Hiro [16]	hiro@affrc.go.jp	National Inst of Crop Science, Tsukuba
Nascimento Jr, Alfredo [11]	alfredo@cnpt.embrapa.br	EMBRAPA–Trigo, Brazil
Nash, Deanna L [15]	deanna@montana.edu	Montana State University, Bozeman
Nass, Hans	nassh@em.agr.ca	AAFC–Prince Edward Island, Canada

Name (year updated)	E-mail address	Affiliation
Nayeem, KA	kanayeem1@rediffmail.com	IARI Regional Sta, Wellington, India
Niedzielski, Maciej [15]	mniedz@obpan.pl	Botanical Garden, Warsaw, Poland
Nelson, Lloyd R	lr-nelson@tamu.edu	Texas A & M University
Nevo, Eviatar	rabi301@haifauvm.bitnet	University of Haifa, Israel
Nicol, Julie M [08]	j.nicol@cgiar.org	CIMMYT–Turkey, Ankara
Noll, John S	jnoll@em.agr.ca	AAFC–Winnipeg, Canada
Nyachiro, Joseph	jnyachir@gpu.srv.ualberta.ca	University of Alberta
O'Donoughue, Louise	em220cyto@ncccot2.agr.ca	AAFC–Canada
Odintsova, TI	musolyamov@mail.ibch.ru	Vavilov Ins Gen Genet, Moscow, Russia
Ogbonnaya, Francis C [08]	F.Ogbonnaya@cgiar.org	ICARDA, Aleppo, Syria
Ogihara, Yasunari	ogihara@kab.seika.kyoto.jp	Kyoto Pref Inst Agric Biotech, Japan
Ohm, Herbert W [10]	hohm@purdue.edu	Purdue Univ, West Lafayette, IN
Ohm, Jay B	jay@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Oman, Jason	jason.oman@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Ortiz-Ávalos, Alma A [11]	ortiz.alma@inifap.gob.mx	INIFAP, Obregon, Mexico
Ortiz Ferrara, Guillermo [08]	oferrara@mos.com.np	CIMMYT, Ramput, Nepal
Osipova, Ludmila V [17]	legos4@yndex.ru	All-Rus Sci Res Inst Agric Chem, Moscow
Osmanzai, Mahmood [08]	m.osmanzai@cgiar.org	CIMMYT, Kabul, Afghanistan
Paelo, Antonio D	adiazpaleo@cnia.inta.gov.ar	CRN INTA Castelar, Argentina
Paling, Joe	jpaling@vt.edu	VA Polytech Inst State Univ, Blacksburg
Papousková, Ludmila [15]	papouskova@vurv.cz	Crop Res Inst, Prague, Czech Republic
Park, SH	seokho@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Pasquini, Mariina [10]	marina.pasquini@entecra.it	CRA–QCE, Roma, Italy
Paux, Etienne [10]	etienne.paux@clermont.inra.fr	INRA, Clermont-Ferrand, France
Payne, Thomas [11]	t.payne@CGIAR.ORG	CIMMYT, México
Penix, Susan	agsusan@mizzou1.missouri.edu	University of Missouri, Columbia
Permyakov, AV	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Perry, Keith	perry@btny.purdue.edu	Purdue University, W. Lafayette, IN
Perry, Sid	sidgsr@southwind.com	Goertzen Seed Research, Haven, KS
Pérez, Beatríz A	baperez@inta.gov.ar	INTA, Castelar, Argentina
Peterson, C James [09]	cjp@oregonstate.edu	Oregon State University, Corvallis
Pickering, Richard	pickeringr@crop.cri.nz	Christchurch, NZ
Piergiovanni, Angela R	angelarosa.piergiovanni@igv.cnr.it	Istituto de Genetica Vegetale, Bari, Italy
Pomazkina, L	agroeco@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Pogna, Norberto	isc.gen@iol.it	Inst Exper Cereal, Rome, Italy
Poland, Jesse [19]	jpoland@k-state.edu	Kansas State University, Manhattan
Poleva, Lina V.	po_linaw@rambler.ru	Agric Res Inst, Moscow, Russian Fed
Porter, David	dporter@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Poulsen, David	davep@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland AU
Poukhalskaya, Nina V [18]	n-v-pooh@ya.ru	Russian Inst for Agrochemistry, Moscow
Prabakaran, AJ	amaljoe@rediffmail.com	Regional Station, Wellington, India
Prasad, Manoj	manoj_pds@yahoo.com	Nat Cent Pl Gen Res, New Delhi, India
Premalatha, S	spr_latha@yahoo.co.in	Bharathiar University, Coimbatore, India
Priillin, Oskar	ebi@ebi.ee	Estonian Agricultural University, Harku
Puebla, Andrea F	apuebla@cicv.inta.gov.ar	INTA, Castelar, Argentina
Pukhalskiy, VA [18]	seo@seomax.ru	Vavilov Inst of General Genetics, Moscow
Pumphrey, Michael O [08]	mop3535@ksu.edu	USDA–ARS, Manhattan, KS
Qualset, Cal	coqualset@ucdavis.edu	University of California–Davis
Quaranta, Fabrizio [10]	fabrizio.quaranta@entecra.it	CRA–QCE, Rome, Italy

Name (year updated)	E-mail address	Affiliation
Quetier, Francis	quetier@genoscope.cns.fr	GENOSCOPE, France
Quick, Jim	jim.quick@colostate.edu	Dakota Grow Pasta Co, Carrington, ND
Rabinovych, Svitlana	bogus@is.kh.ua	Inst Plant Production, Karkiv, Ukraine
Rahman, Sharmin [18]	Sharmin.Rahman@dpird.wa.gov.au	West Australia Grains Res & Innovation
Rajaram, Sanjaya	srajaram@cimmyt.mx	CIMMYT, Mexico
Ram, MS	ramms@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Raman, Harsh	harsh.raman@dpi.nsw.gov.au	Wagga Wagga Agric Institute, Australia
Ratcliffe, Roger H	roger_ratcliffe@entm.purdue.edu	USDA–ARS, W. Lafayette IN
Ratti, C	cratte@tin.it	University of Bologna, Italy
Raupp, W John [19]	jraupp@k-state.edu	Kansas State University, Manhattan
Rawat, Nidhi [17]	nidhirwt@umd.edu	University of Maryland, College Park
Rayapati, John	nanster@iastate.edu	Iowa State University, Ames
Rebetzke, Greg	Greg.Rebetzke@csiro.au	CSIRO, Canberra, Australia
Reddy, V Rama Koti [08]	drvrkreddy@yahoo.com	Bharathiar University, Coimbatore, India
Rekoslavskaya, NI	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Reisner, Alex	reisner@angis.su.oz.au	Australia
Rekoslavskaya, Natalya I	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Riera-Lizarazu, Oscar	oscar.rierd@orst.edu	Oregon State University, Corvallis
Rife, Trevor [16]	trife@k-state.edu	Kansas State University, Manhattan
Rines, Howard [13]	rines001@umn.edu	University of Minnesota, St. Paul
Rioux, Sylvie	sylvie.rioux@cerom.qc.ca	CEROM, Quebec, Canada
Roberts, John	jrobert@gaes.griffin.peachnet.edu	USDA–ARS, Griffin, GA
Rodríguez, Daniel	daniel.rodriguez@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Rogers, W John [18]	rogers@faa.unicen.edu.ar	Univ Nacional, Buenos Aires, Argentina
Rohrer, Wendy L	wrohrer@vt.edu	Virginia Tech, Blacksburg
Romig, Robert W	bobromig@aol.com	Trigen Seed Services LLC, MN
Romsa, Jay [09]	Jay.Romsa@genmills.com	General Mills
Rosa, André	andre@orsementes.com.br	OR Seed Breeding Co., Brazil
Rosa, OS	ottoni@ginet.com.br	OR Seed Breeding Co., Brazil
Rouse, Matthew [12]	Matthew.Rouse@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Rudd, Jackie [08]	j-rudd@tamu.edu	Texas A&M Agric Res Cen, Amarillo
Rubies-Autonell, C	crubies@agrsci.unibo.it	University of Bologna, Italy
Rustgi, Sachin [18]	rustgi2001@yahoo.com	Clemson University, Florence, SC
Safranski, Greg	greg_safranski@entm.purdue.edu	Purdue University, W. Lafayette, IN
Saini, Ram Gopal	sainirg@rediffmail.com	Punjab Agric Univ, Ludhiana, IndiaSher
Sajjad, Muhammad [14]	msajjadpbg@gmail.com	Arid Agri Univ, Rawalpindi, Pakistan
Salyaev, RK	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Santra, Depak [12]	dsantra2@unl.edu	University of NE, Scottsbluff
Sasaki, Takuji	tsasaki@nias.affrc.go.jp	NAIS, Tsukuba, Japan
Sãulescu, Nicolae	saulescu@valhalla.racai.ro	Fundulea Institute, Romania
Schlegel, Rolf [14]	rolf.schlegel@t-online.de	Retired
Schwarzacher, Trude	ts32@leicester.ac.uk	University of Leicester, UK
Schemerhorn, Brandon J [10]	bschemer@purdue.edu	Purdue University, West Lafayette, IN
Scofield, Steven [10]	scofield@purdue.edu	Purdue University, West Lafayette, IN
Seabourn, BW	brad@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Seago, John E [19]	joseago@vt.edu	Virginia Polytechnic Inst, Blacksburg
Sears, Rollie [09]	Rollin.Sears@syngenta.com	AgriPro Wheat, Junction City, KS
See, Deven [08]	deven_see@wsu.edu	USDA–ARS, Pullman, WA
Sehgal, Sunish K [10]	Sunish.Sehgal@sdstate.edu	South Dakota State University, Brookings
Seitz, LM	larry@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS

Name (year updated)	E-mail address	Affiliation
Sendhil, R [19]	R.Sendhil@icar.gov.in	ICAR–IIWBR, Karnal, India
Sessiona, Alan	allen.sessions@syngenta.com	Syngenta, Research Triangle Park, NC
Sethi, Amit P	amit_sethi@hotmail.com	IARI, New Delhi, India
Shafquat, Mustafa N [08]	mshafqat@mx1.cc.ksu.edu	COMSATS Inst Inf Tech, Pakistan
Shah, M Maroof [08]	mmshah@ciit.net.pk	COMSATS Inst Inf Tech, Pakistan
Shaner, Greg	shaner@btny.purdue.edu	Purdue University, W. Lafayette, IN
Sharma, Darshan [18]	Darshan.Sharma@dpird.wa.gov.au	West Australia Grains Res & Innovation
Sharp, Peter	peters@camden.usyd.edu.au	PBI Cobbitty, Australia
Shchipak, GennadiyV [18]	boguslavr@meta.ua	Plant Production Institute, Ukraine
Sheedy, Jason [08]	Jason.Sheedy@dpi.qld.gov.au	Leslie Research Centre, Australia
Sheppard, Ken	ksheppard@waite.adelaide.edu.au	University of Adelaide, Australia
Sherman, Jamie [15]	jsherman@montana.edu	Montana State University, Bozeman
Shields, Phil	shieldsp@phibred.com	Pioneer Hi-Bred, St. Matthews, SC
Shindin, Ivan [09]	shelepa@bk.ru	Inst Comp Anal Reg Prob, Khabarovsk, Russia
Shroyer, Jim	jshroyr@ksu.edu	Kansas State University, Manhattan
Shahzad, Armghan	armghan_shehzad@yahoo.com	University of Wales, Bangor, UK
Shufran, Kevin A	kashufran@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Shukle, Richard [10]	shukle@purdue.edu	Purdue University, West Lafayette, IN
Sibikeev, SN [11]	raiser_saratov@mail.ru	ARISER, Saratov, Russian Federation
Siddiqi, Sabir Z	dirrari@mul.paknet.com.pk	Reg Agr Res Inst, Bahawalpur, Pakistan
Singh, Daljit [16]	singhdj2@k-state.edu	Kansas State University, Manhattan
Singh, Gyanendra P [13]	gyanendrapsingh@hotmail.com	Direct Wheat Research, Karnal, India
Singh, JB	jbsingh1@rediffmail.com	IARI, New Delhi, India
Singh, Nagendra	snagarajan@flashmail.com	IARI, New Delhi, India
Singh, Narinder [18]	nss470@k-state.edu	Kansas State University, Manhattan
Singh, Nirupma	nirupmasingh@rediffmail.com	IARI, New Delhi, India
Singh, Rajender [10]	rajenderkhokhar@yahoo.com	Ch Ch Singh Haryana Agric Univ, India
Singh, Ravi P [15]	R.SINGH@CGIAR.ORG	CIMMYT, México
Singh, SS	singhss@rediffmail.ocm	IARI, New Delhi, India
Singh, Sanjay Kumar [12]	sksingh.dwr@gmail.com	Direct Wheat Research, Karnal, India
Sinnot, Quinn	quinn@prime.ars-grin.gov	USDA–ARS, Beltsville, MD
Síp, Vaclav	sip@hb.vurv.cz	RICP, Prague, Czech Republic
Sivasamy, Muruga [13]	iariwheatsiva@rediffmail.com	IARI, Wellington, India
Skinner, Daniel Z	dzs@wsu.edu	USDA–ARS, Pullman, Washington
Skovmand, Bent	bskovmand@cimmyt.mx	CIMMYT–Mexico
Smith, Joe A	jasmith@frii.com	AgriPro Seeds, Inc., Berthoud, CO
Smith, Rosemary H [18]	Rosemary.Smith@dpird.wa.gov.au	West Australia Grains Res & Innovation
Snape, John [10]	john.snape@bbsrc.ac.uk	JI Centre, Norwich, UK
Sommers, Daryl	SomersD@agr.gc.ca	AAFC, Canada
Sorrells, Mark E [09]	mes12@cornell.edu	Cornell University, Ithaca, NY
Sotnikov, Vladimir V	ncpgru@kharkov.ukrtel.net	Inst Plant Production, Kharkov, Ukraine
Souvorova, Katerine Yu	ncpgru@kharkov.ukrtel.net	Yuriev Pl Prod Inst, Kharkov, Ukraine
Souza, Ed [09]	edward.souza@ars.usda.gov	USDA–ARS, Wooster, Ohio
Spetsov, Penko	iws@eos.dobrich.acad.bg	Inst Wheat and Sunflower, Bulgaria
Spivac, VA [13]	spivac_VA@mail.ru	Chernyshevsky Saratov State Univ, Saratov, Russian Federation
Steffenson, Brian	bsteffen@badlands.nodak.edu	North Dakota State University, Fargo
Stehno, I Zdenek [08]	stehno@vurv.cz	RICP, Prague, Czech Republic
Stein, Lincoln	lstein@cshl.org	Cold Spring Harbor Laboratory, NY

Name (year updated)	E-mail address	Affiliation
Stein, Nils	stein@ipk-gatersleben.de	IPK, Gatersleben, Germany
Stift, G.	stift@ifa-tulln.ac.at	IFA-Tulln, Austria
Stoddard, Fred	stoddard@extro.ucc.edu.oz.ua	University of Sydney, Australia
Stuart, Jeffery J [10]	stuartjj@purdue.edu	Purdue University, West Lafayette, IN
Stupnikova, IV	irina@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Subkova, OV	ariser@mail.saratov.ru	Agric Res Inst SE Reg, Saratov, Russia
Suchy, Jerry	isuchy@em.arg.ca	AAFC–Winnipeg, Manitoba, Canada
Sun, Mei	meisun@hkucc.hku.hk	Hong Kong University
Subramanyam, Subhashree [19]	Subhashree.Subramanyam@usda.gov	USDA–ARS, W. Lafayette, Indiana
Sutherland, Mark	marksuth@usq.edu.au	Univ of Southern Queensland, Australia
Sykes, Stacy [18]	sykes@wsu.edu	USDA–ARS_WWQL, Pullman, WA
Szabo, Les [12]	Les.Szabo@ARS.USDA.GOV	USDA–ARS, University of Minnesota
Talbert, Luther E [15]	usslt@montana.edu	Montana State University, Bozeman
Tewari, Vinod	vinodtiwari_iari@rediffmail.com	IARI, New Delhi, India
Therrien, Mario C	therrien@mbrsbr.agr.ca	AAFC–Manitoba, Canada
Thiessen, Eldon	nass-ks@nass.usda.gov	KS Agric Statistics, Topeka, KS
Thomason, Wade E [10]	wthomaso.vt.edu	VA Polytech & State Univ, Blacksburg
Thompson, John [08]	John.Thompson@dpi.qld.gov.au	Leslie Research Center, Australia
Throne, JE	throne@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Tilley, M	mtilley@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Tinker, Nick	cznt@agradm.lan.mcgill.ca	McGill University, Canada
Tiwari, Vijay [17]	vktiwari@umd.edu	University of Maryland, College Park
Tkachenko, OV[14]	oktkachenko@yandex.ru	Vavilov Saratov State Agrarian Univ, Russian Federation
Tohver, Maimu	maimu.tohver@mail.ee	Estonian Agricultural University, Harku
Tomasović, Slobodan [11]	bc-botinec@bc-institut.hr	Bc Institute, Zagreb, Croatia
Townley-Smith, TF	tsmith@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Trottet, Maxime	mtrottet@rennes.inra.fr	INRA, Le Rheu Cedex, France
Torres, Laura	ltorres@agro.uncor.edu	University of Córdoba, Argentina
Torres, Lorena	letorres_k@yahoo.com.ar	University of Córdoba, Argentina
Tranquilli, Gabriela	granqui@cirn.inta.gov.ar	INTA Castelar, Argentina
Tripathy, Subhash Chandra [11]	subhtripathi@gmail.com	Direct Wheat Research, Karnal, India
Tsehaye, Yemane	yemtse@yahoo.com	Inst Biodiversity Conservation, Ethiopia
Tsujimoto, Hisashi	tsujimot@yokohama-cu.ac.jp	Kihara Institute, Japan
Tverdokhleb, O.V. [11]	etverd@meta.ua	Plant Prod Inst VY Yuryev, Ukraine
Tyagi, BS	bst_knl@yahoo.com	Direct Wheat Research, Karnal, India
Ullah, Naimat [11]	naimat681@gmail.com	Quaid-I-Azam University, Pakistan
Urbano, Jose Maria	urbano@phibred.com	Pioneer Hi-Bred, Sevilla, Spain
D'utra Vaz, Fernando B	ferbdvaz@pira.cena.usp.br	University De Sao Paulo, Brazil
Valenzuela-Herrera V [12]	valenzuela.victor@inifap.g0b.mx	INIFAP, Cd. Obregon, México
Vallega, Victor [14]	vicvall@iol.it	Exp Inst Cerealicoltura, Rome, Italy
Varella, Andrea [15]	andrea.varella@msu.montana.edu	Montana State University, Bozeman
Vassiltchouk, NS	ariser@mail.saratov.ru	ARISER, Saratov, Russia
Van Sanford, David [08]	dvs@uky.edu	University of Kentucky, Lexington
Varshney, Rajeev K [08]	R.K.Varshney@CGIAR.ORG	ICRISAT, India
Varughese, George	g.varughese@cgnet.com	CIMMYT, Mexico
Vecherska, Liudmyla [19]	lyudmila_vecherska@ukr.net	Plant Prod Inst VY Yuryev, Ukraine
Veisz, Ottó	veiszo@penguin.mgki.hu	ARI–HAS, Martonvásár, Hungary
Verhoeven, Mary C	Mary.C.Verhoeven@orst.edu	Oregon State University, Corvallis
Vernichenko, IV [16]	i.vernichenko@gmail.com	Russian State Agrarian Univ, Moscow

Name (year updated)	E-mail address	Affiliation
Vida, Gyula	h8607vid@ella.hu	ARI–HAS, Martonvásár, Hungary
Vilkas, VK [13]	vk.vilkas@rediffmail.com	IARI, Wellington, India
Voldeng, Harvey	voldenghd.ottresb.ottawaem2@agr.gc.ca	AAFC, Ottawa, Ontario, Canada
Von Allmen, Jean-Marc	bvonal@abru.cg.com	Ciba-Geigy, Basel, Switzerland
von Wettstein, Dietrich H [10]	diter@wsu.edu	Washington State University, Pullman
Voss, Márcio	voss@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Vrdoljak, Gustavo	gvrdoljak@nidera.com.ar	Nidera SA, Buenos Aires, Argentina
Waines, Giles [08]	giles.waines@ucr.edu	University of California, Riverside
Walker-Simmons, MK	ksimmons@wsu.edu	USDA–ARS, Pullman, WA
Wanschura, Lucy A [15]	Lucy.Wanschura@ARS.USDA.GOV	USDA–ARS–CDL, St. Paul, MN
Wang, Daowen	dwwang@genetics.ac.cn	Chinese Academy of Science, Beijing
Wang, Richard RC	rrcwang@cc.usu.edu	USDA–ARS, Logan, Utah
Ward, Richard	wardri@msu.edu	Michigan State University, East Lansing
Watanabe, Nobuyoshi [08]	watnb@mx.ibaraki.ac.jp	Ibaraki University, Japan
Webster, James A	jwebster@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Wesley, Annie	awesley@rm.agr.ca	AAFC–Winnipeg, Manitoba
Wicker, Thomas [10]	wicker@botinst.unizh.ch	University of Zurich, Switzerland
Wildermuth, Graham	wilderg@prose.dpi.gld.gov.au	Leslie Research Centre, Australia
Williams, Christie [12]	cwilliams@purdue.edu	USDA–ARS, West Lafayette, IN
Wilson, Dean	trio@feist.com	Trio Research, Wichita, KS
Wilson, Duane L [19]	dlwil@k-state.edu	Kansas State University, Manhattan
Wilson, James A	trio@feist.com	Trio Research, Wichita, KS
Wilson, Jeff D	jdw@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Wilson, Paul	wilsonp@phibred.com	Pioneer Hi-bred, Northants, UK
Wilson, Peter	hwaust@mpx.com.au	Hybrid Wheat Australia, Tamworth
Wise, Kiersten A [10]	kawise@purdue.edu	Purdue University, West Lafayette, IN
Worrall, David	agripro@chipshot.net	AgriPro Seeds, Berthoud, CO
Wu, Shuangye [18]	swu4455@k-state.edu	Kansas State University, Manhattan
Xia, Xian Chun [19]	xiaxianchun@caas.cn	Chinese Acad Sci, Beijing, PR China
Yamazaki, Yukiko [14]	yyamazak@lab.nig.ac.jp	Japan
Yau, Sui-Kwong	sy00@aub.edu.lb	American University Beruit, Lebanon
Yen, Yang	yeny@ur.sdstate.edu	South Dakota State Univ, Brookings
Zeller, Frederich	zeller@mm.pbz.agrar.tu-muenchen.de	Technical University Munich, Germany
Zemetra, Robert [08]	rzemetra@uidaho.edu	University of Idaho, Moscow
Zhanabekova, EH	zhanabek@mail.ru	Agric Res Inst SE Reg, Saratov, Russia
Zhang, Peng [08]	peng.zhang@usyd.edu.au	University of Sydney, Australia
Zhu, Yu Cheng	zhuyc@ag.gov	USDA–ARS, Stillwater, OK
Zhmurko, VV	toshinho@rambler.ru	Kharkov National University, Ukraine

IX. VOLUME 66 MANUSCRIPT GUIDELINES.

The required format for Volume 66 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 44–65 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 66 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. 37–66) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.