ANNUAL WHEAT NEWSLETTER

Volume 67

Contribution no. 22-063-B from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

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Volume 67

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1 September, 2021.

Contribution no. 22-063-B from the Kansas Agricultural Experiment Station, Kansas State University, Manhattan.

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IN DEDICATION TO

SANJAYA RAJARAM

A titan of the wheat world succumbed to COVID-19 on 17 February, 2021. Sanjaya Rajaram, 78, passed away in Ciudad Obregon, Sonora, Mexico. 'Raj', as he was called by those who knew him, carried the mantle of his grand mentors, Norman E. Borlaug and Glenn Anderson, the driving forces of the wheat revolution of the 20th Century. He took over CIMMYT's bread wheat program in the early 1970s and proceeded to lead a 2nd Green Revolution in wheat production into the early 2000s that continues through today.

Rajaram was born and raised in Raipur, a small Indian farming village near the city of Varanasi, Uttar Pradesh. The family was of modest means and Raj was one of the few in the village who went to school. He was a good student and ultimately got a scholarship to study agriculture at the college in Gorakhpur, close to his home. Once finished he went on to IARI, New Delhi for his M.Sc. under the guidance of M.S. Swaminathan and N.L. Dhawan and was then awarded a Ph.D. scholarship to University of Sydney where he studied plant pathology and breeding under I.A. Watson and N. Derera. Upon his return to India, Anderson offered him a postdoctoral fellowship in India and after six months he asked Raj to go to CIMMYT in Mexico.

In Mexico, Rajaram impressed Borlaug and Anderson and went from a postdoctoral fellow in 1969–71 to geneticist in 1971–72 and became head of CIMMYT's Bread Wheat Breeding Program in 1972. In 1996, he was appointed as Director, International Wheat Program. Borlaug and Anderson saw Raj's ability to 'feel' the plants; both how critical it was to have open minded, young scientists for changing the old system and accepting new technology. Raj's photographic memory for wheat cultivars – and humans – and his grasp of handling large numbers of crosses and management of the populations and nurseries was unparalleled.

During Raj's leadership of the CIMMYT Wheat Program, 481 cultivars were released in 51 countries. These cultivars, grown on ca 60 x 10^6 ha, had increased yield stability and potential, broad agronomic adaptation, more efficient input utilization, and improved disease resistance. This increased global wheat production by more than 200 x 10^6 tons during his lifetime across most wheat regions in the world.

Other significant achievements include: increased genetic variability via 'spring x winter' crosses and exploiting synthetic wheats; rust resistance based on slow rusting genes and reduced use of race-specific resistance; development of wheat lines tolerant to acid soils; increased exchange of information via the international nursery system that ultimately led to the International Wheat Information System. This information system increased reliability of data and analysis over time and space; expanded global testing system to identify lines with highest yield potential, disease resistance, and abiotic stress tolerance; and structuring the program according to mega-environments. None of this happened in a vacuum and required outstanding leadership and teamwork from scientists, students, and national staff working in Mexico and cooperating countries.

Human resource development was a critical component to the success of the world wheat effort. Raj interacted and mentored more than 700 young scientists from around the world. It opened up minds and doors that never could have been done otherwise. Further, he supported many advanced projects in the wheat program with universities worldwide. In his efforts with colleagues and students over the years he published more than 419 publications, 119 of which were in refereed journals.

In honor of his lifetime dedication and success in increasing food production and helping to reduce world hunger, Rajaram was awarded the World Food Prize in 2014. Over his career he received numerous honorary degrees and awards and some are mentioned here: the Pravasi Bharatiya Samman award, the highest honor conferred on Indians overseas, and the Padma Shri Award, India; Fellow, IAAS; Presidential Award, Fellow and International Service in Agronomy by ASA and CSSA; the Rank Award, UK; the Friendship Award, China; Crawford Fund Derek Tribe Award, Australia; Khwarizmi International Award, Iran; and the Order of Quetzal Award, Guatemala.

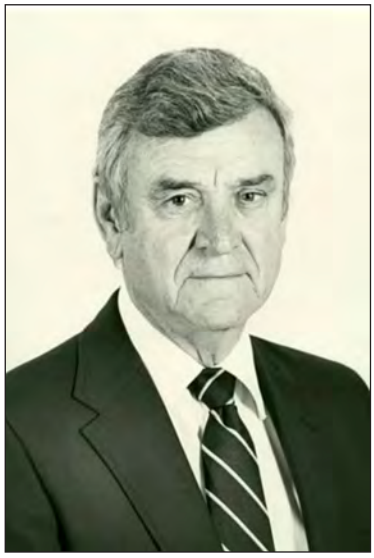
After his retirement from CIMMYT, Rajaram served as Director of the Integrated Gene Management Program at the International Center for Agricultural Research in the Dry Areas (ICARDA) before formally retiring in 2008. In his retirement, he continued as a special scientific advisor to CIMMYT and ICARDA.

In addition to his successful career as a plant scientist, Rajaram launched and operated Resource Seeds International, a company to develop and market seed of improved wheat cultivars. In recent years Raj was serving as President of Fundación Ambiental del Valle del Yaqui A.C, a non-profit foundation in support of environmental improvement in Sonora through afforestation and reforestation with native trees.

The world has lost one of the greatest 'Hunger Fighters' of our time. Rest in peace friend and mentor. Deep condolences are sent to the Rajaram family.

Submitted by H.J. Dubin, H.-J. Braun, R. Singh, and M. Kohli.

BYRD C. CURTIS



The International Maize and Wheat Improvement Center (CIMMYT) sadly notes the passing of Byrd C. Curtis, former Director of the Global Wheat Program, on 7 January, 2021. He was 95 years old and lived in Fort Collins, Colorado, USA, with his wife Eloise Curtis.

From his studies at Oklahoma State University to retiring after a fruitful international career with Colorado State University, Cargill Inc., and CIMMYT, he never got weary of sharing his passion for breeding better, tastier, and sturdier wheat to improve peoples' livelihoods.

He was an innovator at heart and his legacy will live on through Colorado State University's wheat breeding program and the many wheat cultivars he developed. Not only did he start Colorado State University's wheat breeding program in 1963, but he also ensured that the cultivars that were bred by his team reflected the needs of humanity for decades to come, such as the hard, red winter wheat named after himself.

Curtis worked at CIMMYT from 1982 and 1988 as Director of the Global Wheat Program. Together with his team, he worked to position CIMMYT as the leading international research-for-development and breeding organization for wheat for years to come.

"Byrd was very keen to build oral communication skills of scientists, which has been very helpful to me," said Ravi Singh, Head of Global Wheat Improvement at CIMMYT. "He also initiated the Turkey-CIMMYT-ICARDA International Winter Wheat Improvement Partnership's (IWWIP) winter wheat breeding program and even worked there in Turkey in his final year with CIMMYT to ensure it would take off well."

Byrd was instrumental and showed tremendous foresight. IWWIP's establishment in Turkey became first major breeding program within CGIAR that was hosted by a national program. He strongly supported the creation of the Wide Crossing Program. The synthetic wheat varieties developed in this program have had global impact on wheat improvement.

Aside from his remarkable technical legacy, Byrd had a knack for choosing the right people for the job. In the six years as Director of the Global Wheat Program, he hired scientists who held major roles in global wheat improvement: Ravi Singh, Distinguished Scientist and Head of Global Wheat Improvement; Wolfgang Pfeiffer, former leader of spring bread wheat, durum wheat, and triticale crop improvement; and Hans Braun, Director of the Global Wheat Program from 2004 to 2020.

"Byrd not only initiated the winter wheat program," said former Global Wheat Program Director Hans Braun, who was hired by Byrd in 1983. "He was also director when the tropical wheat program was implemented in Thailand." This program's work increased yields up to 1.5 tons per hectare but ultimately did not convince Thai farmers. Nevertheless, Braun said, "One of the oddest experiences I've had was to see our winter wheat material from Turkey grown in the Thai jungle!"

After retiring from his professional life in 1991, Curtis and his wife Eloise moved back to Fort Collins, where his career started in the 1960s and where he will be remembered by his townspeople — and fellow athletes and gym-goers — for his determination and active lifestyle.

I. SPECIAL REPORTS

INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM
http://www.wheatgenome.org/

2.1: New versions of the bread wheat reference sequence assembly and annotation.

As for many around the world, the IWGSC activities were impacted by the closure of laboratories in 2020 and the ongoing inability to travel, meet, and network due to the COVID-19 pandemic. Nonetheless, the Consortium was able to make some progress.

In April 2021, a **revised version** of the reference wheat genome, **IWGSC RefSeq v2.1**, was made available to the community at the IWGSC data repository hosted by URGI-INRAE. The genome assembly of *Triticum aestivum* cv. Chinese Spring (IWGSC RefSeq v1.0) was revised using whole-genome, optical maps and contigs assembled from whole-genome-shotgun (WGS) PacBio SMRT reads. Optical maps were used to detect and resolve chimeric scaffolds, anchor unassigned scaffolds, correct ambiguities in positions and orientations of scaffolds, create super-scaffolds, and estimate gap sizes more accurately. PacBio contigs were used for gap closing. Pseudomolecules of the 21 Chinese Spring chromosomes were reconstructed to develop a new reference sequence, IWGSC RefSeq v2.1. The revisions involved approximately 10% sequence length of the IWGSC RefSeq v1.0. The work was conducted under the leadership of Mingcheng Luo and Jan Dvorak (UC Davis, CA, USA) with funding from the U.S. National Science Foundation and the USDA Agricultural Research Service.

A **new version** of the reference sequence **annotation**, **IWGSC Annotation v2.1**, also was released to accompany RefSeq v2.1. Annotation v1.1 was updated to generate an interim annotation, IWGSC Annotation v1.2, by integrating a set of 117 novel genes and 81 microRNAs, many of which had been curated manually by the wheat community. This interim gene annotation was used to annotate IWGSC RefSeq v2.1. The transposable elements in the resulting assembly IWGSC RefSeq v2.1 were reannotated and gene annotation was updated by transferring the previously known gene models (v1.1) using a fine-tuned, dedicated strategy implemented in the Marker-Assisted Gene Annotation Transfer for Triticeae (MAGATT) pipeline. The newly released IWGSC Annotation v2.1 contains 266,753 genes comprising 106,913 HC genes and 159,840 LC genes. The work was conducted under the leadership of Frédéric Choulet and Hélène Rimbert (INRAE) and with funding from the French the Research National Agency (ANR).

An article outlining these new resources and the improvements to the wheat reference sequence has been published in The Plant Journal and is available on open access.

Reference.

Zhu T, Wang L, Rimbert H, Rodriguez JC, Deal KR, De Oliveira R, Choulet F, Keeble-Gagnère G, Tibbits J, Rogers J, Eversole K, Appels R, Gu YQ, Mascher M, Dvorak J, and Luo M-C. 2021, Optical maps refine the bread wheat *Triticum aestivum* cv. Chinese Spring genome assembly. Plant J https://doi.org/10.1111/tpj.15289.

A collaboration with Arbor Biosciences to provide tools for the community – such as the *myBaits®* Expert Wheat Exome capture panel released in October 2019 – has been delayed in 2020 as Arbor focused its effort on providing tools for the pandemic response. Nevertheless, a promoter capture array has been developed and is currently undergoing tests, with a release anticipated by the end of 2021. Plans and efforts are also underway to develop add-on modules for the exome panel such as low confidence genes from the IWGSC RefSeq v2.1 annotation and an array that captures common introgressions. Arbor Biosciences is also working on the incorporation of the revised and annotated IWGSC RefSeq v2.1 and genome-wide SNPs.

The IWGSC is still looking for collaborators, partners, and funding for the IWGSC **Wheat Diversity project** aimed at sequencing at least eight landraces to characterize the breadth of genetic diversity in bread wheat. In this project, the genomes of eight to twelve landraces, representing the full breadth of genetic diversity in wheat, will be sequenced at

high quality. These, in conjunction with the IWGSC RefSeq v2.1 and subsequent versions as well as other high-quality sequences of elite lines, will serve as the foundation for the diversity panel and haplotype map. Lower quality genome sequences of other landraces and elite lines will be added as available.

The IWGSC also continues its highly successful webinar series to showcase research results, tools, and resources. All webinars are free to attend and are posted subsequently on the IWGSC YouTube channel (see link below).

Data access.

All IWGSC data, including IWGSC RefSeq v2.1, IWGSC Annotation v2.1, and associated resources are publicly available at the IWGSC data repository at URGI-INRAE Versailles, France. Most data are also available at Ensembl Plants, Graingenes, WheatIS and NCBI: https://wheat-urgi.versailles.inra.fr/

Links.

- IWGSC website http://www.wheatgenome.org/
- IWGSC YouTube Channel https://www.youtube.com/c/internationalwheatgenomesequencingconsortium

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 TRIGO
CP 3081, 99.050–970 Passo Fundo, Rio Grande do Sul, Brazil.

Performance of wheat cultivars in the state of Rio Grande do Sul, Brazil, 2019.

Ricardo Lima de Castro, Eduardo Caierão, João Leonardo Fernandes Pires, 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), to support the indications of cultivars. This work evaluated wheat cultivar grain yield performance of the STWC-RS in 2019. The yield grain performance of 30 wheat cultivars (Ametista, BRS 327, BRS Belajoia, BRS Marcante, BRS Reponte, CD 1303, Celebra, Esporão, FPS Amplitude, FPS Certero, Inova, LG Cromo, LG Fortaleza, LG Oro, LG Supra, ORS 1401, ORS 1402, ORS 1403, ORS 1405, ORS Citrino, ORS Madrepérola, ORS Vintecinco, TBIO Audaz, TBIO Iguaçu, TBIO Ponteiro, TBIO Sintonia, TBIO Sinuelo, TBIO Sonic, TBIO Sossego, and TBIO Toruk) was studied in 14 environments (Coxilha, Cruz Alta – seasons 1 and 2, Passo Fundo – seasons 1 and 2, Sertão, Vacaria – season 1, Vacaria – season 2, Vacaria – season 3, Augusto Pestana, Ijuí, Santo Augusto, São Borja, and Três de Maio) in Rio Grande do Sul in 2019. The experiments were in a randomized block design with three or four repetitions. Each plot consisted of five 5-m rows with 0.2 m spacing between rows and a plant density approximaely 330 plants/m^2. Grain yield data (kg/ha^1) were subjected to individual analysis of variance (for each environment) and a grouped analysis of variance (for all environments). The grouped analysis of variance employed a mixed model (fixed cultivar effect and randomized environment effect). Grain yield performance of the wheat cultivars was evaluated by analysis of adaptability and stability, employing the method of distance from the ideal cultivar, weighed by the coefficient of residual variation, as proposed by Carneiro (1988). In this analysis, the ideal cultivar was that with high grain yield, high stability, low sensitivity to adverse conditions of unfavorable environments, and the ability to respond positively to improvement of favorable environments. The general average of the STWC-RS in 2019 was 4,676 kg/ha. Coxilha had the highest average wheat grain yield: 6,589 kg/ha. The maximum wheat grain yield was 7,362 kg/ha in Coxilha (cultivar Inova). Cultivars BRS Reponte, Inova, CD 1303, ORS 1403, and FPS Certero had adaptability and stability in favorable environments (environments with average of wheat grain yield higher than the general average). CD 1303, ORS Citrino, FPS Certero, BRS Reponte, and ORS Vintecinco had adaptability and stability in unfavorable environments (environments with average of wheat grain yield lower than the general average). In general, the average of all environments, CD 1303 (5,130 kg/ha^1), FPS Certero (5,063 kg/ha), BRS Reponte (5,147 kg/ha), ORS Citrino (4,954 kg/ha), and Inova (5,016 kg/ha) were the cultivars that came closest to the ideal cultivar.

Reference.

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

Wheat crop in Rio Grande do Sul state, Brazil, 2019.

Ricardo Lima de Castro, Eduardo Caierão, Aldemir Pasinato, João Leonardo Fernandes Pires, and Pedro Luiz Scheeren.

Rio Grande do Sul is one of the main wheat-producing states in Brazil. This study analyzed the wheat crop in Rio Grande do Sul in 2019. In 2019, Rio Grande do Sul state harvested 760,911 ha of wheat (36.3% of the total area harvested in Brazil), producing 2,287,720 tons of wheat (40.8% of the Brazilian production), with an average of grain yield of 3,007 kg/ha (336 kg/ha above the Brazilian average of 2,671 kg/ha). Among the geographical mesoregions of Rio Grande do Sul (Fig. 1), the RS Northwest mesoregion harvested the largest wheat area, 616,402 ha (81.0 % of the cropped area in the state) and had the largest production, 1,876,590 tons of wheat grain (82.0% of the state production) (Table 1). However, the average wheat grain yield obtained in this mesoregion was the second highest in the state at 3,044 kg/ha (37 kg/ha above the state average) (Table 1). The RS Northeast mesoregion harvested 36,861 ha of wheat (4.8% of the cropped area in the state), produced 124,056 tons of wheat grain (5.4% of state production), and had the highest average wheat grain yield in the state, 3,366 kg/ha (359 kg/ha above the state average) (Table 1). The wheat crop in Rio Grande do Sul, in 2019, had some unfavorable weather conditions, notably a water deficit at the beginning of the crop vegetative development, a high occurrence of powdery mildew, and excessive rainfall at harvest, favoring preharvest sprouting in more susceptible cultivars, especially in the colder regions with later sowing and harvesting. Comparing the wheat crop data with the results of the State Test of Wheat Cultivars in Rio Grande do Sul (STWC-RS) in 2019, we observed that the average of wheat grain yield of commercial crops was 1,669 kg/ha below that of the average of the STWC-RS (4,676 kg/ha).

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

Table 1. Area harvested, production, and average of grain yield of wheat in each of the mesoregions (see Fig. 1) of the state of Rio Grande do Sul, Brazil, in 2019 (Source: IBGE. 2021).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	616,402	81.0	1,876,590	82.0	3,044
RS Northeast	36,861	4.8	124,056	5.4	3,366
RS Western Center	42,978	5.6	120,324	5.3	2,800
RS Eastern Center	7,917	1.0	18,229	0.8	2,303
Porto Alegre Metropolitan	1,000	0.1	2,500	0.1	2,500
RS Southwest	50,550	6.6	135,673	5.9	2,684
RS Southeast	5,203	0.7	10,348	0.5	1,989
Rio Grande do Sul State	760,911	100.0	2,287,720	100.0	3,007

Reference.

IBGE. 2021. Produção Agrícola Municipal. Disponível em: <https://www.ibge.gov.br/estatisticas/economicas/agricultura-e-pecuaria/9117-producao-agricola-municipal-culturas-temporarias-e-permanentes.html?=&t=resultados>. Acesso em: 10 abr. 2021. Nota: Banco de dados agregados de estudos e pesquisas realizados pelo IBGE.

ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK GATERSLEBEN
Correnstraße 3, 06466 Seeland, OT Gatersleben, Germany.
http://www.ipk-gatersleben.de

A. Börner, A.M. Alqudah, D.Z. Alomari, J. Brassac, Yu.V. Chesnokov, I. Draz, N.V. Kocherina, U. Lohwasser, Q.H. Muqaddasi, M.A. Rehman Arif, M.S. Röder, M. Schierenbeck, A. Serfling, S.N. Shevchenko, S. Shokat, M.R. Simón, and R. Tarawneh.

Genetic architecture and genome-wide prediction of grain protein content, grain starch content, and grain hardness revealed via high-density SNP arrays and pan-genome analyses in European winter wheat varieties.

Grain quality traits determine the classification of registered wheat cultivars. Although environmental factors and crop management practices exert a considerable influence on wheat quality traits, a significant proportion of the variance is attributed to the genetic factors. To identify the underlying genetic factors of wheat quality parameters, i.e., grain protein content (GPC), starch content (GSC), and hardness (GH), we evaluated 372 diverse European wheat cultivars in replicated field trials in up to eight environments. We observed that all of the investigated traits hold a wide and significant genetic variation, and significant negative correlation exists between GPC and GSC plus grain yield. Our association analyses based on 26,694 high-quality, single nucleotide polymorphic markers revealed a strong quantitative genetic nature of GPC and GSC with associations on groups 2, 3, and 6 chromosomes. The identification of a known *Puroindoline-b* gene for GH provided a positive analytic proof of our studies. We report that a locus, *QGpc.ipk-6A,* controls both GPC and GSC with opposite allelic effects. Based on wheat's reference and pan-genome sequences, the physical characterization of two loci, *QGpc.ipk-2B* and *QGpc.ipk-6A,* facilitated the identification of the candidate genes for GPC. By exploiting both additive and nonadditive interaction among the loci, we evaluated the prospects of predictive breeding for the investigated traits that suggested its efficient use in the breeding programs.

Linkage mapping identifies a nonsynonymous mutation in FLOWERING LOCUS T (FT-B1) increasing spikelet number per spike.

Total spikelet number per spike (TSN) is a major component of spike architecture in wheat. A major and consistent quantitative trait locus was discovered for TSN in a doubled-haploid, spring wheat population grown in the field over four years. The QTL on chromosome 7B explained up to 20.5% of phenotypic variance. In its physical interval (7B: 6.37 to 21.67 Mb) the gene *FLOWERING LOCUS T* (*FT-B1)* emerged as candidate for the observed effect. In the parental lines, *FT-B1* carried a nonsynonymous substitution on position 19 of the coding sequence. This mutation modifying an aspartic acid (D) into a histidine (H) occurred in a highly conserved position. The mutation was observed with a frequency of ~68% in a set of 135 hexaploid wheat cultivars and landraces, although it was not found in other plant species. *FT-B1* only showed a minor effect on heading (HD) and flowering time (FT), which were dominated by a major QTL on chromosome 5A caused by segregation of the vernalization gene *VRN-A1*. Individuals carrying the *FT-B1* allele with amino acid histidine had, on average, a higher number of spikelets (15.1) than individuals with the aspartic acid allele (14.3) independent of their *VRN-A1* allele. Therefore, the effect of TSN is not mainly related to flowering time, but the duration of pre-anthesis phases may play a major role.

Linkage mapping reveals QTL for yellow rust resistance in spring wheat doubled-haploid populations developed from the German Federal ex situ Genebank genetic resources.

Novel resistance sources to the pathogen *Puccinia striiformis* f. sp. *tritici* (*Pst*) that cause yellow rust (stripe rust), a widespread devastating foliar disease in wheat, are in demand. We tested two doubled-haploid (DH) spring wheat populations derived from the genetic resources for resistance to yellow rust in the field trials in Germany and Egypt. Additionally, we performed tests for all-stage resistances (seedlings resistance). We performed linkage mapping based on the genotyping data of a 15k Infinium SNP-chip that resulted in 3,567 and 3,457 polymorphic markers for DH population-1 (103 genotypes) and DH population-2 (148 genotypes), respectively. In DH population-1, we identified a major and consistent QTL of chromosome 1B that explained up to 28% and 39% of the phenotypic variation in the field and seedling tests, respectively. The identified QTL was (1) contributed by the parental line TRI-5645, (2) located on the short arm of chromosome 1B (1.2 to 1.7 Mb), and (3) harbored several annotated disease resistance proteins, including a known resistance gene *Yr10*. The other parental line, i.e., TRI-11082, contributed several minor QTL on chromosomes 2B and 3A. In DH population-2, a major QTL on chromosome 6B was contributed by line TRI-5310 which represents variety Eureke from France. This QTL was mainly effective in the German environments and explained up to 36% of phenotypic variation. In Egypt, however, only a moderate resistance QTL was identified in the field tests and no resistance QTL was observed in the seedling tests. Nevertheless, the 6B-QTL ranged from 144.9 to 149.4 Mb and harbored several annotated disease resistance genes with no known gene present in the identified interval. Our results demonstrate the usefulness of genetic resources for the identification of novel resistance sources to yellow rust, including the 'Warrior' race *PstS10*.

A Major Facilitator Superfamily Transporter is a putative candidate gene for nutrient mineral accumulation in wheat grains.

Here we report a multi-locus, genome-wide association scan for a set of 369 diverse wheat genotypes, which were genotyped by 90k iSELECT Infinium and 35k Affymetrix arrays and yielded 15,523 SNPs. The panel was grown under the field conditions for three consecutive years: 2015, 2016 and 2017. ICP-OES (Inductively coupled plasma atomic emission spectroscopy) was used to measure the concentration of six nutrient minerals in wheat grains including: Ca, K, Mg, Mn, P, and S. Wide ranges of natural variation among the genotypes in nutrient minerals concentrations were detected. The phenotypic correlation showed strong positive correlation among the nutrient minerals except K that showed opposite correlation trends with other nutrient minerals. The genetic association analysis detected eighty-six significant marker-trait associations (MTAs) underlying the natural variation in nutrient minerals concentration in grains. The major MTA was detected on the long arm of chromosome 5A at 698,510,027 bp that showed a pleiotropic effect on Ca, K, Mg, Mn, and S. Further significant MTAs were distributed among the whole genome except chromosomes 3D and 6D. We identified putative candidate genes, which are potentially involved in metal uptake, transport, and assimilation.

TraesCS5A02G542600 gene at chromosome 5A (698,507,24–698,511,217 bp) annotated as transmembrane transporter activity and belonging to major facilitator superfamily transporter is a putative candidate gene for Ca, K, Mg, Mn, and S grain concentrations. The allelic variation at this gene showed that T allele increased the concentration of nutrient minerals in grain. This gene is highly expressed in seed coat followed by peduncle, awns, and lemma. Furthermore, the genomic prediction findings indicated that genomic selection may be useful for the genetic improvement of nutrient minerals accumulation in wheat. Our study provides crucial insights into the genetic basis of nutrient minerals variation in wheat and serves as an important foundation for boosting nutritional value and for further genetic and molecular mechanisms studies controlling nutrient minerals accumulation in wheat grain.

Genome-wide analysis identified marker trait associations and candidate genes for drought stress tolerance in spring wheat.

Wheat is one of the most important crops worldwide. However, the global climate change and increasing drought stress incidences affected wheat production negatively. The response of 111 spring wheat genotypes to simulated drought stress using chemical desiccation or under rain-out shelter drought were evaluated in order to study the genetic basis of drought response. Analysis showed significant differences between genotypes, chemical desiccation showed strong impacts on yield parameters, where the loss in 1,000-kernel weight reached 35–72% whereas under a rain-out shelter it was 15%.

A genome-wide association analysis revealed high number (263) of significant marker-trait associations (MTAs) for all measured traits after chemical desiccation and under the rain-out shelter. MTAs involved in TKW harbored the *Sugar-Dependent6* gene. Same tolerant genotypes were identified under chemical desiccation and rain-out shelter drought; showing that both approaches are suitable to simulate different drought scenarios.

Genetic dissection for seedling drought stress tolerance in a winter wheat panel.

The future productivity of wheat will be of utmost importance for global food security since it is the most widely grown crop worldwide. Drought or water deficiency is a major yield-limiting factor causing losses of up to 80% of total yield. Our aim was to identify QTL/loci influencing the drought tolerance at the seedling phase. A winter wheat population constituted by 261 accessions was genotyped by 90K Illumina iSelect SNP and used for association mapping and to detect candidate genes associated to drought tolerance-related traits. Plant material was grown at experimental fields of the Leibniz Institute of Plant Genetics and Crop Plant Research in Gatersleben in three environments in 2016, 2017, and 2018. Seeds harvested at these three seasons were used for the experiments. The root length (RL), coleoptile length (CL), shoot length (SL), and root/shoot length ratio (RSR) of ten seedlings per genotype under drought stress (12% PEG 6000) and a control treatment (distilled water) were measured. A tolerance index (TI) was defined for RL, CL, SL, and RSR as the ratio between the mean trait value obtained under stress and the corresponding trait value under control. Data analysis revealed extensive phenotypic variation in all studied traits suggesting the suitability of the used panel for association genetic studies. All variables analyzed were significantly influenced by the years, genotypes and G × Y (environment) interactions ($p<0.001$). In general terms, drought stress induced by PEG reduced SL (–36.3%) and RL (–11.3%) compared with control treatments, while, the CL was increased under drought conditions by 11%. A genome-wide association analysis was performed using 17,093 SNPs passing quality control. FARM-CPU model using GAPIT R-package was applied to avoid any false-negative and control for the false-positive associations by preventing model overfitting. Results revealed 80 stable QTL in at least two environments across 17 chromosomes. Furthermore, seven multi-traits-associated SNPs were found in chromosomes 1B, 2A (2), 2B, 4B, 7A, and 7B. The identified candidates genes showed strong involvement in controlling two or more traits related to drought stress tolerance during the seedling phase. Markers linked to the loci obtained through this project could then be used for marker-assisted selection in wheat breeding programs and be a source of drought tolerance in new genotypes.

QTL analysis of yield and yield related traits in durum wheat recombinant-inbred line population under irrigated and drought conditions in Pakistan.

Durum wheat is the hardest of all wheats. The density, high protein content, and gluten strength makes it an ideal choice for producing quality products including bread, couscous, frekeh, bulgur, and pasta. Durum wheat global consumption, however, is ahead of its production. Durum wheat is primarily grown under rain-fed conditions where the frequent drought combined with heat stress is the major aspect of grain yield reduction. Breeding for resistance to drought is complicated by the lack of fast, reproducible screening techniques and the inability to routinely create defined and repeatable water stress conditions where large populations can be evaluated efficiently. In spite of the available maps, populations, and marker technologies, progress in transferring knowledge from QTL studies on yield under drought conditions to breeding remains slow. We undertook an investigation in durum wheat recombinant-inbred lines (RILs) population for yield and yield related traits under drought and irrigated conditions at Nuclear Institute for Agriculture and Biology (NIAB) in Pakistan. These RILs were developed from a cross between a drought tolerant cultivar Omrabi5 (P1) and a high temperature and salinity tolerant breeding line Belikh2 (P2) at ICARDA, by repeated selfing of F_1 using single seed descent. Moreover, the population was genotyped with 265 microsatellites comprising of 159 GWM, 62 BARC, and 44 WMC markers spanning a distance of 2,864 cM at IPK Gatersleben, Germany. Our analyses revealed following: a total of 221 (160 with LOD > 2 ≤ 3 and 61 with LOD > 3) QTL distributed on all 14 durum wheat chromosomes; from which 109 (78 with LOD > 2 ≤ 3 and 31 with LOD > 3) were observed in season 1; 112 (82 with LOD > 2 ≤ 3 and 30 with LOD > 3) were observed in season 2; and a total of 53 clusters of QTL. The data provides a base line to improve drought tolerance in durum wheat. For example, allelic profiles of yield QTL on chromosome 2A and 7B indicate that allele A of *Xgwm895* and allele B of *Xbarc276* can enhance the yield up to 6.16% in control and 5.27% under drought. Moreover, if combined, a yield gain of up to 11% would be possible.

Evaluation of ITMI mapping population lines and QTL mapping in spring bread wheat in the Middle Vogla region environment.

During 2013–18 in the conditions of the Middle Volga region (Bezenchuk, Samara District, Russian Federation), 112 RILs of the ITMI mapping population were evaluated. The lines were characterized by the averaged biennial feature values. QTL analysis was performed using the MAPMAKER/QTL computer program. The mapping data published in the GrainGenes database (http://www.greengenes.cit.cornell.edu) were used to recalculate distances on the map using the MAPMAKER/EXP 3.0 program. The obtained phenotypic analysis data were integrated into the existing basemap of chromosomes created for the ITMI population. Localization of QTL on the genetic map and the comparison of the obtained linkage groups with the existing chromosome maps was performed using the QGENE computer program. Of note, under the conditions of the Middle Volga region, on the basis of ecological and genetic tests, redefinition of genetic formulas was shown for some quantitative traits, and molecular markers genetically linked to the identified QTL were established. Based on the data obtained, a Catalog was published, which presents the results of genetic tests of the ITMI mapping population under the conditions of Bezenchuk in Middle Vogla region environment (Gulaeva NV et al. 2020). Information was gathered on the localization of the identified QTL on linkage groups; data on the influence of seed reproduction on the manifestation of quantitative traits, but also the characteristics of the best lines of ITMI, are given according to some features, which showed themselves in the conditions of Bezenchuk location. The results of one-way analysis of variance for the year of research indicaties the reliability of the localization of the identified QTL and establishing the influence of the experiment setting factor on the variability of the studied traits, depending on the year of its manifestation. The Catalog was compiled to help breeders and scientists to familiarize themselves with the diverse and promising genetic and breeding material, as well as for scientific use of information on molecular genetic identification and chromosomal localization. Genetic factors that determine the control of economically valuable traits in spring bread wheat in the ecological and geographical conditions of the Middle Volga region of the Russian Federation were identified.

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ITEMS FROM INDIA

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Current Research Activities.

Yield and pathological evaluation for yellow rust (stripe) resistant mutants in the background of elite cultivars of the North Western Plains Zone of India.

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Yellow rust of wheat (*Puccinia striiformis* f. sp. *tritici*) is a major disease of concern for the North Western Plains Zone of India. New pathotypes of *P. striiformis* have emerged overcoming the resistance provided by *Yr* genes deployed in recent high-yielding cultivars of this zone. One such cultivar, DBW-88, which despite being high-yielding, became susceptible to yellow rust race 110S119. Mutation breeding using gamma rays was initiated for improvement of DBW-88 during 2014–15 with the objective to obtain mutants with resistance to yellow rust races in field conditions. Putative mutants (M2) were identified for yellow rust resistance (2015–16) at IIWBR, Karnal, and then further confirmed and stabilized (M3–M8, 2016–20) at both IIWBR, Karnal, and the IIWBR summer nursery at Dalang, HP, India. Mutants showed resistance-type reactions (Immune to 5MS) compared to parent (susceptible reaction; 60–80S). Being direct mutants, these genotypes have the added advantage, apart from being resistant, that they are very phenotypically and genotypically similar to the parent the same as DBW-88, thus amenable to acceptance by farmers. Preliminary yield evaluation of selected mutant lines were carried out at IIWBR, Karnal, and superior lines in yield and resistance were advanced to multilocation testing. During Rabi 2020–21, three advance lines were tested in station trials at IIWBR, Karnal, and two promising lines were identified, which will be further tested in multilocation trials for their yield and resistance superiority. Two other popular cultivars, HD-2967 and WH-1105, also were included for mutation breeding-based improvement for yellow rust (2016–17), and putative resistant mutants (M2) were identified (2017–18). These mutants were confirmed and stabilized (M3-M6, 2017–20) at both IIWBR, Karnal, and the IIWBR summer nursery at Dalang, HP, India. Currently, stable mutants (M6) are being evaluated in preliminary yield trials at IIWBR, Karnal, for their agronomic performance.

Improved sharbati wheat mutants suitable for cultivation in the Central Zone of India.

G. Vishwakarma and and B.K. Das, J.B. Singh and S.V. Sai Prasad (ICAR-Indian Agriculture Research Institute, Regional Station, Indore, India), and D.A. Gadekar (MPKV Agriculture Research Station–Niphad, Nashik, India).

Sharbati wheat cultivar of the Central Zone of India are very popular among consumers and farmers due to their excellent *Chapati* making quality and fetch premium prices for farmers. These cultivars have a few agronomic defects, (tall height, susceptibility to lodging, and lower yield potential, but are still cultivated by farmers in large areas due to their wider acceptance and market prices. *Sharbati* wheats HI-1500 (Amrita) and HI-1531 (Harshita) are among two of the most popular cultivars of this category with good yield and quality aspects. However, these cultivars have a tall plant type and, hence, susceptible to lodging during heavy irrigation, hailstorms, unseasonal rains, and heavy winds at maturity. Mutation breeding using gamma rays of these two *sharbati* wheats was initiated to improve agronomic traits and keep the genotypic background as similar to the parents for acceptance by farmers. Gamma ray-treated M1 seeds were raised (2016–17) at Trombay, Mumbai, and the subsequent M2 generation grown and screened for desired traits at the IARI regional station, Indore, in the Central Zone. Putative mutants with an improved plant type, reduced height, increased tillering, and early maturity, were identified, and these mutants were advanced to a stable mutant generation (M3–M6, 2017–20) at Indore. Multi-environment (restricted irrigation and irrigated) station trials of selected mutants was at IARI

RS Indore, MP, and promising lines with reduced height, increased tillering, and increased yield were identified. These lines will be tested under multilocation trials in the coming season and assessed for adaptability and stability.

Improvement of wheat cultivar C-306 using mutation and molecular breeding approaches.

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C-306 is an important landmark cultivar in India, released in 1969, and still cultivated by many farmers of different agroclimatic zones of India. C-306 has a high demand among consumers, primarily for its excellent *Chapati*-making quality and resilience for yield in marginal conditions. However, being more than 5 decades old, C-306 suffers from a few agronomic defects, such as susceptibility to wheat rusts and a semi-late maturity, which is effected by terminal heat stress. In view of the popularity and demand of C-306 to the flour making industry and farmers, induced mutation breeding for improving C-306 was initiated at NA&BTD, BARC, Mumbai, and an early maturing (~25 days) mutant (TWM-89-2) was developed, which could easily escape terminal heat stress. To further improve rust resistance, TWM-89-2 was crossed with HW-2004 (a NIL of C-306) having rust resistance genes *Sr24*/*Lr24*. Using marker-assisted selection, recombinant lines with early maturity and resistance to rust were developed. Selected mutant-derived recombinant lines were tested for yield, agronomic traits (maturity), and rust resistance at multiple (3–4) locations in the Central and Plains Zones of India. Promising lines with improved yield, early maturity, and rust resistance better than C-306 were identified and will be advanced to station trials at IGKV–Bilaspur, MPKV ARS–Niphad, and IARI RS Indore.

Induced mutation breeding for developing spot blotch resistance in popular cultivars of North Eastern Plains Zone of India.

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The North East Plains Zone (NEPZ) of India, consisting of 30% of total wheat area in India, is an important zone for national food safety. Spot blotch of wheat, caused by *Bipolaris sorokiniana* (Sacc. In Sorok) Shoem syn. *Helminthosporium sativum* Pamm, is the most important disease in the NEPZ and remains the major concern for this area with 20–40% yield loss as well as affecting end use quality. Although a number of efforts to improve resistance towards spot blotch have been carried out using recombination breeding, their success was limited due to the quantitative nature of inheritance in most sources. Mutation breeding-based improvement of spot blotch disease was attempted for wheat cultivar HI-1563, and M1 using gamma rays was raised (2018–19). Subsequently, the M2 was screened (2019–20) at a hot-spot for spot blotch, Pundibari farm, UBKV, and Coochbehar, under artificial epidemic conditions. Putative mutants were identified showing field level resistance compared to the parent. The M3 generation (2021) was screened for spot blotch resistance and confirmed resistant mutants identified. Confirmed mutants will be stabilized further for resistance, and yield trials will be carried out in coming years. These putative mutants hold promise to be used in direct or indirect source for resistance to spot blotch in the NEPZ.

Optimization of a proton (H^+) beam mutagen for induced mutation breeding in Indian wheat.

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Mutation breeding history dates to 1960s and, since then, has contributed significantly in plant breeding activities across globe in all types of crops. With the initial start using X-rays, slowly, many other mutagen-like chemicals, gamma rays, and particle beams were added to the arsenal of the mutation breeder. However, to date, the most common physical mutagen used world-wide are gamma rays, originating from isotopic sources such as Co-60 or Cs-137. Over the years, many countries, such as China, Japan, and South Korea, have explored the use of ion beams as mutagens owing to their high Relative Biological Effect (RBE) and Linear Energy Transfer (LET). However, their wide-spread use has remained limited, due to concerns of availability of high-energy accelerators and related facilities. In India, at BARC, H^+ ion beam mutagenesis for plants was initiated. Using the BARC–TIFR Pelletron LINAC facility, (TIFR, Mumbai), a 14 MeV

energy, accelerated H^+ ion was used for mutation breeding in wheat. Initially, seed geometry and the spread of the ion beam for irradiation was optimized. Subsequently, radio-sensitivity studies were carried out in important wheat cultivars (HI-1563, DBW-173, and NIAW-1994). Proton beams as mutagens showed 50% lethality (LD50) at ~175 Gy compared to 350 Gy for gamma rays, showing an RBE of 1.5–2.0. Mutagenic populations for HI-1563 and DBW-173 were created (2019–20) by irradiating at 150 Gy, and the M1 raised at BARC, Mumbai, and IIWBR, Karnal, respectively. These populations will be screened for desired traits in the coming year. Proton beam irradiation holds the promise to develop novel mutants that could hold solutions to current and future challenges in agriculture.

Optimization of thermal neutrons (n) as a mutagen for induced mutation breeding in Indian wheat.

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In the history of mutation breeding over the years, many sources of physical mutagens have been used for mutagenizing explants. Noncharged particle radiation, i.e., neutrons, have been especially interesting due to their very high LET and, hence, potentially better mutagens compared to others. However, due to limited useful neutron sources and strict radio safety constraints, their widespread use has been very limited. At BARC Mumbai, neutron irradiation for mutation breeding in wheat was initiated using a thermal neutron (25 meV energy) source at the Dhruva research reactor. Seed preparation, geometry, and packaging was optimized. Further radio-sensitivity studies with two wheat were carried out with a neutron flux of ~10^7 neutron/cm/sec and passive thermo-luminescence dosimeter (TLD). Initial results indicated an LD50 value ~21 Gy, compared to 350 Gy for gamma, showing an RBE of 16–17. In the future, this irradiation procedure will be refined further for bulk irradiation, and large-scale seed irradiation will be carried out for the mutation breeding program. Neutron-based irradiation will further be explored to use fast neutrons as a mutagen. Overall the use of neutrons as a mutagen provides an exciting option for plant mutation breeders with potentially novel mutant traits to be obtained.

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http://molbiolabccsumrt.webs.com/founder.htm; http://ccsubiflaboratory-com.webs.com/

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Genetic, molecular breeding, and epigenetic studies for a variety of traits in wheat.

CCS University Meerut is located in the Northern Plain Zone of India. For more than five decades, a team of scientists at the Department of Genetics and Plant Breeding of this university has been engaged in studies involving cytogenetics and genetics of a variety of traits in wheat (mainly spring bread wheat). During the last 25 years, there has been a shift towards the use of molecular markers for genetic/cytogenetic studies (both QTL interval mapping and GWAS; development of genetic and physical maps) for a variety of traits related to abiotic and biotic stresses, grain yield and quality, biofortification, and N/K use efficiency. More recently, during the last 10 years, the group also has been utilizing bioinformatics for identifying and chracterizing a variety of useful genes, utilizing whole-genome sequences of wheat and a range of software/tools that have become available. A major emphasis, in recent years, was the study of epigenetic control of plant immunity (leaf rust resistance). All aspects of epigenetic control, including DNA methylation, histone modifications (both acetylation and methylation), and ncRNAs (both miRNAs and lncRNAs), have been utilized for the study of epigenetic regulation of (i) leaf rust resistance mediated by two different genes, the seedling resistance gene

Lr28 and the adult plant resistance gene *Lr48*; and (ii) spot blotch resistance caused by *Bipolaris sorokiniana*, using two different systems, one involving R genes following a gene-for-gene relationship and the other involving sensitivity genes (e.g., *Tsn1*) following an inverse gene-for-gene relationship. The majority of recent work was undertaken through funds made available in the form of multi-institutional collaborative projects by different funding agencies in India and abroad (including USAID and NIH of USA). The work carried out in all these areas during 2020–21) is described briefly.

Genetics of tolerance to abiotic stresses: heat, drought, and preharvest sprouting.

Meta-QTL analysis for heat stress tolerance. Heat tolerance is a complex trait, which adversely affects grain yield and yet remains relatively unexplored. Heat stress affects 40% of the wheat-growing area of the world. Every 1°C rise in temperature above the optimal 28°C reduces wheat yield by 3–4%. To date, more than 1,000 QTL are reported for several traits responsive to heat stress. However, these QTL have large confidence intervals and, thus, closely associated markers are only rarely available. The present study on meta-QTL (MQTL) analysis for heat tolerance traits in wheat was planned to identify robust QTL with closely linked markers, which may be useful for developing heat-tolerant wheat cultivars. For this purpose, we retrieved 826 mapped QTL from 28 different studies (published up to 2020), which utilized different mapping populations. These QTL control a number of different traits, including morphological traits, canopy temperature, chlorophyll content, cell membrane thermostability, and grain yield and yield related traits. The MQTL analysis used the software BioMercator V4.2. Only as many as 411 QTL (out of the available 826 QTL) were retained by the software (due to inadequate information for the remaining QTL) and were used for the MQTL analysis. A consensus map consisting of 50,310 markers (SNP, SSRs, RFLP, and DArT) was prepared for the MQTL analysis using four reference maps available in the GrainGenes database and also the maps used in earlier QTL studies. The above 411 QTL were projected onto the consensus map leading to identification of 85 MQTL distributed on all the 21 wheat chromosomes. The confidence intervals for each of the 85 MQTL was narrower than the original QTL, suggesting greater precision in the mapping of MQTL. We are currently examining these MQTL using the following different criteria: low CI, high average PVE (>20%), control of more than two traits, and those with more than two initial QTL, which will help us identify MQTL for their potential application in breeding for heat tolerance following MQTL pyramiding. Putative candidate genes underlying the most refined MQTL regions also are being mined using different databases.

Meta-QTL analysis for drought tolerance. We made an effort to identify robust, key genomic regions associated with yield and related traits under drought using a trait-wise QTL meta-analysis approach. Using LPmerge software, a high-density consensus map consisting ~50,000 markers (SNP, SSRs, RFLP, and DArT) was prepared using different reference maps available in GrainGenes database. The initial QTL reported in the individual studies published earlier were projected on to this map using BioMercatorV4.2 software for conducting meta-analysis. Using 379 yield-related, original QTL from 16 different studies, a meta-analysis was performed resulting in 70 meta-QTL (MQTL) located on 18 different chromosomes. The maximum MQTL belonged to 1,000-kernel weight (16), followed by MQTL for grain weight/spike (15), grain number/spike (12), plant height (10), spikes/plant (7), grain yield (4), and days to maturity and days to heading (3 each). The confidence intervals for each of these MQTL were mostly narrow relative to the original QTL. We are currently using these MQTL for analyzing ortho-metaQTL and underlying candidate genes for drought tolerance across a number of cereal species.

GWAS for heat stress-responsive traits. The genetic architecture of 11 heat stress-responsive traits (eight agronomic and three physiological traits) was examined using an association mapping panel (273 diverse wheat genotypes) using three different models, namely CMLM, SUPER, and FarmCPU. The data also was used for genomic prediction using rrBLUP. Phenotypic data were recorded at Meerut (Uttar Pradesh) and Powerkheda (Madhya Pradesh; heat-prone region) under timely sown and late-sown conditions. Genotype data involved 17,937 SNP markers (genotyping work was outsourced to Kilian Andrzej of DArT Pvt Ltd, Australia, and funded by CIMMYT, Mexico). Twenty-one marker-trait associations (MTAs) identified using GWAS (17 at Powerkheda and four at Meerut) may prove useful for MAS while breeding for heat tolerance. Eight of the 21 MTAs overlapped known QTL for different traits. Forty-seven candidate genes associated with important MTAs also were identified and will be validated using qRT-PCR expression studies.

Expression of genes involved in starch metabolism. Starch content in wheat is directly correlated to grain size/grain weight and accounts for 65–70% of the total dry weight. This study was planned using two wheat genotypes (Seri82, thermotolerant, and KSG132, relatively thermosensitive) to study changes in the expression pattern of nine important genes involved in starch metabolism under two different temperature regimes: control temperature (24°C/16°C) and high temperature (34°C/16°C). The effect of heat stress on sugar and starch concentration also was examined. The experiment

was conducted at three grain development stages, including 14, 21, and 28 days after anthesis (DAA). Of the nine genes, eight (*AGPaseLS*, *AGPase SS*, *SSSI*, *SSSIII*, *GBSSI* and *GBSSII, ISAI*, and *SBEI*) are involved in starch biosynthesis and one (*BMY*) is involved in starch degradation. The results of starch content revealed an initial increase at 14 DAA, followed by a decline at 21 DAA in both genotypes. The decline was further intensified at 28 DAA in KSG132, but not in Seri82.

These results suggest that different genes differ in their expression pattern at individual time-points within the two selected genotypes (KSG132 and Seri82) and also that individual genes differ in their temporal expression. Overall, downregulation of genes was more conspicuous as revealed through 25 of the 54 different gene-genotype-stage combinations (nine genes x three stages x two genotypes). At 21 DAA, a decline in starch content may be attributed to decreased expression or no change in expression of almost all the genes except *SSSIII* in Seri82, which showed upregulation. Overall, the results of gene expression allowed us to identify two genes encoding for AGPaseSS and SSSIII, which either showed no change or showed upregulation at all the three stages in the thermotolerant cultivar Seri82. Therefore, these two genes may be further explored for their role in thermotolerance and may be potential candidates for development of thermotolerant wheat cultivars. This study may serve as a template for conducting future experiments involving enzyme assays and estimating amylose/amylopectin content, which may provide better insight into the role of these nine genes in developing thermotolerant wheat genotypes. This study was carried out by Gautam Saripalli during his visit to Kansas State University, Manhattan, Kansas, USA, in 2016.

GWAS, genomic prediction and candidate genes involved in preharvest sprouting tolerance. Preharvest sprouting (PHS) is a serious problem in wheat, as untimely rain at the time of crop maturity leads to germination of grains in the spike. In India, PHS occurs in many wheat-producing states, but northern and eastern parts are predominantly affected. Generally, red-grained wheat possesses greater PHS tolerance than white-grained wheat. Various tests, such as wetting treatment of physiologically matured spikes, threshed seed germination counts, and alpha-amylase activity (measured by falling number), are used to evaluate wheat genotypes for PHS tolerance and to dissect the genetic control of PHS. This study identified potential chromosome regions associated with tolerance to PHS-related traits, sprouting score (SS), falling number (FN), and grain color (GC). For this purpose, a GWAS was conducted using 190 accessions of Spring Wheat Reference Set grown at Meerut over two seasons, and genotyped using 9,904 polymorphic SNP markers.

The frequency distribution largely showed normal distribution for all the three traits (SS, FN and GC) suggesting that they are under polygenic control. A correlation analysis revealed significant ($P < 0.05$) negative correlations of PHS with FN and GC, indicating that PHS tolerance is associated with high FN and white grain. We identified MTAs using CMLM and SUPER (single-locus analyses) and FarmCPU (a multi-locus analysis) that were available in the GAPIT software. Using principal component analysis, we showed that ~14% of the variation was explained by the first three principal components. A total of 188 significant ($p < 0.001$) MTAs were detected in two environments using all the three statistical methods as follows: 48 in CMLM (14 for SS +16 for FN + 18 for GC); 78 in SUPER (23 for SS +33 for FN +22 for GC); and 62 in FarmCPU (15 for SS +24 for FN +23 for GC). These MTAs were mapped on all the 21 wheat chromosomes, except 4B and 4D. The phenotypic variance explained (estimated only using CMLM) due to individual MTAs for the three traits ranged from 5.9% to 9.4%. As many as 33 MTAs (8 for SS+ 14 for FN + 11 for GC) were common and detected by each of the three methods; these MTAs may be more important for use in breeding for tolerance to PHS.

This study further suggests that, out of 188 MTAs, 40 were co-localized with the previously reported QTL/genes controlling different traits associated with PHS. For example, two SNP markers, M10478 and M1920 on chromosome arm 4AL, were reported in the close vicinity to *PhsA1*, a QTL for seed dormancy, QTL for PHS tolerance reported in previous studies. Over 40 candidate genes underlying MTAs also were identified for the three traits. Some important candidate genes that are known to be involved in controlling the three PHS-associated traits include genes encoding for serine/threonine protein kinase, F-box like domain, GRASS TF, WRKY TF, and leucine rich repeats. These results may lead to an improved understanding of the complex genetic architecture of PHS/dormancy. Besides GWAS, three genomic prediction models for predicting SS, FN, and GC using a cross-validation approach for each environment are also being tried.

Genetics for tolerance to biotic stresses.

GWAS and interval mapping for resistance to cereal cyst nematodes (*H. avenae*). GWAS and QTL interval mapping is being conducted to detect significant MTAs/QTL for resistance against cereal cyst nematode. For this purpose, phenotypic data for resistance to cereal cyst nematode was recorded under controlled environmental conditions for two years with a minimum of five replicates. The following plant material was used: (i) an association mapping panel consisting of a worldwide collection of 100 spring and 80 winter wheat genotypes obtained from IPK, Gatersleben, Germany; (ii) an association mapping panel consisting of 143 Indian wheat genotypes; (iii) the novel, doubled-haploid ITMI mapping population (114 individual lines) derived from the cross 'synthetic wheat M6 / Opata'; and (iv) an RIL mapping population consisting of 149 lines derived from the cross 'C-306 / HUW-468'.

Expression studies using transcriptome for nematode resistance. Whole-genome transcriptome analysis is underway to quantify differences in gene expression between resistant and susceptible interactions involving wheat roots and nematodes. The study also includes the evaluation of histological responses of susceptible and resistant wheat genotypes to *H. avenae* infection, which was performed using an acid fuchsin dye following staining of infected plant roots at different time points after inoculation.

GWAS for resistance to spot blotch. For resistance to spot blotch, an association mapping panel (303 diverse wheat genotypes) using SUPER and FarmCPU model (available in GAPIT) was used. The association mapping panel was genotyped for 12,160 DArT SNP markers, and the phenotypic data on the panel were recorded on the following disease-related traits: (i) area under disease progress curve (AUDPC), (ii) incubation period (IP), and (iii) lesion number (LN), at BHU, Varanasi (in Uttar Pradesh), and the BISA Farm, Samastipur (in Bihar). Model-based cluster analysis of the association mapping panel used the software STRUCTURE version 2.3.4, and four subpopulations (G1 with 31, G2 with 49, G3 with 50, and G4 with 173 genotypes) were identified using ΔK. Based on the principal component analysis, the first three principal components explained 7.8%, 4.53%,, and 3.19% of the variation within all genotypes. The SUPER model captured a maximum number of MTAs at (P <0.001) followed by FarmCPU (45 at Varanasi and 39 at Samastipur using SUPER, and 32 at Varanasi and 31 at Samastipur using FarmCPU). The MTAs/QTL identified may prove useful for molecular breeding leading to development of spot blotch tolerant wheat cultivars.

GWAS for powdery mildew resistance. GWAS also is being conducted for resistance to powdery mildew using an association panel comprising 224 SWRS genotypes that were genotyped for 17,937 SNP markers (generated using DArT-seq at Diversity Array Technology Pvt. Ltd., Australia, under the 'Seed for Discovery' project at CIMMYT). The phenotypic data for GWAS on powdery mildew was recorded for two years at a single location (Eternal University, Baru Sahib) in Himachal Pradesh. This location was used because powdery mildew disease is common in this region.

Meta-QTL analysis for leaf rust resistance. Using GWAS and interval mapping, a large number of QTL and MTAs were identified during the last two decades. We utilized 260 QTL for leaf rust resistance from 47 studies for a meta-QTL (MQTL) analysis. A high-density integrated linkage map with 71,778 markers (3,026 DArT, 61,569 SNP, 3,385 SSR, and 3,798 other types of markers) was used for projection of 260 QTL. As a result, 135 QTL were clustered into 32 MQTL consisting of 2 to 8 initial QTL. Out of these 32 MQTL, four were large (PVE > 15%) each based on 4–8 initial QTL, indicating their importance in molecular breeding for leaf rust resistance in wheat. As many as 108 candidate genes also were identified. The proteins encoded by these candidate genes contained domains related to the disease resistance. Only 10 showed differential gene expression during leaf rust infection, indicating their importance in providing resistance against leaf rust. Some of the genes also encoded proteins that were similar to the proteins encoded by known *Lr* or *Yr* genes, including genes containing the following domains: NBS-LRR (NLR), ABC transporter, or protein kinase domain. Overall, our results provid useful genomic resources, including robust MQTL and underlying candidate genes that may be potential targets for molecular breeding for development of leaf rust-resistant cultivars.

Meta-QTL analysis for stripe rust resistance. As many as 61 important meta-QTL (MQTL) involving 184 out of 353 QTL were identified using a dense consensus map consisting of 76,753 markers. Ten important genomic regions, including six breeders' MQTL (PVE >20%) and four MQTL hotspots, were selected for use by wheat breeders. As many as 409 important candidate genes also were identified, which either encoded known R proteins (265) or showed differential expression (144) due to stripe rust infection, includeing genes encoding for proteins NBS-LRR, WRKY domains, ankyrin repeat domains, and sugar transporters. Overall, this study provides robust MQTL and underlying candidate gene, which may be potential targets for molecular breeding for development of stripe rust resistant wheat cultivars or may be the target for future molecular studies to understand the mechanism of stripe rust resistance.

Genetics of some other traits: nitrogen-use efficiency, yield, grain morphology, Fe/Zn content, and quality traits.

Interval mapping for nitrogen-use efficiency (NUE). NUE and its component traits are inherently complex and influenced by environmental factors, N management practices, and genotypic variation. The genetics underlying NUE and its component traits was studied using a bi-parental mapping population comprising of 149 RILs, which were grown in an augmented block design under four different N levels (0, 60, 120, and 180kg/ha) for three years. The population was derived from a cross between previously identified high NUE parent (HUW468) and a low NUE parent (C306). Phenotypic data was collected on RILs and the parental lines for 14 traits. The RIL population was genotyped using a genotyping-by-sequencing platform. Using this data, a genetic map of the RIL population was constructed using Multipoint software. The genetic map contained 518 loci and 26 linkage groups with a length of 2,837.24 cM. The size of the individual linkage groups ranged from 9.24 cM (chromosome 4D) to 391.39 cM (chromosome 5A). Chromosome 5A had the maximum number of loci (67), whereas chromosome 6D had the minimum (3). The genetic map and phenotypic data are being currently used for QTL interval mapping for 14 traits including NUE.

GWAS for yield and its component traits. GWAS for 10 yield and yield component traits was conducted using a panel of 225 diverse spring wheats that were genotyped using 10,904 SNPs and evaluated for three years (2016–19). The MTAs were worked out for each trait using four different approaches, including three single-trait approaches (CMLM, FarmCPU, and SUPER) and one multi-trait approach (mvLMM). Hundreds of MTAs were obtained using each approach, but after Bonferroni correction, only six MTAs for three traits were available using CMLM, and 21 MTAs for four traits were available using FarnCPU. None of the 525 MTAs obtained using SUPER could qualify after Bonferroni correction. Epistatic interactions involving 28 pairs of MTAs also were available for seven of the 10 traits. As many as 134 putative candidate genes (CGs) were identified. This study has provided markers for MAS for the development of wheat cultivars with improved agronomic traits.

GWAS for grain morphology. We identified MTAs for the following six grain traits: (i) grain area size, (ii) grain perimeter length, (iii) grain length, (iv) grain width, (v) grain length-width ratio, and (vi) factor form density. A spring wheat reference set comprised of 225 diverse accessions was genotyped using 10,904 SNPs and phenotyped for the above six traits over two consecutive years (2017–18 and 2018–19). GWAS used four different models involving two single-locus models (CMLM and SUPER), one multi-locus model (FarmCPU), and one multi-trait model (mvLMM). The 'Q x Q' epistatic interactions also were identified. The false discovery rate (FDR) and Bonferroni correction (corrected p value <0.05) were applied to eliminate false positives due to multiple testing. This exercise gave 79 main effect and 48 epistatic MTAs after FDR, but after the Bonferroni correction, five main effect and 12 epistatic MTAs were identified. We then identified 53 candidate genes. *In silico* expression analysis of the candidate genes in different tissues at different development stages was also carried out. MTAs and candidate genes identified during the study are a useful addition to available resources for MAS to supplement wheat breeding programs after due validation and also for future research program.

GWAS for grain hardness. The spring wheat reference set association panel comprised of 224 genotypes (for which SNP genotyping data was available from earlier studies), also is being used to study the genetics of grain hardness. The available SNP genotyping data and the phenotypic data for grain hardness, collected using Perten Single Kernel Characterization System (SKCS4100), for two years at a single location (Meerut, UP, India) are currently being used for GWAS.

Study of modifiers for plant height. In wheat, 25 *Rht* genes for dwarfness are known, which include both GA-insensitive and GA-responsive genes. The GA-insensitive *Rht* genes are widely used, although their suitability under abiotic stress conditions has been questioned. This necessitated a search for alternative GA-responsive, spontaneous, and induced dwarfing genes. We earlier reported an induced dwarf mutant *dwarf mutant-30* (44 cm); the mutant allele was named *Rht4c* allele (2BL). This dwarf mutant was not suitable for cultivation due to its extra-dwarf nature. Therefore, we searched for naturally occurring QTL that would modify the phenotype of *dwarf-mutant-30* using a mutant-assisted gene identification and characterization (MAGIC) approach. For this purpose, *dwarf mutant-30* was crossed with the tall wheat cultivar NP114. Homozygous mutant F_2 plants (~25% of the progeny) were selected, which were phenotyped for plant height and genotyped using SSR markers. The data were utilized for QTL analysis for plant height. Six modifier QTL were identified on chromosomes 2A, 2B, and 4A. Two QTL, each on 2A and 2B, were responsible for increase in plant height (described as 'enhancer modifiers'), whereas the remaining two QTL on 4A were responsible for reducing plant height (described as 'suppressor modifiers'). We hypothesized that the enhancer QTL could be exploited for the development of semidwarf, high-yielding genotypes containing the *Rht4c* allele. This is the first study of its kind in wheat

demonstrating that the MAGIC approach could be used to identify modifiers of the mutant phenotypes of other traits for wheat improvement.

Genetics of grain iron (Fe) and zinc (Zn). A GWAS is being used to study the genetic architecture of Fe and Zn concentrations in wheat grains utilizing a wheat diversity panel (WDP) of 288 genotypes. This WDP was evaluated in alpha lattice design at Meerut during 2019–20 crop season and is being currently (2020–21 crop season) evaluated again an alpha lattice design at three different locations (Meerut, Ludhiana, and Pantnagar). Grain Fe and Zn concentrations were estimated for first year using inductively coupled plasma mass spectrometry (ICPMS) and X-ray Fluorescence (EDXRF spectrometer X-Supreme 8000) methods. Similar data for the second year will be recorded after harvesting of the crop. Genotyping of the WDP is being performed through 90k iSelect Infinium high-density SNP array through outsourcing. Phenotypic and genotypic data will be used for the association mapping using FarmCPU. Efforts also are underway to pyramid 3–4 alien genes for Fe and Zn homeostasis using introgression lines prepared in the background of cultivar PBW343 using *Aegilops kotschyi* as a donor.

Meta-QTL analysis for grain Fe and Zn. A large number of QTL for grain micronutrient concentration are reported in different interval mapping studies. Using these QTL, a meta-QTL analysis for GFe and GZn was performed. For this purpose, information of 159 QTL (93 for GFe and 66 for GZn) was retrieved from 12 earlier studies on interval mapping. This information was used for MQTL analysis conducted using Biomercator software V4. A high-density consensus map with >100,000 SSR, SNP, and DArT markers was developed and used for MQTL analysis. Of 159 QTL, only 32 could be projected on the consensus map; 10 MQTL distributed across four wheat chromosomes (5A, 6A, 5B, and 7A) were identified. Of the 10 MQTL, eight were localized on the A genome and two on the B genome. Of 10 MQTL, eight were identified for both GFe and GZn and two only for GZn. The 95% confidence intervals (0.51–15.75 cM) of the identified genomic regions were significantly narrower than the average of their corresponding original QTL and these genomic regions contained 12 candidate genes for GFe and GZn that will be validated through wet-lab experiments. Our results indicate that majority of the MQTL identified are hotspots for GFe and GZn concentration. This study also suggests a possible correlation between levels of Fe and Zn in wheat grains, because eight of the ten MQTL each controlled both GFe and GZn.

Breeding using marker-assisted selection.

MAS for drought tolerance. A major QTL (*Qyld.csdh.7AL*) for grain weight/spike (under drought conditions) was introgressed into two high-yielding, drought-sensitive, Indian wheat cultivars HD2967 and DBW88 through MAS, using the genotype SQ1 as the donor parent. Foreground MAS used the SSR marker *Xwmc273* and heterozygous/homozygous plants in the BC_1F_1 , BC_2F_2, and BC_3F_3 populations were selected. Finally, 94 BC_2F_6 homozygous progenies (72 BC_2F_6 progenies from 'HD2967 / SQ1' and 22 BC_2F_6 progenies from 'DBW88 / SQ1') for *Qyld.csdh.7AL* were selected. A preliminary yield trial of these selected progenies along with nine high-yielding checks under irrigated and rainfed conditions (only one irrigation, 40 DAS) is being carried out during the current crop season (2020–21) at the Research Farm of CCS University, Meerut. Phenotypic data on the following nine agronomic/physiological traits is being recorded: days to heading, days to anthesis, days to maturity, plant height, chlorophyll content, grains/spike, 1000-kernel weight, grain yield, biomass, and harvest index. The progenies also were tested for resistance to yellow and brown rusts under high disease pressure in field conditions at IIWBR, Karnal. Multi-location trails of the selected lines will be conducted in the next crop seasons.

MAS for heat stress tolerance. A MAS program was initiated to transfer desirable alleles of ten QTL reported earlier for six different heat-responsive traits from the high-yielding, heat-tolerant, Egyptian cultivar Giza168 into the background of the popular Indian wheat PBW343 following a MABC scheme. BC_2F_1 plants phenotypically similar to the recipient parent and with 3–8 QTL were selected in 2018–19 and backcrossed. Foreground selection followed by phenotypic selection in the BC_3F_1 generation during the 2019–20 crop season identified plants containing a combination of a maximum number of desirable QTL and also a high phenotypic similarity with PBW343. These BC_3F_1 plants were selfed and the BC_3F_2 obtained. Foreground MAS in the BC_3F_2 progenies will select plants carrying combination of different QTL in homozygous condition. The progenies of these plants carrying different combinations of QTL will be evaluated in preliminary yield trials under heat stress conditions to identify desirable progenies.

MAS for pyramiding of genes/QTL for grain quality and rust resistance. We are using the following improved prebreding material: (i) HD2967 (*Gpc-B1/Yr36 + Lr24*), (ii) HD2967 (*Lr19/Sr25 + Yr10 + Lr34*), and (iii) Lok1 (*Gpc-*

B1/Yr36+ Lr24 + Qphs.dpivic.4A.2). Using these three genotypes, we attempted the two crosses 'HD2967 (*Gpc-B1/Yr36 + Lr24*) / HD2967 (*Lr19/Sr25 + Yr10 + Lr34*)' and 'Lok1 (*Gpc-B1/Yr36+ Lr24 + Qphs.dpivic.4A.2*) / HD2967 (*Lr19/ Sr25 + Yr10 + Lr34*)'. Foreground MAS for all the genes/QTL was carried out in F_2, F_3, and F_4 generations. Selected F_5 plants of crosses 1, homozygous for seven QTL/genes, and cross 2, homozygous for eight (except for *Lr19/Sr25*), were raised simultaneously at the Research Farm of CCS University, Meerut, for seed multiplication, and for screening for rust resistance under high-disease pressure in field conditions at IIWBR, Karnal. F_6 populations with pyramided QTL/genes were raised at Wellington, Tamil Nadu, to evaluate disease resistance and for seed multiplication. A preliminary yield trial is being conducted for the F_7 population of both crosses at the Research Farm of CCS University, Meerut, during the 2020–21 crop season. High-yielding progenies with improved grain quality and rust resistance will be identified and eventually be submitted for testing under national varietal development trials.

Pyramiding of rust resistance genes in genotypes with improved grain quality also is being exercised in parallel for two new crosses involving a widely adapted cultivar PBW723 (*Lr37*/*Yr17*/*Sr38* + *Lr76*/*Yr70*) as donor and HD2967 (*Lr19*/*Sr25* + *Yr10* + *Lr34*) and Lok1 (*Gpc-B1*/*Yr36*+ *Lr24* + *Qphs.dpivic.4A.2*) as recipients. Their F_2 populations are being raised during 2020–21 crop season for MAS for pyramiding of a number of genes.

MAS for white-grain PHS-tolerant, protein-rich leaf rust resistant cultivars. A major QTL for PHST was introgressed into an elite Indian wheat Lok1, which is PHS susceptible. These PHST lines also were pyramided with one gene each for high grain protein content (*Gpc-B1*) and leaf rust resistance (*Lr24*). For introgression of the PHST QTL, initially Lok1 was separately crossed with two donors, PHS tolerant white-grained lines AUS1408 and CN19055. Backcrossing in each generation was followed by foreground and background selections using SSR markers. In advanced lines, a KASP assay also was carried out for the candidate gene *TaMKK3-A* underlying the PHST QTL. The MAS-derived lines homozygous for the PHST QTL were screened for PHS using simulated rain chambers resulting in the selection of ten PHST lines. For pyramiding PHST QTL, *Gpc-B1*, and *Lr24*, MABB-derived BC_4F_2 plants (from the cross 'Lok1 / CN19055') were crossed with a MAS-derived BC_2F_5 line (Lok1 (*Gpc-B1+Lr24*)) we developed earlier in the same background of Lok1. After foreground MAS followed by PHS screening, four advanced lines carrying all the three QTL/ genes in homozygous condition were selected. These lines exhibited high level of PHST (PHS score 2–3) associated with significant improvement in grain protein content with no yield penalty and resistance against leaf rust under artificial epidemic conditions.

In silico identification and characterization of genes in wheat.

***In silico* identification and characterization of the 20S proteasome gene family**. The ubiquitin-mediated, proteolysis system sustains cellular homeostasis by preventing the accumulation of damaged or misfolded proteins. Although whole-genome-based identification and analysis of the 20S proteasome gene family is reported in Arabidopsis and rice, the genes encoding the α (PA) and β (PB) subunits of the 20S proteasome in common wheat are unknown. In this study, we investigated and characterized 67 genes of the *T. aestivum* 20S proteasome α (TaPA) and β (TaPB) family utilizing the current wheat genome sequences. These 67 TaPA and TaPB genes were distributed in all the 21 wheat chromosomes. A majority of genes (20) were in triplicate. Comparative analysis showed that 67 wheat genes (34 TaPA+ 33 TaPB) were orthologues to 23 rice genes (13 OsPA +10 OsPB), and to 24 Arabidopsis genes (13 AtPA + 11 AtPB). A single α- and β-type domain belonging to the 20S proteasome was identified in each of the protein encoded by the 67 genes. Phylogenetic analysis constructed seven clusters belonging to each of the seven α (α1-7) and β (β1-7) subunits along with the conserved motifs in proteins. *In silico* expression data revealed that 10 of the 67 genes were involved in heat stress response, whereas four showed maximum expression under drought stress at the seedling stage. Nine genes (*TaPAD2-5A*, *TaPAC1-7B*, *TaPAC1-7D*, *TaPAD1-7A*, *TaPAD1-7B*, *TaPBB1-1D*, *TaPBD1-4D*, *TaPBG1-5A*, and *TaPBC1-7B*) were expressed under combined stresses of heat and drought, suggesting their involvement in response to multiple abiotic stresses. These findings lay the foundation of future research on the potential role of each of the TaPA and TaPB genes of the 20S proteasome family in response to different environment stresses aimed at improving wheat for climate resilience.

Epigenetic regulation of leaf rust resistance.

DNA methylation due to *Lr28* using BiS-seq. Continuing our earlier studies, the dynamics of DNA methylation was examined in the wheat–leaf rust pathosystem utilizing genome-wide BiS-seq of the susceptible wheat cultivar HD2329 and the resistant NIL (HD2329 + *Lr28*) at 0 hours before infection (hbi) and 96 hours after infection (hai). BiS-seq was

carried out for the following four treatments though outsourcing to Nucleome Informatics Pvt. Ltd., Hyderabad: susceptible HD2329 (0 hbi (S0) and 96 hai (S96)) and resistant NIL HD2329+*Lr28* (0 hbi (R0) and 96 hai (R96)). Differentially methylated regions (DMRs) and differentially methylated genes (DMGs) were identified in the following four pairs of treatments: (i) S0 vs. S96, (ii) S0 vs. R0, (iii) S96 vs. R96, and (iv) R0 vs. R96. In each pair, there were more DMRs with a CHH-context than with CG and CHG contexts.

In addition, we also examined (i) chromatin states, (ii) transposable elements, (iii) common regions undergoing histone modifications, and (iv) DNA methylation. Eighteen chromatin states were available, which provided sufficient resolution to understand the biologically meaningful patters across four different treatment pairs. Comparing DMGs with DEGs revealed 6,322 were commonly identified in transcriptome data involving the same four treatment pairs. Of these 6,322 DMGs, nearly half (3,429) showed expected relationship with gene expression where methylation in promoter and TTS regions repressed gene expression and methylation in introns and exons promoted gene expression. Comparison of DMGs with genes undergoing histone methylation (available from our earlier ChIP-seq analysis) revealed 435 unique DMGs having H3K4me3 mark and 28 unique DMGs having H3K27me3 mark across all the four treatment pairs. A set of 29 genes also were selected for further validation using qRT-PCR. These 29 genes belonged to the four treatment pairs as follows: S0 vs. S96 (8 genes), S0 vs. R0 (6 genes), S96 vs. R96 (8 genes), and R0 vs. R96 (7 genes). Each of these genes showed methylation in either of the above three contexts.

Identification of miRNAs and lncRNAs during *Lr28*-mediated resistance against leaf rust. In this study, miRNAs and lncRNAs associated with the wheat-leaf rust pathosystem were identified using RNA-seq data for a pair of NILs, which differed for the gene *Lr28* in the background of wheat cultivar HD2329. The study is a continuation of our earlier transcriptome study involving the same pathosystem. A total of 50 miRNAs and 1,178 lncRNAs were identified through *in silico* analysis of RNA-seq data. Of these, 16 miRNAs and 22 lncRNAs were differentially expressed. Expression of as many as eight miRNAs was induced in resistant NILs (expression of remaining DE miRNAs induced in susceptible NIL); these differentially expressed miRNAs targeted several important genes, which include disease-response genes. As many as 49 lncRNAs were found to be the targets for miRNAs; one functioned as a precursor of two mature miRNAs and three acted as target mimics (which mimic and, therefore, compete with the mRNA targets for miRNA), thus regulating the expression of target genes. The results were also validated using qRT-PCR analyses.

Differential DNA methylation due to *Lr48* using MeDIP and Bis-seq. Differential DNA methylation due to *Lr48*, an APR gene for leaf rust resistance, in wheat cultivar CSP44 was examined at the preadult-plant (P-AP) susceptible stage and adult-plant (AP) resistant stages at 0 hbi and 96 hai. As many as 52,872 DMRs carrying 897 DMGs and many intergenic regions were identified. The DMRs included exons/introns, promoters, and UTRs. Within the DMRs, transposable elements (TEs) were identified, which included DNA transposons (DNA/CMC-EnSpm) representing the most widely occurring TE family, followed by the LTR retrotransposons *gypsy* and *Copia*. Of the 897 DMGs, 340 also were available in the transcriptome data based on RNA-seq analysis. Susceptibility (at P-AP) was found to be governed by activation (due to hypomethylation) of relatively more genes, whereas resistance (at AP) involved silencing of relatively large number of genes. Using GO terms, DMGs were found to belong to a variety of biological processes, including transcription regulation, protein synthesis, signal transduction, defense, photosynthesis, and lipid and carbohydrate metabolism. Finally, a set of 15 DMGs also were selected for further validation using qRT-PCR analysis and expression pattern of 11 of these 15 genes revealed expected inverse relationship with DNA methylation.

In order to understand the context-specific DNA methylation at the single-nucleotide level (CG, CHG, and CHH), bisulphite sequencing (Bis-seq) was undertaken. The raw Bis-seq data will be subjected to detailed analysis in order to identify the context-dependent downstream DMGs. Validation of 29 DMGs also was undertaken using qRT-PCR during the P-AP and AP stages. The above results of DNA methylation using MeDIP and Bis-seq together will improve our understanding of the epigenetic control of APR for leaf rust in wheat.

QTL database.

WheatQTLdb: A QTL database. During the last three decades, QTL analysis in wheat has been conducted for a variety of individual traits, so that thousands of QTL, along with the linked markers, their genetic positions, and contribution to phenotypic variation, for concerned traits are now known. However, no exhaustive database for wheat QTLs is currently available on a single platform. Therefore, we prepared a database that is an exhaustive information resource for wheat QTL data curated for known QTL from the published literature up to May 2020. QTL data from interval mapping/GWAS

have been included for the following classes of traits: (i) tolerance to abiotic stresses including drought, water logging, heat stress, preharvest sprouting, and salinity; (ii) resistance to biotic stresses including bacterial, fungal, nematode, and insects; (iii) traits for biofortification (Fe, K, Se, and Zn content); (iv) developmental traits; (v) morphological traits; (vi) N/P use efficiency; (vii) physiological traits; (viii) quality traits; and (ix) yield and yield-related traits. For the preparation of the database, literature was searched for data on QTL/MTAs, curated, and then assembled in the form of WheatQTLdb. The available information on metaQTL, epistatic QTL, and candidate genes, wherever available, is also included in the database. Information on QTL in WheatQTLdb includes QTL names, traits, associated markers, parental genotypes, crosses/mapping populations, association mapping panels, and other useful information. To our knowledge, WheatQTLdb prepared by us is the largest collection of QTL (11,644), epistatic QTL (107), and metaQTL (330) data for hexaploid wheat to be used by geneticists and plant breeders for further studies involving fine mapping, cloning and marker assisted selection (MAS) during wheat breeding.

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Promotion and impact evaluation of improved bread wheat cultivars at the farmers' field in India – the case of DBW 222.

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Food grain production in India has witnessed a rapid transformation – from 'net imports' to 'net exports' – after the wide adoption of Green Revolution technologies, especially in rice and wheat. Wheat, a *Rabi* season crop (October/November–March/April), has undergone rapid strides in terms of production as evident from the quantum jump since the inception of the All-India Coordinated Research Project (Ramdas 2012; Ramadas et al. 2019). Yet, the seed and varietal replacement rate is low in a majority of regions (Singh 2015; Dirisala et al. 2018) and attributed to the demand–supply gap. Seed of crop cultivars, being the prime channel of modern technology and a crucial input in crop farming, requires continuous replacement to take advantage of the incremental yield and associated benefits (Witcombe et al. 1998; Sendhil et al. 2021a). Capitalizing on the potential benefits of frontline demonstrations, seed of the latest cultivars have been distributed to farmers across India for promoting the cultivars and enlightening the farmers on the advantages of seed and/or cultivar replacement (Singh et al. 2019). The process helps to reduce the yield gap between attainable and observed yield levels (Sendhil et al. 2014), strengthen the seed value chain by bringing potential cultivars (Pavithra et al. 2017) through trained seed production to the frontline demonstration beneficiaries, and empower the farmers.

The Indian Institute of Wheat and Barley Research has been instrumental in developing and promoting the recent wheat and barley cultivars across India (Singh 2019). For the 2020–21 crop season, seed of the newly released bread variety DBW 222 (Mishra et al. 2020) was distributed to 160 farmers under a project entitled 'Promotion and impact evaluation of ICAR-IIWBR technologies at farmers' field' with financial support from the Scheduled Caste Sub-Plan (SCSP) program executed at the ICAR-Indian Institute of Wheat and Barley Research, Karnal. Adopting the experimental approach using the randomized controlled trial (RCT) at farmers' fields in Haryana and Punjab, seed of DBW 222 (40 kg/beneficiary to cover one acre (0.4 ha) of land) were distributed during November 2020 (Fig. 1, p. 26). In total, 160 acres of land (64 ha) were covered in Haryana and Punjab to promote DBW 222 among the farmers. The pretrial experiment under this project was registered at the 'Global Registry' of the RCTs for registration (https://doi.org/10.1257/rct.7102-1.2000000000000002; Sendhil et al. 2021b). Under this project, crop cutting experiments were conducted (FAO 2017) during April 2021 at random plots in Haryana to assess yield levels in farmers' fields (Fig. 2, p. 26) and compared with full-plot harvests (Kosmowski et al. 2021). In addition, we supplied 10 kg of DBW 222 seed to 20 randomly selected farmers in the Phurlak village of the Karnal district and trained them to raise the seed crop. The seed was used to sow 0.5 acres (0.2 ha) under the supervision of experts for quality seed production. Monitoring and evaluating experimental seed plots were carried out at regular intervals to issue advisories, if needed (Fig. 3, p. 26).

This project, which has been planned for a 5-year duration (2020–21 to 2024–25), is to extensively promote the latest and improved wheat cultivars (DBW 222 in 2020–21 crop season) among farmers to re-establish the fact that adopting recent cultivars results in a quantum jump leading to enhance farmers' livelihood. In addition, the project also aims to develop a 'seed value chain model' in the experimental village (Phurlak) during 2020–21, assess multi-dimensional potential benefits to the beneficiaries, and replicate its success to other wheat-growing regions to empower farmers, especially small-holders. The reflections during the course of the project period will facilitate the researchers, extension personnel, and policy makers to devise a framework for strengthening the seed system in India.

Fig. 1. Experimental plot for the promotion and evaluation of DBW 222 in the farmer's field.

Fig. 2. The crop-cutting experiment of DBW 222 conducted in the farmer's field.

Fig. 3 Capacity building for farmers on quality wheat seed production and monitoring of the seed production plot.

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Breeding wheat for early maturity, disease resistance, nutrition, and heat tolerance in the western Himalayas.

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Evaluation of wheat germplasm under the All India Co-ordinated Research Programme on Wheat (AICRP Wheat), 2020–21 crop season. As one of the voluntary funded centres in the Northern Hill Zone for evaluation of advanced wheat breeding lines before their release as cultivars, a set of 16 advanced breeding lines received under the Initial Varietal Trails were evaluated in four replications. A set of six advanced breeding lines received under Advanced Varietal Traits were evaluated in six replications in a randomized, complete-block design. These lines were evaluated for a variety of morphological traits, including plant height, number of tillers, spike length, spikelets/spike, days to flowering, days to maturity, 1,000-kernel weight, and grain yield. These lines also were screened for leaf blight and yellow rust resistance. Lines that were found to be early maturing, disease resistant, and high yielding were selected for further evaluation and release as cultivars for the Kashmir Valley. In addition, a segregating stock nursery also was evaluated and several promising segregants have been selected for a variety of traits.

Genome-wide association study for mapping genes for culm cellulose content and related traits in wheat. Lodging in cereal crops, in general, and wheat, in particular, is a severe problem in agricultural production that has developed as a barrier to meeting predetermined productivity objectives, degrades quality criteria, and prevents mechanized harvesting. Lodging-resistant wheat cultivars have better chance of on-time harvest, which is typically hampered by biotic and abiotic stresses. Keeping this in view, we conducted a study to assess the lodging resistance and culm strength of 256 Indian wheat cultivars released over the last 100 years. Trials were conducted at two locations during 2019–20 and

2020–21 in an augmented block design. Phenotypic data was recorded on 13 important traits, including plant height, tillers/plant, spike length, spikelets/spike, spike weight, test weight, basal internode length, culm/stem diameter, basal internode weight, culm wall thickness, pith diameter, and cellulose content. The data was subjected to standard statistical analysis. Efforts also were made to validate genes/QTL previously identified in earlier studies for lodging and related traits. The findings of this study will serve as a benchmark for future efforts in breeding wheat cultivars with enhanced culm strength. The identified candidate lines will be a valuable resource for transcriptomics studies and for other wheat hybridization programs.

Genetic study of 'spring × winter' wheat crosses for yield and yield-related traits. Introgression from the winter wheat gene pool into spring wheat is a potential approach to improve yield and yield-related traits. Winter wheats carry enormous variability for tillering, spike length, grain number, grain size, and biotic and abiotic stress tolerance. However, very little is known about the combining ability and segregation pattern of these two groups. Moreover, development of early maturing wheat cultivars is an important breeding objective in the Kashmir region to ensure a double cropping system (rice–wheat crop rotation). Therefore, we attempted crosses between spring and winter wheats during 2019–20. The spring wheat material was obtained from CIMMYT, Borlaug Institute of South Asia (BISA), Ludhiana, and winter wheat material from Punjab Agriculture University, India. The F_1 seed obtained from the crosses was sown in pots in polyhouse of Division of Genetics and Plant Breeding, Faculty of Agriculture, Wadura Sopore, SKUAST-Kashmir, India. The F_2 seed was sown in the experimental fields of the faculty during the 2020–21 cropping season. The F_2 population of about 1,000 plants from 'spring × winter' wheat combinations was used to assess the segregation pattern for yield and yield related traits. Data were recorded on 9 important traits on each F_2 generation segregants, including the presence/absence of awns, days to flowering, days to maturity, number of tillers/plant, spike length, spikelets/spike, and 1,000-kernel weight. In addition, an F_2 population was evaluated for brown rust disease. Early maturing, disease resistant, and high-yielding segregants were identified from the F_2 population. The F_2 population was single-plant harvested and will be evaluated as F_2 derived F_3 populations next year.

Fig. 1. A set of 4,560 diverse wheat genotypes was evaluated for cold tolerance in 2020–21 at the research farm of the Faculty of Agriculture, SKUAST-Kashmir.

Genetic analysis for cold/freezing tolerance in wheat. A set of 4,560 diverse wheat genotypes were evaluated for cold tolerance during the Rabi season of 2020–21 under field conditions at the research farm of Faculty of Agriculture (SKUAST-Kashmir) on a rating scale of 0–4 as grades of cold tolerance (Fig. 1). Large phenotypic variation was observed in response to cold stress. Most of the genotypes were susceptible to cold stress. On the 0–4 scale, several genotypes were tolerant to cold with a score of 0. In addition, several genotypes were moderately tolerant and given a cold tolerance score of 1. A set of 20 selected genotypes, with contrasting trait performance for cold tolerance and early maturity, was selected and involved in a crossing program. Approximately 100 crosses were made (Fig 2). The F_1 seeds were harvested and sown in pots under controlled conditions at SKUAST-K. The F_2 seeds will be harvested soon and will be allowed to grow under field conditions to obtain the F_2 generation. The germplasm is being further assessed for chilling injury in the laboratory with an electrolyte leakage test from leaf tissues damaged by cold stress. Electrolyte leakage of cold stressed plants grown under natural (field) conditions was measured based on protocol of Bajji et al. (2002).

Fig. 2. Crossing of 20 genotypes with contrasting trait performance for cold tolerance and early maturity.

Germplasm characterization and introgression of *GPC B1* allele into early maturing wheats. Besides quality, improving early maturity is one of the important objectives in wheat breeding programs in the western Himalayas of the Kashmir Valley. In this region, successful rice–wheat crop rotation is considered very crucial to achieve self-sufficiency in food production. Here, the wheat crop

takes ~8 months from sowing to harvest (October–June) and, thus, does not vacate land in time for rice cultivation (before 21 June). The release of two, early maturing wheat cultivars WW-101 (SKUA-101) and WW-102 (SKUA-102) identified recently by the Faculty of Agriculture, Wadura, SKUAST-K, are expected to make sure timely availability of land for sowing of next crop (i.e., rice) and increase the rate of adoption of rice–wheat cropping system in the valley. We evaluated a set of 450 germplasm lines for early maturity and quality traits at three different locations in the valley. Substantial genetic variation was found for almost all the traits in the set. Crossing was done to introgress grain protein content (*Gpc-B1*) allele from the cultivar Lok1 into the early maturing wheat WW101 during the main wheat cropping season of 2020–21. The F_1 seed was sown in pots in the polyhouse as an off-season crop on 15 June 2021. The F_2 seed, expected to be harvested in October–November, will be sown in the main field in November 2021. The F_2 population will be screened for early maturity through visual observation and genotyped for *Gpc-B1* allele using the linked markers. Segregants containing both early maturity and *Gpc-B1* allele will be advanced through further generations to obtain the desired genotypes with multiple target traits.

Evaluation of Indian wheat cultivars for foliar leaf blight. Leaf blight of wheat is caused by the fungus *Alternaria triticina*. In the recent past, with the change in cropping system, foliar blight has now become a major disease in our country. This study evaluated Indian wheat cultivars for foliar blight and find promising candidate genotypes for leaf blight. A set of 262 Indian wheat cultivars were evaluated for their tolerance to foliar blight disease at four different locations in the Kashmir Valley in an augmented block design. These locations include Faculty of Agriculture, Wadura; Dryland Agriculture Research Station, Budgam; and MRCFC Khudwani, MARES Gurez. Disease severity at six different growth stages, from tillering to maturity, was recorded. Infected leaves showing typical symptoms of circular concentric rings were collected from all four locations. Fresh samples of infected leaves were collected and used to isolate the pathogen. These lines also were grown in the greenhouse for conducting pathogenicity tests to ensure that the actual pathogen, *Alternaria* spp., was responsible for disease development in all locations. Of the 262 genotypes screened for resistance to foliar blight, no genotypes showed 100% resistance to leaf blight in all locations. However, 22 genotypes showed 90–99% resistance and 50 genotypes showed 70–89% resistance. The remaining genotypes were susceptible to the leaf blight.

Evaluation of Indian wheat cultivars for stripe rust resistance. Wheat production in the western Himalayan region is affected by various biotic and abiotic stresses, of which yellow (or stripe) rust, caused by *Puccinia striiformis* f. sp. *tritici,* is the most serious threat. Under conducive weather conditions, stripe rust can cause yield losses up to 100%, but the damage is usually between 10–70%, depending upon crop stage, disease severity, and cultivar susceptibility. This study screened wheat germplasm for stripe rust resistance in multiple locations of the western Himalayan region of the Kashmir Valley. We investigated spontaneous variation in 262 Indian wheat cultivars released in India over the last 100 years (1906–2006) for adult-plant stripe rust resistance during autumn (October–March) 2020–21 in three different location of the western Himalayan region, Faculty of Agriculture, SKUAST-K, DARS, Budgam SKUAST-K; and MRCFC, khudwani, SKUAST-K). The wheat germplasm was evaluated in augmented block design (ABD) (Fig. 3). Weather conditions for screening of the wheat germplasm were favourable during 2020–21 in the western Himalayan region. A modified Cobb scale was used for evaluating rust severity. Large variation was observed in response to disease severity and infection at all three locations. Based on this evaluation, crosses were made between resistant and susceptible genotypes (2020–21 crop season). In the greenhouse, F_1 seed will be grown and harvested (2021 off-season). Greenhouse F_2 seed will be harvested and grown in the field/greenhouse (2022 main season).

Fig. 3. The stripe rust resistant wheatWL 711 in the evaluation nursery.

Development and use of SSRs for heat-responsive miRNAs in wheat. Terminal heat stress is an important abiotic stress constraint to successful wheat production worldwide and is regulated by different molecular mechanisms. During the last two decades, the importance of microRNAs (miRNAs) in gene expression under various biotic and abiotic stresses is well studied. Molecular markers, especially co-dominant markers such as simple sequence repeats (SSRs), play an important role in marker-assisted breeding. The discovery of SSR markers from non-coding regions has been a

challenge. Therefore, developing novel markers from the conserved regions will be useful for studying genetic diversity of heat-responsive miRNA genes in wheat.

We mined SSR markers from 96 members of heat-responsive miRNA genes of wheat and validated 37 contrasting panels of tolerant and susceptible wheat genotypes, each with 26 and 11 genotypes, respectively. Of the seven polymorphic miRNA-SSRs, only three were found to be very informative (HT-169j, HT-160a, and HT-160b), able to differentiate the tolerant and susceptible genotypes in two different groups. We also been found that miRNA genes were more diverse in susceptible genotypes than the tolerant ones (as indicated by polymorphic index content), which might interfere with form the stem-loop structure of premature miRNA and their subsequent synthesis in susceptible genotypes. We concluded that length variations of the repeats in salt responsive miRNA genes may be responsible for a possible sensitivity to heat adaptation. This is the first report of characterization of trait specific miRNA-derived SSRs in wheat.

Characterization and evaluation of wheat germplasm lines for biotic stress resistance. Under the DBT-funded network project 'Germplasm Characterization and Trait Discovery in Wheat using Genomics Approaches and its Integration for Improving Climate Resilience, Productivity and Nutritional quality', a large, diverse germplasm set of wheat comprised of 4,560 landraces were evaluated in the temperate conditions of Kashmir at Faculty of Agriculture (FOA), SKUAST-K, Wadura under supervision of Dr. Reyazul Rouf Mir (Associate Professor), Department of Genetics and Plant Breeding. These diverse landraces were sown in November 2020 at the research farms of the Faculty of Agriculture in an augumented block design. Five released cultivars were replicated as checks after 20 genotypes/line. This diverse set was screened for two fungal diseases, stripe rust (*P. striiformis*) and leaf blight (*A. triticina*), and great variability for these diseases were recorded in the germplasm (Fig 4). Using DUS guidelines released by IIW&BR, Karnal, growth habit, days to flowering, days to maturity, plant height, awn character, and seed traits were recorded. Substantial variability for lodging also was observed in this diverse set. We identified various landraces that matured in the first week of June, which are suitable for future reci–wheat crop rotation. Crosses were made between genotypes possessing different traits of interest, such as cold tolerance, early maturity, disease resistance, and high yield.

Fig. 4. Nursery fharacterization and evaluation of wheat germplasm for stripe rust and leaf blighty resistance at SKUAST Kasmir.

Wheat field day. The Faculty of Agriculture (FOA), Wadura campus, SKUAST-Kashmir, organized a Wheat field day on 28 May, 2021. This particular occasion was inaugurated by Hon'ble Vice Chancellor, Prof. J.P Sharma, SKUAST- J&K, along with the Director Extension, Registrar of SKUAST-K. The Joint Director Agriculture, Department of Agriculture along with other field functionaries, farmers, and students participated in the Wheat Field Day. The main aim of function was to acquaint the farmers and public about research programs being carried out by the faculty and release of wheat cultivars WW101 and WW102 developed by the Faculty of Agriculture, SKUAST-K. These cultivars are early maturing and ready to harvest by the first week of June; thus playing a big role in benefiting the farmers with a double-cropping system. Various schemes and salient features of the Wheat Day were elaborated to farmers. They were encouraged to cultivate wheat after paddy to double their income. Furthermore, farmers were made aware of wheat germplasm currently being bred at FOA for high nutrition to mitigate hidden hunger and malnutrition; biotic (leaf blight resistance and rust resistance) and abiotic stresses (cold tolerance and high temperature); and physical stress (lodging resistance), with the aim to prevent yield losses. In the future, these germplasm lines can be released for cultivation by farmers to increase their income.

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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.

INIFAP, CAMPO EXPERIMENTAL VALLE DE MÉXICO (CEVAMEX)
km 13.5 Carret. Los Reyes-Texcoco, Coatlinchán, Texcoco, Edo. De México.

Evaluation of elite bread wheat lines from the 16th National Bread Wheat Trial in southern Sonora, Mexico.

Huizar Leonardo Díaz-Ceniceros, Alberto Borbón-Gracia, Guillermo Fuentes-Dávila, and Gabriela Chávez-Villalba; and Héctor Eduardo Villaseñor-Mir, Eliel Martínez-Cruz, and René Hortelano-Santa Rosa (CEVAMEX).

Abstract. Wheat breeding programs implement strategies that generate and identify superior lines. Through the National Bread Wheat Trial for Irrigated Conditions in Mexico, INIFAP's breeding program focuses on the phenotypic effect of each cultivar through multiple environments. This research was to determine high-yielding, advanced bread wheat lines with desirable agronomic traits and resistance to leaf and stripe rusts, as candidates for commercial cultivar release for the southern region in the state of Sonora. The trial consisted of 39 experimental lines and 11 control cultivars evaluated in an alpha-lattice experimental design with two replications under restricted and normal irrigation. The experimental unit consisted of two 3.0-m rows with 0.8 m between rows and a 100 kg/ha density. Under normal irrigation, lines 27, 21, 15, and 13 produced a greater grain yield than that of the check cultivar Borlaug 100 (11 to 156 kg/ha). For restricted irrigation, lines 23, 21, and 13 showed a 31 to 219 kg/ha greater grain yield than that of Borlaug 100. Line 24 had the highest protein content (12.5%) and lines 21 and 13 the lowest (11.6%).

Introduction. Cereals are the most important source of human food energy (Serna-Saldívar 2010). Wheat has the second highest production worldwide, just behind that of corn. In 2017, wheat reached a world production of 771 x 10^6 tons with an average yield of 3.5 t/ha (FAOSTAT 2019). During the 2017–18 crop season, in the state of Sonora, Mexico, 223,373 ha were sown with wheat. An average grain yield of 6.5 t/ha made Sonora the main producing region in the country. During the last 3 years (2016–18), bread wheat cultivation increased from 30,958 to 41,965 ha in this region (SIAP 2019). The area with bread wheat is expected to increase, since the government has implemented economic incentives for producers in order to reduce imports. Therefore, genotypes with high yield potential, quality, resistance to diseases, in particular to leaf and stripe rusts which are endemic in the region and threaten production (Huerta et al. 2014), and that are quickly adopted by producers, are importnt. Our objective was to evaluate advanced bread wheat lines from the 16th National Bread Wheat Trial for grain yield, resistance to leaf rust, and protein content, which could qualify as candidate lines for new cultivars for southern Sonora.

Materials and methods. The 16th National Bread Wheat Trial for Irrigated Conditions was sown on 18 December, 2018, at the Norman E. Borlaug Experimental Station of INIFAP (National Institute of Forestry, Agricultural, and Livestock Researcher), in the Yaqui Valley during the 2018–19 season. The trial consisted of 39 experimental lines and 11 check cultivars (50 genotypes in total). The trial was evaluated in an alpha-lattice design with two replications under restricted (two) and normal (four) irrigations. The experimental unit consisted of two 3.0-m beds spaced 0.8 m apart, each with two rows, and a density of 100 kg/ha. Agronomic management followed the technical recommendations of the guide to produce wheat in southern Sonora (Figueroa et al. 2011). Grain yield, protein content, reaction to leaf and stripe rusts under natural conditions, and agronomic characteristics were recorded. The experimental unit was harvested using an experimental Wintersteiger combine. A combined analysis of variance was performed with the SAS 9.4 statistical pack-

age (2013), in which the variables were the number of irrigations and genotypes. Mean comparison was carried out with Tukey's test (0.05).

Results and discussion. Grain yield is one of the traits most affected by the lack of water and should be considered when selecting new genotypes as possible cultivars in response to the number of irrigations. When irrigation was restricted by 50%, losses ranging from 745 up to 1,630 kg/ha were detected. Thirteen outstanding lines were identified in this nursery (Table 1); four had a general performance superior to the best check cultivar Borlaug 100, and eight were superior to the second best control Tacupeto F2001. Under normal irrigation, lines 27, 21, 15, and 13 stand out with 8,953, 8,896, 8,849, and 8,807 kg/ha, respectively, whereas lines 23, 21, and 13, with 7,839, 7,792, and 7,651 kg/ha, respectively, under restricted irrigation. In both cases, the average grain yield was greater than that of Borlaug 100. The importance of the genotypic effect as a response to water limitation is seen in line 15, which under normal irrigation had excellent performance (8,849 kg/ha), but was 7,219 kg/ha under restricted irrigation, a 1,630 kg difference and 401 kg less than the best check cultivar. Lines 27, 21, and 13 showed a similar response under normal irrigation, but with restricted irrigation, grain yield was the most affected in line 27. Although yield potential is the main selection criteria in breeding programs, disease resistance and grain quality are also very important. In this case, the lines evaluated did not show any symptoms of leaf or stripe rust infection. Grain protein content is an important quality trait in wheat. Line 24 showed the highest protein content (12.5%), followed by that of lines 23 and 41 with a protein percentage of 12.3; lines 27, 15, 38, and 49 with 12.2; and lines 21, 13, and 22 had the lowest protein content (11.6%) (Table 1), which can be improved by nitrogen-based agronomic management.

Table 1. Average grain yield (GY) under normal (NI) and restricted irrigation (RI), and protein percentage (PPT) of the best lines of the 16th National Bread Wheat Trial during the 2018–19 crop season. Best control cultivars are indicated with a •; ≠ indicates the difference in kilograms with the best check cultivar Borlaug 100; PPT is the protein percentage of lines under normal irrigation; LSD = least significant difference; CV = coefficient of variation.

No.	Line/cultivar	GY	≠	NI	≠	RI	≠	PPT
21	KSW/SAUAL//SAUAL/3/2*BORL14	8,344	136	8,896	99	7,792	172	11.6
23	WBLL1*2/BRAMBLING///2*BORL14	8,266	57	8,693	–104	7,839	219	12.3
27	KACHU/BECARD///TECUE #1	8,245	37	8,953	156	7,537	-83	12.2
13	WHEAR/KUKUNA/3//9/KACHU	8,229	21	8,807	11	7,651	31	11.6
7	BORLAUG 100 •	8,208	0	8,797	0	7,620	0	12.3
15	KSW/SAUAL//SAUAL/3/REEDLING #1	8,034	–174	8,849	52	7,219	–401	12.2
24	WBLL1*2/BRAMBLING//.../3/2*BORL14	8,016	–193	8,552	–245	7,479	–141	12.5
38	KACHU/BECARD//.../KACHU/KIRITATI	8,000	–208	8,719	–78	7,281	–339	12.2
22	SUP152/BAJ#1/4/…./5/SUP152/BAJ #1	7,997	–211	8,594	–203	7,401	–219	11.6
30	BORL14*2/3/KBIRD//WBLL1*2/KU-RUKU	7,971	–237	8,344	–453	7,599	–21	11.9
49	BORL14*2/NAVJ07	7,945	–263	8,438	–359	7,453	–167	12.2
17	NELOKI//SOKOLL/EXCALIBUR	7,919	–289	8,615	–182	7,224	–396	11.8
25	ATTILA/3*BCN//…BECARD/QUAIU #1	7,878	–331	8,495	–302	7,261	–359	12.1
1	TACUPETO F2001 •	7,872	–336	8,276	–521	7,469	–151	11.8
41	BORL14*2//MUNAL #1/FRANCOLIN #1	7,823	–385	8,349	–448	7,297	–323	12.3
	Tukey ($p < 0.05$)	LSD 676						0.47
		CV 3.2						0.96

Conclusions. Thirteen lines from the 16th National Bread Wheat Trial were selected for irrigated conditions in the breeding program at the Norman E. Borlaug Experimental Station. These are high-yielding lines, with desirable agronomic traits and resistance to leaf and stripe rusts. Within this group, lines 21 (KSW/SAUAL//SAUAL/3/2*BORL14), 23 (WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14), 27 (KACHU/ BECARD//WBLL1*2/BRAMBLING/3/FRNCLN*2/TECUE#1), and 13 (WHEAR/ KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/8/VEE#8//JUP/BJY/3/F3.71/TRM/4/BCN/5/KAUZ/6/MILAN/KAUZ/7/SKAUZ/PARUS//PARUS/9/KACHU), which overcame the general grain yield performance of check cultivar Borlaug 100, are considered new candidates for release as commercial cultivars. Six lines showed a protein content between 12.2 and 12.3%, similar to that of Borlaug 100 (12.3%).

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Evaluating the synergistic effect of 2X POTENCIOR F with the fungicides Velficur (tebuconazole) and Sanazole (propiconazole) for control of leaf rust in durum wheat in the southern Sonora.

Huizar Leonardo Díaz-Ceniceros, César Martín Armenta-Castro, Guillermo Fuentes-Dávila, Alberto Borbón-Gracia, and Elizabeth García-León.

Abstract. Leaf rust of wheat caused by *Puccinia triticina* is widely distributed in Mexico, where it can cause yield losses up to 84%. CIRNO C2008 is the durum wheat cultivar most widely cultivated in Northwestern Mexico, despite being susceptible to the races of leaf rust present in the region; however, many growers still prefer this cultivar due to its high grain yield, stability, and industrial quality. This work evaluated the biological effectiveness and the possible phytotoxicity of the fungicides Velficur 25 EW (tebuconazole) and Sanazole 250 EC (propiconazole), individually and in combination with the enhancer 2X POTENCIOR F, for control of *P. triticina* in CIRNO C2008. The trial was carried out at the Mayo Valley Experimental Site (SEMAY-INIFAP), in Navojoa, Sonora, using a complete block experimental design with four replications. Five readings of leaf rust severity per experimental unit were recorded, the biological efficiency of each treatment was determined, and the area under the disease progress curve. The data was analyzed with the Statistical Analysis System Ver. 9.4 program. The best treatments were Velficur, Velficur + Potencior, and Sanazole + Potencior, reaching grain yields of 7,304, 7,010, and 6,998 kg/ha, respectively. Sanazole showed minimum for control of leaf rust, but it increased its effectiveness when it was combined with Potencior. No phytotoxicity was detected in any of the treatments.

Introduction. Wheat after corn is the cereal with the second highest production worldwide. In 2017, the world production was 771.72 x 10^6 tons (MT) with an average of 3.5 t/ha (FAOSTAT 2019). In Mexico, wheat production was 3.5 MT with a national average around 5.3 t/ha[1]; 1.8 t more than the world average (SIAP 2019). Wheat is mainly grown during the autumn-winter crop season in the Northwest and Bajio regions in Mexico, where irrigated conditions prevail that render high wheat yields with good quality (SFA 2011). This crop has been affected by important diseases such as leaf rust, which is a widely distributed and devastating disease in Mexico and the world (Huerta-Espino et al. 2011), causing yield losses up to 84%. Early infections decrease the number of grains/spike, test weight, and affect grain quality (Delgado-Sánchez et al. 2016). During the 2019–20 crop season, 216,462 ha of wheat were established in southern Sonora, of which 122,005 ha were sown with durum wheat cultivar CIRNO C2008. Despite its loss of resistance to leaf rust, the cultivar is still grown in the region due to its high yield, stability, and industrial quality (Pérez-López et al. 2017). Our objective was to evaluate the biological effectiveness of the fungicides Velficur 25 EW (tebuconazole) and Sanazole 250 EC (propiconazole), individually and in combination with the enhancer 2X POTENCIOR F, for the control of *P. triticina* in CIRNO C2008 and also detect the possible phytotoxicity of fungicides with the enhancer.

Materials and methods. The experiment was planted on 18 December, 2019 at the Mayo Valley Experimental Site (SEMAY), which belongs to the National Institute for Forestry, Agriculture, and Livestock Research located in Navojoa, Sonora (27°00'40" N 109°30'04" W), on a clay soil. A complete-block, experimental design with four replications was used, where the experimental plot consisted of four 5-m beds separated by 0.8 m (16.0 m^2) and the experimental unit consisted of two 5-m beds (8.0 m^2). The susceptible durum wheat cultivar CIRNO C2008 was sown at a density of 100

kg/ha. Fertilization was applied using the formula 287–52–00, fractioning 50% of the nitrogen and 100% phosphorus in presowing and the rest during the first irrigation. Sowing was on moist soil. Weed control was with Situi XP (30 g c.p./ha) and Axial XL (1 L c.p./ha). Three complementary irrigations were applied during the crop season. Five treatments (Velficur 25 EW, Velficur 25 EW + 2X Potencior F, Sanazole 250 EC, Sanazole 250 EC + 2X Potencior F, and the untreated check) of a single application were evaluated. Application was made when the first rust pustule was detected in the trial (4 March, 2020) at a rate of 500 cc of commercial product (Velficur 25 and Sanazole). The enhancer 2X Potencior F was added at ratio of 1 ml for every 10 ml of active ingredient of the commercial product. Treatments were applied with a motorized sprayer (Honda) with a four-nozzle boom Teejet 8002 to cover two beds with two rows. Additionally, the pH regulator (acid flo plus) was applied in all treatments at a rate of 1 ml/L water until a reading of 5 was reached. The phytotoxicity of 2X POTENCIOR F was recorded based on the scoring scale proposed by the European Weed Research Society (Champion 2000). Grain yield was estimated in kilograms per hectare. Five readings of leaf rust severity were recorded per experimental unit in order to calculate the biological effectiveness per treatment and the area under the disease progress curve (AUDPC). Harvest was with an experimental Wintersteiger combine taking only the two central beds. The data were analyzed with the Statistical Analysis System Ver. 9.4 program (SAS 2013) to obtain the analysis of variance, and mean comparison was performed with Tukey's test ($p < 0.05$).

Results and discussion. The results of the analysis of variance for grain yield, AUDPC, and biological effectiveness, where the coefficients of variation were low, allowed us to generate precise conclusions (Table 2). A highly significant difference was detected between treatments. The best treatments were Velficur, Velficur + Potencior, and Sanazole + Potencior, reaching grain yields of 7,304, 7,010, and 6,998 kg/ha, respectively, and which are statistically similar (Table 3). The application of Velficur produced 823 kg/ha more than the application of Sanazole and 1,640 kg/ha more than that of the untreated check. In the case of Sanazole, the loss of effectiveness during the grain-filling and reinfection by *P. triticina* caused a reduction of the photosynthetic area of the flag leaf, affecting yield. This fungicide, in combination with Potencior, caused a lengthening of the protection period, which in turn had lower grain yield losses (Table 3). Although Velficur and Velficur + Potencior had a similar effect on performance, the enhancer lengthened the protection period (as with the Sanazole), but they had a very similar biological effectiveness, which means that the enhancer for this fungicide did not make any improvement. Grain yields obtained with the application of Velficur and Sanazole were 7,304 and 6,481 kg/ha, respectively, 11.27% greater with the first fungicide; indicating an important difference between the active ingredients for the control of *P. triticina*. The AUDPC is the indicator that determines the efficiency in the control of the disease. Velficur and Velficur + Potencior showed the lowest mean AUDPC values (Table 3 and Fig. 1, p. 37), which consequently allowed the plant to be protected during grain formation and filling, thus producing higher grain yields.

Table 2. Square means from the analysis of variance for grain yield, area under the disease progress curve (leaf rust) (AUDPC), and biological effectiveness of two fungicides with and without the enhancer 2X Potencior F, during the crop season 2019-2020 in the Mayo Valley, Sonora, Mexico. DF = degrees of freedom; CV = coefficient of variation; ** = highly significant; * = significant.

Source of variation	DF	Grain yield	AUDPC	Biological effetiveness (%)
Treatments	4	1,670,607.20**	3,857,900.90**	6,873.66**
Block	3	69,049.70	58,119.41*	88.42
Error	12	69,823.80	15,818.30	63.8
Total	19			
R2		0.98	0.89	0.97
CV (%)		3.94	16.00	14.00

Table 3. Mean comparison between treatments for grain yield, area under the disease progress curve (leaf rust), and biological effectiveness of two fungicides with and without the enhancer 2X Potencior F, during the 2019–20 crop season in the Mayo Valley, Sonora, Mexico. AUDPC = area under the disease progress curve; LSD = Least significant difference.

Treatment	Grain yield	AUDPC	Biological effectiveness (%)
Velficur	7,304 a	87 c	92 a
Velficur + Potencior	7,010 ab	61 c	93 a
Sanazole + Potencior	6,998 ab	227 c	76 a
Sanazole	6,481 b	1,054 b	30 b
Untreated check	5,664 c	2,356 a	0 c
Tukey ($p < 0.05$)	595	283	18

Conclusions. The fungicide Sanazole 250 EC showed minimum for control of leaf rust in the durum wheat CIRNO C2008, but an increased effectiveness when combined with the enhancer 2X POTENCIOR F. The fungicide Velficur was highly effective for the control of leaf rust in CIRNO C2008 when applied individually and with the enhancer 2X POTENCIOR F. No phytotoxicity was detected in any of the treatments.

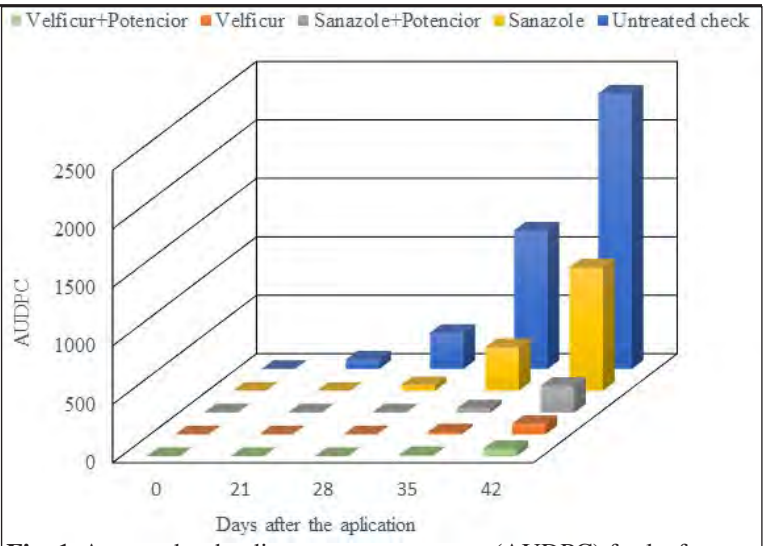

Fig. 1. Area under the disease progress curve (AUDPC) for leaf rust after the applicaton of Velficur and Sanazole aungicides with and without the enhancer 2X Potencior F during the 2019–20 crop season in the Mayo Valley, Sonora, Mexico.

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Morphologic and molecular description of bread wheat cultivar Onavas F2009.

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Abstract. Characterization of bread wheat cultivar Onavas F2009 was visual, following the UPOV guidelines, and by the evaluation of 13 genes: *Lr34* (resistance to leaf rust); *Sr2*, *Sr22*, *Sr24*, *Sr25*/*Lr19*, *Sr26*, *Sr35*, and *Sr39* (resistance to stem rust); *Pin-a* and *Pin-b* (grain hardiness); *Rht-D1* and *Rht-B1* (plant height); and the translocation T1BL·1RS (resistance to drought). Onavas F2009 showed an average height of 97 cm and reached physiological maturity in 121 days, being sown in December. Growth habit is spring type and intermediate; grain color is white and semi-elliptical. Onavas F2009 shows resistance to stem rust and immunity to diverse strains of Ug99, conferred by the presence of genes *Sr2* and *Sr35*. Considered a soft wheat, the wild-type alleles *PinA-D1a* and *PinB-D1a* have been identified in Onavas F2009.

Introduction. Bread wheat is a cereal of great importance in Mexico, particularly for human consumption, the transformation industry and for the economy of the country (Peña Bautista et al. 2008). However, a high deficit in bread wheat production only satisfies 25% of the national need and, therefore, wheat has to be imported (National Strategic Plan 2016) (Villaseñor Mir et al. 2011). Before the 1990s, bread wheat predominated in northwestern Mexico, but due to its susceptibility to *Tilletia indica,* the causal agent of Karnal bunt, and grain yield inestability, among other economic fac-

tors, the area grown with this species was reduced considerably. Statistical data provided by the Agri-food and Fishery Information Service (2021), indicate that in the state of Sonora 236,472.08 ha were sown with wheat, of which 23.8% was bread wheat. Therefore, the federal government initiated programs to try to increase wheat productivity but without aparent success, due to market prices and the low grain yield compared to durum wheat. During this time, new cultivars were generated. Onavas F2009 (Figueroa-López et al. 2013) a bread wheat, which is the result of the cross 'KAMBARA1*2/BRAMBLING' carried out by the Global Wheat Program from the International Maize and Wheat Improvement Center (CIMMYT), and later by the selection as advanced line by the National Institute for Forestry, Agriculture, and Livestock Research (INIFAP) at the Norman E. Borlaug Experimental Station (CENEB). The cross and selection history of Onavas F2009 is CGSS01B00069T099Y-099M-099M-099Y-099M-20Y-0B. The individual and bulk selections were carried out between the experimental stations of El Batán, state of Mexico (B) (19°30'N and 2,249 msnm); San Antonio Atizapán, state of Mexico (M) (19°17'N and 2,640 msnm); and CENEB in the Yaqui Valley (Y) (27°20'N and 40 msnm) in Sonora. Onavas F2009 has the registration TRI-121-100910 in the National Catalogue of Plant Cultivars (CNVV) from the National Service for Seed Inspection and Certification (SNICS, 2021).

Materials and methods. Phenotypic characterization was performed according to the International Union for the Protection of New Varieties of Plants (UPOV 1994), and using the manual of Applied Molecular Genetics (Hoisington et al. 1994) from CIMMYT. The molecular part consisted in identifying the presence of resistance genes to leaf rust, stem rust, grain hardiness, plant height, and drought resistance. The markers used are described (Table 4, p. 39). DNA was isolated following Saghai-Maroof et al. (1984) using seed from the crop season 2020–21. PCR was based on the program of each of the markers used (described in Table 5, p. 40).

Fig. 2. Onavas F2009 is a spring bread wheat cultivar with an intermediate growth habit and a very high frequency of recurved flag leaves. The glaucosity of the flag leaf blade is strong and the culm neck is medium. Spike glaucosity is medium before physiological maturity with a weak hairiness of the first rachis segment. The grain shape is semi-elliptical.

Results. The phenotypic characteristics shown by bread wheat cultivar Onavas F2009 were growth habit intermediate (Fig. 2) with very high frequencey of plants with curved flag leaves. Before maturity, the glaucosness of the flag leaf blade is strong, and the culm neck is medium. Upon maturity, the pith of the straw in cross section (halfway between the base of the ear and the stem node below) is thin. Ear glaucosness is medium before physiological maturity with a weak hairiness of the first rachis segment. The shoulder width of the lower glume is absent or very narrow, with a short and slightly curved beak; the hairiness on the external surface is weak. Grain color is white and semi-elliptical. The molecular characterization indicated the presence of gene *Sr2,* which confers resistance to stem rust. *Sr2* has been used as a durable source and of a wide-spectrum adult-plant resistance. The result is the absence of pustules in plant tissue between nodes, and it includes resistance to the Ug99 race and related isolates. *Sr2* confers recesive resistance. The traditional breeding using *Sr2* has been difficult due to its nature, and the fact that the phenotype is only evident in adult plants and can be influenced by the genetic antecedent and the environment. A morphological marker partially dominant related to *Sr2* is the pseudo-black chaff (PBC), which has been used in reproduction programs. PBC is a dark pigmentation that is produced in the glumes, peduncle, and in the lower nodes of the stem, but the level of expression varies according to the genetic antecedent and the environment. The *Sr2* gene shows parallelism with *Lr34* and *Lr46*, because it is associated with the resistance to multiple pathogens (Suaste Franco et al. 2015). This resistance gene currently is effective against all strains of *P. graminis* f. sp. *tritici* in all the wheat-producing regions of the world (Haile et al. 2013). The presence of gene *Sr35* in Onavas F2009 provides immunity against Ug99 and has been selected because it is effective against all virulent races, when it is transferred to hexaploid wheat either by hibridization or recombination (Saintenac et al. 2013). According to Morris et al. (2001), wheat cultivars are classified as

Table 4. Functional markers used for molecular characterization of bread wheat cultivar Onavas F2009.

Locus	Marker	Heredity	Primer sequence (5" 3")	Allele	Fragment size	Chromosome	Reference
STEM RUST RESISTANCE GENES							
Sr2	Cssr2	Polymorphic	F: 5' -CAA GGG TTG CTA GGA TTG GAA AAC -3' R: 5' -AGA TAA CTC TTA TGA TCT TAC ATT TTT CTG -3'	Cssr2	172/112/53	3BS	Mago et al. 2011
Sr22	CFa2123	Codominant	F: 5' -CGG TCT TTG TTT GCT CTA AAC C -3' R: 5' -ACC GGC CAT CTA TGA TGA AG -3'	CFa2123	245/260	7A	Khan et al. 2005
Sr24	Sr24#12	Dominant	F: 5' -CAC CCG TGA CAT GCT CGT A -3' R: 5' -AAC AGG AAA TGA ACG ACG ATG T -3'	Sr24#12	600	3DL	Mago et al. 2005
Sr25/Lr19	Gb	Dominant	F: 5' -CAT CCT TGG GGA CCT C -3' R: 5' -CCA GCT CGC ATA CAT CCA -3'	Gb	130	7D	Prins et al. 2001
Sr26	Sr26#43	Dominant	F: 5' -AAT CGT CCA CAT TGG CTT CT -3' R: 5' -CGC AAC AAA ATC ATG CAC TA -3'	Sr26#43	207	6AL	Mago et al. 2005
Sr35	CFa2193	Polymorphic	F: 5' -ACA TGT GAT GTG CGG TCA TT -3' R: 5' -TCC TCA GAA CCC CAT TCT TG -3'	cfa2193	243/230	3AL	Zhang et al. 2010
Sr39	Sr39 #22r	Dominant	F: 5' -AGA GAA GAT AAG CAG TAA ACA TG -3' R: 5' -TGC TGT CAT GAG AGG AAC TCT G -3'	Sr39 #22r	487	2B	Gold et al. 1999
LEAF RUST RESISTANCE GENES							
Lr34	csLV34	Codominant	F: 5' -GTT GGT TAA GAC TGG TGA TGG -3' R: 5'-TGC TTG TTG CTA CTG AAT AGT -3'	csLV34	~150	7D	Lagudah et al. 2006
GRAIN HARDNESS GENES							
Pin-a	Pina	Dominant	F: 5' -CCC TGT AGA GAC AAA GCT AA -3' R: 5' -TCA CCA GTA ATA GCC AAT AGT G -3'	Pina-D1a	450	5D	Gautier et al. 1994
		Dominant	F: 5' -CCC TGT AGA GAC AAA GCT AA -3' R: 5' -TCA CCA GTA ATA GCC AAT AGT G -3'	Pina-D1b	450	5D	Gautier et al. 1994
Pin-b	Pinb	Dominant	F: 5' -ATG AAG ACC TTA TTC CTC CTA -3' R: 5' -TCA CCA GTA ATA GCC ACT AGG GAA -3'	Pinb-D1	250	5D	Giroux and Morris 1997
DWARFING GENES							
Rht-D1	DF2-WR2	Dominant	F: 5' -GGC AAG CAA AAG CTT CGC G -3' R: 5' -GGC CAT CTC GAG CTG CAC -3'	Rht- D1a	264	4D	Ellis et al. 2002
	DF-MR2	Dominant	F: 5' -CGC GCA ATT ATT GGC CAG AGA TAG -3' R: 5' -CCC CAT GGC CAT CTC GAG CTG CTA -3'	Rht- D1b	254	4D	Ellis et al. 2002
Rht-B1	BF-WR1	Dominant	F: 5' -GGT AGG GAG GCG AGA GGC GAG -3' R: 5' -CAT CCC CAT GGC CAT CTC GAG CTG -3'	Rht- B1a	237	4B	Ellis et al. 2002
	BF-MR1	Dominant	F: 5' -GGT AGG GAG GCG AGA GGC GAG -3' R: 5' -CAT CCC CAT GGC CAT CTC GAG CTA -3'	Rht- B1b	237	4B	Ellis et al. 2002
TRANSLOCATION GENE							
T1BL·1RS	RIS	Dominant	F: 5' -TAA TTT CTG CTT GCT CCA TGC -3' R: 5' -ACT GGG GTG CAC TGG ATT AG -3'	RIS	500	1R	Weng et al. 2007

Table 5. PCR conditions used to characterize bread wheat cultivar Onavas F2009.

Trait–locus	Marker	PCR Conditions
Stem rust resistance genes		
Sr2	Cssr2	Denaturing step: 95°C, 2 min Amplification step (30 cycles): 95°C, 30 sec, 60°C, 40 sec, 72°C, 50 sec Extension step: 72°C, 5 min
Sr22	CFa2123	Denaturing step: 95°C, 3 min Touchdown cycles (decrease 1°C/cycle for 15 cycles): 95°C, 45 sec, 65-51°C, 45 sec, 72°C, 60 sec Amplification cycles (25 cycles) 95°C, 45 sec, 50°C, 45 sec, 72°C, 60 sec Extension step: 72°C, 4 min
Sr24	Sr24#12	Denaturing step: 94°C, 5 min Touchdown step 1 (7 cycles, 1ºC down each cycle): 92°C, 30 sec, 62°C, 30 sec, 72°C, 30 sec Amplification step (30 cycles): 92°C, 30 sec, 59°C, 30 sec, 72°C, 30 sec Extension step: 72°C, 10 min
Sr25/Lr19	Gb	Denaturing step: 94°C, 4 min Amplification step (35 cycles): 94°C, 45 sec, 50°C, 30 sec, 72°C, 45 sec Extension step: 72°C, 7 min
Sr26	Sr26#43	Denaturing step: 94°C, 3 min Amplification step (35 cycles): 94°C, 60 sec, 60°C, 60 sec, 72°C, 120 sec Extension step: 72°C, 10 min
Sr35	CFa2193	Denaturing step: 94°C, 5 min Amplification step (30 cycles): 94°C, 30 sec, 60°C, 30 sec, 72°C, 30 sec Extension step: 72°C, 10 min
Sr39	Sr39 #22r	Denaturing step: 94°C, 5 min Amplification step (30 cycles): 92°C, 30 sec, 58°C, 30 sec, 72°C, 40 sec Extension step: 72°C, 10 min
Leaf rust resistance genes		
Lr34	csLV34	Denaturing step: 94°C, 5 min Amplification step (40 cycles): 94°C, 45 sec. 55°C, 30 sec, 72°C, 60 sec Extension step: 72°C, 7 min
Grain hardness genes		
Pin-a	Pina	Denaturing step: 94°C, 3 min Amplification step (37 cycles): 94°C, 90 sec, 55°C, 90 sec, 72°C, 2 min Extension step: 72°C, 10 min
Pin-b	Pinb	Denaturing step: 94°C, 3 min Amplification step (37 cycles): 94°C, 90 sec, 55°C, 90 sec, 72°C, 2 min Extension step: 72°C, 10 min
Dwarfing genes		
Rht- D1	DF2-WR2 DF-MR2	Denaturing step: 94°C, 2 min Amplification step (30 cycles): 94°C, 1 min, 60°C, 2 min, 72°C, 2 min Extension step: 72°C, 7 min
Rht-B1	BF-WR1	Denaturing step: 94°C, 4 min Amplification step (30 cycles): 94°C, 1 min, 58°C, 2 min, 72°C, 2 min Extension step: 72°C, 7 min
Translocation gene		
T1BL·1RS	RIS	Denaturing step: 94°C, 4 min Amplification step (30 cycles): 94°C, 15 sec, 65°C, 45 sec, 72°C, 45 sec Extension step: 72°C, 7 min

'soft' when the alleles of the wild types *PinA-D1a* and *PinB-D1a* are present. Both alleles interact in the determination of the grain texture; the presence of both mutations determines softness, whereas the abscence of any of the two determines hardiness. As indicated by Suaste Franco et al. (2015), all cultivars that carry *PinB-D1a* in 40 or 50% and 70% of *PinA-D1a* can be considered soft wheats.

Conclusions. The bread wheat cultivar Onavas F2009 is a feasible option in the future for farmers in southern Sonora, because it carries genes that confer resistance to stem rust, and also quality that is required by the elaboration and transformation industry.

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Genes of agricultural importance present in bread wheat cultivar Villa Juárez F2009.

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Abstract. Currently, in Mexico, there is a demand of bread wheats with better quality for the milling industry. The production of this cereal is estimated in 3.4 x 10^6 t, which does not suffice the national need of 6.3 x 10^6 t. Therefore, cultivars are needed with high grain yield, better milling and baking quality, resistance to diseases, and tolerance to adverse environmental factors. We characterized the bread wheat cultivar Villa Juárez F2009 at the molecular level using 13 markers: *Lr34* (resistance to leaf rust); *Sr2*, *Sr22*, *Sr24*, *Sr25*/*Lr19*, *Sr26*, *Sr35*, and *Sr39* (resistance to stem rust); *Pin-a* and *Pin-b* (grain hardness); *Rht-D1* and *Rht-B1* (plant height); and the T1BL·1RS translocation (resistance to drought). We detected the presence of the *Sr2* gene which confers resistance to stem rust. The analysis to determine the PINA genes (*Pina-D1a* and *Pina-D1b*) detected the presence of the *pina-D1b* mutation, related to texture of the endosperm, which determines its final use.

Introduction. Mexico currently has a great demand for bread wheats with better milling quality for the industry (Espitia et al. 2008). The production of this cereal is estimated in 3.4 x 10^6 t, which does not fulfill the national need of 6.3 10^6 t (SIAP 2009). Therefore, cultivars are needed with high grain yield, better milling and baking quality, resistance to diseases, and tolerance to adverse environmental factors (Shan et al. 2007). From the genetic breeding point of view, the most valuable genomic contribution is the discovery of genes that are agronomically important, including: 1) genes for adaptation, *Vrn-1*, *Vrn-3*, *Q*, *Rht-1*, and *Ppd-1* (Pearce et al. 2011); 2) genes that confer resistance to diseases, *Lr34*, *Lr10*, and *Lr21* (Lagudah et al. 2009); and 3) genes for quality, *Glu-A1*, *Pin-A*, *Pin-B*, and *Gpc-B1* (Uauy et al. 2006). A simple strategy to capitalize on this knowledge in breeding is to develop molecular markers from allelic sequences of genes and then utilize this tool to characterize material and/or marker-assisted selection. Our objective was to molecularly characterize the bread wheat cultivar Villa Juárez F2009 (Fig. 3) using 13 markers for *Lr34*, *Sr2*, *Sr22*, *Sr24*, *Sr25*/*Lr19*, *Sr26*, *Sr35*, *Sr39*, *Pin-a*, *Pin-b*, *Rht-D1*, *Rht-B1*, and T1BL·1RS (Table 4, p. 39).

Fig. 3. Villa Juárez F2009 is a spring bread wheat with a semiprostrate growth habit and a high frequency of recurved flag leaves. The glaucocity of the flag leaf blade is strong and the culm neck is medium. Spike glaucosity is strong before physiological maturity with a very weak or absent hairiness of the first rachis segment. Grain shape is semi-elliptical.

Materials and methods. The genetic material was obtained at the Norman E. Borlaug Experimental Station (CENEB) from the National Institute for Forestry, Agriculture, and Livestock Research (INIFAP), located in Block 910 in the Yaqui Valley (27º22'N, 109º55'W, 37 masl), during the 2018-19 and 2019-20 crop seasons, using the spring bread wheat cultivar Villa Juárez F2009 (Valenzuela-Herrera et al. 2012). DNA was extracted from foliar tissue, selecting areas without lesions or necrosis that could be present in the leaves. Samples were kept in 1.5-mL tubes at –20°C and later at –85°C previous to lyophilization (Hoisington et al. 1994). DNA was extracted (Saghai-Maroof et al. 1984) and the PCR analysis was based on the

program of each of the markers used (Table 5, p. 40). After that, electrophoresis was used to determine the presence of genes of interest.

Results. The presence of gene *Sr2* was identified through molecular analysis. This gene is effective against all strains of stem rust (*Puccinia graminis* Pers.:Pers. *tritici* Eriks. and E. Henn.) in all the wheat-producing regions of the world (Haile et al. 2013). A few adult-plant genes with individual minor effects are catalogued and designated, including *Sr2*/*Lr27*/*Yr30*/*Pbc1*, *Sr57*/*Lr34*/*Yr18*/*Pm38*/*Stb1*/*Ltn1*, *Sr58*/*Lr46*/*Yr29*/*Pm39*/*Ltn2*, and *Sr55*/*Lr67*/*Yr46*/*Pm46* show a pleiotropic effect, that is they confer resistance to multiple disesases such as stem rust, leaf rust (*P. triticina* Erikss.), yellow rust (*P. striiformis* Westend. f. sp. tritici Eriks.), and powdery mildew (*Blumeria graminis* (DC.) Speer f. sp. *tritici* emend. É. J. Marchal) (Herrera-Foessel et al. 2014). Before posible mutations in the pathogen occur with changing climatic conditions, we need genetic material with resistance. At least 75% of the wheat cultivars recommended for commercial cultivation in the country base their resistance on the *Sr2* gene (Singh et al. 2011). Our analysis determined the *PINA* gene (*Pina-D1a* and *Pina-D1b*) and detected a of the mutation *pina-D1b*, which is related to endosperm hardness or softness, thus determining the end-use. Grains with a hard texture require more energy for milling than those with a soft texture. therefore a greater number of starch granules are physically damaged. Because the damaged starch granules absorb more wáter than undamaged ones, flour from hard wheat for baking bread with yeast is preferred, whereas flour from soft wheat is preferred for cookies and cakes. Molecular markers associated to the agronomic characters of interest facilitate a quick and precise identification of individuals with favorable allelic combinations in segregating populations, independent of the phenotypic expression and, therefore, accelerate the process of generating new cultivars. However, it is necessary to amplify the presence of genes in new wheat materials in order to create greater resistance to diseases.

Conclusions. It was detected the presence of the *Sr2* gene in the bread wheat cultivar Villa Juárez F2009, which confers resistance to stem rust. This cultivar also has the gene that provides characteristics that require the milling industry.

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Effect of growth regulators on wheat yield in the Yaqui Valley during the 2016–17 and 2017–18 crop seasons.

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Abstract. The main cost of wheat production in southern Sonora, Mexico, is fertilization, in which 25% of the total production cost is invested. Nitrogen and phosphorus are the most defficient elements in this region. However, wheat producers generally apply different products along with herbicides, and some of these are growth regulators as well as major and minor elements, but little or no information is available regarding their efficiency. During the 2016-17 and 2017-18 crop seasons, plant growth regulators Moddus 1.0 L/ha^{1}, Hormovit Frio 1.0 L/ha^{1}, and X-Cyte 0.5 L/ha^{1}, and an untreated check, were evaluated to determine their effect on wheat grain yield. The application of these growth regulators was during stem elongation. Durum wheat cultivars CIRNO C2008 and Baroyeca Oro C2013 were used during the first and second seasons, respectively. No statistical differences were found between growth regulators and the untreated check in both crop seasons. We recommended to increase the rates of the products and to make evaluations during different phenological stages of the wheat plants, using one durum wheat cultivar.

Introduction. The state of Sonora has the largest area grown with wheat in Mexico, with an average of 257,655 ha for the last 5 years, and an average grain yield of 6.57 t/ha^{1}. Ninety percent of that area is establised in southern Sonora, which comprises the counties of Cajeme, Navojoa, Benito Juárez, Etchojoa, Bacúm, San Ignacio Río Muerto, Huatabampo, Guaymas, and Empalme. The average grain yield for the 2019–20 crop season was 6.64 t/ha^{1}, with a range of 6.07 to 7.06 t/ha^{1} (SIAP 2021). The main cost of wheat production is fertilization, in which 25% of the total production cost is invested. Nitrogen and phosphorus are the most defficient elements in this region (Cortés et al. 2011). However, wheat producers generally apply different products along with herbicides, and some of these are growth regulators as well as major and minor elements, but little or no information is available regarding their efficiency. These products are considered as supplies of plant nutrition. By April 2021, the Federal Comission for Protection against Sanitary Risks (COFEPRIS) had a list of 4,222 products classified as plant nutrients, which have a registration for the following functions: synthetic growth regulators, nonsynthetic growth regulators, inorganic fertilizer, organic fertilizer, organic-mineral fertilizer, inorganic soil improver, organic soil improver, biological soil improver, inoculant (micro-organisms), and moisturizer (COFEPRIS 2021). Plant growth regulators are compounds chemically synthesized or obtained from other organisms, are similar to phytohormones, and have an important role in regulating different biochemical processes at

the celular level (Lluna 2006). They can be classified according to their molecular structure, activity in the plant, and inhibitory or stimulating effects, among other classifications (Alcántara-Cortes et al. 2019). These important compounds are responsible for the genetic expression of diverse growth and development events and participate in the regulation of multiple physiologic processes, such as seed germination, rooting, tropic movements, tolerance to different types of biotic and abiotic stresses, flowering stage, and fruit maturity and senescence (McCourt 1999; cited by Cruz et al. 2010). Generally, these registered products are not commonly used in evaluations at INIFAP; however, foliar plant nutrition has received little importance, so farmers in the southern Sonora suggested to evaluate them to determine their efficiency. Our objective was to evaluate the effect of growth regulators on durum wheat grain yield.

Materials and methods. Plant growth regulators Moddus 1.0 L/ha, Hormovit Frio 1.0 L/ha, and X-Cyte 0.5 L/ha, and an untreated check, were evaluated during the 2016–17 and 2017–18 crop seasons at the Norman E. Borlaug Experimental Station in the Yaqui Valley in a clay soil, to determine their effect on grain yield. According to the products technological specifications, X-Cyte contains 0.04% g/L natural cytokinin as active ingredient, is a phytoregulator recommended to stimulate celular division during growth and fruit development, inhibits premature plant death, increases pollen viability during high temperature, increases the resistance to abiotic and biotic stresses, promotes regeneration of new roots when plants are affected by pathogens, and retards premature maturity and early senescence of plant tissue (Stoller 2021). Hormovit Frio is a biostimulator that contains 70 ppm of auxin, 700 ppm of gibberellin, and 1,000 ppm of cytokinin and recommended for application when the temperature is higher than the maximum required. Hormovit Frio helps to balance the plant metabolism under high temperature, regulates the excesive loss of moisture by transpiration caused by the temperature, protects the plant from auxin degradation caused by the temperature excess, and induces greater and balanced plant growth and development (Quimia 2021). Moddus is a growth regulator with trinexapac-ethyl 25.50% w/w as active ingredient and recommended for small grain cereals such as wheat and barley. Moddus prevents plant growth, the distance between nodes is shortened and the thickness of the stem increases, which helps avoid lodging (Syngenta 2021).

Crop season 2016–17. Durum wheat cultivar CIRNO C2008 (Figueroa-López et al. 2010) was sown on 8 December, 2016, at the rate of 150 kg/ha. The experimental plot consisted of 12 beds with three 110-m rows, and the experimental unit was two 3-m beds with three replications. The application of growth regulators was during stem elongation using a tractor with a 12 nozzle sprayer and a container of 600 L. In this season, three complementary irrigations were applied.

Crop season 2017–18. Durum wheat cultivar Baroyeca Oro C2013 (Chávez-Villalba et al. 2015) was sown on 7 December, 2017, at the rate of 100 kg/ha. The experimental plot consisted of four beds with two 110-m rows, and the experimental unit consisted of two 3-m beds with three replications. The application of growth regulators was during stem elongation using a 20 L back pack Swissmex sprayer. In this season, four complementary irrigations were applied.

For both crop seasons, agronomic crop management followed technical recommendations by INIFAP for the region (Figueroa-López et al. 2011). Statistical analysis was performed using Mstat 2.0 and the mean comparison with Tukey's test (0.05).

Results and discusion. We observed no statistical differences in grain yield between treatments with growth regulators and the untreated check in both crop seasons (Table 6). During the 2016–17 crop season, the treatment with Moddus showed the lowest grain yield and X-Cyte the highest, a difference of 316 kg. The untreated check was 178 kg greater than that of Moddus and 138 and 48 kg lower than that of X-Cyte and Hormovit Frio, respectively. During the 2017–18 crop season, growth regulators X-Cyte, Moddus, and the untreated check showed the same grain yield (6.462 ha), whereas Hormovit Frio had the lowest grain yield with 281 kg lower than those of the other three treatments. These results also might indicate a 'genotype x environment' (growth regulator, irrigation) interaction, because Hormovit Frio and Moddus caused a differential response by the durum wheat cultivars used. The overall mean of Baroyeca Oro C2013, which had four complementary irrigations, was greater by 116 kg than

Table 6. Growth regulators evaluated on durum wheat cultivars and its effect on grain yield, during the 2016–17 and 2017–18 crop seasons at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. No statistical differences were found between growth regulators and the untreated check (Tukey, 0.05).

	Grain yield (t/ha)	
Growth regulator	CIRNO C2008	Baroyeca Oro C2013
X-Cyte	6.412	6.462
Hormovit Frio	6.322	6.181
Moddus	6.096	6.462
Untreated check	6.274	6.462
Mean	6.276	6.392

the mean of CIRNO C2008, which had three complementary irrigations. The difference in the evaluation between the 2016–17 and 2017–18 crop seasons was the use of a different cultivar, CIRNO C2008 during the first and Baroyeca Oro C2013 during the second, and the number of complementary irrigations. Baroyeca Oro C2013 could be more susceptible to lodging, it is taller than CIRNO C2008; however, the effect of Moddus could not be detected because there were no lodging problems. An overview of the wheat crop during physiological maturity can be observed (Fig. 4). The Hormivit Frio treatment had a maize plot to the west during the 2017–18 crop season, which would limit solar radiation during the afternoon and could cause a reduction in grain yield compared to the other treatments with other growth regulators and the untreated check, because solar radiation is required by crops for their development (Lluna 2006; McCourt 1999; cited by Cruz et al. 2010). The results indicate additional evaluations, but using one cultivar, applying the same number of complementary irrigations, increasing seed density, applying growth regulators at different phenological stages and, perhaps, increasing the rate of the products.

Fig. 4. Overview of the crop at physiological maturity during the 2017–18 crop season at the Norman E. Borlaug Experimental Station, Yaqui Valley, Sonora, Mexico.

Conclusion. We observed no statistical differences in grain yield between the application of growth regulators (X-Cyte, Homovit Frio, and Moddus) and an untreated check during the 2016–17 and 2017–18 crop seasons using durum wheat cultivars CIRNO C2008 and Baroyeca Oro C2013, respectively.

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Effect of Convolvulus arvensis on yield components of durum wheat in an organic production system in the Yaqui Valley, Sonora, Mexico.

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Abstract. *Convolvulus arvensis* is considered the most important limiting factor to organic wheat productivity. The effect of competition between the durum wheat cultivar CIRNO C2008 and field bindweed was evaluated during the 2020–21 autumn-winter crop season in a clay soil located in block 910 of the Yaqui Valley, Sonora, Mexico (27°22´4.9"N latitude and 109°55´36.86"W longitude, 40 masl). Sowing date was 1 December, 2020, using 69 kg/ha of seed in 100-m beds with two rows spaced 80 cm apart. Treatments were wheat in a bindweed-free area of the field and wheat in an infested area. *C. arvensis* was controlled manually twice during the growing season, before the first and second irrigations. To determine wheat grain field, four replications (0.8 m^2 each) per treatment were harvested. The average wheat dry biomass obtained in the treatments without *C. arvensis* competition was 17.667 t/ha, whereas it was 8.837 with competition; grain yield was 9.073 and 4.158 t/ha, respectively. The average *C. arvensis* dry biomass obtained was 1.186 t/ha. Other yield components negatively affected were grains/m^2, grains/spike, and spikes/m^2. These results indicate that with an efficient organic method for control of *C. arvensis*, organic wheat production will be economically feasible in this region of northwest Mexico.

Introduction. Grain yield is the product of plant density, tiller number, number of spikes/plant, number of spikelets/spike, number of kernels/spikelet, and kernel weight. Spike number/plant depends on plant density, cultivar, sowing date, availability of moisture and nutrients, and temperature. The number of spikelets is determined when stem elongation is initiated. Stress caused by weed competition, heat, cold, drought, nutrient deficiency and diseases during this period, reduces the number of spikelets formed (University of California 2021). In many agricultural systems around the world, competition from weeds is one of the major factors reducing crop yield and farmers' income (Cousens and Mortimer 1995; cited by Labrada 2003). Height, early-season growth, tillering capacity, and leaf area are plant traits that may confer competitive ability in wheat grown in organic systems (Mason and Spaner 2006). In addition, weeds increase the cost of production and reduce the quality of the harvested products (Tamayo 2020). A great demand exists for new technologies that encourage environmental sustainability, society-oriented development, and long-term management of natural resources (Leff 2002). Conventional agriculture has rendered a significant increase in agricultural productivity along with damage to natural resources such as soil, water, and the biodiversity of plants and animals. Therefore, proposals have emerged that seek a better harmony between agriculture and the environment (Restrepo et al. 2000).

Organic Agriculture is a production system that sustains the health of soils, ecosystems, and people, relying on ecological processes, biodiversity, and cycles adapted to local conditions, without the use of inputs that have adverse effects. Combining tradition, innovation, and science to benefit the environment that we share and promote fair relationships and a good quality of life for all involved (IFOAM 2008), organic agriculture is based on the principles of health, ecology, equity, and precaution (IFOAM 2005). In monocultures, as the population increases, the average production per plant decreases due to competition for the resources necessary for growth (Willey and Heath 1969), which is reflected in a growth reduction of individuals under a more unfavorable competitive situation. Plants can have negative effects on each other through allelopathy (Weiner 1993). In organic agriculture, weeds are considered the main obstacle to higher crop productivity (Abouziena and Haggag 2016). In the Yaqui Valley, Sonora, Mexico, *C. arvensis* dramatically affects wheat yield in conventional production systems. This situation turns even more serious in an organic production system where herbicides are forbidden. Without any control, bindweed reduced wheat yield by 90% compared with a bindweed-free area of the field (Cortes-Jimenez et al. 2020a). This fact requires immediate action to sort out bindweed competition in an organic wheat production system. Our objective was to determine grain yield and production of durum wheat biomass, with and without competition from *C. arvensis* in an organic production system.

Materials and methods. The effect of competition between durum wheat cultivar CIRNO C2008 (Figueroa-López et al. 2010) and field bindweed was evaluated during the 2020–21 autumn–winter crop season in a clay soil at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico (27°22'4.9"N latitude and 109°55'36.86' W longitude, 40 masl). This region has a warm climate (BW (h)) and extreme heat according to Koppen's classification, modified by

Garcia (1988). Sowing date was 1 December, 2020, using 69 kg/ha of seed in 100-m beds with two rows spaced 80 cm apart. The plot used has organic certification (AGRICERT MEXICO-SENASICA 2019; BIOAGRICERT 2019a, b). For agronomic management, INIFAP's technical recommendations were followed (Figueroa-López et al. 2011): application of 9 t/ha of poultry manure, soil preparation with a harrow, mechanical cultivation, and two manual weeding of all species 39 and 76 days after the sowing date. One presowing and three complementary irrigations and the use of beneficial insects for pest control (Cortés and Ortiz, 2018) were employed.

To determine wheat grain field and biomass, four replications (0.8/m^2 each) per treatment were harvested. The biomass obtained in the treatment with competition was separated into weed and wheat biomass, then dried for 48 h in a stove with continued air circulation at 65°C. Nutrient content in the *C. arvensis* biomass was determined. The experimental design was a randomized complete block with four replications, and the mean comparison was performed using Tukey's test (0.05). The experimental unit (EU) consisted of one bed with two 1-m rows. Harvest was manually with a hand sickle, and each EU was weighed (EUW), and spikes (S) counted and threshed in a Pullman stationary thresher. Samples were cleaned from plant debris and grain weighed (GW). The 100-kernel weight was recorded (W 100 grains). Grain yield components were obtained through the following formulas: grain/m^2 = ((GW*100)/(W 100 grains))/0.8 m; number of grains/spike = (GW/EUW)/(S); number of spikes/m^2 = (S)/(0.8 m); grain yield/ha = ((GW)/(0.8 m))*10,000; dividing by 1,000 the outcome is t/ha (Ortiz-Avalos et al. 2020). Microsoft Excel was used to obtain the relationship between yield components. Data from the *C. arvensis* treatment were used to graph the relationship between yield components and wheat yield. The statistical analysis was performed using the MSTAT (Michigan State University) version 2.10.

Results and discussion. Average wheat dry biomass was 17.667 t/ha in treatments without *C. arvensis* competition and 8.837 with no weeds. Average grain yield was 9.073 with and 4.158 t/ha, without *C. arvensis*. Therefore, yield loss was 4.915 t/ha (54%) in this evaluation. The *C. arvensis* dry biomass obtained was 1.186 t/ha. Other yield components significatively affected were spikes/m^2, grains/m^2, and grains/spike. Grain quality, expressed as yellow berry percent, was 40.5 and 85.5 without and with competition, respectively (Table 7). The infestation level by *C. arvensis* in the evaluation site is shown (Fig. 5, p. 49). Based on the growth of *C. arvensis* after the manual weedings, we observed that a third weeding would be necessary. Yield components are shown (Fig. 6, p. 50). According to previous results, biomass and grains/m^2 remained the components that are better correlated with wheat yield (Ortiz-Avalos et al. 2020; Sañudo et al. 2019; Quiñones et al. 2019). Integrated weed management methods used to control the maximum quantity of weed ultimately increase the grain and straw yield in a wheat field (Dnyandeo et al. 2021). In this experiment, it was clear that *C. arvensis* affected both yield and grain quality. At harvest time, bindweed infestation was observed in the wheat crop, and a high percentage of yellow berry in grain as compared with the plot without the weed (Fig. 7, p. 50). Another alternative evaluated to decrease bindweed infestation was to increase the wheat seeding rate. The biomass and weed

Table 7. Effect of *Convolvulus arvensis* on yield components of durum wheat cultivar CIRNO C2008 under an organic production system in the Yaqui Valley, Sonora, Mexico, during the 2020–21 crop season. Numbers with different letters are statistically different (Tukey, 0.05).

Variable	Wheat control	Wheat with *C. arvensis*	Probability	CV
Wheat biomass (t/ha)	17.667 a	8.837 b	0.0006	6.07
Grain yield (t/ha)	9.073 a	4.158 b	0.0004	6.00
Spikes/m^2	288 a	206 b	0.0320	12.42
Grains/spike	46 a	30 b	0.0024	6.17
Grains/m^2	13171 a	6135 b	0.0007	7.04
Volumetric weight (kg/hl)	81.02 a	80.57 a	0.2388	0.54
100-kernel weight (g)	6.66 a	6.58 a	0.4321	1.95
Yellow berry (%)	40.5 a	85.5 b	0.0026	10.80
C. arvensis biomass (t/ha)	0.0	1.186		

Table 8. Nutrient content in *Convolvulus arvensis* biomass under an organic production system in the Yaqui Valley, Sonora, Mexico.

Nutrient	Concentration in *C. arvensis*	Nutrient content in biomass (kg/t)
Nitrogen (%)	3.28	32.80
Phosphorus (%)	0.24	0.24
Potassium (%)	2.53	25.30
Calcium (%)	1.28	12.80
Magnesium (%)	0.44	0.44
Sodium (%)	0.53	0.53
Cupper (ppm)	20.00	0.02
Iron (ppm)	404.00	0.40
Manganese (ppm)	111.00	0.11
Zinc (ppm)	71.90	0.07

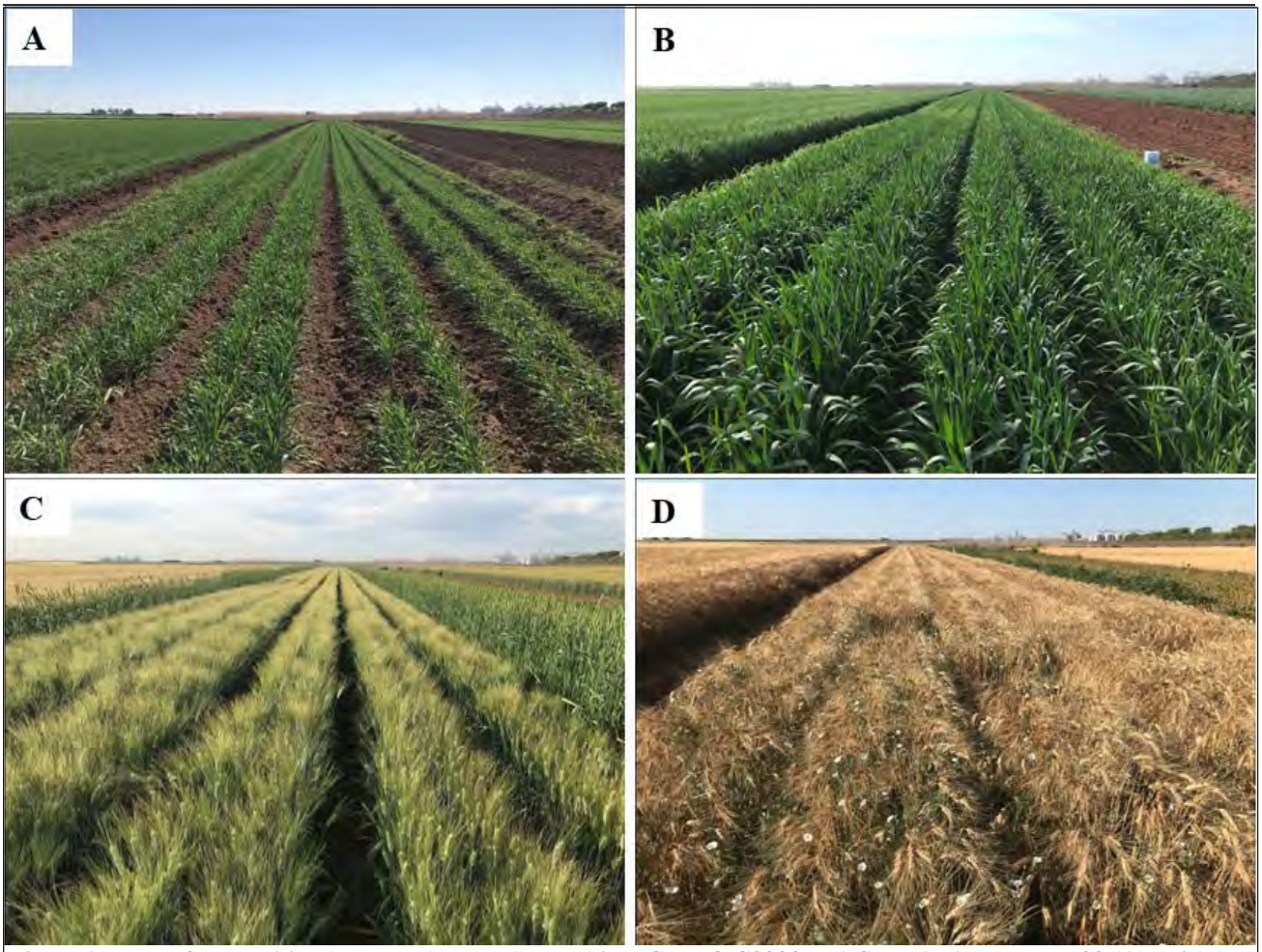

Fig. 5. Aspects of competition between durum wheat cultivar CIRNO C2008 and *Convolvulus arvensis* 39 (A), 76 (B), 188 (C), and 169 (D) days after sowing.

seed production was reduced and the wheat grain yield remained the same (Walsh 2019). The biomass of bindweed contains essential nutrients whose concentration and kg of nutrients/t of biomass are shown (Table 8, p. 48). Nitrogen was the element in the highest concentration, followed by potassium and calcium. These results are related with the nutrient competition between wheat and bindweed. According with Ilker et al. (2021), losses in productivity can be preventable by supplying those minerals in adequate amounts. We point out that with three or more weedings to control *C. arvensis* and with additional fertilization, organic wheat production will be feasible in the future in this region of northwest Mexico, which in turn is very important to maintain the organic certification (Cortes-Jimenez et al. 2020b).

Conclusions. The competition between the durum wheat cultivar CIRNO 2008 and *C. arvensis* under the conditions of this evaluation, caused a severe reduction in wheat biomass production and grain yield and quality.

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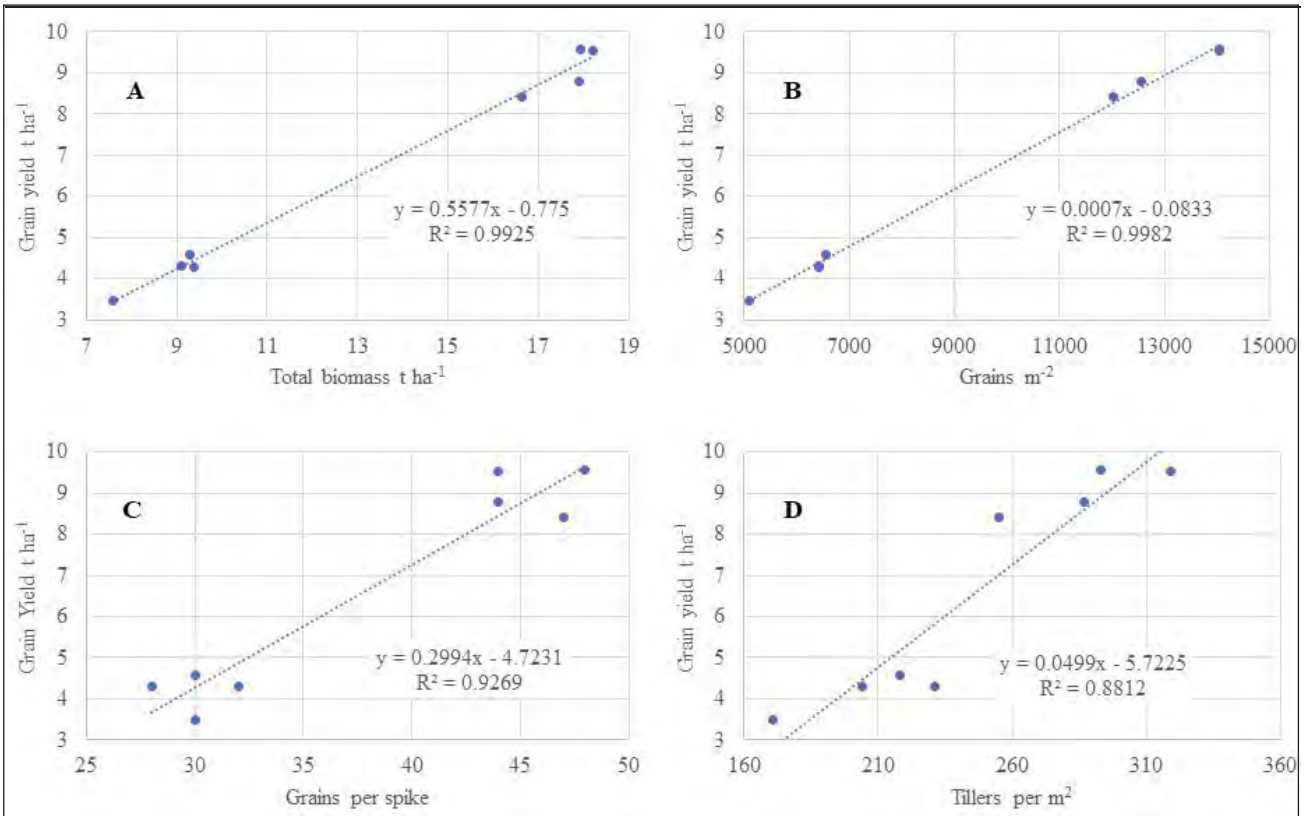

Fig. 6. Yield components of durum wheat cultivar CIRNO C2008: A –total biomass (tha), B – grains/m^2, C – grains/spike, and D – tillers/m^2.

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Fig. 7. Crop appearance before harvest and wheat grain quality of durum wheat cultivar CIRNO C2008: A–B – with bindweed competition and C–D – without bindweed competition.

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Field evaluation of durum wheat advanced lines during the 2019–20 crop season.

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Abstract. Seven durum wheat advanced lines were evaluated for spike weight (g), spike length (cm), number of grains/spike, grain weight/spike (g), grain length (cm), 1,000-kernel weight (g), and grain yield/ plot (t/ha), during the 2019–20 crop season. Sowing date was 14 December, 2019, at the Norman E. Borlaug Experimental Station in Yaqui Valley, Sonora, Mexico. Plots consisted of three 100-m beds, 0.80 m apart, with two rows; seed density was 100 kg/ha. The most oustanding lines were 1) SILVER_14/MOEWE//BISU_1/PATKA_3/3/PORRON_4/YUAN_1/9/USDA595/3/ D67.3/

RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR, which had the highest spike weight, grain weight/spike, 1,000-kernel weight, and grain yield/plot and 2) GUAYACANINIA/POMA_2//SN ITAN/4/D86135/ACO89//PORRON_4/3/SNITAN/7/CAMAYO//HYDRANASSA30/ SILVER_5/3/SOOTY_9/RASCON_37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4, which had the highest spike and grain length and was second in spike weight, grain weight/spike, 1,000-kernel weight, and grain yield/plot. These lines are the most promising candidates to become commercial cultivars among the seven lines evaluated.

Introduction. Wheat is one of the staple crops in Mexico. The national production in 2019 was estimated around 3.2 x 10^6 ton generated from 598,233 ha. The states of Baja California, Guanajuato, Michoacán, Sinaloa, and Sonora stand out as the major producers under irrigated conditions during the autumn–winter crop season, and the states of Guanajuato, México, Oaxaca, Puebla, and Tlaxcala under rainfed conditions during the spring–summer crop season (SIAP 2019). Out of the total wheat production, 40% corresponds to bread wheat and 60% to durum wheat. Because Mexico has to import several million tons per year to suffice its demand, generating more cultivars for domestic use with resistance to pests and diseases, tolerance to adverse environmental factors, and high grain yield and better milling and baking quality is important (Peña et al. 2002; Branlard et al. 2003; Shan et al. 2007). During the breeding process, characterization and selection of germplasm is of primary importance. Some of the most desirable traits include earliness, resistance to diseases, tolerance to adverse environmental factors, higher grain yield, better milling and baking quality, and adaptation (Velasco et al. 2012). Our objective was to evaluate seven advanced lines of durum wheat in order to determine the best in terms of grain yield and other yield components.

Materials and methods. Seven durum wheat advanced genotypes (Table 9) were evaluated for spike weight (g), spike length (cm), number of grains/spike, grain weight/spike (g), grain length (cm), 1,000-kernel weight (g), and grain yield/plot (t/ha), during the 2019–20 crop season. Sowing was 14 December, 2019, at the Norman E. Borlaug Experimental Station in a clay soil located in block 910 of the Yaqui Valley, Sonora, Mexico, at 27°22'4.9"N latitude and 109°55'36.86:W longitude, 40 masl. Plots consisted of three 100-m beds, 0.80 m apart, with two rows. Seed density was

Table 9. Advanced durum wheat lines evaluated at the Norman E. Borlaug Experimental Station, during the 2019-2020 crop season in the Yaqui Valley, Sonora, Mexico.

#	Pedigree and selection history
1	SILVER_14/MOEWE//BISU_1/PATKA_3/3/PORRON_4/YUAN_1/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR CDSS12B00145T-099Y-014M-14Y-3M-0Y
2	HUBEI//SOOTY_9/RASCON_37/3/2*SOOTY_9/RASCON_37/4/CRAKE_10/RISSA/11/TATLER_1/TARRO_1/3/ALTAR84/BISU_1//PLATA_2/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBAD/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CHEN/ALTAR84/3/HUI/POC//BUB/RUFO/4/FNFOOT/12/TOPDY_18/F CDSS11B00325T-049Y-054M-39Y-0M
3	GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN/7/ C AMAYO//HYDRANASSA30/SILVER_5/3/SOOTY_9/RASCON_37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4 CDSS09Y00259S-099Y-016M-1Y-0M-04Y-0B
4	AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOMBRA_20/4/SNITAN/5/ SOMAT_4/INTER_8/6/GUAYACANINIA/POMA_2//SNITAN/7/SOOTY_9/RASCON_37//JUPAREC2001/3/SOOTY_9/RASCON_37//CAMAYO/4/SOOTY_9/RASCON_37//SOMAT_3.1/3/SOOTY_9/RAENTE/MEXI_2/3/AEGILOPSSQUARROSA(TAUS)/4/WEAVER CDSS13Y00451T-099Y-019M-19Y-4M-0Y
5	CBC509CHILE/6/ECO/CMH76A.722//BIT/3/ALTAR84/4/AJAIA_2/5/KJOVE_1/7/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/8/SOOTY_9/RASCON_37//WODUCK/CHAM_3/9/ODIN_15/WITNEK_1//ISLOM_1/5/TARRO_1/TISOMA_2//TARRO_1/3/COMB DUCK_2/ALAS//4*COMB DUCK_2 /4/SHAG_9/BU CDSS12B00124T-099Y-019M-24Y-3M-0Y
6	SOOTY_9/RASCON_37//JUPAREC2001/3/SOOTY_9/RASCON_37//GUAYACANINIA/9/WID22209/6/ADAMAR_15//ALBIA_1/ALTAR84/3/SNITAN/4/SOMAT_4/INTER_8/5/SOOTY_9/RASCON_37/8/KALKA/7/PLATA_7/ILBOR_1/5/BR12*3//BH1146*6/ALD/3/MUSK_1/4/MUSK_4 CDSS13Y00458T-099Y-013M-24Y-4M-0Y
7	CBC509CHILE/6/ECO/CMH76A.722//BIT/3/ALTAR84/4/AJAIA_2/5/KJOVE_1/7/AJ AIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/8/SOOTY_9/RASCON_37//WODUCK/CHAM_3/12/1A.1D 5+1 CDSS13Y00281S-099Y-018M-20Y-2M-0Y

100 kg/ha. For agronomic management, INIFAP's technical recommendations were followed (Figueroa-López et al. 2011).

Results and discussion. The average spike weight was 4.15 g with a range of 3.8 to 4.5 g. Lines with the highest spike weight were those that showed a grain yield above 5.8 t/ha, whereas those with less spike weight showed the lowest grain yield. Lines 'SILVER_14/MOEWE//BISU_1/PATKA_3/3/PORRON_4/YUAN_1/9/USDA595/3/ D67.3/RABI//CRA/4/ ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT// SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR' and 'GUAYACANINIA/POMA_2 //SNITAN/4/D86135/ACO89// PORRON_4/3/SNITAN/7/CAMAYO//HYDRANASSA30/ SILVER_5/3/SOOTY_9/RASCON_37/5/DUKEM_15/3/ BISU_1/PLATA_16//RISSA/4/ SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4' had the highest spike weight (Fig. 8A, lines 1 and 3). The line 'GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89// PORRON_4/3/ SNITAN/7/CAMAYO//HYDRANASSA30/SILVER_5/3/SOOTY_9/RASCON_37/5/ DUKEM_15/3/ BISU_1/PLATA_16//RISSA/4/SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4' had the longest spike with 8.2 cm, and 'CBC 509 CHILE/6/ECO/CMH76A.722//BIT/3/ALTAR84/4/AJAIA_2/5/KJOVE_1/7/ AJAIA_12/F3 LOCAL(SEL.ETHIO.135.85)//PLATA_13/8/SOOTY_9/RASCON_37//WODUCK/ CHAM_3/9/ ODIN_15/WITNEK_1//ISLOM_1/5/TARRO_1/TISOMA_2//TARRO_1/3/COMB' the lowest at 6.9 cm (Fig. 8B). The greatest number of grains/spike was line 4 (AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOM-BRA _20/4/SNITAN/5/SOMAT_4/INTER_8/6/GUAYACANINIA/POMA_2//SNITAN/7/SOOTY_9/RASCON_37// JUPAREC2001/3/SOOTY_9/RASCON_37//CAMAYO/4/SOOTY_9/RASCON_37//SOMAT_3.1/3/SOOTY_9/RAS-CON_37//STORLOM/8/SOOTY_9/RA (CDSS13Y00451T-099Y-019M-19Y-4M-0Y) with 67 (Fig. 8C); the range was 60 to 67 grains/spike. The greatest grain weight/spike was in line 'SILVER_14/ MOEWE//BISU_1/PATKA_3/3/POR-RON_4/YUAN_1/9/USDA595/3/D67.3/RABI// CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/ TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR' with 3.77 g, followed by 'GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89// PORRON_4/3/SNITAN/7/CAMAYO//HY-DRANASSA30/SILVER_5/3/SOOTY_9/ RASCON_37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/SOOTY_9/ RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4' with 3.66 g (Fig. 8D). The average grain length was 0.71 cm; 'GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89// PORRON_4/3/SINTAN/7/CAMAYO//HYDRANAS-

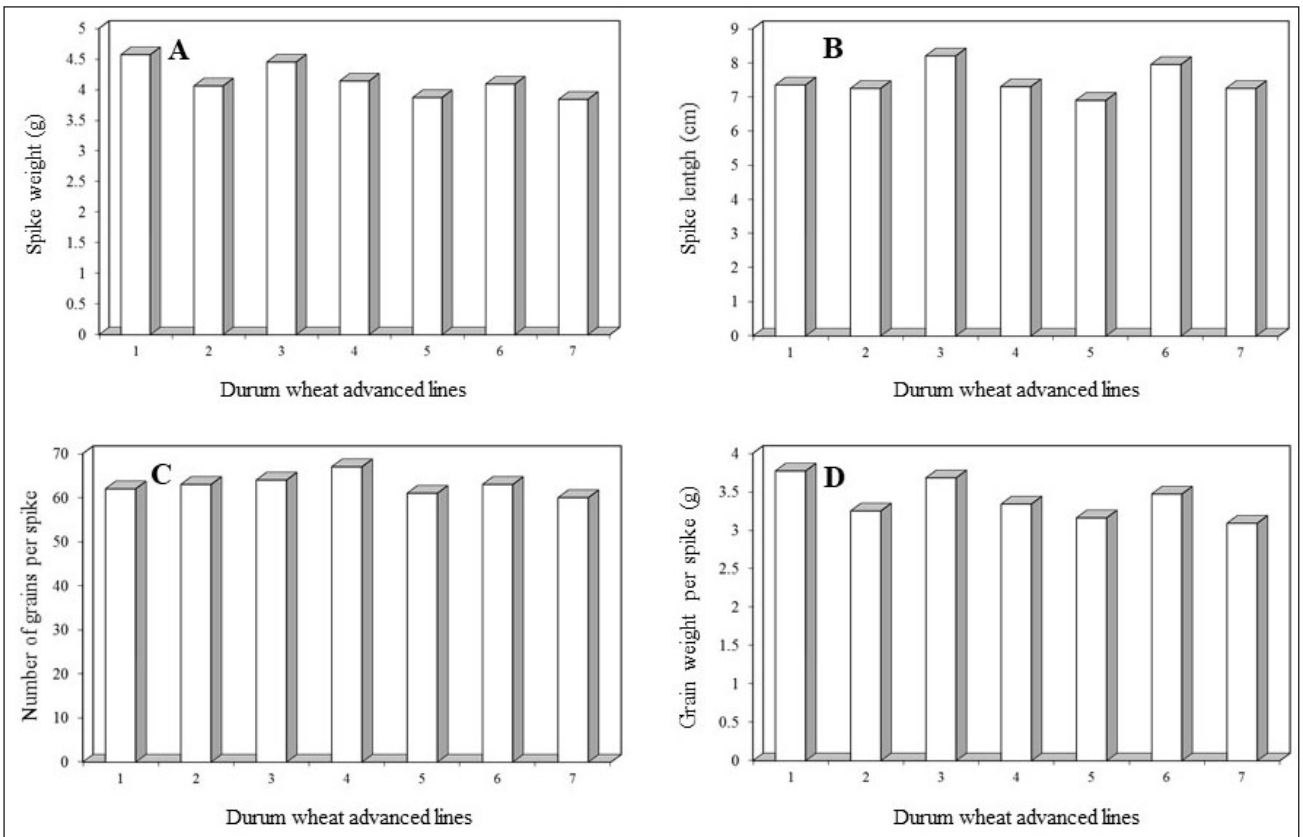

Fig. 8. Spike weight (A), spike length (B), grains/spike (C), and grain weight/spike (D) of seven advanced durum wheat lines (Table 9, p. 52) evaluated during the 2019–20 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

SA30/SILVER_5/3/SOOTY_9/ RASCON_37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/SOOTY_9RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4' had the longest average with 0.74 cm (Fig. 9A). Grain size is an important component of yield, but also in the market price (Takanari-Tanabata et al. 2012) and has an influence on test weight, seed vigor and, therefore, commercialization. The average 1,000-kernel weight (53.4 g) was the trait with the greatest difference among lines, with a range of 50.6 to 57.0 (Fig. 9B). 'SILVER_14/MOEWE//BISU_1/PATKA_3/3/PORRON_4/YUAN_1/9/USDA595/3/D67.3 /RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO _1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR' had the highest weight at 57.0 g, followed by 'GUAYACANINIA/ POMA_2 //SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN/7/CAMAYO//HYDRANASSA30/ SILVER_5/3/SOOTY_9/RASCON_37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/ SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4' with 56.6 g. The average grain yield/plot was 5.83 t/ha with a range of 5.3 to 6.5 t/ha (Fig. 9C). The highest grain yield was in line 'SILVER_14/MOEWE//BISU_1/PATKA_3/3/ PORRON_4/YUAN_1/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR' with 6.5 t/ha, followed by 'GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN/7/ CAMAYO//HYDRANASSA30/SILVER_5/3/SOOTY_9/RASCON_37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37// TILO_1/LOTUS_4' with 6.3 t/ha. Grieve et al. (1992) reported that greater grain yield was determined by a greater number of spikelets, greater number of grains/spike, and grains with higher weight, but these yield components also are affected by weather factors.

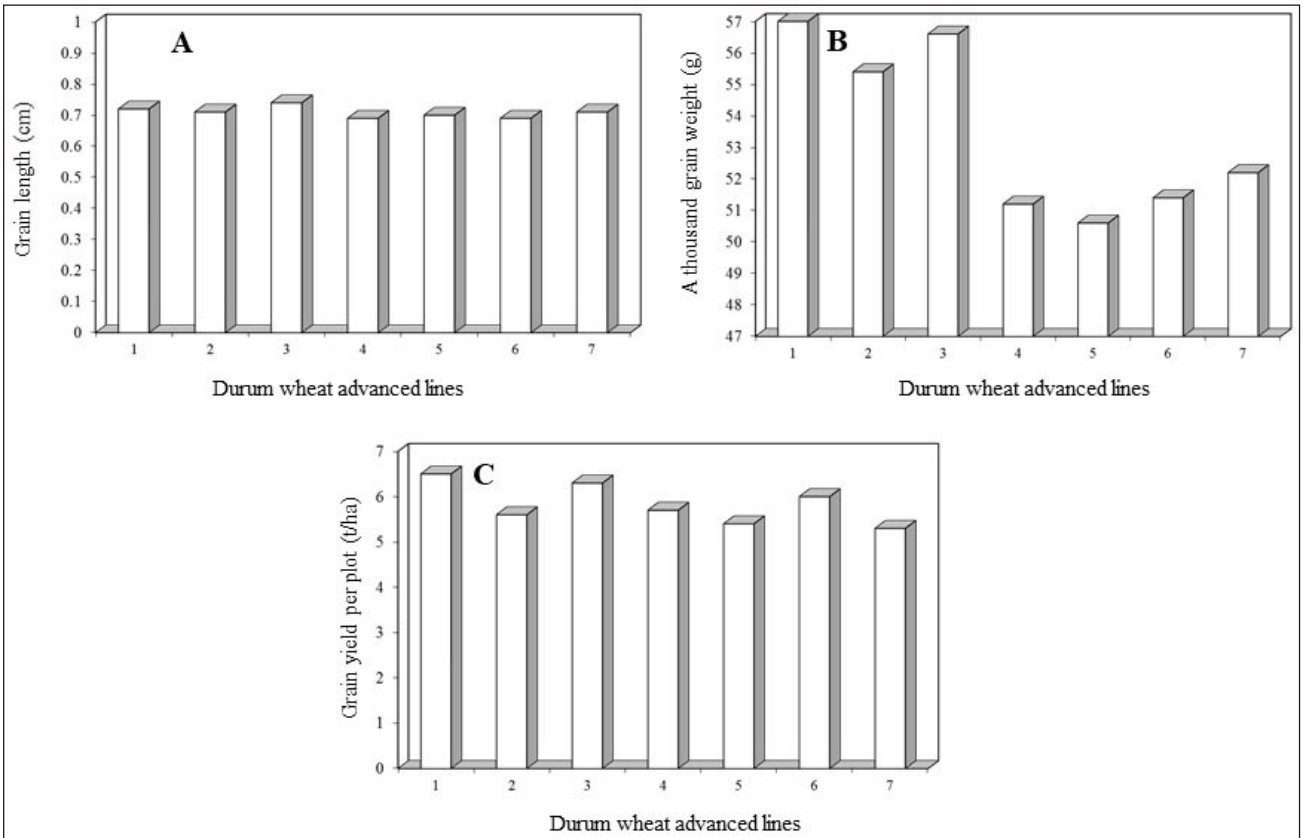

Fig. 9. Grain length (A), 1,000-kernel weight (B), and grain yield/plot (C) of seven advanced durum wheat lines (Table 9, p. 52) evaluated during the 2019–20 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Conclusion. Durum wheat advanced lines 'SILVER_14/MOEWE//BISU_1/PATKA_3/3/ PORRON_4/YUAN_1/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ALTAR' and 'GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89//PORRO N_4/3/SNITAN/7/CAMAYO//HYDRANASSA30/SILVER_5/3/SOOTY_9/RASCON_ 37/5/DUKEM_15/3/BISU_1/PLATA_16//RISSA/4/SOOTY_9/RASCON_37/6/SOOTY_9/RASCON_37//TILO_1/LOTUS_4' are the most promising candidates to become commercial cultivars

among the seven lines evaluated, based on grain yield, which was 6.5 and 6.3 t/ha, respectively, as well as other yield components.

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Yield and quality evaluation of two wheat Triticum turgidum subsp. durum cultivars under organic production system in the Yaqui Valley, Sonora, Mexico.

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Abstract. One of the most important factors affecting yield, grain quality, and food safety in organic farming is the selection of cultivars. Grain yield and its components were evaluated in cultivars Baroyeca Oro C2013 and CENEB Oro C2017 during the 2020–21 autumn–winter crop season in a clay soil at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico (27°22'4.9"N latitude and 109°55'36.86"W longitude, 40 masl). Sowing was on 1 December, 2020, using 69 and 77 kg/ha of seed, respectively, in 100-m beds with two rows 80 cm apart in a plot with organic certification. To determine grain yield, four replications (2.4 m^2) were evaluated for each cultivar. The average dry biomass was 17.865 t/ha for Baroyeca and 16.349 for CENEB Oro; grain yields were 8.203 and 8.422 t/ha, and straw yields 9.835 and 8.107 t/ha, respectively. The average yellow berry was 16.75% in Baroyeca Oro and 7.75% in CENEB Oro. Results indicate that for organic wheat production, CENEB Oro has better quality and grain yield, however, Baroyeca Oro has better performance when cultivars are prone to lodging.

Introduction. During 2020, 477,638 ha of wheat were harvested in Mexico; 230,082 in the state of Sonora, and 151,122 in the Yaqui Valley. Average grain yields were 5.868 in Mexico, 6.661 in Sonora, and 6.892 t/ha in the Yaqui Valley (SIAP 2020). Durum wheat had 59.79% of the total production, which complies with the national need, and also positions Mexico as the third exporter of this product worldwide (SAGARPA 2017). Wheat quality is a very important factor in the organic wheat market and grain protein content and percentage of yellow berry are some of the main quality characteristics considered. A high percentage of yellow berry is highly correlated (r = –0.98) with low protein content in the wheat grain (Miravalles et al. 2013) and, therefore, is of commercial interest. Yellow berry refers to the nonvitreous nature of the wheat kernel. Individual kernels may be vitreous, nonvitreous (yellow berry), or have varying proportions of each (mottled). Although cultivars differ somewhat in their predisposition to yellow berry, the over-riding cause relates to N fertility and, secondarily, biotic and abiotic stresses on the wheat plant. In general, N applied or available during late grain filling and yield-reducing stresses (drought, high temperature) reduce the incidence of yellow berry (WSU 2021).

One of the most important factors affecting yield, grain quality, and food safety in organic farming is the selection of cultivars. A study determined the suitability of 13 cultivars of spring wheat for cultivation in organic farming according to their competitive potential against weeds, susceptibility to fungal diseases, and grain yield. A synthesis of results of the 3-year study, showed the six most useful cultivars for organic farming (Feledyn-Szewczyk et al. 2020). The conventional approach to agriculture has produced significant increases in productivity; however, this model has damaged natural resources, such as soil, water, and the biodiversity of plants and animals. In the last two decades, proposals have emerged that seek a better harmony between agriculture and the environment, with Agroecology as the main focus (Restrepo et al. 2000). Organic agriculture is a production system that sustains the health of soils, ecosystems, and people, relying on ecological processes, biodiversity, and cycles adapted to local conditions, without the use of inputs that have adverse effects. Organic agriculture combines tradition, innovation, and science to benefit the environment that we share and promote fair relationships and a good quality of life for all involved (IFOAM 2008). Organic agriculture is based on the principles of health, ecology, equity, and precaution (IFOAM 2005). Constraints that may be associated with organic grain production include reduced yields due to soil nutrient deficiencies and competition from weeds. Global wheat breeding efforts over the past 50 year have concentrated on improving yield and quality parameters. In Canada, disease resistance and grain quality have been the major goals. Wheat cultivars selected before the advent of chemical fertilizers and pesticides may perform differently in organic, low-input management systems than in conventional, high-input systems. Height, early-season growth, tillering capacity, and leaf area are plant traits that may confer competitive ability in wheat grown in organic systems (Mason and Spaner 2006). Yadav et al. (2020) demonstrated that the performance of durum wheat cultivars was significantly better than the bread wheats under an organic production system in India. Our objective evaluated the quality and grain yield and its components of two durum wheat cultivars in an organic production system.

Materials and methods. Grain yield and its components of durum wheat cultivars Baroyeca Oro C2013 (Chávez et al. 2015) and CENEB Oro C2017 (Chávez et al. 2018) were evaluated during the 2020–21 autumn–winter crop season in a clay soil, at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico (27°22'4.9"N latitude and 109°55'36.86"W longitude, 40 masl). This region has a warm climate (BW (h)) and extreme heat according to Koppen's classification, modified by Garcia (1988). Sowing date was 1 December, 2020, using 69 (Baroyeca Oro C2013) and 77 (CENEB Oro C2017) kg/ha of seed, in 100-m beds with two rows spaced 80 cm apart. Seed was not treated with any type of organic fungicide. The plot used has an organic certification (AGRICERT MEXICO–SENASICA 2019; BIO-AGRICERT 2019a, b; Cortes-Jimenez et al. 2020b). For agronomic management, INIFAP's technical recommendations were followed. Application of 9 t/ha of poultry manure, soil preparation with a harrow, mechanical cultivation, and two manual weedings of all species made 39 and 76 days after sowing. One presowing and three complementary irrigations were applied (Cortes and Ortiz 2018). During the past crop season, there was no incidence of rust and aphids, therefore, application of organic fungicides and insecticides was not necessary. To determine wheat grain yield and its components, four replications (2.4/m^2) per treatment were harvested. The experimental design was a randomized complete block with four replications, and the mean comparison was performed using Tukey's test (0.05). Variables analyzed were total biomass (t/ha), grain and straw yield (t/ha), grain/biomass relationship, grains/m^2, spikes/m^2, grains/spike, 100 grain weight, test weight (kg/hl), and yellow berry (%). Statistical analysis was performed using MSTAT (Michigan State University) version 2.10.

Results and discussion. The average wheat biomass was 17.865 t/ha for Baroyeca Oro C2013 and 16.349 for CENEB Oro C2017 (Table 10) and average grain yield was 8.203 and 8.422 t/ha, respectively, so they were statistically similar. Baroyeca produced significatively more straw than CENEB with a difference of 1.728 t/ha; however, the harvest index (grain yield/bio-

Table 10. Evaluation of two durum wheat cultivars under an organic production system in the Yaqui Valley, Sonora, Mexico, during the 2020–21 crop season. Numbers with the same letters, are not statistically different (Tukey, 0.05).

Variable	CENEB Oro C2017	Baroyeca Oro C2013	Probablilty	CV (%)
Wheat biomass (t/ha)	16.349 a	7.865 a	0.1623	6.79
Grain yield (t/ha)	8.422 a	8.203 a	0.7271	9.71
Straw yield (t/ha)	8.107 a	9.835 b	0.0097	4.60
Grain/biomass (%)	50.42 a	44.87 b	0.0179	3.48
Spikes/m^2	309 a	284 a	0.3365	10.14
Grains/spike	53 a	57 a	0.2901	7.51
Grains/m^2	13,954 a	12,883 a	0.3563	10.38
Test weight (kg/hl)	84.0 a	84.5 a	0.4481	0.96
100-kernel weight (g)	5.11 a	5.22 a	0.4265	3.21
Yellow berry (%)	7.75 a	16.75 a	0.3623	96.90

mass) was higher in CENEB. We noticed that the percentage of grains with yellow berry observed in Baroyeca (Fig. 10) was double that of CENEB (16.75% and 7.75%, respectively). Previous results showed that the grain protein content variation was mostly explained by the baking quality grade of the cultivar, crop nitrogen status, and weed density at flowering (Casagrande et al. 2009). An attempt was made to identify and localize the genes controlling yellow berry in wheat. Monosomic analysis using Chinese Spring monosomic lines showed the presence of two major dominant genes on chromosomes 1A and 7A, and four modifiers on 4A, 4B, 6A, and 6D, which influence the expression of yellow berry in bread wheat (Dhaliwal et al. 1986). Recently, a set of 36 wheat cultivars were grown for two consecutive years under low and high nitrogen conditions. The interactions of cultivars with different environmental factors, suggested the presence of a wider genetic variability which may be utilized for the genetic improvement of the desired trait (Tyagi et al. 2020). No significant differences were observed in the rest of the yield components (spikes/m^2, grains/m^2 and grains/spike); however, Baroyeca has a stronger stem than CENEB, which prevents lodging (Fig. 11). CENEB showed some lodging in previous evaluations, which is undesirable when the objective is to produce organic seed. On the other hand, CENEB has less susceptibility to yellow berry, which is more desirable in the organic market. In addition, CENEB showed a higher yield potential. Every cultivar has different advantages. With proper agronomic management, organic wheat production will be feasible in the future in this region of Northwest Mexico.

Fig. 10. Grain quality expressed as % yellow berry in CENEB Oro C2017 (A) and Baroyeca Oro C2013 (B).

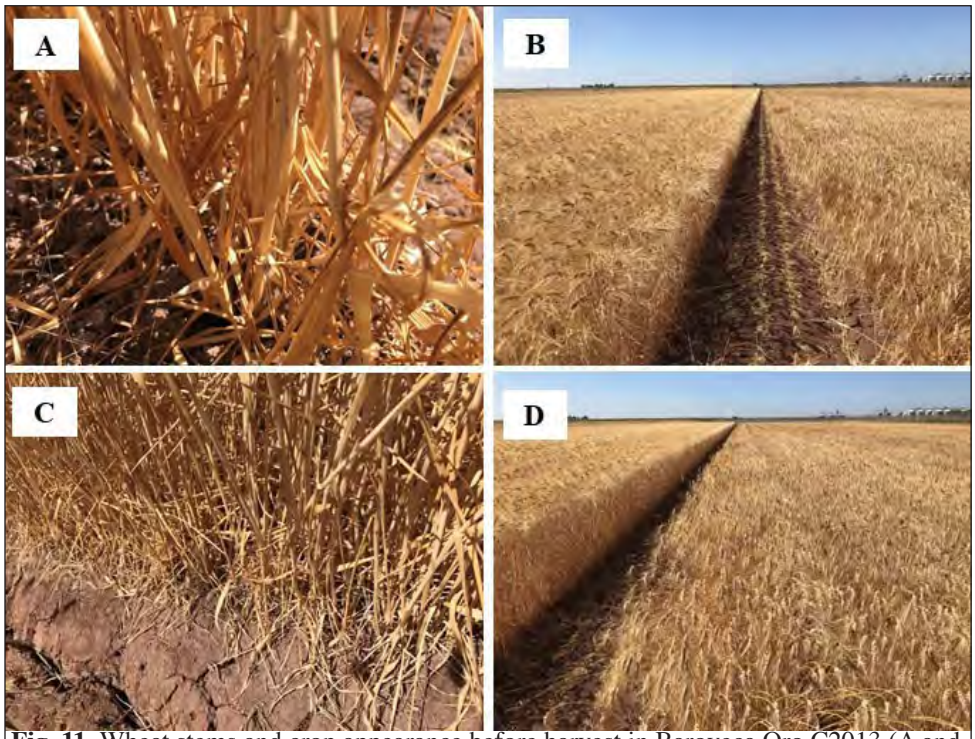

Fig. 11. Wheat stems and crop appearance before harvest in Baroyeca Oro C2013 (A and B (left)) and CENEB Oro C2017 (C and D, B (right)).

Conclusions. For organic wheat production, CENEB Oro C2017 has better quality and grain yield, however, Baroyeca Oro C2013 has better performance when cultivars are prone to lodging.

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Effectiveness of biofungicides on wheat leaf rust (Puccinia triticina) in the Yaqui Valley.

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Abstract. Leaf rust is the most important disease of wheat in Mexico, historically and economically, which has caused significant economic losses that vary from 30 to 60%, according to the cultivar and environmental conditions. The extensive use of chemical compounds for disease control, the outbreak of pathogens with resistance to fungicides, and the deterioration of farmer's health and consumers, has promoted the search for viable alternatives that guaranty greater sustainability in agricultural production, minimizing the negative impact on the environment. In this work, the biofungicides ROYA OUT® and BEST ULTRA®F, and a mixture of both, were evaluated for control of leaf rust. Significant statistical differences were found with the untreated check. The effect of ROYA OUT® provided the best control, although it was

not statistically different from the other treatments. The presence of leaf rust was low in comparison to previous crop seasons.

Introduction. Leaf rust is the most important disease of wheat in Mexico, historically and economically, which has caused significant economic losses that vary from 30 to 60%, according to cultivar and environmental conditions (Villaseñor et al. 2003). In Mexico, durum wheat maintained resistance to leaf rust until 2001, when a new race designated BBG/BN was detected. More than 80% of all the durum wheat collections of the International Maize and Wheat Improvement Center (CIMMYT) are susceptible to this new race, including the cultivar Altar C84, which was the most popular in southern Sonora with a longevity of more than 20 years (Herrera et al. 2005). The extensive use of chemical compounds for disease control, the outbreak of pathogens with resistance to fungicides, and the deterioration of farmer and consumer health, has promoted the search for viable alternatives that guaranty greater sustainability in agricultural production, minimizing the negative impact on the environment. Biological control of diseases with microbial agents, such as fungi and plant extracts, are one of these sustainable alternatives, because they not only diminish agrochemical use (reducing costs) but crop management also renders good production, reduced disease incidence, and secure health of field workers (Janisiewicz and Korsten 2002). Our objective was to evaluate biofuncides for control of leaf rust on wheat.

Materials and methods. The evaluation was carried out at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, during the wheat season autumn–winter 2020–21 in a clay soil with organic certification (AGRICERT MEXICO–SENASICA 2019; BIOAGRICERT 2019a, b). Land preparation consisted of three passes of disc harrowing and the application and incorporation of 5 t/ha of chicken manure. Durum wheat cultivar CIRNO C2008, which is susceptible to leaf rust, was sown on 1 December, 2020, at the rate of 100 kg/ha. Weeds were controlled by scarification between rows and two manual weedings. One presowing irrigation and three complementary irrigations were applied to the crop. The products evaluated were ROYA OUT®, a microbial organic fungicide, which consists of clove extract + *Bacillus subtilis* (1 x 10^8 cfu/mL) + emulsifier, condicioners and thinners (GREENCORP BIORGANIKS DE MEXICO, 2020a); BEST ULTRA®F, *Bacillus* spp. (1 x 10^7 cfu/mL) + *Azotobacter* spp. (1 x 10^5 cfu/mL) + *Pseudomonas* spp. (1 x 10^5 cfu/mL) + plant extracts + conditioners and stabilizers (GREENCORP BIORGANIKS DE MEXICO, 2020b); and a mixture of both products (2 + 2 L each). An untreated check was included (Table 11). The experimental design was randomized complete blocks with three replications. The experimental units consisted of three 5-m beds with two rows 0.8 m apart. Biofungicides were applied with a 10 L back pack Swissmex with a volume of 300 L/ha. Disease severity was evaluated visually, taking at random 10 flag leaves for each replication and each treatment. The values obtained based on the modified Cobb's scale (Peterson et al. 1948) were analyzed with the SAS program and the mean comparison with the Duncan's multiple range test ($\alpha = 0.05$).

Table 11. Biofungicides evaluated in foliar applications for control of leaf rust on durum wheat cultivar CIRNO C2008, at the Norman E. Borlaug Experimental Station, during the 2020–21 season in the Yaqui Valley, Sonora, Mexico.

Treatment	Product	Rate (L/ha)	Date of application	Phenological stage
1	BEST ULTRA®F	2	22 February and 22 March 2021	Heading
2	ROYA OUT®	2	22 February and 22 March 2021	Heading
3	Mixture of both products	2+2	22 March, 2021	Physiological maturity
4	Untreated check			

Results. Disease severity by *P. triticina* on durum wheat CIRNO C2008 was lower on plants treated with the biofungicides than on the untreated check in the last evaluation, being statistically different (Table 12). ROYA OUT® had the lowest average disease severity value with 0.66 and a range of 0 to 1.5, but it was not statistically different from BEST ULTRA®F (average 1.0 and a range of 0.5–1.5) and the mixture of both products (average of 1.1 and a range of 1.0–1.5). The untreated check was statistically different to the products and their mixture with a severity disease average of 4.9 and a range of 4.6–5.3 (Fig. 12, p. 60). The

Table 12. Mean comparison (Duncan, α=0.05) between the different treatments evaluated for control of leaf rust on durum wheat cultivar CIRNO C2008, during the 2020–21 season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Duncan grouping	Mean	Treatment
B	0.66	ROYA OUT®
B	1.00	BEST ULTRA®F
B	1.16	Mixture of products
A	4.90	Untreated check

incidence of leaf rust in this particular season was lower than in previous seasons in southern Sonora, which, unless there was not enough inoculum present, could be related to weather conditions and the sowing date. Grageda-Grageda et al. (2014) reported that a study conducted to assessed possible scenarios of temperatures in southern Sonora from 2000 to 2050, that would be favorable for leaf rust of wheat, the number of days conducive for disease development would range between 10 and 110, being the Mayo Valley with more prevalence of favorable temperatures for the pathogen.

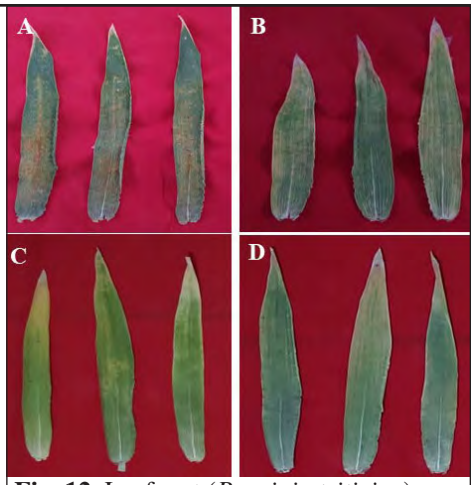

Fig. 12. Leaf rust (*Puccinia triticina*) severity on durum wheat cultivar CIRNO C2008 after treatment with biofungicides, untreated check (A), BEST ULTRA®F (B), ROYA OUT® (C), and a mixture of both products (D).

Conclusion. The lowest disease severity by *P. triticina* on durum wheat cultivar CIRNO C2008 was the treatment with the biofungicide ROYA OUT®, but it was not statistically different from BEST ULTRA®F and a mixture of both products.

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Effect of some climatic factors on wheat grain yield and leaf rust (Puccinia triticina) in southern Sonora.

Alma Angélica Ortiz-Avalos, Juan Manuel Cortés-Jiménez, Guillermo Fuentes-Dávila, Ivón Alejandra Rosas-Jáuregui, and José Luis Félix-Fuentes.

Abstract. Evaluation of grain yield and severity of leaf rust on durum wheat cultivar CIRNO C2008 was carried out at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, during the autumn–winter 2018–19 and 2020–21 wheat seasons. During 2018–19, the biofungicide Fubagro was applied 98, 110, and 115 days after sowing during the grain filling period and during physiological maturity, for control of leaf rust, while in 2020–21, two preventive applications for leaf rust with the biofungicide CYR MEGA were applied during heading and physiological maturity, 83 and 111 days after sowing, respectively. The average grain yield was 6.975 and 9.225 t/ha, respectively, and infection by leaf rust

was recorded in both seasons with a severity grade of 10 during grain filling and and 20 at physiological maturity, in the first season, and 5 in the second using Cobb's modified scale. However, during the second season, it was neccesary to apply a fourth complementary irrigation to induce a favorable environment for disease development. Some climatic variables that might have an effect on grain yield and development of leaf rust were analyzed during the two wheat seasons; these were recorded in the weather station Block 910-CIANO from the automated weather station network in southern Sonora. Wheat season 2020–21 had 725 cold units recorded, while season 2018–19 had 458.

Introduction. In the state of Sonora, the area harvested during the autumn–winter 2019–20 wheat season was 230,087 ha with a grain production of 1,532,757 t and an average yield of 6.08 t/ha. In the District of Rural Development (DDR) 148-Cajeme (Yaqui Valley), which comprises the counties of Benito Juárez, Bácum, Cajeme, Etchojoa, Guaymas, Navojoa, Huatabampo, and San Ignacio Río Muerto, 213,538 ha were harvested with a production of 1,451,962 t, and the average grain yield was 6.74 t/ha. Grain yield by county was 6.96 (Benito Juárez), 6.78 (Bácum), 7.06 (Cajeme), 6.61 (Etchojoa), 6.23 (Guaymas), 6.69 (Navojoa), 6.07 (Huatabampo), and 6.75 (San Ignacio Río Muerto) t/ha, (SIAP 2021). The highest grain yield in Mexico was in Sonora, followed by South Baja California, and Baja California (north), with average yields of 5.98 and 5.79 t/ha, respectively (SIAP 2021). Climate, soil, and agronomic management together propitiate high grain yield in wheat in the region (Cortés et al. 2019).

Wheat grain yield is the result of the relationship and development of the different components during the crop season, and the relationship between genotype, management, and environmental factors (Hall 1980). Because the process of cultivar release has been very dynamic, farmers have at hand wheat cultivars adapted to the agroecology of southern Sonora. Recommendations for agronomic management of wheat have been stable through the years, but it is neccesary to update the technology when a new agrochemical is available in the market or if tnew outbreaks of pests or diseases effect the crop (Cortés et al. 2011). Mexico and the world are facing climate change, which is considered one of the most important problems of our time. Variation in climate is attributed directly or indirectly to human activity (CEDRSSA 2019). Agriculture is extremely vulnerable to the climate change. Temperature rise causes a reduction in crop productivity and, at the same time, proliferation of weeds, pests, and diseases (IFPRI 2019). Since 1997, a drastic reduction in water capture by dams has occurred, making farmers have a two-year rotation in a monocrop system, where wheat was, and still is, dominant. Another drastic reduction in the dam system in this same region prohibited water use for agriculture during the 2003–04 wheat season (Cortés et al. 2013). A similar event occurred with the climate during the 2010–11 season, where 1,800 ha of wheat were damaged due to the low temperatures during January 2011 (SIAP 2021). During the 2014–15 wheat season, economic losses for more than 100 x 19^6 USD were estimated, due to low grain yield attributed to high temperatures during the wheat season, mainly during grain filling (Cortés et al. 2016).

The use of weather data has allowed to develop studies which result to be tools for the decisión-making in agriculture. Through the analysis of weather data, hthe influence of the climatic variables, mainly temperature but on pest and disease appearance and differences in grain yield as well as been demonstrated (Coscollá 1980; Matamoros et al. 2017; Grageda et al. 2014; Castellarín et al. 2018). Soto et al. (2009) evaluated the influence of temperature on the phenological stages of wheat and triticale and reported that the temperature has an important influence on duration of the season, regardless of the plant species studied. In southern Sonora, an automated weather station network (REMAS 2021) has 42 stations. With these data, it has been possible to interpolate with the technique of 'your closest neighbor', in order to create maps of spatial variability of evapotranspiration values, cold units, and rainfall (Ortiz et al. 2009), and the spatial variability of the percentage of clay, electric conductivity in soils of the Yaqui Valley, and salt content, anions and cations of the aquifer of the same Valley (Cortés et al. 2008). Our objective evaluated the effect of temperature and relative humidity on wheat grain yield and on the proliferation of leaf rust during two crop seasons.

Materials and methods. The evaluation was at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, during the 2018–19 and 2020–21 autumn–winter wheat seasons, in a clay soil with organic certification (AGRICERT MEXICO–SENASICA 2019; BIOAGRICERT 2019a, b). In both seasons, durum wheat cultivar CIRNO C2008 (Figueroa-López et al. 2010), susceptible to leaf rust was used, as was the same field preparation, which consisted of three passes of disc harrow. Fertilizer incorporation was during the third disc harrowing. Chicken manure was broadcast at the rate of 10 and 9 t/ha for the 2018–19 and 2020–21 seasons, respectively.

Crop season 2018–19. Sowing was on 14 December, 2018, at the rate of 100 kg/ha. The experimental plot consisted of 12 110-m beds with two rows spaced 0.80 m apart. One presowing and three complementary irrigations were applied. For phytosanitary management, two applications of Bio Crack were carried out 45 and 65 days after sowing, during late tillering and at initiation of stem elongation, respectively, for control of aphids (*Schizaphis graminum*). The product

contains 87% garlic (*Allium sativum*) aqueous extract, 10% chamomile (*Matricaria chamomilla*) aqueous extract, and rue (*Ruta graveolens*). The product is an organic formulation that contains chemical messengers (allomonas), specialized in repelling and deterring the feeding by insects, and attracts beneficial ones to improve the productivity of a crop (Berni Labs 2021).

Fubagro was applied 98, 110, and 115 days after sowing during grain filling and during physiological maturity for control of leaf rust. Fubagro is a fungicide–bactericide of wide spectrum that contains 36% creosote bush (*Larrea tridentata*) extract, 10% pine tree extract (*Pinus pinaster*), and 0.6% citric acid (*Citrus limonum*, *Citrus aurantium*). Because Fubagro is formulated based on plant extracts, it is friendly with the sorrounding environment (Agrorgánicos Nacionales 2021). Both products have the OMRI (Organic Materials Review Institute, https://www.omri.org/) registration. In both cases, a rate of 1.0 L/ha of product in 200 L of water was applied.

Crop season 2020–21. Sowing was on 1 December, 2020 at the rate of 70 kg/ha. The experimental plot consisted of three 5-m beds with two rows and separated by 0.8 m. One presowing and four complementary irrigations were applied to the crop. Weeds were controlled with three manual weedings. Two preventive applications for leaf rust were applied during heading and physiological maturity, 83 and 111 days after sowing, respectively, with the organic fungicide CYR MEGA, which contains 95% creosote bush (*Larrea tridentata*) extract. This product is considered to be a botanic bactericide and fungicide (CYR Agro química, 2018). The rate was 6 L/ha in 300 L of water.

Despite the application of biofungicides, leaf rust appeared on the wheat crop in both seasons. To assess the level of infection, 10 flag leaves per replication were evaluated visually and the results were compared with Cobb's modified scale. In both seasons, the products used for pest and disease control were applied with a 10-L, back pack Swissmex sprayer. The experimental design was a randomized complete block with six replications during the first season and three during the second. The experimental unit consisted of one bed with two 1-m rows. Harvest was manually with a sickle and threshed with an stationary Pullman thresher. To complement the study, we used climatic variables (average, minimum, and maximum temperature (°C); relative humidity (%); and cold units (number) reported on the REMAS webpage from the weather station at Block 910-CIANO at 27.36959 N, -109.92892 W, located within the facilities of the Norman E. Borlaug Experimental station. A cold unit was considered when the temperature is equal to or below 10°C, recorded by a given weather station during one hour (Félix et al. 2009). The data set analyzed was from 15 November to 15 May during the 2018–19 and 2020–21 wheat seasons. The analysis of descriptive statistics and graphs was done with Microsoft Excel 2016.

Table 13. Average value, maximum, minimum, and standard deviation of grain yield of durum wheat cultivar CIRNO C2008 at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, during the 2018–19 and 2020–21 crop seasons.

Crop season	Mean	Grain yield (t/ha)		SD
		Maximum	Minimum	
2018–19	6.975	7.375	6.475	0.3271
2020–21	9.225	9.425	8.950	0.2462

Results and discussion. Grain yield and the relationship with climatic variables. Sowing dates for this evaluation were based on the report by Félix et al. (2009) who indicate that sowing between 15–30 November present a grain yield loss between 0 and 6%. No losses during 1–15 December; a 7 to 13% loss during 16–30 December; and reaching 28% when sowing was 1–15 January. Grain yield during the 2020–21 season was > 24.39% that of 2018–19. The average grain yield during 2020–21 was 9.225 with a range of 8.950 to 9.425 t/ha, whereas in 2018–19 it was 6.975 with a range of 6.475 to 7.375 (Table 13). The 2020–21 wheat season accumulated 725 cold units, 36.82% more than in 2018–19 with 458 (Fig. 13). Several studies conducted in south Sonora confirm the positive correlation between cold units and grain yield of wheat (Félix et al. 2008; Félix et al. 2009; Cortés et al. 2011; Moreno et al. 2018) and plant development according to the sowing date (Ortiz et al. 2012). Frequency histograms of minimum temperatures in both seasons show that 50.5% of the minimum temperatures during 2018–19 were ≤ 10°C and 63% in 2020–21. From these temperatures cold units are generated (Fig. 14, p. 63).

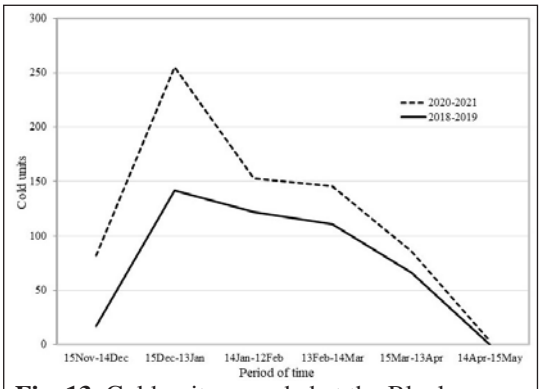

Fig. 13. Cold units recorded at the Block 910-CIANO weather station located at the Norman E. Borlaug Experimental Station during the 2018–19 and 2020–21 wheat seasons.

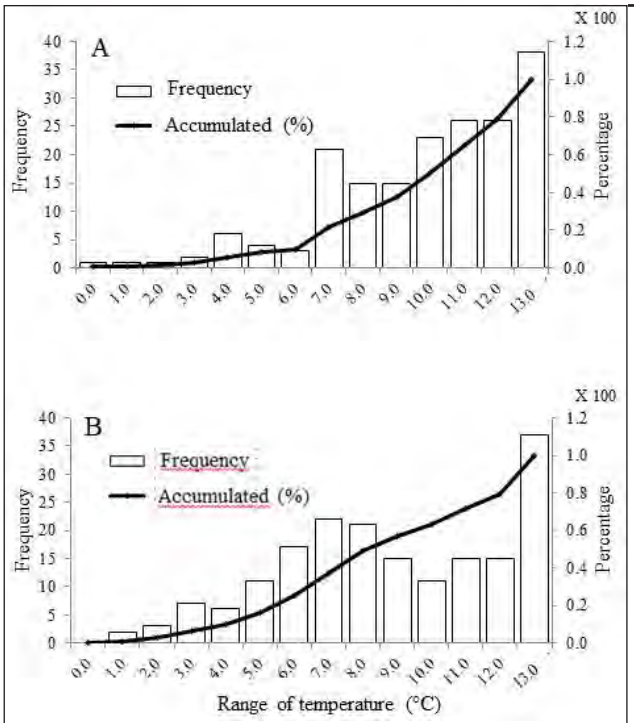

Fig. 14. Frequency of minimum temperatures recorded at the Block 910-CIANO weather station during the 2018–19 (A) and 2020–21 (B) wheat seasons at the Norman E. Borlaug Experimental Station.

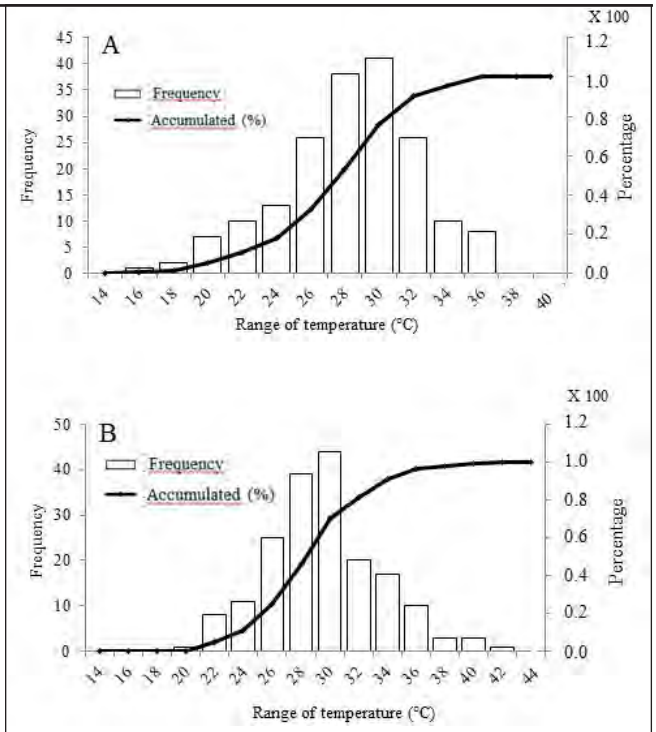

Fig. 15. Frequency of maximum termperatures recorded at the Block 910-CIANO weather station during the 2018–19 (A) and 2020–21 (B) wheat seasons at the Norman E. Borlaug Experimental Station.

Leaf rust and the relationship with climatic variables. The presence of leaf rust with a severity of grade 5 on Cobb's modified scale was observed 98 days after sowing during the 2018–19 crop season when Fubagro was applied, and repeated after the last irrigation 110 and 115 days after sowing, during grain filling and physiological maturity and with infections of 10 and 20, respectively. During the 2020–21 wheat season, leaf rust was not observed. Therefore, we decided to apply a fourth complementary irrigation because greater humidity creates favorable conditions for disease development (Harel et al. 2014). Thereafter, urediospores were present at a grade 5 level of severity according to Cobb's modified scale. The fourth irrigation could have accounted for an increase in grain yield of about 0.2% in 2020–21. Dìaz-Ceniceros et al. (2020) found an increase of 0.18% in grain yield with four complementary irrigations in comparison with two at a 15 December sowing date. According to the Plant Health Council of the Yaqui Valley, during 2018–19, leaf rust was detected in 46 fields during week 15 (8–14 April) out of a total of 242 (JLSV 2021). Up to 19 March, 2021, during the 2020–21 season, no fields showed the presence of leaf rust (JLSV 2021). However, the SIMROYA webpage reported a total of nine out of 263 sampled fields with leaf rust (SIMROYA 2021). During the wheat seasons in the Yaqui Valley in general, temperature, relative humidity, and dew formation are conducive for leaf rust development as long as inoculum is present. During the two seasons, the frequency of temperatures greater than

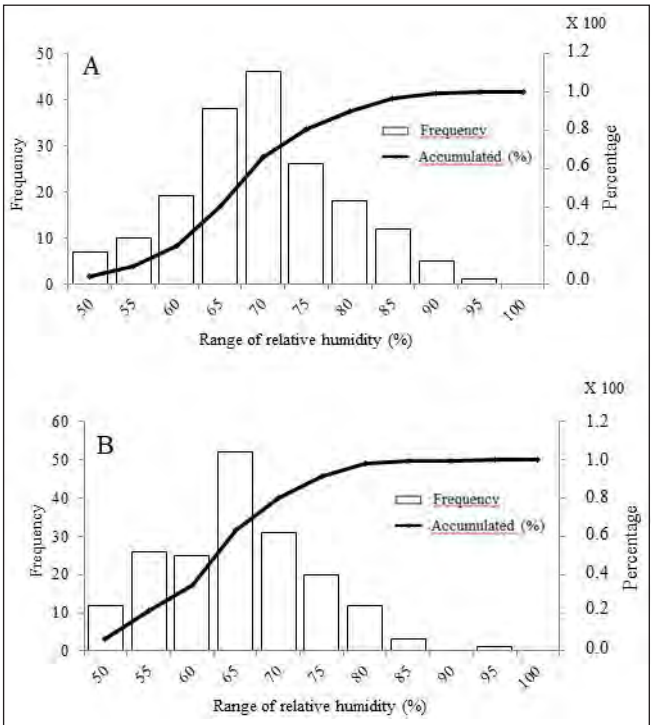

Fig. 16. Frequency of relative humidity recorded at the Block 910-CIANO weather station during the 2018–19 (A) and 2020–21 (B) wheat seasons at the Norman E. Borlaug Experimental Station.

24°C was high (Fig. 15, p. 63), although the average temperature recorded for the station Block 910-CIANO in both seasons was 17.8°C (REMAS, 2021). In relationship to relative humidity, the crop season 2018–19 seemed better suited for rust development since it had 56% more more probability for leaf rust development since the range was equal or greater than 80% (Fig. 16, p. 63). Favorable conditions for development of leaf rust is a temperature around 20°C and dew for several hours (Roelfs et al. 1992). Magaña (2007) cited by Grageda et al. (2014) reported that in Sonora there will be an increase of the average annual temperature that will oscillate between 1 and 2°C for the year 2020 and from 1.5 to 3°C for 2050. As the temperature will increase, favorable conditions for leaf rust would be reduced, which in turn, the forecast would be that favorable conditions for disease development will be diminished in 2020 and thereafter (Grageda et al. 2014).

Conclusion. The weather station at Block 910-CIANO from the automated weather station network in southern Sonora recorded in both seasons an average temperature of 17.8°C, 458 cold units during the 2018–19 and 725 during the 2020–21 wheat seasons. The average grain yield was 6.975 t/ha in 2018–19 and 9.225 in 2020–21. Infection by leaf rust was recorded in both seasons with a severity grade of 10 and 20 during grain filling and physiological maturity, respectively, in 2018–19, and a severity grade of 5 in 2020–21 using Cobb's modified scale.

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Effect of Opus, Folicur, Juwel, and Bemistop on some yield components of bread wheat.

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Abstract. The effect of Opus, Folicur, Juwel, and Bemistop fungicides, evaluated for their biological effectiveness to control Karnal bunt of wheat, also was evaluated on some yield components of the bread wheat cultivar Tacupeto F2001. For spike length, 20 spikes/replication were used with a total of 80/treatment. Five spikes/replication were evaluated to determine the number of spikelets/spike with a total of 20/treatment. For grain length, diameter, and weight, 200 grains/replication were evaluated with a total of 800/treatment. To determine the number of grains/spike, five spikes/replication were evaluated with a total of 20/treatment. The greatest spike length was obtained with the application of Bemistop, with an average of 11.6 cm followed by that of Jewel with 11.55. The highest number of spikelets/spike was obtained with the treatment with Opus with 8, followed by those of Folicur with 7.95 and Jewel with 7.88. The greatest grain length was obtained with Bemistop at 0.717 cm, followed by those of Opus with 0.713 and Jewel with 0.712. The greatest diameter was obtained with Jewel, which recorded an average of 0.322 cm, followed by 0.319 cm for Folicur and Opus. A small difference was detected among treatments regarding grain weight; Jewel showed an average of 0.058 g, Opus and Folicur 0.057 g, Bemistop 0.055 g, and the check 0.057 g. The highest number of grains/spike was obtained with Folicur at 48.65, followed by Opus with 47.90, Jewel with 47.15, Bemistop with 46.35, and the check with 44.30.

Introduction. Karnal bunt, caused by the fungus *Tilletia indica* Mitra, is the most important disease of wheat seed and grain in northwest Mexico (Fuentes-Dávila 1997). The negative effect of Karnal bunt on flour quality and the quarantine regulations are the main cause of economic loss (SARH 1987; Brennan et al. 1990; SAGARPA 2002). Chemical control applied during the heading–flowering–anthesis of the wheat plant is considered an important measure of an integrated management program of the disease (Singh and Prasad 1980; Singh and Singh 1985; Smilanick et al. 1987; Figueroa and Valdés 1991; Salazar-Huerta et al. 1997; Figueroa-López and Alvarez-Zamorano 2000; Fuentes-Dávila 2007; Fuentes-Dávila et al, 2005, 2016). In 2018, Fuentes-Dávila et al. reported that the biological effectiveness of the products Opus, Juwel, Bemistop, and Folicur against *T. indica* was 98.2%, 97.7%, 95.4%, and 95.2%, respectively. We now report the effect of those products on spike length, number of spikelets/spike and grains/spike and grain length, diameter, and weight of the bread wheat cultivar Tacupeto F2001.

Materials and methods. The experiments, in the field during the 2017–18 crop season at the Norman E. Borlaug Experimental Station, located in block 910 of the Yaqui Valley, are described in Fuentes-Dávila et al. (2018), and the bread cultivar Tacupeto F2001 is described in Camacho-Casas et al. (2003). The products used were Opus SC (BASF, epoxiconazol 12% a.i. in weight), as the regional check, Folicur 25 EW (Bayer, tebuconazole), Juwel (BASF, epoxyconazol 11.50% + kresoxim-metil 11.50% CS), and Bemistop (Arysta Lifescience, propiconazol 25.50 EC). The experiment included an untreated check. To evaluate spike length, 20 spikes/replication were used with a total of 80/treatment and a grand total of 400. Average spike length and the average of the other yield components was calculated in order to make comparisons through histograms. Five spikes/replication were evaluated to determine the number of spikelets/spike with a total of 20/treatment and a grand total of 100. For grain length, diameter, and weight, 200 grains/replication were evaluated with a total of 800/treatment and a grand total of 4,000. To determine the number of grains/spike, five spikes/replication were evaluated with a total of 20/treatment and a grand total of 100.

Results. *Spike length*. The greatest spike length was obtained with the application of Bemistop with an average of 11.6 cm, followed by that of Jewel at 11.55 cm (Fig. 17A, p. 67). The average spike length obtained with the fungicides Opus (11.41 cm) and Folicur (11.16 cm) were inferior to the check (11.5 cm). Although Opus and Folicur showed the shortest spike length, in some replications they had spike lengths greater than the average of Bemistop. For example, spike length was 11.98 cm after the fourth replication of Folicur, wherease 11.90 cm after the third of Opus.

Number of spikelets/spike. The highest number of spikelets/spike was obtained with the Opus treatment at 8, followed by those of Folicur (7.95) and Jewel (7.88) (Fig. 17B, p. 67). The check showed 7.65 spikelets/spike; Bemistop showed 7.55, although two replications had 7.7 and 7.9 spikelets/spike.

Grain length, diameter and weight. The greatest grain length was obtained using Bemistop with 0.717 cm, followed by thse for Opus (0.713 cm) and Jewel (0.712 cm) (Fig. 17C, p. 67). Folicur showed 0.710 cm and was shorter than that of the check (0.712 cm); however, in some replications, Folicur was above the average length of the check (one replication

was 0.728 cm). The greatest diameter was obtained with Jewel, which recorded an average of 0.322 cm, followed by those of Folicur and Opus (0.319 cm) (Fig. 18A). Bemistop showed an average of 0.310 cm and the check was 0.315 cm. Small differences were detected among treatments for grain weight (Fig. 18B). Jewel showed an average of 0.058 g, Opus and Folicur 0.057 g, Bemistop 0.055 g, and the check 0.057 g.

Number of grains/spike. The highest number of grains/spike was obtained with Folicur at 48.65, followed by Opus with 47.90, Jewel with 47.15, Bemistop with 46.35, and the check with 44.30 (Fig. 18C).

Conclusions. The relative effects of fungicides Opus, Juwel, Bemistop, Folicur, and an untreated check on spike length, number of spikelets/spike and grains/spike and grain length, diameter, and weightr of the bread wheat cultivar Tacupeto F2001 were small. Bemistop had the greatest spike and grain length, but the lowest number of spikelets/spike, grain diameter and weight and, more importantly, the lowest number of grains/spike. Jewel had the highest grain diameter and weight. Opus followed by Folicur had the highest number of grains/spike.

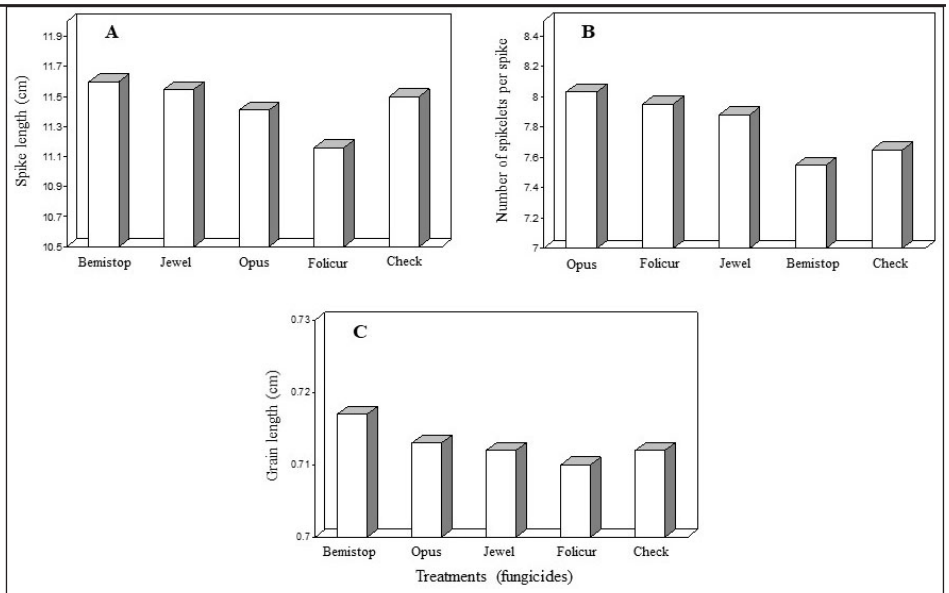

Fig. 17. Spike length (A), number of spikelets/spike (B), and grain length (C) of the bread wheat cultivar Tacupeto F2001 after two applications with fungicides for control of Karnal bunt at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, during the 2017–18 crop season.

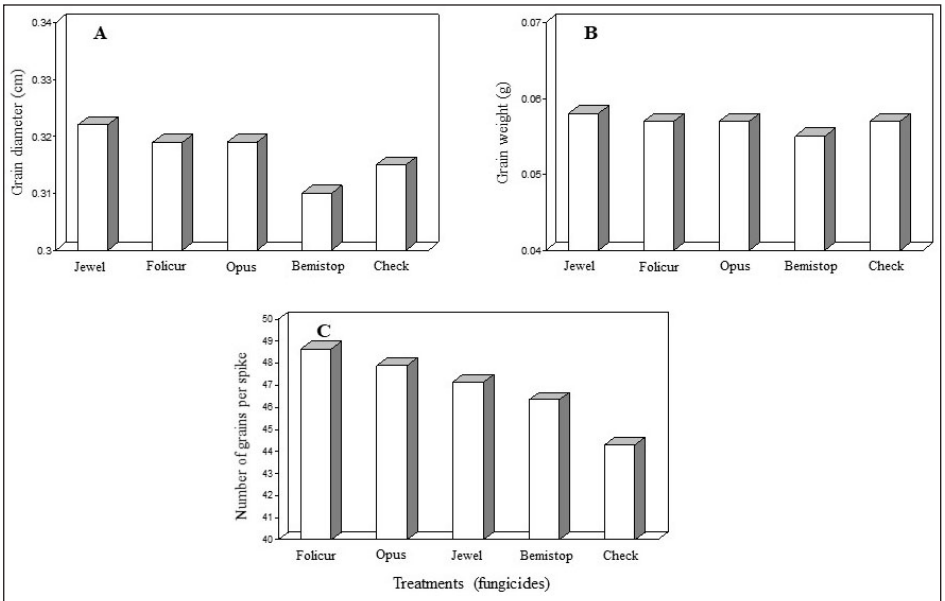

Fig. 18. Grain diameter (A), grain weight (B), and number of grain/spike (C) of the bread wheat cultivar Tacupeto F2001 after two applications with fungicides for control of Karnal bunt at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, during the 2017–18 crop season.

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

H.E. Bockelman, Agronomist and Curator.

Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN–Global): https://npgsweb.ars-grin.gov/gringlobal/search.aspx?. Certain accessions may not be available from the National Small Grains Collection due to intellectual property rights (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
693617 PVP	*Triticum aestivum*	DE2001192	United States	Illinois
693618 PVP	*Triticum aestivum*	DE2001154	United States	Illinois
693619 PVP	*Triticum aestivum*	DE2001152	United States	Illinois
693620 PVP	*Triticum aestivum*	DE2001095	United States	Illinois
693628 PVP	*Triticum aestivum* subsp. *aestivum*	Devote	United States	Washington
693629 PVP	*Triticum aestivum* subsp. *aestivum*	Scorpio	United States	Washington
693632 PVP	*Triticum aestivum*	TCG-Heartland	United States	North Dakota
693663	*Aegilops tauschii*	ARM2010-01	Armenia	Ararat
693664	*Aegilops tauschii*	ARM2010-06	Armenia	Armavir
693665	*Aegilops columnaris*	ARM2010-08	Armenia	Ararat
693666	*Aegilops columnaris*	ARM2010-10	Armenia	Ararat
693667	*Aegilops tauschii*	ARM2010-14	Armenia	Erevan
693668	*Triticum aestivum* subsp. *aestivum*	ARM2010-19	Armenia	Erevan
693669	*Triticum timopheevii* subsp. *armeniacum*	ARM2010-28	Armenia	Kotayk
693670	*Triticum timopheevii* subsp. *armeniacum*	ARM2010-29	Armenia	Kotayk
693671	*Triticum monococcum* subsp. *aegilopoides*	ARM2010-30	Armenia	Kotayk
693672	*Aegilops tauschii*	ARM2010-43a	Armenia	Syunik
693673	*Aegilops neglecta*	ARM2010-46	Armenia	Syunik
693674	*Aegilops neglecta*	ARM2010-47	Armenia	Syunik
693675	*Aegilops neglecta*	ARM2010-49	Armenia	Syunik
693676	*Aegilops neglecta*	ARM2010-53	Armenia	Syunik
693677	*Aegilops tauschii*	ARM2010-56a	Armenia	Syunik
693678	*Aegilops tauschii*	ARM2010-57	Armenia	Syunik
693679	*Aegilops columnaris*	ARM2010-63	Armenia	Erevan
693680	*Triticum urartu*	ARM2010-64	Armenia	Kotayk
693681	*Triticum monococcum* subsp. *aegilopoides*	ARM2010-65	Armenia	Kotayk
693682	*Triticum monococcum* subsp. *aegilopoides*	ARM2010-66	Armenia	Erevan
693783 PVP	*Triticum aestivum* subsp. *aestivum*	OK Corral	United States	Oklahoma
693934 PVP	*Triticum aestivum*	KS Dallas	United States	Kansas
693935 PVP	*Triticum aestivum*	KS Western Star	United States	Kansas
693936 PVP	*Triticum aestivum*	KS Silverado	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
693939 PVP	*Triticum turgidum* subsp. *durum*	TCG-Bright	United States	Colorado
694038 PVP	*Triticum aestivum* subsp. *aestivum*	AP18 AX	United States	Colorado
694042 PVP	*Secale cereale*	KWS Serafino	Germany	
694043 PVP	*Secale cereale*	KWS Tayo	Germany	
694045 PVP	*X Triticosecale* spp.	APT1426023	United States	Texas
694047 PVP	*X Triticosecale* spp.	Caesar	Canada	Ontario
694048 PVP	*X Triticosecale* spp.	APB269	United States	Arizona
694049 PVP	*Triticum aestivum* subsp. *aestivum*	MN-Washburn	United States	Minnesota
694051 PVP	*Triticum aestivum* subsp. *aestivum*	Buckhorn AX	United States	Colorado
694052 PVP	*Triticum aestivum* subsp. *aestivum*	CP 7017 AX	United States	Colorado
694053 PVP	*Triticum aestivum* subsp. *aestivum*	CP 7050 AX	United States	Colorado
694054 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Atomic AX	United States	Colorado
694055 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Helix AX	United States	Colorado
694056 PVP	*Triticum aestivum* subsp. *aestivum*	VI Bulldog	United States	Colorado
694057 PVP	*Triticum aestivum* subsp. *aestivum*	VI Frost	United States	Colorado
694058 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Blackjack	United States	Colorado
694059 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Diesel	United States	Colorado
694060 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Julep	United States	Colorado
694061 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Buster	United States	Colorado
694062 PVP	*Triticum aestivum* subsp. *aestivum*	MS Ranchero	United States	Colorado
695071 JPR	*Triticum aestivum* subsp. *aestivum*	GA06343-13E2 (TX-EL2)	United States	Texas
695072 PVP	*Triticum turgidum* subsp. *durum*	Lustre	United States	Montana
695087 PVP	*Triticum aestivum* subsp. *aestivum*	2016W20221	United States	Virginia
695088 PVP	*Triticum aestivum* subsp. *aestivum*	SSI30-06	United States	Virginia
695093 PVP	*Triticum aestivum* subsp. *aestivum*	AG Radical	United States	Colorado
695094 PVP	*Triticum aestivum* subsp. *aestivum*	HRW 144	United States	Colorado
695095 PVP	*Triticum aestivum* subsp. *aestivum*	AG Golden	United States	Colorado
695100 PVP	*Triticum aestivum*	Draper	United States	South Dakota
695101 PVP	*Triticum aestivum*	Winner	United States	South Dakota
695149 PVP	*Triticum aestivum*	Tam 115	United States	Texas
695150 PVP	*Triticum aestivum*	Tam 205	United States	Texas
695151 PVP	*Triticum aestivum*	Guardian	United States	Colorado
695152 PVP	*Triticum aestivum*	Fortify	United States	Colorado
695157	*Triticum turgidum* subsp. *durum*	VA05WD-12	United States	Virginia
695158	*Triticum turgidum* subsp. *durum*	VA05WD-16	United States	Virginia
695159	*Triticum turgidum* subsp. *durum*	VA05WD-42	United States	Virginia
695160	*Triticum turgidum* subsp. *durum*	VA15WD-4	United States	Virginia
695161	*Triticum turgidum* subsp. *durum*	VA15WD-53	United States	Virginia
695162	*Triticum turgidum* subsp. *durum*	VA15WD-113	United States	Virginia
695163	*Triticum turgidum* subsp. *durum*	VA15WD-68	United States	Virginia
695164	*Triticum turgidum* subsp. *durum*	VA16WD-22	United States	Virginia
695165	*Triticum turgidum* subsp. *durum*	VA16WD-42	United States	Virginia
695166	*Triticum turgidum* subsp. *durum*	VA16WD-43	United States	Virginia
695167	*Triticum turgidum* subsp. *durum*	VA16WD-67	United States	Virginia
695168	*Triticum turgidum* subsp. *durum*	VA17WD-3	United States	Virginia
695169	*Triticum turgidum* subsp. *durum*	VA17WD-6	United States	Virginia
695170	*Triticum turgidum* subsp. *durum*	VA17WD-10	United States	Virginia
695171	*Triticum turgidum* subsp. *durum*	VA17WD-17	United States	Virginia
695172	*Triticum turgidum* subsp. *durum*	VA17WD-18	United States	Virginia
695173	*Triticum turgidum* subsp. *durum*	VA17WD-21	United States	Virginia

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
695174	*Triticum turgidum* subsp. *durum*	VA17WD-29	United States	Virginia
695175	*Triticum turgidum* subsp. *durum*	VA17WD-30	United States	Virginia
695176	*Triticum turgidum* subsp. *durum*	VA17WD-76	United States	Virginia
695177	*Triticum turgidum* subsp. *durum*	VA18WD-4	United States	Virginia
695178	*Triticum turgidum* subsp. *durum*	VA18WD-6	United States	Virginia
695179	*Triticum turgidum* subsp. *durum*	VA18WD-11	United States	Virginia
695180	*Triticum turgidum* subsp. *durum*	VA18WD-17	United States	Virginia
695181	*Triticum turgidum* subsp. *durum*	VA18WD-18	United States	Virginia
695182	*Triticum turgidum* subsp. *durum*	VA18WD-20	United States	Virginia
695183	*Triticum turgidum* subsp. *durum*	VA18WD-24	United States	Virginia
695184	*Triticum turgidum* subsp. *durum*	VA18WD-31	United States	Virginia
695185	*Triticum turgidum* subsp. *durum*	VA18WD-33	United States	Virginia
695186	*Triticum turgidum* subsp. *durum*	VA18WD-34	United States	Virginia
695187	*Triticum turgidum* subsp. *durum*	VA18WD-45	United States	Virginia
695188	*Triticum turgidum* subsp. *durum*	VA18WD-52	United States	Virginia
695189	*Triticum turgidum* subsp. *durum*	VA19WD-25	United States	Virginia
695190	*Triticum turgidum* subsp. *durum*	VA19WD-26	United States	Virginia
695191	*Triticum turgidum* subsp. *durum*	VA19WD-27	United States	Virginia
695192	*Triticum turgidum* subsp. *durum*	VA19WD-28	United States	Virginia
695193	*Triticum turgidum* subsp. *durum*	VA19WD-30	United States	Virginia
695194	*Triticum turgidum* subsp. *durum*	VA19WD-33	United States	Virginia
695195	*Triticum turgidum* subsp. *durum*	VA19WD-36	United States	Virginia
695196	*Triticum turgidum* subsp. *durum*	VA19WD-37	United States	Virginia
695197	*Triticum turgidum* subsp. *durum*	VA19WD-40	United States	Virginia
695198	*Triticum turgidum* subsp. *durum*	VA19WD-50	United States	Virginia
695199	*Triticum turgidum* subsp. *durum*	VA18WD-31	United States	Virginia
695200	*Triticum turgidum* subsp. *durum*	Snowglenn sel	United States	Virginia
695201	*Triticum turgidum* subsp. *durum*	OAC Amber	United States	Virginia
695202	*Triticum turgidum* subsp. *durum*	VA05WD-1	United States	Virginia
695203	*Triticum turgidum* subsp. *durum*	VA05WD-17	United States	Virginia
695204	*Triticum turgidum* subsp. *durum*	VA05WD-22	United States	Virginia
695205	*Triticum turgidum* subsp. *durum*	VA05WD-26	United States	Virginia
695206	*Triticum turgidum* subsp. *durum*	VA05WD-31	United States	Virginia
695207	*Triticum turgidum* subsp. *durum*	VA05WD-39	United States	Virginia
695208	*Triticum turgidum* subsp. *durum*	VA20WD-2	United States	Virginia
695209	*Triticum turgidum* subsp. *durum*	VA20WD-5	United States	Virginia
695210	*Triticum turgidum* subsp. *durum*	VA20WD-6	United States	Virginia
695211	*Triticum turgidum* subsp. *durum*	VA20WD-10	United States	Virginia
695212	*Triticum turgidum* subsp. *durum*	VA20WD-11	United States	Virginia
695213	*Triticum turgidum* subsp. *durum*	VA20WD-17	United States	Virginia
695214	*Triticum turgidum* subsp. *durum*	VA20WD-20	United States	Virginia
695215	*Triticum turgidum* subsp. *durum*	VA20WD-22	United States	Virginia
695216	*Triticum turgidum* subsp. *durum*	VA20WD-23	United States	Virginia
695217	*Triticum turgidum* subsp. *durum*	VA20WD-26	United States	Virginia
695218	*Triticum turgidum* subsp. *durum*	VA20WD-27	United States	Virginia
695219	*Triticum turgidum* subsp. *durum*	VA20WD-29	United States	Virginia
695220	*Triticum turgidum* subsp. *durum*	VA20WD-31	United States	Virginia
695221	*Triticum turgidum* subsp. *durum*	VAKS20WD-33	United States	Virginia
695222	*Triticum turgidum* subsp. *durum*	VAKS20WD-36	United States	Virginia
695319 PVP	*Triticum aestivum* subsp. *compactum*	Castella	United States	Washington

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
695320 PVP	*Triticum aestivum* subsp. *aestivum*	NuMont	United States	Montana
695321 PVP	*Triticum aestivum* subsp. *aestivum*	6PDLD01B	United States	Iowa
695322 PVP	*Triticum aestivum* subsp. *aestivum*	6PELS91B	United States	Iowa
695323 PVP	*Triticum aestivum* subsp. *aestivum*	6PHD88B	United States	Iowa
695324 PVP	*Triticum aestivum* subsp. *aestivum*	6PJBN05B	United States	Iowa
695325 PVP	*Triticum aestivum* subsp. *aestivum*	6PJRS71B	United States	Iowa
695326 PVP	*Triticum aestivum* subsp. *aestivum*	6PLKV03B	United States	Iowa
695327 PVP	*Triticum aestivum* subsp. *aestivum*	6PMQL91B	United States	Iowa
695328 PVP	*Triticum aestivum* subsp. *aestivum*	6PPNA89B	United States	Iowa
695329 PVP	*Triticum aestivum* subsp. *aestivum*	6PAGP65B	United States	Iowa
695330 PVP	*Triticum aestivum* subsp. *aestivum*	6PCQS35B	United States	Iowa
695331 PVP	*Triticum aestivum* subsp. *aestivum*	6PUCY79B	United States	Iowa
695332 PVP	*Triticum aestivum* subsp. *aestivum*	6PVEJ41B	United States	Iowa
695333 PVP	*Triticum aestivum* subsp. *aestivum*	6PVML12B	United States	Iowa
695334 PVP	*Triticum aestivum* subsp. *aestivum*	6PWBD39B	United States	Iowa
695335 PVP	*Triticum aestivum* subsp. *aestivum*	6PYMG52B	United States	Iowa
695336 PVP	*Triticum aestivum* subsp. *aestivum*	6PZNF07B	United States	Iowa
695337 PVP	*Triticum aestivum* subsp. *aestivum*	6PZRK73B	United States	Iowa
695338 PVP	*Triticum aestivum* subsp. *aestivum*	6PQZV26B	United States	Iowa
695339 PVP	*Triticum aestivum* subsp. *aestivum*	6PSQD81B	United States	Iowa
695360 PVP	*Triticum aestivum* subsp. *aestivum*	OR2X2 CL+	United States	Oregon
695361 PVP	*Triticum aestivum* subsp. *aestivum*	Appleby CL+	United States	Oregon
695399 PVP	*X Triticosecale* spp.	759484305	United States	Montana
695400 PVP	*X Triticosecale* spp.	419606537	United States	Montana
695404 PVP	*Triticum aestivum*	122016W	United States	Iowa
695405 PVP	*Triticum aestivum*	AP EverRock	United States	Iowa
695408 PVP	*Triticum aestivum*	WB4401	United States	Minnesota
695409 PVP	*Triticum aestivum*	WB2606	United States	Minnesota
695410 PVP	*Triticum aestivum*	WB4309	United States	Minnesota
695415 PVP	*Triticum aestivum*	AP Iliad	United States,	Iowa
695416 PVP	*Triticum aestivum*	AP Dynamic	United States	Iowa
696395 PVP	*Triticum aestivum*	Nixon	United States	Oregon
697028 PVP	*Triticum aestivum* subsp. *aestivum*	KWS Helium	Germany	Niedersachsen
697029 PVP	*Triticum aestivum* subsp. *aestivum*	KWS Expectum	Germany	Niedersachsen
697274	*Triticum aestivum* subsp. *aestivum*	PI595379-1	United States	Oklahoma
698115 PVP	*Triticum aestivum* subsp. *aestivum*	Velocity	United States	North Dakota
698116 PVP	*Triticum aestivum* subsp. *aestivum*	TCG-Wildcat	United States	North Dakota
698166 PVP	*X Triticosecale* spp.	344	United States	Montana
698170 PVP	*Triticum aestivum* subsp. *aestivum*	AB32N40RG	United States	California
698201 PVP	*Triticum aestivum* subsp. *aestivum*	AP Murdock	United States	Iowa
698202 PVP	*Triticum aestivum*	AP Smith	United States	Iowa
698203 PVP	*Triticum aestivum*	AP Gunsmoke CL2	United States	Iowa
698204 PVP	*Triticum aestivum*	M-IDAS	United States	Iowa
698205 PVP	*Triticum aestivum*	MN-Torgy	United States	Minnesota
698232 PVP	*Triticum aestivum*	LCS Steel AX	United States	Colorado
698300 PVP	*Triticum aestivum* subsp. *aestivum*	Net CL+	United States	Washington
698301 PVP	*Triticum aestivum* subsp. *aestivum*	Uncharted	United States	Oklahoma
698302 PVP	*Triticum aestivum* subsp. *aestivum*	Strad CL Plus	United States	Oklahoma
698303 PVP	*Triticum aestivum* subsp. *aestivum*	Big Country	United States	Oklahoma
698304 PVP	*Triticum aestivum* subsp. *aestivum*	Butler's Gold	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
698305 PVP	*Triticum aestivum* subsp. *aestivum*	Breakthrough	United States	Oklahoma
698306 PVP	*Triticum aestivum* subsp. *aestivum*	DE2101207	United States	Illinois
698307 PVP	*Triticum aestivum* subsp. *aestivum*	DE2101213	United States	Illinois
698308 PVP	*Triticum aestivum* subsp. *aestivum*	DE2101191	United States	Illinois
698309 PVP	*Triticum aestivum* subsp. *aestivum*	ND Noreen	United States	North Dakota
698310 PVP	*Triticum aestivum* subsp. *aestivum*	ND Frohberg	United States	North Dakota
698311 JPR	*Triticum turgidum* subsp. *durum*	A0709-BX05	Canada	Saskatchewan
698456 PVP	*Triticum turgidum* subsp. *durum*	AAC Stronghold	Canada	Saskatchewan
698467 PVP	*Triticum aestivum* subsp. *aestivum*	TW Starlite	Canada	Québec
698469 JPR	*Triticum aestivum* subsp. *aestivum*	Sarta	Lithuania	Kedainiai
698470 JPR	*Triticum aestivum* subsp. *aestivum*	Eldija	Lithuania	Kedainiai

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2021 SUPPLEMENT

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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, 2018, 2019, and 2020 also are available at those sites as well as the *Annual Wheat Newsletter*.

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.

Henceforth, loci are designated in uppercase italic script; alleles are described as previously.

Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

9. Brittle Culm

BRC3.

Add note at end of section:

A further recessive mutation in *T. monococcum* accession Pau 5088 was named *brc5* (11505). **ma:** *Xcfd-5AL* – 2.6 cM – *brc5* – 4.8 cM – *Xgwm126-5AL* {11505}.

16. Corroded

CO1.

co1.

Add: *wsl* {11535}.

v: Add references '{1293,1297}' to previous germplasm entry'. Add: Guomai Mutant {11535}.

ma: *Xgwm508-6B* – 5.1 cM – *Xgwm519-6B* – 8.2 cM – *CO1* {11535}; *Xgwm508-2* – 8.7 cM – *CO1* – *Xgpw7651-6B* {11534}.

CO2.

co2.

v: Add: Shannong 33 Mutant I30 {11534}.

ma: *Xcfd190-6D* – *CO2* – 9.1 cM – 6DS-5 {11534}.

30. Glume Color and Awn Color

30.1. Red (brown/bronze/black) glumes

RG-B1.

Rg-B1a. *TraesCS1B02G005200*.

Rg-B1b. **v:** Add: Jagger {11538}; Norin 60 {11538}; Red glume spelts {11538}.

c: Encodes an R2R3-MYB transcription factor {11538}. *TraesJAG1B01G000800* and *TraesNOR1B01G001100* in red glume Jagger and Norin 40, respectively, carried the same *Rg-B1b_h1* sequence; haplotype comparisons revealed that a specific group of MYB alleles was conserved in red glume genotypes {11538}.

38. Hairy Glume

HG1. Redesignate *HG* as *HG1*.

HG2.

Hg2 {11508}. 2BS {11508}. **v:** CIGM86.944 [syn. Croc_1 / *Ae. tauschii* 518].

tv: Croc_1 {11508}.

ma: *XicsH020* – 1.18 cM – *HG2* – 0.84 cM – *XicsHS358*, corresponding to physical interval 740.0–741.1 Mb in cv. Svevo {11508}.

46. Hybrid Weakness

46.1. Hybrid necrosis

NE1.

Ne1. **ma:** Mapped to a 4.06 Mb region (383.03–3.87.10 Mb) that was deleted in all tested non-*Ne1* carriers {11517}. Co-segregation with the null allele of indel marker *5B-InDel385* {11517}. Mapped to a 4.45 Mb interval represented by *Xwgrc3074-5B* – 0.07 cM – *NE1/5markers* – 0.12 cM – *Xwgrc3009-5B* {11518}. *Xbarc216-5B* – 3.8 cM – *Xwgrc3030* – 0.3 cM – *NE1/Xwgrc1426/3009* – 4.8 cM – *Xbarc74-5B* {11537}; *Xgwrc3030* – 1.4 cM – *Ne1/Xwgrc3146/3147/3150/Xmag1426* – 0.12 cM – *Xwgrc3150* {11537}; markers *Xwgrc3146*, *Xwgrc3147*, and *Xwgrc3150* were dominant {11537}.

NE2. *TraesCS2B01G182800* {11530, 11531, 11532}; also predicted in {11529}.

ma: *Xgwm148-2B* – 5.2 cM – *Xwgrc1713/Xwgrc1736-2B* – 1.3 cM – *NE2/3 markers* {11518}; *Xgwm148-2B* – 5.4 cM – *Ne2/Xwgrc1774/1775/1739* – 3.0 cM – *Xwmc474-2B* {11537}.

Ne2m. **v:** Add: Liaochun 10 {11530}; Zhoumai 22 {11531}.

c: Encodes a CC-NBS-LRR protein {11531; 11532; 11533}. One of two *Ne2m* haplotypes is *Lr13* {11531}. GenBank MW756036 {11532}.

57. Meiotic Characters

57.2. Pairing Homoeologous

PH2. *TraesCS3D02G119400*.

ph2a. **ma:** *ph2a* is a 120–125 Mb deletion {11526}.

ph2b. **c:** Contains a G to A transition at position 74,359,312 in the *TaMSH7-3D* gene {11527}. *TaMSH7* is a plant-specific member of the DNA mismatch repair (MMR) family {11527}.
Wide cross hybrids involving *ph2* mutants have a 5.5-fold increase in homoeologous pairing {11516}.

70. Response to Vernalization

VRN-B1.

Vrn-B1d **[**{11520}**].** *Vrn-B1c* {11520}.

v: Paragon and 24 others {11520}; Saratovskaya 29 and 5 others {11521}.

c: Carries a 0.8-kb deletion and 0.4-kb duplication in intron 1 relative to *vrn-B1* {11520, 11521}.

Vrn-B1e [{11522}]. *Vrn-B1d* {11522}. **v:** Hongchunmai {11522}.
c: Differs from *vrn-B1* by 2 deletions, a SNP and TTTT to ACAA change in in intron 1 {11522}; GenBank HQ130482 {11520}; HQ593668 {11521}.

Vrn-B1f {11523}. **v:** Barta {11523}.
c: Has a partially duplicated 837-bp sequence in intron 1 {11523}.

Proteins

86. Proteins
86.3. Endosperm storage proteins
86.3.1. Glutenins
86.3.1.1. *Glu-1*

GLU-A1.
Add:

Glu-A1bb [{11540}]. **tv:** *T. turgidum* subsp. *turgidum* BGE019307 {11540}.

Glu-A1-1.
Add:

Glu-A1-1y [{11540}]. **tv:** *T. turgidum* subsp. *turgidum* BGE019307 {11540}.

GLU-B1.
Add:

Glu-B1cq [{11492}].	7+8* {11492}.	**tv:** *T. turgidum* subsp. *turgidum* BGE048494 {11492}.
Glu-B1cr [{11492}].	8*.1+20y {11492}.	**tv:** *T. turgidum* subsp. *durum* BGE045649 {11492}, BGE047535 {11492}.
Glu-B1cs [{11492}].	20x {11492}.	**tv:** *T. turgidum* subsp. *durum* BGE045673 {11492}.
Glu-B1ct [{11540}].	6+(8) {11540}.	**tv:** *T. turgidum* subsp. *durum* Langdon {11540}.

Glu-B1-2.
Add:

Glu-B1-2an [{11492}].	8*.1 {11492}.	**tv:** *T. turgidum* subsp. *durum* BGE045649 {11492}, BGE047535 {11492}.
Glu-B1-2ao [{11540}].	(8) {11540}.	**tv:** *T. turgidum* subsp. *durum* Langdon {11540}.

86.3.1.3 Glu-3.

GLU-A3.
Replace the note associated with allele *Glu-A3ax* with the following: The designation of this protein (subunit 6.1) as encoded by *Glu-A3*, previously deduced from its electrophoretic mobility {10116}, was confirmed through mapping studies {11492}. According to {11492}, this subunit is equivalent to that designated 7* in {11539}.

Add:

Glu-A3bd [{11492}].	5+22 {11492}.	**tv:** *T. turgidum* subsp. *turgidum* BGE047532 {11492}.
Glu-A3be [{11492}].	5* {11492}.	**tv:** *T. turgidum* subsp. *turgidum* BGE048495 {11492}.
Glu-A3bf [{11492}].	5*+20 {11492}.	**tv:** *T. turgidum* subsp. *turgidum* BGE048498 {11492}.
Glu-A3bg [{11539}].	5*+11+20 {11539}.	**tv:** *T. turgidum* subsp. *turgidum* BGE018646 {11539}.
Glu-A3bh [{11539}].	10 {11539}.	**tv:** *T. turgidum* subsp. *durum* BGE013622 {11539}.
Glu-A3bi [{11539}].	5*+11+22 {11539}.	**tv:** *T. turgidum* subsp. *turgidum* BGE013089 {11539}.
Glu-A3bj [{11540}].	5* {11540}.	**tv:** *T. turgidum* subsp. *durum* Fanfarron {11540}.
Glu-A3bk [{11540}].	8* {11540}.	**tv:** *T. turgidum* subsp. *durum* BGE019300 {11540}.
Glu-A3bl [{11540}].	5+8* {11540}.	**tv:** *T. turgidum* subsp. *durum* BGE013718 {11540}.

GLU-B3.

Add:

Glu-B3aw [{11492}]. 1+3+8+13+15+18 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047502 {11492}.

Glu-B3ax [{11492}]. 1+3+13*+19 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047504, BGE047506 {11492}.

Glu-B3ay [{11492}]. 1+3+14+15 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047521 {11492}.

Glu-B3az [{11492}]. 1+16 {11492}. **tv:** *T. turgidum* subsp. *dicoccum* BGE045645, BGE047503 {11492}.

Glu-B3ba [{11492}]. 2+4+7+13*+15+19 {11492}. **tv:** *T. turgidum* subsp. *durum* BGE045651 {11492}.

Glu-B3bb [{11492}]. 2+4+15 {11492}. **tv:** *T. turgidum* subsp. *durum* BGE047516 {11492}.

Glu-B3bc [{11492}]. 2+4+15+17+21 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE048494 {11492}.

Glu-B3bd [{11492}]. 4+(7**)+13+15+19 {11492}. **tv:** *T. turgidum* subsp. *dicoccum* BGE045628 {11492}.

Add note: The designation of subunit 7** as encoded by *Glu-A3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies {11492}; the subunit was therefore referenced by {11492}.

Glu-B3be [{11492}]. 4+(7**)+13+15+21 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047511 {11492}.

Add note: The designation of subunit 7** as encoded by *Glu-A3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies {11492}; the subunit was therefore referenced by {11492}.

Glu-B3bf [{11492}]. 4+(7**)+15+19 {11492}. **tv:** *T. turgidum* subsp. *dicoccum* BGE045629, BGE045676, BGE047499, BGE048499 {11492}.

Add note: The designation of subunit 7** as encoded by *Glu-A3* was deduced from its electrophoretic mobility and awaits confirmation by mapping studies {11492}; the subunit was therefore referenced by {11492}.

Glu-B3bg [{11492}]. 4+7***+13+16 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047531 {11492}.

Glu-B3bh [{11492}]. 4+7***+15+19 {11492}. **tv:** *T. turgidum* subsp. *durum* BGE045657 {11492}.

Glu-B3bi [{11492}]. 7+9+14+16 {11492}. **tv:** *T. turgidum* subsp. *durum* BGE047533 {11492}.

Glu-B3bj [{11492}]. 7+13*+15+18 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047512 {11492}.

Glu-B3bk [{11492}]. 7***+8a*+14+17 {11492}. **tv:** *T. turgidum* subsp. *durum* BGE047507 {11492}.

Glu-B3bl [{11492}]. 7***+8a*+14*+15+19 {11492}. **tv:** *T. turgidum* subsp. *turgidum* durum wheat landrace BGE048495 {11492}.

Glu-B3bm [{11492}]. 7***+8a*+14*+16+21 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047535 {11492}.

Glu-B3bn [{11492}]. 8+9+14+18 {11492}. **tv:** *T. turgidum* subsp. *durum* BGE045667 {11492}.

Glu-B3bo [{11492}]. 8+13+18 {11492}. **tv:** *T. turgidum* subsp. *dicoccum* BGE048901 {11492}.

Glu-B3bp [{11492}]. 8+13*+16 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047510 {11492}.

Glu-B3bq [{11492}]. 8a*+13*+15+19 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047519 {11492}.

Glu-B3br [{11492}]. 8a*+13*+16 {11492}. **tv:** *T. turgidum* subsp. *dicoccon* BGE047498 {11492}.

Glu-B3bs [{1149}]. (13**)+14+18 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE045632, BGE047532, BGE048498 {11492}.

Add note: The designation of subunit 13** as encoded by *Glu-B3* was deduced from its electrophoretic mobility and awaits confirmation by mapping studies {11492}; the subunit was therefore referenced by {11492}.

Glu-B3bt [{11492}]. (13**)+14+19 {11492}. **tv:** *T. turgidum* subsp. *turgidum* BGE047513, BGE048496 {11492}.

Add note: The designation of subunit 13** as encoded by *Glu-B3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies {11492}; the subunit was therefore referenced by {11492}.

Glu-B3bu [11539]. 7***+8a*+14*+16+19 {11539}. **tv:** *T. turgidum* subsp. *turgidum* BGE013100 {11539}.

Glu-B3bv [11539]. 13+15+19 {11539}. **tv:** *T. turgidum* subsp. *turgidum* BGE020942 {11539}.

Glu-B3bw [11539]. 13+17+19 {11539}. **tv:** *T. turgidum* subsp. *durum* BGE013622 {11539}.

Glu-B3bx [{11539}]. 1+3+7*+15+19 {11539}. **tv:** *T. turgidum* subsp. *durum* BGE013590 {11539}.

Add note: According to {11492}, this subunit (subunit 7*) is equivalent to 6.1 in {10116}.

Glu-B3by [{11539}]. 1**+2+4+15+17+19 {11539}. **tv:** *T. turgidum* subsp. *durum* BGE08366 {11539}.

Glu-B3bz [{11539}]. 1*+2+4+15+16 {11539}. **tv:** *T. turgidum* subsp. *turgidum* BGE12537 {11539}.

Glu-B3ca [{11540}]. 1+3+13+19 {11540}. **tv:** *T. turgidum* subsp. *durum* BGE018639 {11540}.

Glu-B3cb [{11540}]. 13*+18 {11540}. **tv:** *T. turgidum* subsp. *durum* BGE018657 {11540}.

Glu-B3cc [{11540}]. 13+14+18 {11540}. **tv:** *T. turgidum* subsp. *durum* BGE013724 {11540}.

Glu-B3cd [{11540}]. 2+4+13+15+17 {11540}. **tv:** *T. turgidum* subsp. *durum* BGE030927 {11540}.

Disease/Pest Reaction

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

PM1.

Pm1a. **c:** Encodes a nucleotide-binding, leucine rich repeat protein with close similarity to *Pm21* {11509}.

Add at end of section: Reference {M2011} provides further evidence for a non-recombinogenic region in distal chromosome arm 7AL. The region appeared to have rearrangements involving all three homoeologous group-7 chromosomes. This casts doubt regarding an allelic series at the *PM1* locus {11509}.

PM2. *TraesCS5D01G044600 {11503}.*

Pm2a. **c:** GenBank: Correct to LN999386, protein CZT14023.1. The *TraesCS5D01G044600* allele in susceptible CS and Taichung 29 differed from the *Pm2a* allele by a 7-bp deletion in the first intron {11503}. Several alleged alleles at the *Pm2* locus are likely *Pm2a* {11503}.

Pm2b. Add note at end of section: Identified as *Pm2a* {11503}.

Pm2c. Add note at end of section: Identified as *Pm2a* {11503}.

Add note at end of entire *PM2* section: Several alleged alleles at the *Pm2* locus are likely *Pm2a* {11503}.

PM4.

Pm4a. **c:** Similar structure to Pm4b {11525}.

Pm4b. Closest homologue of the C2 domain of *Pm4b* in CS is *TraesCS2A01G557900*.

c: Encodes a putative chimeric protein of a serine/threonine kinase and multiple C2 domains and transmembrane regions; *Pm4b* undergoes alternative splicing to generate two isoforms, both of which are essential for resistance function {11525}. Genbank: Pm4b_V1 CDS: MT783929; Pm4b_V2 CDS, MT783930.

Pm4d. **v:** Add: SYMattis {11525}.

PM5. *TraesCS7B02G441700* (susceptible allele) (chr7B: 706.811–706.816 Mb) {11533}.

Pm5a. **c:** GenBank MK955160.

Pm5b. **c:** GenBank MK955159.

Pm5d. **c:** Same sequence as *Pm5e* {11533}.

Pm5e. **v:** Add: Baiyouyantiao (previously published as *PmBYYT* {11533}); Hongquanmong (previously published as *PmH* {11533}; Mazhamai (previously published as *Mlmz* {11533}); Tangmai 4 (previously published as *PmTm4* {11533} {10961, 11533}); Xiaobaidongmai (previously published as *Pmxbd* {0258, 11533}.

c: Identified as a CC-NBS-LRR {11533}. GenBank MK955156.

pm5. **c:** CS (susceptible allele): *TraesCS7B02G441700* (chr7B: 706.811–706.816 Mb); GenBank MK955157.

99. Reaction to *Magnaporthe oryzae*.

RMG6.

Rmg6 (11504). Add: [*Rwt3* {11504}]. **v:** Add: Chinese Spring *Rmg9* {11504}.

ma: *Xwmc432-1D – RMG9* – 5.0 cM – *RMG6 – Xwmc222-1D* {11504}.

RMG9.

Rmg9 {11504}. *Rwt6* {11504}. 1D {11504}.

v: Add: Chinese Spring *Rmg6* {11504}.

ma: *Xwmc432-1D – RMG9* – 5.0 cM – *RMG6 – Xwmc222-1D* {11504}.

Add note at end of section: *Rmg1*, *Rmg6*, and *Rmg9* were identified in two *Ae. tauschii* accessions (KU-2108, KU-2158) from the southern coast of the Caspian Sea, the likely region of origin of common wheat, offering the possibility that all three genes were simultaneously introduced to wheat {11504}.

100. Reaction to *Mayetiola destructor*

H7.

H7. 6AS {11511}; 5D {026}.
ma: Mapped as a major QTL (PVE 0.61 – 0.78) in a 6-Mb interval flanked by GBS6A205 and GBS6A215 {11511}.

With relocation of *H7* to chromosome arm 6AS there are issues of overlap with *H31*.

H8.

H8. 2B {11511}.
ma: Mapped as a minor QTL (PVE, 0.03– 0.05) {11511}.

The *H7* and *H8* genes were variously described as duplicate {026}, complementary and additive {11511}.

H35 in chromosome arm 3BS and *H36* in chromosome arm 7AS were named for one major and one minor QTL in common wheat line SD06165 {11512}.

QTL
QH.icd-2A {11510}. 2AL. Putatively derived from *T. turgidum* subsp. *dicoccum* {11510}.
tv: DWHF01 {11510}.
ma: Linked with *Ax-94980581I* {11510}.
QH.icd-5B {11510}. 5BS. **tv:** DWHF01 {11510}. Possible overlap with *H31* {11510}.
Qhara.icd-6B {11510}. 6BS {11510}.
tv: *T. turgidum* subsp. *armeniacum* derivatives: DWHF02 {11510}; Chaoui {11510}; Icamoram7d {11510; Marouane {11510}; Nassira {11510}.
ma: Linked with *Ax-95181449* {11510}.

***Mayetiola destructor* tolerance QTL**
QTL
QHft.nc-7D in chromosome arm 7DS conferring tolerance to Hessian fly in line LA03136E71 is reported in {11513}.

103. Reaction to *Pratylenchus* spp.

103.2. Reaction to *Pratylenchus thornei*

Add: ', 11501' to present reference. Add: These QTL were fine mapped in a 'Sokoll (MR) / Krichauff' DH population and further crosses: *QRlny.sk-2B* was mapped to a 1.4 cM/2.19-Mbp region; *QRLnt.sk-6D* was mapped to a 3.5 cM/1.77-Mbp region {11501, 11502}.

105. Reaction to *Puccinia graminis* Pers.

SR22.

Sr22b {11514}. *SrTm5* {11208} $7A^{m}L$ {11208}.
i: PI 306540 / Kronos // Clear White // *3 Fielder {11514}.
dv: *T. monococcum* subsp. *monococcum* PI 277131-2 *Sr21 Sr60* {11208, 11385}; PI 306540 *Sr21 Sr22b Sr60 SrTm4* {11208, 11385}.
ma: *SrTm5/IWB25012/IWB44281/IWB405527/Sr22GMF/GMR* – 0.8 cM – *IWB6942* {11208}; *pkw4995* (RefSeq v1.1 *TraesCS7A02G499500*) – 0.04 cM – *SrTm5* – 0.04 cM – *pkw4999* (RefSeq v1.1 *TraesCS7A02G499900*) {11514}.
c: The predicted *Sr22b* NLR protein is 95.7 to 96.7% identical to proteins translated from six *Sr22a* resistant haplotypes {11514}.

Allelism of *Sr22a* and *Sr22b* was based on more than 2,200 gametes {11514}.

SR26.

Sr26. **c:** Encodes an NLR protein; GenBank MN531843 {11528}.

SR61.

Sr61. **c:** Encodes an NLR protein; GenBank MN531844 {11528}.

SR62.

Sr62 {11524}. *Sr1644-1Sh* {11519}. 1B (T1S^{sh}S·1S^{sh}L–1BL) {11524}.
v: Zahir*4 / *Ae. sharonensis* AS_1644, JIC DPRM0081 {11524}.
1D (1SShS.1SShL-1DL) {11524}.
al: *Ae. sharonensis* AS_1644 {11519}.
ma: Mapped in *Ae sharonensis* to a 480-kb interval on chromosome arm 1S^{sh}S {11519}.
c: Cloned from *Ae. sharonensis* and validated in transformed wheat with *Sr62* {11524}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

LR13. *TraesCS2B01G182800* {11530, 11531}; also predicted in {11529}.
Lr13. *LrLC10* {11529}; *LRZH22* {11531}.
v: Add: Liaochun 10 {11530}; Zhoumai 22 {11531}.
c: Encodes a CC-NBS-LRR protein {11531; 11532} that is identical to that produced by one of the *Ne2m* haplotypes {11531}. GenBank MW756036 {11532}.

LR59.
Lr59. Add note: Further study of this translocation (*Lr59*-Full) identified a T1AS·1L^{P}–6S^{P}–6BS structure. Another round of recombination identified the following types: T1AS·1L^{P}–1AL; T1AS·1L^{P}–6S^{P}–6BS; and T1AS·1AL–1L^{P}–6S^{P}–6BS (Line *Lr59*-151 had the shortest alien segment). Recombinants with 6BS retained the wheat *GLI-B2* locus {11499}.

LR65 .
Lr65. **ma:** *LR65* – 0.5 cM – *Alt-64* – 0.05 cM – *Alt 21* – 1.7 cM – *Xbarc212-2A* {11536}; *AltID-11* – 0.7 cM – *Lr65* – 0.02 cM – *Alt-64* – 1.1 cM – *Alt21* {11536}. *TraesCS2A02G001500* was predicted as the candidate position for *LR65* {11536}.

107.3. QTL for reaction to *P. triticina*

AGS 2038 (R) / UG111729 (MR) RIL population. Seedling and adult-plant resistance was controlled by several QTL, the most important of which was designated *QLr.ags-1AL* spanned by *IWB20487* and *IWA4022* {11507}.

26R61 (S) / AGS 2000 (R): RIL population. A single QTL (*QLr.uga-2BS*) flanked by *wPt-666389* and *wPt-2600* on chromosome arm 2BS was designated *LrA2K* {11507}. *LrA2K* – 2.9 cM – *Xwmc770-2B* {11507}.

112. Reaction to *Schizaphis graminum*

GB5.
Gb5 {1515, 1514}. 7S#1L(7A) {391}; T7S#1L·7S#1S–7S {389}.
tr: CI 17883; CI 17884; CI 17885 {1515}; UCRBW98-1 and UCRBW98-2 (PI 603919) have a shortened alien segment {11515}.
ma: KASP markers are reported in {11516}.

115. Reaction to Soil-borne Cereal Mosaic Virus

SBM1.
Sbm1. **v2:** Cadenza *Sbm2* {add: , 11500}.

Sbm2 {11500}. 2BS {11500}. **v:** Xi19 {11500}.
v2: Cadenza *Sbm1* {11500}.

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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

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IX. VOLUME 68 MANUSCRIPT GUIDELINES.

The required format for Volume 68 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 previous volumes 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 email to jraupp@ksu.edu.

DISTRIBUTION:

The only method of distribution of Volume 68 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) or Research Gate (https://www.researchgate.net/profile/W_Raupp).

The *Annual Wheat Newsletter* also will continue to be available (Vol. 37–67) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.

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The synthesis of new donors and sources of valuable traits in spring bread wheat: resistance to leaf and stem rusts and grain productivity. The study of the Puccinia triticina population structure.

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

Using artificial infection with leaf and stem rust pathogens in the greenhouse and strong natural stem rust epidemics in the experimental field, we evaluated resistance to these diseases in original, spring bread wheat, near-isogenic lines with alien translocations and their combinations and in a set of introgression lines with genes from various relatives of bread wheat. Genes *Lr9*, *Lr24*, *Lr28*, *Lr29*, *Lr41*, *Lr51*, and *Lr57* and unidentified *LrSatu* and *LrSp*; transfers from durum wheat cultivars Saratovskaya 57 and Zolotaya Volna; *T. kiharae* (6X, artificial amphidiploid of *T. timopheevii* x *Ae. tauschii*); *T. turgidum* subsp. *dicoccoides*; and *T. timopheevii* subsp. *timopheevii*.

Six combinations of *Sr* genes were highly resistant to *P. graminis*, including the genes *Sr11, Sr13, Sr17, Sr22, Sr25, Sr28, Sr31, Sr38,* and *Sr57*. Basically, the combinations are built on *Sr25* with one or two of these genes. Effective combinations of *Sr* genes (mainly *Sr25*) with unidentified *Sr* genes from the durum wheat cultivars Saratovskaya Zolotaya, NICK, and Zolotaya Volna, and from *T. kiharae*, *T. persicum*, *T. timopheevii*, *T. turgidum* subsp. *dicoccum* (k13659 and k10456) were obtained.

The structure of the leaf rust pathogen population for 2017–19 was studied and analyzed. Isolated, monopustule clones of *P. triticina* were avirulent to the Thatcher lines with genes *Lr9, Lr19, Lr41, Lr42, Lr43+24,* and *Lr53* and virulent to *Lr1, Lr2a, Lr2b, Lr2c, Lr3, Lr3bg, Lr3ka, Lr10, Lr11, Lr12, Lr13, Lr14a, Lr14b, Lr15, Lr16, Lr17, Lr18, Lr21, Lr22a, Lr22b, Lr25, Lr28, Lr 30, Lr32, Lr33, Lr34, Lr35, Lr36, Lr37, Lr38, Lr40, Lr44, Lr45, Lr B, Lr W, Lr Erph, Lr Kanred, Lr57,* and *Lr67*. Significant variation for virulence to genes *Lr20, Lr23, Lr24, Lr26, Lr29*, and *Lr47* was observed. The population structure of *P. triticina* in 2017–19 revealed a partial loss of efficiency of gene *Lr47*.

In the 2020 growing conditions in the set near-isogenic lines, a statistically insignificant increase in grain productivity was obtained for translocation combinations T7DS–7DL-7Ae#1L + T1BL–1R#1S (*Lr19*/*Sr25*+*Lr26*/*Sr31* genes) and T7DS–7DL–7Ae#1L + T2AL·2AS–2MV#1 (*Lr19*/*Sr25* + *Lr37*/*Sr38*/*Yr17* genes). A positive effect on grain productivity was observed in the following introgression lines: 'Favorit/*T. persicum**2//Favorit (substitution 6D(6Agi) + *T. persicum* genetic material)' at 3,190 kg/ha, 'L505/Taro 1//L505/3/L505 (T7DS–7DL–7Ae#1L + genetic material of durum wheat cultivar Taro 1) at 3,324 kg/ha, and 'Voevoda/*T. petropavlovsky* (6D (6Agi) substitution + genetic material of *T. petropavlovsky*) at 3,152 kg/ha, compared with that of Favorite, the standard cultivar, at 2,749 kg/ha.

Among the set of spring bread wheat lines obtained from crossing CIMMYT synthetics with Saratov-bred cultivars, the following lines showed a significant increased in grain productivity compared with Favorite (2,781 kg/ha): L369 (pedigree: Dob/3/Croc/*Ae. tauschii* (205)//Weaver/4/Dob) at 3,191 kg/ha, L373 (pedigree: L505/3/Croc/*Ae. tauschii* (205)//Weaver/4/L505/5/C68) at 3,203 kg/ha, L375 (pedigree: L505/3/Croc/*Ae. tauschii* (205)//Weaver/4/L505/5/L505) at 3,277 kg/ha, and L380 (pedigree: Dob/3/Altar84/*Ae. tauschii* (224)//Pgo*2/4/Dob/5/Cel20) at 3,330 kg/ha. L373 and L375 are resistant to leaf, stem, and stripe rusts. DNA marker analysis in L373 showed the presence of *Lr19*/*Sr25*+*Lr26*/*Sr31* combinations, which are translocations T7DS–7DL–7Ae#1L + T1BL–1R#1S, and L375 showed the presence of combinations *Lr19*/*Sr25*+*Lr26*/*Sr31*+*Lr41*, (translocations T7DS–7DL–7Ae#1L + T1BL–1R#1S + 2DS–*Ae. tauschii*-2DL).

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Subhashree Subramanyam, Jill A. Nemacheck, Victor Bernal-Crespo, and Nagesh Sardesai.

Insect-derived extra-oral GH32 plays a role in susceptibility of wheat to Hessian fly.

Phytophagous insects produce an array of plant cell wall degrading enzymes (PCWDEs) that target cell wall components and have major effects on wall architecture. In insects, PCWDEs primarily include enzyme families such as glycoside hydrolases, polysaccharide lyases, and carbohydrate esterases. Glycoside hydrolases (GHs) constitute one of the largest families (GH1-GH167) of PCWDEs, as catalogued in the CAZy database (http://www.cazy.org).

The Hessian fly (*Mayetiola destructor* [Say]), a dipteran gall midge (family: Cecidomyiidae), is an obligate pest on host wheat causing significant monetary losses. This gene-for-gene, plant-insect interaction triggers either a resistant (incompatible interaction) or susceptible (compatible interaction) reaction in the plant. During incompatible interactions, the larvae die within 4–5 days after feeding on resistant plant. In contrast, during compatible interactions, within 3 days after feeding on susceptible plants, the larvae alter host metabolic pathways upregulating susceptibility-associated genes resulting in the formation of a sugar and protein-rich nutritive tissue that provides the larvae a steady source of readily available nutrients. Therefore, the efficient utilization of wheat host nutrients, following induced susceptibility, is key to successful development of Hessian fly larvae.

Here, we report increased expression of *MdesGH32*, a gene belonging to the GH32 family in virulent Hessian fly larvae feeding on susceptible wheat. *MdesGH32* in the Hessian fly is acquired via horizontal gene transfer. The localization of the Hessian fly-derived MdesGH32 protein within the feeding sites of the susceptible host, indicates extra-oral secretion (Fig. 1). The MdesGH32 protein shows levanase/inulinase/sucrase activities that aid in the breakdown of the plant cell wall inulin polymer into monomers and converting sucrose, the primary transport sugar in plants, to glucose and fructose, resulting in the formation of a nutrient-rich tissue benefitting the developing virulent larvae. Further studies also indicated the presence of a glucose transporter system within the Hessian fly larvae that may be responsible for transporting the plant and larval-derived glucose from the lumen of the larvae into the hemocoel. Our findings elucidate the molecular mechanism of nutrient sink formation and establishment of susceptibility (Fig. 2, p. 71) leading to further downstream applications for efficient management and control of this and other devastating insect pests of economically important cereal crops.

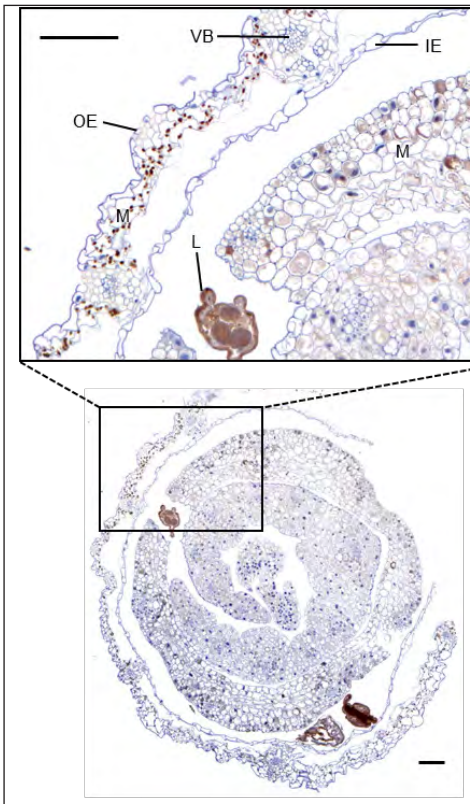

Fig. 1. Immunohistochemical localization of MdesGH32 in wheat tissues. Biotype L-infested Newton crown tissue collected 7 DAH showing MdesGH32 localized (brown spots) throughout the mesophyll cells (M) between the outer epidermis (OE) and inner epidermis (IE) of the leaf sheath (inset) being fed on by larvae (L). VB–vasular bundle; scale bar = 100 μm.

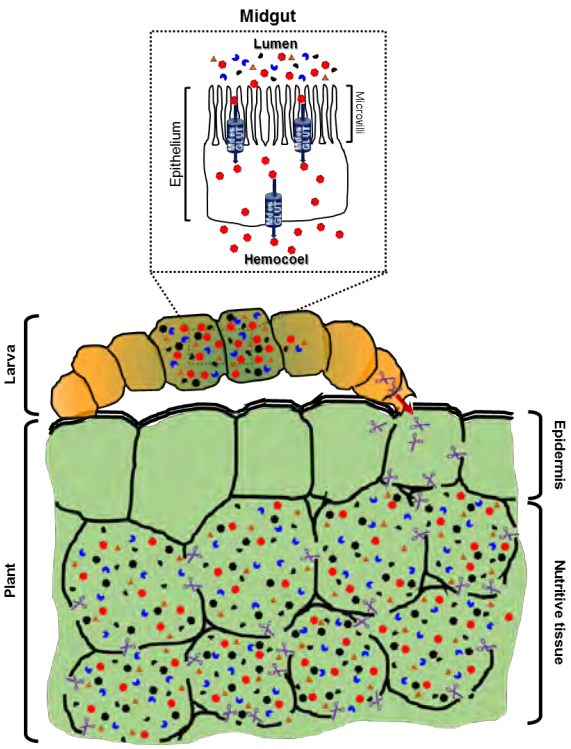

Fig. 2. Model highlighting the role of MdesGH32 in the wheat–Hessian fly interaction. Virulent larva initiates feeding on the leaf sheath and secrets (red arrow) MdesGH32 (purple scissors) extra-orally into the plant tissue. MdesGH32 contributes towards the formation of a nutritive tissue by thinning and lysis of the epidermal and mesophyll cell walls by the inulinase activity against the plant cell wall inulin fructose polymers. Invertase activity of MdesGH32 converts sucrose, the main transport sugar, into glucose (red-filled hexagons) and fructose monomers that get phosphorylated (black-filled hexagons). Rupture of the cell walls along with down-regulation of cell wall-associated genes increases permeability of the leaf tissue and creates a nutritive tissue rich in hexose sugar monomers, free amino acids (blue-filled semicircles), polyamines (black-filled semicircles), and miscellaneous solutes (orange-filled triangles) that diffuse to the leaf surface where they are sucked up by the larva. Within the larval midgut (inset), the glucose transporter MdesGLUT (blue-filled cylinder) actively transports plant- and insect-derived glucose from the lumen across the microvilli of the epithelial layer into the hemocoel.

Publication.

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Microplastics from agriculture.

M.B. Kirkham.

Since the middle of the 1950s, plastics have been widely used in agriculture, and they have allowed farmers to increase crop production. To face the food needs of the growing population, it is predicted that consumption of plastics will increase by 50% (9.5 x 10^6 metric tons) by 2030. By then, waste from agricultural plastics will increase as well, up to 17 x 10^6 metric tons. The polymers used in agricultural plastics are nondegradable by microorganisms, and the plastics break down into microplastics (particles less than 5 mm in size) that contaminate the environment.

Plastics are used in many ways in agriculture, including by wheat producers. For example, plastic bags hold fertilizer and seed. Farmers who irrigate use plastic irrigation equipment. Few studies have been done to determine the

effects of microplastics on soil organisms and plants. Nothing is known about the uptake of microplastics by food crops and their potential hazard to human health.

The disposal of agricultural plastics presents a huge problem. Incineration is no longer an option in many places, because burning has been banned due to the production of carcinogenic dioxins and other air pollutants. Recycling is not often done by farmers, because it is difficult to recycle plastics with debris on them, there are few recycling centers, and the cost of transportation to recycling centers is great. Agricultural plastics are put in landfills, resulting in the potential for microplastics to contaminate the groundwater. The ability of photodegradable and biodegradable plastics to degrade into carbon dioxide and water has been questioned.

Because plastics remain in the environment for hundreds of years, alternatives to agricultural plastics are needed. Methods used before plastics were developed should be considered. Earthen tiles might be used instead of plastic tubing for irrigation. Gunny sacks might be used instead of plastic bags. Before hemp was made illegal in the USA in 1937, textiles used to be made out of hemp. However, the 2018 Farm Bill legalized production of hemp, and it might be grown to produce gunny sacks. Measures to counter microplastic pollution need to be enacted immediately to benefit the environment and future generations.

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New sources of resistance to Fusarium head blight and DON in wheat.

Bernd Friebe.

Our objective was to introgress *Fhb6*, derived from *Elymus tsukushiensis* in the form of a T1AL·1AS-1E^{ts}#1S into the adapted winter wheat cultivars Everest, Lyman, and Overland with native resistance to Fusarium head blight (FHB). Unfortunately, during the backcrossing we lost *Fhb6* in Everest background and only recovered introgressions in Overland and Lyman backgrounds. All lines are BC_1F_6 and were confirmed to be homozygous for *Fhb6* by both molecular marker (BE426771/RsaI and AK357509/HaeIII) and genomic *in situ* hybridization analyses. the FHB evaluations were performed in our Rocky Ford scab nursery. The *Fhb6* introgressions in Overland background are looking excellent in both FHB incidence and DON accumulation (Table 1, Fig. 1, p. 74), whereas the Lyman introgression line little improved compared to pure Lyman.

Table 1. *Fhb6* introgressions into Overland and Lyman (NT = not tested).

Line	FHB incidence		Heading		Height	1,000-kernel weight	DON	
	2019	2020	2019	2020	2020 (cm)	2020 (g)	2019	2020
Everest	80	100	5/29	5/12	81	—	NT	34.8
Lyman	80	80	5/30	5/20	101	23.4	9.5	12.7
Overland	80	80	5/30	5/21	91	19.6	24.5	22.7
Lyman/*Fhb*	60	80	5/26	5/17	114	23.9	20.9	11.7
Overland/*Fhb6*	40	50	5/31	5/21	104	26.3	12.5	NT
Overland/*Fhb6*	40	60	5/31	5/18	108	24.8	14.8	NT
Overland/*Fhb6*	40	60	5/31	5/21	98	24.1	4.7	NT
Overland/*Fhb6*	50	60	5/29	5/16	114	28.3	14.1	10.2
Overland/*Fhb6*	30	70	5/29	5/19	109	26.3	16.8	12.6

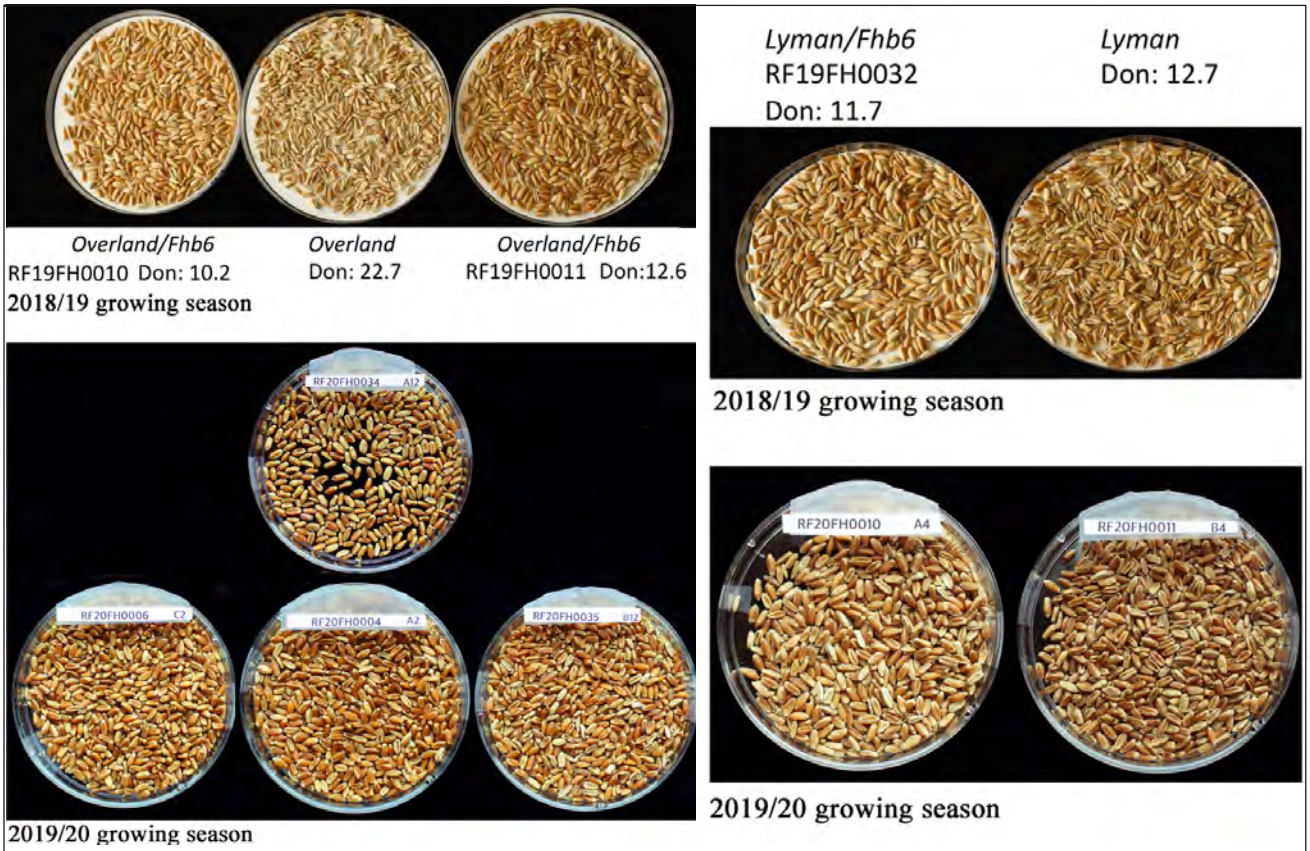

Fig. 1. *Fhb6* introgressions into Overland and Lyman.

Phenotypic evaluation of stripe rust, leaf rust, and stem rust resistance in the A-genome, diploid relatives of wheat.

Buket Sahin, Duane Wilson, Bernd Friebe, and Jesse Poland; and Robert Bowden (USDA–ARS, Manhattan, KS).

Global food security relies on increasing production of two main grain crops – rice and wheat. Among these, wheat has greater significance in terms of tonnage. The various rust diseases that attack this crop – leaf rust (*Puccinia triticina*), stripe rust (*P. striiformis* Westend. f. sp. *tritici*) and stem rust (*P. graminis* Pers. f. sp. *tritici*) are important limitations for increasing wheat production in the world. In order to stay ahead of constantly evolving rust pathogens, increasing genetic diversity by identifying genetic resistance from sources besides common wheat is necessary. Wild relatives of wheat are tractable sources of wheat rust resistance genes. A mini-core collection of diploid A-genome species covering about 90% of the genetic variation of these species, including 59 accessions of *Triticum monococcum* subsp. *aegilopoides*, 24 accessions of *T. monococcum* subsp. *monococcum*, and 26 accessions of *T. urartu*, spanning their whole area of geographic distribution, was established using genotype-by-sequencing. These accessions are being evaluated for their seedling resistance to leaf, stripe, and stem rust under greenhouse conditions and also for adult-plant resistance under both greenhouse and field conditions. This information will be crucial for directed gene transfer from these accessions into advanced wheat breeding lines.

Development and application of genome-specific SNP markers for tracing alien introgressions in the polyploid wheat genome.

Tatiana Danilova, Wei Zhang, Mingyi Zhang, Xianwen Zhu, Jason D. Fiedler, and Xiwen Cai (Department of Plant Science, North Dakota State University, Fargo); and Jesse Poland and Bernd Friebe.

New traits can be introduced into crops through interspecific hybridization. This approach has been successfully applied for wheat improvement. Detection of wheat–alien introgressions requires screening large populations and is time and labor consuming. With next-generation sequence resources available for wheat and related species, single nucleotide polymorphism (SNP) markers provide an effective tool for detecting alien introgressions. The allopolyploidy of the wheat genome (2n=6x=42, AABBDD) makes introgressions and chromosome manipulations possible, but complicates the development of genome-specific, co-dominant molecular markers. We found that the four genome-specific allelic SNPs needed for developing molecular markers are rare, whereas closely located two genome-specific SNPs are more common. These 'shifted' SNPs do not need much sequence data to discover and can be used for developing genotyping assays. Chromosomal locations of sequences containing SNPs are important for tracing recombination events by molecular markers. The wheat cDNA cytogenetic map is a useful resource for developing molecular markers with known positions. Mapped cDNAs cover all chromosomes of the three wheat subgenomes, and orthologous sequences can be found in sequenced genomes of related species. PCR Allelic Competitive Extension genotyping assays with co-dominant shifted SNP markers were developed using mapped sequences and applied to trace barley, *Aegilops speltoides*, *Thinopyrum elongatum*, and *Th. intermedium* introgressions in hexaploid wheat background. This approach improved the throughput and accuracy in detecting homoeologous recombinants and tracing alien introgressions in wheat.

Fishing eccDNA elements that defy chromosome control of mitosis and meiosis and drive rapid adaptive evolution.

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

Mitosis ensures accurate copying of identical genomic material to daughter soma cells during the growth of an organism. In germ cells, meiosis requires pre-alignment of homologous chromosomes. Any aberrant chromosome(s) that may have arisen during numerous mitotic divisions, will misalign and not be passed on to the progeny. Thus, the processes of mitosis and meiosis have evolved to ensure organismal genomic integrity. While this has evolutionary advantages, it is also a liability in cases where an organism is faced with adverse stress or a xenobiotic agent such as a drug or an herbicide? Apparently, organisms have renegade genetic elements in the form of extrachromosomal circular (ecc) DNAs that are ubiquitous and can defy controls of mitosis and meiosis. The eccDNAs may arise as structural mutations (via intrachromosomal recombination as an example) during cell division leading to soma cell heterogeneity. In response to the xenobiotic agent (e.g. herbicide), rare soma cells with eccDNAs harboring target gene, can increase in copy number, fight the stress, and acquired resistance is passed on to the progeny for rapid adaptive evolution. We will describe the FISHing and visualization of eccDNA molecules, show how they defy the controls of mitosis and meiosis and lead to acquired herbicide resistance in Amaranthus palmeri (Koo et al. PNAS 115:332-337).

Prediction of wheat–rye 1RS translocations (T1AL·1RS and T1BL·1RS) and the impact on wheat breeding.

, and Jesse Poland; and M. Timothy Rabanus-Wallace, Martin Mascher, and Nils Stein (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany).

The whole arm (Robertsonian) translocations of rye 1RS to wheat chromosomes 1A and 1B are known to possess various biotic and abiotic resistance traits, yet with reduced bread making quality particularly for the translocation on wheat 1B. The availability of a rye reference genome enabled us to examine the group 1 wheat-rye translocations in detail. We first delineated the wheat-rye T1BL·$1RS_{Kavkaz}$ and T1AL·$1RS_{Amigo}$ translocation segment to be approximately 269Mb, directly at the projected centromere positions, confirming whole-chromosome arm translocations. From this we developed a bioinformatics pipeline to predict the presence or absence of the wheat-rye translocations based on GBS or exome sequenc-

ing data for various wheat panels globally. We detected T1BL·1RS in varying frequencies (6.5–31%) for central US winter wheat panels (>4,000 lines), European WHEALBI panel (>500 lines) and CIMMYT spring wheat breeding panel (>900 lines). In contrast, T1AL·1RS translocation is only detected at 4–10% in central US materials but not in European or CIMMYT panels. We called SNPs and calculated the identity by state percentages among various 1RS lines. Our results suggest that the two 1R translocations found in thousands of breeding lines lines in different panels globally likely share a single common origin designed at $1RS_{Kavkaz}$ and $1RS_{Amigo}$. We found positive correlations for 1RS and grain yield for central US winter wheat materials. Importantly, we identified a novel 1R recombination line between T1BL·$1RS_{Kavkaz}$ and T1AL·$1RS_{Amigo}$ that shows high yield and is not associated with very poor bread making quality. The 1RS prediction pipeline developed will enable breeding programs to monitor the presence of rye translocations. Our work also demonstrates the potential of targeted breeding of 1RS and other rye translocations to advance wheat breeding for productivity, resilience, and good quality.

Genome-wide association mapping of glume color in A-genome wheat species.

Laxman Adikari, Shuangye Wu, John Raupp, and Jesse Poland; and Simon Krattinger and Michael Abrouk (King Abdullah University of Science and Technology, Saudi Arabia).

Glume color in the A-genome progenitor species of wheat can be an important trait to classify the species and differentiate accessions for core collections. Glume color also might be an important trait influencing grain properties. However, the genetic basis of glume coloration in these species is not illustrated yet. We performed an association analysis of glume coloration in three A-genome species, *T. urartu* and *T. monococcum* subsps. *monococcum* and *aegilopoides*, using genotyping-by-sequencing (GBS) SNP to understand the genetic architecture of the trait in these different species. Nine 96-plexed GBS libraries with *PstI-MspI* were constructed for 848 A-genome accessions, including 172 *T. urartu*, 117 subsp. *monococcum*, and 559 subsp. *aegilopoides*. The raw sequence data (pair-end 150 bp) were processed using the TASSEL5 GBSv2 pipeline, where reads were aligned to a *T. urartu* reference (tu2.0). The filtered SNPs and binary coded (0 = white, 1=color) phenotype were tested for genome-wide association within each species using GAPIT, and the result was verified using an rrBLUP mixed model. The top genome-wide association hit for all three species was observed on the short arm of chromosome 1 at ~5 Mb. When a functional query sequence of a wheat MYB aligned to the tu2.0 using BLAST, the best hit also was observed at ~5 Mb of chromosome 1. These results indicate that the wheat MYB ortholog on chromosome 1 could be a potential candidate gene for glume coloration in the A-genome species.

Evaluation of Two Cycles of Genomic Selection in an Intermediate Wheatgrass Breeding Program.

Jared Crain and Jesse Poland, and Lee DeHaan (The Land Institute, Salina, KS).

Perennial grains could provide a host of ecosystem and environmental services, yet large-scale adoption of perennial grains require having economically viable crop yields. Intermediate wheatgrass (*Th. intermedium*) has been undergoing domestication as a perennial grain crop since the mid 1980s. While phenotypic breeding has produced large breeding gains, over 10% genetic gain per cycle, it is estimated that another 20 and 110 years of equal breeding gains will be required to reach the grain yield and seed size of annual wheat, respectively. Beginning in 2017, genomic selection (GS) has been used in The Land Institute's breeding program to overcome the long-estimated times to achieve a comparable product as annual wheat. Each year over 4,500 genotypes have been profiled using genotyping-by-sequencing, with GS used to predict genotype performance. The 100 best genotypes have been moved immediately to the crossing block for intermating allowing one cycle to be completed per year. An additional 1,000 genotypes are planted in the field as the GS training population. Correlation between the seedling predicted genotype performance and the observed field observations have ranged from 0.14 to 0.73. The realized selection differential has ranged from 10–23% superior for the selected parents compared to the random training population. Utilizing the GS pipeline has resulted in reducing cycle time by half which should theoretical double the rate of genetic gains. Our current results indicate that greater than 10% genetic gain per year can be achieved for selected traits using GS, speeding the development of perennial grains.

OneKK: A high throughput seed phenotyping Android application.

Trevor Rife, Megan Calvert, Chaney Courtney, Mitchell Neilsen, and Jesse Poland.

Seed size and morphology has an important effect on the end uses of crops. Rapidly measuring morphological phenotypes and utilizing this information for indirect selection within breeding programs could lead to increased yields and improved end use quality. High-throughput approaches are useful for many crops since they can provide rapid and accurate measurements, but commercial solutions are expensive and outside the budgets of most plant breeding programs. OneKK, a new app that runs on Android smartphones and tablets, makes rapid seed phenotyping accessible, portable, and cost effective. OneKK uses an established algorithm to calculate length and width and a novel watershed algorithmic approach to estimate the number of seeds within the image – even when seeds are immediately adjacent. To validate the accuracy of OneKK, seeds from common crops were manually measured for length and width. The same samples were processed using OneKK to measure the average length, average width, and sample count. A high correlation between both morphological measurements and seed counts was observed, and measurements from OneKK were collected considerably faster. To validate the utility of OneKK for genomic research, the Synthetic/Opata doubled haploid wheat population was utilized for QTL mapping. Seed measurements taken with OneKK were successfully used to map a QTL for seed length and width. OneKK is a free and flexible app that will provide all plant breeding and genetics research programs with the data necessary to perform both phenotypic selection and genomic analysis.

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Wheat leaf rust in the United States in 2020.

Occurrence. In 2020, leaf rust caused by *Puccinia triticina* was widespread at low to moderate levels of infection throughout the soft red winter wheat area of the southeastern states, the Ohio Valley, and the hard red winter wheat and hard red spring wheat areas of the Great Plains. Throughout most of the wheat-growing regions, temperatures were much above average in March (NOAA). In April, temperatures were near average in the southern plains and southeastern region and cooler in the northern Great Plains and the Ohio Valley. Temperatures in March and April allowed infections of *P. triticina* to increase and spread across the winter wheat regions. In June, temperatures were higher than normal in the Great Plains, southeastern states, and the Ohio Valley, followed by average temperatures in July. The above-average temperatures contributed to the spread of *P. triticina* across the spring wheat region of the northern Great Plains.

Leaf rust was observed in mid-March in southern Texas and bacame prevalent in the first week of April. Leaf rust was common across Oklahoma by early May and was at moderate levels in Kansas in May. Leaf rust was observed in winter wheat plots in Nebraska and South Dakota in early June and in North Dakota in late June. In late July, leaf rust was widespread on susceptible spring wheat plots in Minnesota and North Dakota, and at lowere levels in plots of the regional cultivars. Leaf rust also was reported at various levels in Louisiana, Kentucky, Virginia, Wisconsin, and Washington in 2020.

In Oklahoma, losses due to leaf rust were estimated to be 5%, with losses of 2% in Texas and 2.8% in Kansas. Losses in the other states were estimated at 1% or less. Overall, estimated losses in wheat in the U.S. due to leaf rust in 2020 were 15 x 10^6 bushels.

Races and virulence to *P. triticina*. In 2020, 36 races of *P. triticina* were identified in collections of leaf rust-infected leaves that were sent to the USDA–ARS Cereal Disease Laboratory. A total of 260 isolates was processed for race identification. Travel restrictions due to COVID19 reduced the number of collections received in 2020. Race TBBGS was the most common race overall at 23.5% and was found almost entirely in the spring wheat region of Minnesota and North Dakota. TBBGS is virulent to *Lr21*, which is in some of the spring wheat cultivars in the region and, in addition, has virulence to *Lr39*, which is in many hard red winter wheat cultivars.

Race MNPSD was the second most common race at 20.8% of all isolates. MNPSD was found in the soft red winter regions of the southeastern states, the Ohio Valley, and the winter and spring wheat region of the Great Plains. MNPSD and the closely related race MPPSD, at 7.3% of all isolates, are virulent to the hard red winter wheat SY Monument, which is widely grown in Kansas and Nebraska. In addition, MNPSD and MPPSD are virulent to genes *Lr24*, *Lr37*, and *Lr39*, that are in many of the hard red winter wheat cultivars. In the southeastern states, MBTNB is virulent to *Lr11*, which is in many soft red winter wheat cultivars, and MCTNB is virulent to *Lr11* and *Lr26*.

In the Rio Grande Valley of Texas, a large number of isolates were the durum leaf rust type race BBBQD, which is avirulent to most leaf rust resistance genes in common wheat, but highly virulent to durum wheat cultivars. These collections came from sentinel winter wheat plots for detection of virulent stem rust races. The durum-type races are virulent to *Lr39* that is present in TAM111, TAM112, TAM114, Winterhawk, and other commonly grown hard red winter wheat cultivars. The durum-type races could potentially spread and infect some of the winter wheat cultivars, in addition

to any winter durum crops.

Virulence to *Lr24* and *Lr39* are highest in the southern to mid Great Plains regions. Virulence to *Lr11* and *Lr26* are highest in the southeastern states and Ohio Valley region. Virulence to *Lr18* was detected at low frequencies in all regions. Virulence to *Lr2a* and *Lr21* was highest in Minnesota, South Dakota, and North Dakota.

The complete race frequency and virulence frequency to individual *Lr* genes are give in Tables 1 and 2 (p. 80),

Table 1. Number and frequency (%) of the predominant virulence phenotypes of *Puccinia triticina* in the United States in 2020 identified by virulence to 20 lines of Thatcher wheat with single genes for leaf rust resistance.

Race	Virulence combination (ineffective *Lr* genes)	Southeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBQD	*B,10,39*	0	0.0	0	0.0	25	54.3	0	0.0	0	0.0	0	0.0	25	9.6
LBDSG	*1,17,B,10,14a,28*	1	3.0	0	0.0	0	0.0	0	0.0	0	0.0	3	50.0	4	1.5
LCDJG	*1,26,17,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	16.7	1	0.4
LCDSG	*1,26,17,B,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	16.7	1	0.4
MBDSD	*1,3,17,B,10,14a,39*	0	0.0	0	0.0	1	2.2	2	9.5	8	5.7	0	0.0	11	4.2
MBTNB	*1,3,3ka,11,17,30,B,14a*	8	24.2	4	28.6	0	0.0	0	0.0	0	0.0	0	0.0	12	4.6
MCDSB	*1,3,26,17,B,10,14a*	2	6.1	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.8
MCDSD	*1,3,26,17,B,10,14a,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	0.7	0	0.0	1	0.4
MCJSB	*1,3,26,11,17,B,10,14a*	1	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
MCTNB	*1,3,26,3ka,11,17,30,B,14a*	8	24.2	0	0.0	1	2.2	1	4.8	0	0.0	0	0.0	10	3.8
MLPSD	*1,3,9,3ka,17,30,B,10,14a,39*	0	0.0	0	0.0	1	2.2	0	0.0	0	0.0	0	0.0	1	0.4
MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	3	9.1	1	7.1	12	26.1	13	61.9	25	17.9	0	0.0	54	20.8
MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	0	0.0	1	7.1	3	6.5	3	14.3	12	8.6	0	0.0	19	7.3
MPTSD	*1,3,9,24,26,3ka,11,17,30,B,10,14a,39*	0	0.0	1	7.1	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
MSBJG	*1,3,9,16,24,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	1	0.7	0	0.0	1	0.4
TBBGS	*1,2a,2c,3,10,21,28,39*	0	0.0	0	0.0	2	4.3	0	0.0	59	42.1	0	0.0	61	23.5
TBBJS	*1,2a,2c,3,10,14a,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	0.7	0	0.0	1	0.4
TBRKG	*1,2a,2c,3,3ka,11,30,10,14a,18,28*	0	0.0	0	0.0	1	2.2	0	0.0	4	2.9	0	0.0	5	1.9
TBTDB	*1,2a,2c,3,3ka,11,17,30,14a*	0	0.0	1	7.1	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TBTNB	*1,2a,2c,3,3ka,11,17,30,B,14a*	3	9.1	3	21.4	0	0.0	0	0.0	0	0.0	0	0.0	6	2.3
TCBGS	*1,2a,2c,3,26,10,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	2	1.4	0	0.0	2	0.8
TCGJG	*1,2a,2c,3,26,11,10,14a,28*	1	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TCJTB	*1,2a,2c,3,26,11,17,B,10,14a,18*	2	6.1	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.8
TCSQB	*1,2a,2c,3,26,3ka,11,17,B,10*	1	3.0	0	0.0	0	0.0	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	0	0.0	0	0.0	0	0.0	0	0.0	1	16.7	1	0.4
TCTNB	*1,2a,2c,3,26,3ka,11,17,30,B,14a*	1	3.0	2	14.3	0	0.0	0	0.0	0	0.0	0	0.0	3	1.2
TCTQB	*1,2a,2c,3,26,3ka,11,17,30,B,10*	1	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TDBGS	*1,2a,2c,3,24,10,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	0.7	0	0.0	1	0.4
TFPSB	*1,2a,2c,3,24,26,3ka,17,30,B,10,14a*	0	0.0	1	7.1	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TFTSB	*1,2a,2c,3,24,26,3ka,11,17,30,B,10,14a*	1	3.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TGBGS	*1,2a,2c,3,16,10,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	0.7	0	0.0	1	0.4
TNBGJ	*1,2a,2c,3,9,24,10,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	5	3.6	0	0.0	5	1.9
TNBGS	*1,2a,2c,3,9,24,10,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	7	5.0	0	0.0	7	2.7
TNBJJ	*1,2a,2c,3,9,24,10,14a,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	5	3.6	0	0.0	5	1.9

respectively. Information on the individual collections, location, date, cultivar collected from, and race designations of the derived isolates are given.

The postulated leaf rust resistance genes in the ten most common hard red winter wheat cultivars in Texas, Oklahoma, and Kansas in 2020 are listed in Table 3 (p. 80). The postulated *Lr* genes in the ten most common hard red spring wheat cultivars in Minnesota and North Dakota in 2019 are listed in Table 4 (p. 80). When possible, an *Lr* gene was postulated.

Table 2. Frequency (%) of isolates of *Puccinia triticina* collected in 2020 in the United States with virulence to Thatcher lines of wheat with single genes for leaf rust resistance.

	Southeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		Washington		Total	
Resistance gene	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	33	100.0	14	100.0	21	45.7	21	100.0	140	100.0	6	100.0	235	90.4
Lr2a	10	30.0	7	50.0	3	6.5	2	9.5	93	66.4	1	16.7	116	44.6
Lr2c	10	30.3	7	50.0	3	6.5	2	9.5	93	66.4	1	16.7	116	44.6
Lr3	32	97.0	14	100.0	21	45.7	21	100.0	140	100.0	1	16.7	229	88.1
Lr9	3	9.1	3	21.4	16	34.8	18	85.7	63	45.0	0	0.0	103	39.6
Lr16	0	0.0	0	0.0	0	0.0	0	0.0	2	1.4	0	0.0	2	0.8
Lr24	4	12.1	4	28.6	15	32.6	18	85.7	64	45.7	0	0.0	105	40.4
Lr26	18	54.5	5	35.7	4	8.7	5	23.8	15	10.7	3	50.0	50	19.2
Lr3ka	26	78.8	14	100.0	18	39.1	17	81.0	41	29.3	1	16.7	117	45.0
Lr11	27	81.8	11	78.6	2	4.3	1	4.8	4	2.9	1	16.7	47	18.1
Lr17	32	97.0	14	100.0	18	39.1	19	90.5	46	32.9	6	100.0	135	51.9
Lr30	25	75.8	14	100.0	18	39.1	17	81.0	41	29.3	1	16.7	116	44.6
LrB	32	97.0	13	92.9	43	93.5	19	90.5	46	32.9	4	66.7	157	60.4
Lr10	13	39.4	4	28.6	45	97.8	20	95.2	140	100.0	5	83.3	227	87.3
Lr14a	31	93.9	14	100.0	19	41.3	20	95.2	65	46.4	5	83.3	154	59.2
Lr18	2	6.1	0	0.0	1	2.2	0	0.0	4	2.9	0	0.0	7	2.7
Lr21	0	0.0	0	0.0	2	4.3	1	4.8	79	56.4	0	0.0	82	31.5
Lr28	2	6.1	0	0.0	3	6.5	2	9.5	94	67.1	5	83.3	106	40.8
Lr39	3	9.1	3	21.4	44	95.7	20	95.2	135	96.4	0	0.0	205	78.8
Lr42	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 2020 (+ indicates that the cultivar was resistant to all isolates tested).

Texas	Oklahoma	Kansas	Nebraska
TAM 114–*Lr18*	Gallagher–*Lr26*	SY Monument	SY Monument
Gallagher–*Lr26*	Smith's Gold–*Lr34 Lr37 Lr77*	Zenda–*Lr37*	Husker Genetics: Ruth–*Lr37*
TAM 112–*Lr39*	Doublestop CL Plus–no *Lr* gene	WB Grainfield–*Lr39*	Husker Genetics: Settler CL–*Lr11*
TAM 111–*Lr37 Lr39*	Bentley–*Lr21 Lr39*	Winterhawk–*Lr39*	Brawl CL Plus–*Lr3, Lr14a*
TAM 204 +	SY Monument	Everest–*Lr1 Lr14a*	LCS Link
SY Monument	WB 4515	T158–*Lr37 Lr39*	Husker Genetics: Robidoux–no *Lr* gene
WB Cedar–*Lr10 Lr14 Lr37*	Endurance–*Lr1 Lr26*	LCS Mint	AP503 CL
Winterhawk–*Lr39*	Iba–*Lr34 Lr37*	TAM 114–*Lr18*	Husker Genetics: Freeman–no *Lr* gene
TAM 105	LCS Chrome–*Lr37 Lr39*	TAM 111–*Lr37 Lr39*	Pronghorn
TAM 304–*Lr16 Lr24*	WinterHawk–*Lr39*	Doublestop CL Plus–no *Lr* gene	Langin– no *Lr* gene

Table 4. Hard red spring wheat cultivars grown in 2020 (+ indicates that the cultivar was resistant to all isolates tested).

Minnesota		North Dakota	
SY Ingmar +	Faller–*Lr21*	Linkert +	MN–Washburn +
SY Valda +	Bolles +	SY Valda +	WB Mayville
WB9590	WB9479–*Lr21*	WB9590	SY Ingmar +
SY Soren +	Shelly–*Lr21*	WB9479–*Lr21*	Bolles +
Glenn–*Lr21*		Shelly–*Lr21*	

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5019.1	20VA5019 - 1	TCGJG	*1,2a,2c,3,26,11,10,14a,28*	VA	Richmond	Carl Griffey	MI16W0102 & MI17W0121	1
5019.2	20VA5019 - 2	TCGJG	*1,2a,2c,3,26,11,10,14a,28*	VA	Richmond	Carl Griffey	MI16W0102 & MI17W0121	1
5019.3	20VA5019 - 3	TBTNB	*1,2a,2c,3,,3ka,11,17,30,B,14a*	VA	Richmond	Carl Griffey	MI16W0102 & MI17W0121	1
5020.1	20VA5020 - 1	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Richmond	Carl Griffey	VA16W-5-LR-Check	1
5020.1	20VA5020 - 1	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Richmond	Carl Griffey	VA16W-5-LR-Check	1
5020.2	20VA5020 - 2	TBTNB	*1,2a,2c,3,,3ka,11,17,30,B,14a*	VA	Richmond	Carl Griffey	VA16W-5-LR-Check	1
5020.3	20VA5020 - 3	MCJSB	*1,3,26,11,17,B,10,14a*	VA	Richmond	Carl Griffey	VA16W-5-LR-Check	1
5021.1	20VA5021 - 1	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Richmond	Carl Griffey	OH14-112-34	1
5021.2	20VA5021 - 2	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Richmond	Carl Griffey	OH14-112-34	1
5021.3	20VA5021 - 3	TFTSB	*1,2a,2c,3,24,26,3ka,11,17,30,B, 10,14a*	VA	Richmond	Carl Griffey	OH14-112-34	1
5022.2	20VA5022 - 2	TBTNB	*1,2a,2c,3,,3ka,11,17,30,B,14a*	VA	Nottoway	Carl Griffey	Massey	1
5023.1	20VA5023 - 1	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Nottoway	Carl Griffey	Sus Border Mix	1
5023.2	20VA5023 - 2	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Nottoway	Carl Griffey	Sus Border Mix	1
5023.3	20VA5023 - 3	MCDSB	*1,3,26,17,B,10,14a*	VA	Nottoway	Carl Griffey	Sus Border Mix	1
5023.3	20VA5023 - 3	MCDSB	*1,3,26,17,B,10,14a*	VA	Nottoway	Carl Griffey	Sus Border Mix	1
5024.2	20VA5024 - 2	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Nottoway	Carl Griffey	Jagger	1
5024.3	20VA5024 - 3	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Nottoway	Carl Griffey	Jagger	1
5025.1	20VA5025 - 1	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	KWS 242	1
5025.2	20VA5025 - 2	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	KWS 242	1
5025.3	20VA5025 - 3	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	KWS 242	1
5026.1	20VA5026 - 1	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	Massey	1
5026.2	20VA5026 - 2	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	Massey	1
5026.3	20VA5026 - 3	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	Massey	1
5027.1	20VA5027 - 1	TCTNB	*1,2a,2c,3,26,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	Massey	1
5027.2	20VA5027 - 2	LBDSG	*1,,17,B,10,14a,28*	VA	Accomack	Carl Griffey	Massey	1
5027.3	20VA5027 - 3	MBTNB	*1,3,,3ka,11,17,30,B,14a*	VA	Accomack	Carl Griffey	Massey	1
5028.1	20VA5028 - 1	TCTQB	*1,2a,2c,3,26,3ka,11,17,30,B,10*	VA	Suffolk	Carl Griffey	Massey	1
5028.2	20VA5028 - 2	TCSQB	*1,2a,2c,3,26,3ka,11,17,B,10*	VA	Suffolk	Carl Griffey	Massey	1
5028.3	20VA5028 - 3	MCTNB	*1,3,26,3ka,11,17,30,B,14a*	VA	Suffolk	Carl Griffey	Massey	1
5032.1	20VA5032 - 1	TCJTB	*1,2a,2c,3,26,11,17,B,10,14a,18*	VA	Richmond	Carl Griffey		1
5032.1	20VA5032 - 1	TCJTB	*1,2a,2c,3,26,11,17,B,10,14a,18*	VA	Richmond	Carl Griffey		1
5033.1	20VA5033 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	VA	Richmond	Carl Griffey	Tribute	1
5033.2	20VA5033 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	VA	Richmond	Carl Griffey	Tribute	1
5033.3	20VA5033 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	VA	Richmond	Carl Griffey	Tribute	1
5036.1	20WI5036 - 1	MPTSD	*1,3,9,24,26,3ka,11,17,30,B,10, 14a,39*	WI	Green	Adrian Barta	Comm	3
5037.1	20WI5037 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,1 4a,39*	WI	Rock	Adrian Barta	Comm	3
5121.1	20IN5121 - 1	MBTNB	*1,3,,3ka,11,17,30,B,14a*	IN	Gibson	Sam Tragesser	25R46	3
5122.1	20IN5122 - 1	TBTDB	*1,2a,2c,3,,3ka,11,17,30,14a*	IN	Gibson	Sam Tragesser		3
5122.2	20IN5122 - 2	TBTNB	*1,2a,2c,3,,3ka,11,17,30,B,14a*	IN	Gibson	Sam Tragesser	25R46	3

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5123.1	20IN5123 - 1	MBTNB	*1,3,,3ka,11,17,30,B,14a*	IN	Allen	Sam Tragesser	KWS050	3
5123.2	20IN5123 - 2	MBTNB	*1,3,,3ka,11,17,30,B,14a,*	IN	Allen	Sam Tragesser	KWS050	3
5124.1	20IN5124 - 1	MBTNB	*1,3,,3ka,11,17,30,B,14a*	IN	Allen	Sam Tragesser	KWS050	3
5124.2	20IN5124 - 2	TFPSB	*1,2a,2c,3,24,26,3ka,17,30,B,10 ,14a*	IN	Allen	Sam Tragesser	KWS050	3
5138.1	20IN5138 - 1	TCTNB	*1,2a,2c,3,26,3ka,11,17,30,B,14a*	IN	Tipton	Sam Tragesser		3
5138.2	20IN5138 - 2	TBTNB	*1,2a,2c,3,,3ka,11,17,30,B,14a*	IN	Tipton	Sam Tragesser		3
5139.1	20IN5139 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	IN	Tipton	Sam Tragesser		3
5139.2	20IN5139 - 2	TCTNB	*1,2a,2c,3,26,3ka,11,17,30,B,14a*	IN	Tipton	Sam Tragesser		3
5139.3	20IN5139 - 3	TBTNB	*1,2a,2c,3,,3ka,11,17,30,B,14a*	IN	Tipton	Sam Tragesser		3
5001.1	20TX5001 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5001.2	20TX5001 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5001.3	20TX5001 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5002.1	20TX5002 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5002.2	20TX5002 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5002.3	20TX5002 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5003.1	20TX5003 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5003.2	20TX5003 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5003.3	20TX5003 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5004.2	20TX5004 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5004.3	20TX5004 - 3	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,1 4a,39*	TX	Hidalgo		Line E	4
5005.1	20TX5005 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5005.2	20TX5005 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5005.3	20TX5005 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5006.1	20TX5006 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5006.2	20TX5006 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5006.3	20TX5006 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5007.3	20TX5007 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5008.1	20TX5008 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5008.2	20TX5008 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Morocco	4
5009.2	20TX5009 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5009.3	20TX5009 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5010.1	20TX5010 - 1	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5010.2	20TX5010 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5011.2	20TX5011 - 2	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5011.3	20TX5011 - 3	BBBQD	*,,,B,10,39*	TX	Hidalgo		Line E	4
5012.1	20OK5012 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	OK	Payne	Bob Hunger	OK Bullet	4
5012.2	20OK5012 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	OK	Payne	Bob Hunger	OK Bullet	4
5012.3	20OK5012 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	OK	Payne	Bob Hunger	OK Bullet	4
5013.1	20OK5013 - 1	MBDSD	*1,3,,17,B,10,14a,39*	OK	Payne	Bob Hunger	wheat breeder line 62-80	4
5013.2	20OK5013 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	OK	Payne	Bob Hunger	wheat breeder line 62-80	4
5013.3	20OK5013 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	OK	Payne	Bob Hunger	wheat breeder line 62-80	4
5014.1	20TX5014 - 1	MLPSD	*1,3,9,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	Patton	4

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5014.2	20TX5014 - 2	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	Patton	4
5014.3	20TX5014 - 3	MCTNB	*1,3,26,3ka,11,17,30,B,14a,*	TX	McLennan	Gigi Opena	Patton	4
5015.2	20TX5015 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TAM 205	4
5015.3	20TX5015 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TAM 205	4
5016.1	20TX5016 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TX15V70627	4
5016.2	20TX5016 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TX15V70627	4
5016.3	20TX5016 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TX15V70627	4
5017.1	20TX5017 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TX17A001134	4
5017.2	20TX5017 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	TX	McLennan	Gigi Opena	TX17A001134	4
5029.1	20OK5029 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	OK	Major	Bob Hunger	Bentley	4
5029.2	20OK5029 - 2	TBRKG	*1,2a,2c,3,,3ka,11,30,10,14a,18,28*	OK	Major	Bob Hunger	Bentley	4
5029.3	20OK5029 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	OK	Major	Bob Hunger	Bentley	4
5031.3	20OK5031 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	OK	Major	Bob Hunger	Jagalene	4
5034.1	20NE5034 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	NE	Lancaster	S Wegulo	Wesley	5
5034.2	20NE5034 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	NE	Lancaster	S Wegulo	Wesley	5
5034.3	20NE5034 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	NE	Lancaster	S Wegulo	Wesley	5
5104.1	20KS5104 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Saline	Eric DeWolf		5
5104.2	20KS5104 - 2	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	KS	Saline	Eric DeWolf		5
5105.1	20KS5105 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Harper	Eric DeWolf		5
5105.2	20KS5105 - 2	MCTNB	*1,3,26,3ka,11,17,30,B,14a,*	KS	Harper	Eric DeWolf		5
5106.1	20KS5106 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	KS	Barber	Eric DeWolf	SY Roggee	5
5107.1	20KS5107 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Pratt	Eric DeWolf	LCS Yeti	5
5107.2	20KS5107 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Pratt	Eric DeWolf	LCS Yeti	5
5108.1	20KS5108 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	KS	Pratt	Eric DeWolf	SY Benefit	5
5108.2	20KS5108 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Pratt	Eric DeWolf	SY Benefit	5
5109.1	20KS5109 - 1	TPBGJ	*1,2a,2c,3,9,24,26,,10,28,39*	KS	Kingman	Eric DeWolf	Paradise	5
5109.2	20KS5109 - 2	MBDSD	*1,3,,17,B,10,14a,39*	KS	Kingman	Eric DeWolf	Paradise	5
5110.1	20KS5110 - 1	MBDSD	*1,3,,17,B,10,14a,39*	KS	Sedgwick	Eric DeWolf	Rock Star	5
5111.2	20KS5111 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Sedgwick	Eric DeWolf		5
5111.3	20KS5111 - 3	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	KS	Sedgwick	Eric DeWolf		5
5113.1	20KS5113 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Clay	Eric DeWolf		5
5113.2	20KS5113 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Clay	Eric DeWolf		5
5114.1	20KS5114 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Barton	Eric DeWolf		5
5116.1	20KS5116 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	KS	Clay	Eric DeWolf		5
5038.1	20MN5038 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	CP 3915	6
5039.1	20MN5039 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Waseca	Jim Kolmer	CP 3055	6
5039.2	20MN5039 - 2	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Waseca	Jim Kolmer	CP 3055	6
5039.3	20MN5039 - 3	TNBGJ	*1,2a,2c,3,9,24,,10,28,39*	MN	Waseca	Jim Kolmer	CP 3055	6
5040.1	20MN5040 - 1	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Waseca	Jim Kolmer	Dyna Grow Ballistic	6
5040.2	20MN5040 - 2	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Waseca	Jim Kolmer	Dyna Grow Ballistic	6

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5040.3	20MN5040 - 3	TNBJJ	*1,2a,2c,3,9,24,,10,14a,28,39*	MN	Waseca	Jim Kolmer	Dyna Grow Ballistic	6
5041.1	20MN5041 - 1	TBRKG	*1,2a,2c,3,,3ka,11,30,10,14a,18,28*	MN	Waseca	Jim Kolmer	SY Longmire	6
5041.2	20MN5041 - 2	MBDSD	*1,3,,17,B,10,14a,39*	MN	Waseca	Jim Kolmer	SY Longmire	6
5041.3	20MN5041 - 3	MBDSD	*1,3,,17,B,10,14a,39*	MN	Waseca	Jim Kolmer	SY Longmire	6
5042.1	20MN5042 - 1	TNBJJ	*1,2a,2c,3,9,24,,10,14a,28,39*	MN	Waseca	Jim Kolmer	Morocco	6
5042.2	20MN5042 - 2	TNBJJ	*1,2a,2c,3,9,24,,10,14a,28,39*	MN	Waseca	Jim Kolmer	Morocco	6
5042.3	20MN5042 - 3	TNBJJ	*1,2a,2c,3,9,24,,10,14a,28,39*	MN	Waseca	Jim Kolmer	Morocco	6
5043.1	20MN5043 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Waseca	Jim Kolmer	Morocco	6
5044.1	20MN5044 - 1	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Waseca	Jim Kolmer	Glenn	6
5044.3	20MN5044 - 3	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Waseca	Jim Kolmer	Glenn	6
5045.1	20MN5045 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	SY 611 CLZ	6
5045.2	20MN5045 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	SY 611 CLZ	6
5045.3	20MN5045 - 3	TDBGS	*1,2a,2c,3,24,,10,21,28,39*	MN	Waseca	Jim Kolmer	SY 611 CLZ	6
5046.1	20MN5046 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	Marshall	6
5046.2	20MN5046 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	Marshall	6
5046.3	20MN5046 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	Marshall	6
5047.1	20MN5047 - 1	MBDSD	*1,3,,17,B,10,14a,39*	MN	Waseca	Jim Kolmer	MN 16136-2	6
5047.2	20MN5047 - 2	MBDSD	*1,3,,17,B,10,14a,39*	MN	Waseca	Jim Kolmer	MN 16136-2	6
5047.3	20MN5047 - 3	MBDSD	*1,3,,17,B,10,14a,39*	MN	Waseca	Jim Kolmer	MN 16136-2	6
5048.1	20MN5048 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	Prosper	6
5048.2	20MN5048 - 2	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Waseca	Jim Kolmer	Prosper	6
5048.3	20MN5048 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	Prosper	6
5049.1	20MN5049 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	LCS Cannon	6
5049.2	20MN5049 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Waseca	Jim Kolmer	LCS Cannon	6
5050.1	20MN5050 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Le Sueur	Jim Kolmer		6
5051.1	20MN5051 - 1	TBRKG	*1,2a,2c,3,,3ka,11,30,10,14a,18,28*	MN	Redwood	Jim Kolmer	Marshall	6
5051.2	20MN5051 - 2	TBRKG	*1,2a,2c,3,,3ka,11,30,10,14a,18,28*	MN	Redwood	Jim Kolmer	Marshall	6
5051.3	20MN5051 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Redwood	Jim Kolmer	Marshall	6
5052.1	20MN5052 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Redwood	Jim Kolmer	Prosper	6
5052.2	20MN5052 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Redwood	Jim Kolmer	Prosper	6
5052.3	20MN5052 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Redwood	Jim Kolmer	Prosper	6
5053.1	20MN5053 - 1	TNBGJ	*1,2a,2c,3,9,24,,10,28,39*	MN	Redwood	Jim Kolmer	Glenn	6
5053.3	20MN5053 - 3	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	MN	Redwood	Jim Kolmer	Glenn	6
5054.1	20MN5054 - 1	MBDSD	*1,3,,17,B,10,14a,39*	MN	Redwood	Jim Kolmer	Morocco	6
5054.2	20MN5054 - 2	TBRKG	*1,2a,2c,3,,3ka,11,30,10,14a,18,28*	MN	Redwood	Jim Kolmer	Morocco	6
5054.3	20MN5054 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Redwood	Jim Kolmer	Morocco	6
5055.2	20MN5055 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Redwood	Jim Kolmer	Morocco	6
5055.2	20MN5055 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Redwood	Jim Kolmer	Morocco	6
5055.3	20MN5055 - 3	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,1 4a,39*	MN	Redwood	Jim Kolmer	Morocco	6
5056.2	20MN5056 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5056.3	20MN5056 - 3	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,1 4a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5057.1	20MN5057 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5057.2	20MN5057 - 2	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,1 4a,39*	MN	Stevens	Jim Kolmer	Marquis	6

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5057.3	20MN5057 - 3	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5058.1	20MN5058 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5061.1	20MN5061 - 1	MCDSD	*1,3,26,17,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5061.2	20MN5061 - 2	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5061.3	20MN5061 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Marquis	6
5062.1	20MN5062 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Morocco	6
5062.2	20MN5062 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Morocco	6
5062.3	20MN5062 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Stevens	Jim Kolmer	Morocco	6
5067.1	20SD5067 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	SD	Brookings			6
5076.1	20MN5076 - 1	MSBJG	*1,3,9,16,24,,10,14a,28*	MN	Washington	Jim Kolmer	Morocco	6
5077.1	20MN5077 - 1	TBBGS	*1,2a,2c,3,10,21,28,39*	MN	Washington	Jim Kolmer	Morocco	6
5077.2	20MN5077 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Washington	Jim Kolmer	Morocco	6
5080.1	20MN5080 - 1	TNBGJ	*1,2a,2c,3,9,24,,10,28,39*	MN	Polk	Jim Kolmer	LCS Rebel	6
5080.2	20MN5080 - 2	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Polk	Jim Kolmer	LCS Rebel	6
5080.3	20MN5080 - 3	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	MN	Polk	Jim Kolmer	LCS Rebel	6
5081.1	20MN5081 - 1	TCBGS	*1,2a,2c,3,26,,10,21,28,39*	MN	Polk	Jim Kolmer	CP 3903	6
5081.2	20MN5081 - 2	TBBJS	*1,2a,2c,3,,,10,14a,21,28,39*	MN	Polk	Jim Kolmer	CP 3903	6
5082.1	20MN5082 - 1	TNBGJ	*1,2a,2c,3,9,24,,10,28,39*	MN	Polk	Jim Kolmer	ND ARS 16-14-126	6
5082.2	20MN5082 - 2	TNBGJ	*1,2a,2c,3,9,24,,10,28,39*	MN	Polk	Jim Kolmer	ND ARS 16-14-126	6
5082.3	20MN5082 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	ND ARS 16-14-126	6
5083.1	20MN5083 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	Marshall	6
5083.2	20MN5083 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	Marshall	6
5084.1	20MN5084 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	Glenn	6
5084.2	20MN5084 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	Glenn	6
5084.3	20MN5084 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	Glenn	6
5085.1	20MN5085 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	CP 3055	6
5085.2	20MN5085 - 2	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	CP 3055	6
5085.3	20MN5085 - 3	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	CP 3055	6
5086.1	20MN5086 - 1	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2030	6
5086.2	20MN5086 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2030	6
5086.3	20MN5086 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2030	6
5087.1	20MN5087 - 1	MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5087.2	20MN5087 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5087.3	20MN5087 - 3	MBDSD	*1,3,,17,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5088.1	20MN5088 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2055	6
5088.2	20MN5088 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2055	6

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5088.3	20MN5088 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2055	6
5089.1	20MN5089 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	Thatcher	6
5089.2	20MN5089 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Thatcher	6
5089.3	20MN5089 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Thatcher	6
5090.1	20MN5090 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Thatcher	6
5090.2	20MN5090 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Thatcher	6
5090.3	20MN5090 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Thatcher	6
5091.1	20MN5091 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5091.2	20MN5091 - 2	MBDSD	*1,3,,17,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5091.3	20MN5091 - 3	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5092.2	20MN5092 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2052	6
5092.3	20MN5092 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2052	6
5093.1	20MN5093 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2010	6
5093.2	20MN5093 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2010	6
5093.3	20MN5093 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	MN	Polk	Jim Kolmer	AY-2 Plot 2010	6
5094.1	20MN5094 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	MN	Polk	Jim Kolmer	Morocco	6
5095.1	20ND5095 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5095.2	20ND5095 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5096.1	20ND5096 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5096.2	20ND5096 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5096.3	20ND5096 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5097.1	20ND5097 - 1	TNBJS	*1,2a,2c,3,9,24,,10,14a,21,28,39*	ND	Cass	Jim Kolmer		6
5097.2	20ND5097 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5097.3	20ND5097 - 3	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5098.1	20ND5098 - 1	TCBGS	*1,2a,2c,3,26,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5098.2	20ND5098 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5098.3	20ND5098 - 3	TNBJJ	*1,2a,2c,3,9,24,,10,14a,28,39*	ND	Cass	Jim Kolmer		6
5099.1	20ND5099 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5099.2	20ND5099 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5100.1	20ND5100 - 1	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5101.2	20ND5101 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5101.3	20ND5101 - 3	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5102.1	20ND5102 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5102.2	20ND5102 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5103.1	20ND5103 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5103.2	20ND5103 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Jim Kolmer		6
5118.1	20SD5118 - 1	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	SD	Codington			6
5118.2	20SD5118 - 2	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	SD	Codington			6
5119.1	20SD5119 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	SD	Codington			6
5119.2	20SD5119 - 2	TGBGS	*1,2a,2c,3,16,,10,21,28,39*	SD	Codington			6
5120.2	20SD5120 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	SD	Brookings			6
5128.1	20ND5128 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Matt Brieland		6
5129.1	20ND5129 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Matt Brieland		6
5129.2	20ND5129 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cass	Matt Brieland		6
5130.1	20ND5130 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Foster	Matt Brieland		6
5130.2	20ND5130 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Foster	Matt Brieland		6

Table 5. Information on individual collections and race designations of derived leaf rust isolates.

Collection / Isolate	Full collection number	Race	VirulenceFormula	Survey state	Survey county	Collector	Cultivar	Survey area
5131.1	20ND5131 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	ND	Foster	Matt Brieland		6
5131.2	20ND5131 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	ND	Foster	Matt Brieland		6
5132.1	20ND5132 - 1	TNBGS	*1,2a,2c,3,9,24,,10,21,28,39*	ND	Foster	Matt Brieland		6
5133.1	20ND5133 - 1	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	ND	Cavalier	Matt Brieland		6
5133.2	20ND5133 - 2	MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	ND	Cavalier	Matt Brieland		6
5135.1	20ND5135 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cavalier	Matt Brieland		6
5135.2	20ND5135 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cavalier	Matt Brieland		6
5137.1	20ND5137 - 1	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cavalier	Matt Brieland		6
5137.2	20ND5137 - 2	TBBGS	*1,2a,2c,3,,,10,21,28,39*	ND	Cavalier	Matt Brieland		6
5071.1	20WA5071 - 1	LCDJG	*1,26,17,10,14a,28*	WA	Skagit	XM Chen	Ars/PI195097 Line 177	8
5071.2	20WA5071 - 2	LBDSG	*1,,17,B,10,14a,28*	WA	Skagit	XM Chen	Ars/PI195097 Line 177	8
5071.3	20WA5071 - 3	LBDSG	*1,,17,B,10,14a,28*	WA	Skagit	XM Chen	Ars/PI195097 Line 177	8
5073.1	20WA5073 - 1	LBDSG	*1,,17,B,10,14a,28*	WA	Skagit	XM Chen	Ars/Yr15 NIL	8
5073.2	20WA5073 - 2	LCDSG	*1,26,17,B,10,14a,28*	WA	Skagit	XM Chen	Ars/Yr15 NIL	8
5073.3	20WA5073 - 3	TCTBB	*1,2a,2c,3,26,3ka,11,17,30*	WA	Skagit	XM Chen	Ars/Yr15 NIL	8

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Fine tuning the genetic control of chromosome pairing in polyploid common wheat.

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Wheat is the primary food staple for 20% of the world's population as it is an affordable source of nutrition (Koo et al. 2020). About 50% of the wheat produced in the U.S. is exported, which brings it into the category of the world's lead wheat-exporters. With the steadily increasing world population, a consistent increase in wheat demand is experienced, which is difficult to meet due to stagnating wheat grain yield over the last two decades (Schauberger et al. 2018). Monoculture of selected genotypes and inbreeding within the adapted wheat germplasm is one of the reasons behind the observed stagnancy.

Wheat is produced on over 110,000 acres in South Carolina, which is valued at $23 million in 2020. The current wheat yield in the State (51 bushels acre^{-1}) is at par with the average national winter wheat yield of 52 bu/acre but significantly lower than the average winter wheat yield reported in the U.S. Pacific Northwest (74.7 bu/acre) (USDA NASS 2021). Wheat is well adapted to the edaphoclimatic conditions of the State and fits well in the practiced crop rotations. It suggests that there is great potential to increase wheat yield in South Carolina. Thus, it is imperative to adopt new breeding strategies to reduce the potential and observed wheat yield gap to meet future wheat demand. In this direction, we set out to use the knowledge of the recombination process to achieve the foremost objectives of plant breeding of creating

genetic diversity and selecting for the agronomically desirable alleles (Taagen et al. 2020; Kuo et al. 2021).

Control of chromosome pairing in common wheat. Genetic recombination is a vital inherent cellular process in all eukaryotes that occur during gametogenesis and gives rise to new allelic combinations. As we know, each cell possesses two sets of chromosomes, one each from mother and father, and during gametogenesis, the genetic information between these two sets of chromosomes gets reshuffled, giving rise to all extant genetic diversity (Appels et al. 1998). This process also reduces the number of chromosomes to half to keep transgenerational consistency in the chromosome number (Appels et al. 1998). For the exchange of genetic information, each chromosome finds and pairs with its partner; failing to do so results in infertility to lethality in an organism. Specific genes regulate this pairing process, and their transcriptional silencing leads to pairing among related (homoeologous) chromosomes (Taagen et al. 2020; Kuo et al. 2021). For instance, in natural conditions, wheat chromosomes 1A, 1B, and 1D pair exclusively with their counterparts in the nucleus, but upon silencing of the regulatory genes, these chromosomes not only pair with each other but also with the corresponding chromosomes from related species, such as *Aegilops*, rye (1R), or other wild/cultivated wheat relatives, allowing transfer of genetic information among them (Koo et al. 2020).

Stable silencing of the *Asynopsis1* (*Asy1*) gene induces pairing among homoeologous chromosomes very similar to the *Pairing homoeologues1* (*Ph1*) mutant in Chinese Spring background (Boden et al. 2009). In addition to the phenotypic similarity, transcriptional up-regulation of the *Asy1* gene in the *Ph1* mutant suggested that *Asy1* functions downstream to *Ph1* in the genetic recombination pathway (Boden et al. 2009; Able et al. 2009). Earlier research in Arabidopsis revealed that another gene, *DMC1* (*disrupted meiosis cDNA1*), is involved in the homologous recombination process and functions downstream to the *Asy1* gene (Sanchez-Moran et al. 2007). Later, it was shown that the product of *Asy1* physically interacts with the coiled-coil protein Asy3 to form the chromosome axis (known as the lateral element in the synaptonemal complex), which facilitates homologous chromosome pairing and promotes loading of DMC1 onto the chromosome axis to ensure exchange of genetic material between the homologous chromosomes, i.e., non-sister chromatids (Ferdous et al. 2012; Pradillo et al. 2014). Parallelly research in common wheat revealed that in due course of events, Asy1 facilitates loading of Zyp1 (Zipper1 – a component of the transverse filament of the synaptonemal complex) that holds the homologous chromosomes together until they separate and get packaged in daughter cells destined to give rise to gametes (Khoo et al. 2012).

Recombinase DMC1 and its paralogue RAD51 both participate in the exchange of genetic material during the homologous recombination at meiotic prophase I. In maize, wheat, and *Arabidopsis*, it has been reported that in the absence of one nucleoprotein, another nucleoprotein takes over the repair process; however, the outcome of the repair process is different in both cases. For instance, in *DMC1* knockout plants, RAD51 drives the repair process and uses sister chromatids as the template for repair, which manifests cytologically as chromosome univalents at the meiotic metaphase I. Whereas, in the *RAD51* knockout plants, DMC1 takes over the process, and the repair takes place exclusively using non-sister chromatids as template resulting in chromosome multivalents at meiotic metaphase I (Li et al. 2007; Bennypaul et al. 2012; Pradillo et al. 2014).

Meiotic recombination in eukaryotes initiates with the induction of double-stranded breaks (DSBs) in the chromosomal DNA by SPO11 (SPOrulation 11), a protein that belongs to the family of type II topoisomerases. *SPO11* was first isolated from yeast in a screen for mutants showing reduced sporulation. Later on, the protein was discovered as an essential component of the double-strand break repair (DSBR) pathway. Mutation in *SPO11* displayed decreased ability to generate DSBs and showed corresponding defects in SC formation. These defects were caused by a decline in the number of ZIP3 (HEI10) complexes, thought to represent sites of SC initiation via their role in promoting the recruitment of the transverse filament protein ZIP1 (MacQueen and Roeder 2009).

Unique from other eukaryotes, plants possess multiple copies of *SPO11*: *Arabidopsis* and maize have three copies, while the rice genome contains four copies. Out of the three *Arabidopsis* homologs, only *SPO11-1* and *SPO11-2* have a meiotic function (Stacey et al. 2006; Grelon et al. 2001). The phenotypes of *Arabidopsis spo11-1* and *spo11-2* mutants appear to overlap considerably. None of the above two mutants formed crossovers or could synapse chromosomes and only produced univalents at metaphase I (Stacey et al. 2006; Grelon et al. 2001). More recently, identification of mutations in the *SPO11-1* and *SPO11-2* genes and stacking mutants in the homoeologous copies of each of these genes in the common wheat provided convincing evidence for the conservation of SPO11 function in Arabidopsis and wheat (Benyahya et al. 2020; Da Ines et al. 2020). The lack of functional redundancy between these two *SPO11* genes suggested that DSB formation is catalyzed by a SPO11 heterodimer in plants and not a homodimer as is thought to occur

in other eukaryotes. In *S. cerevisiae*, SPO11 requires nine other proteins to catalyze DSB formation. Only four of these are conserved in plants (Rad50, Mre11, Nbs1, Ski8), but none has a conserved function in this recombination step.

The *Poor Homologous Synapsis1* (*PHS1*) is another gene involved in coordinating chromosome pairing and early recombination events, ensuring pairing fidelity and proper repair of meiotic DSBs. In *phs1* mutant, chromosomes exhibit early recombination defects and frequently pair with non-homologous chromosomes instead of pairing with their homologs. It was shown earlier that PHS1 is a cytoplasmic protein that functions by controlling the transport of RAD50 from the cytoplasm to the nucleus. RAD50 is a component of the MRN protein complex that processes DNA DSBs and facilitates the production of the stranded DNA ends, which act in the homology search and recombination (Ronceret et al. 2009; Pawlowski et al. 2004).

It is apparent from the above description that *SPO11*, *Asy1, DMC1,* and *PHS1* play a central role in chromosome pairing and recombination process, and modulating their expression level may permit the exchange of genetic material between homoeologous (related) chromosomes. Given this knowledge, we transiently silenced these genes in common wheat to induce/repress homo-/homoeologues pairing to allow the exchange of genetic material between homoeologous chromosomes, which is otherwise not possible due to recombination barrier(s).

Virus-induced gene silencing (VIGS) of wheat meiotic genes. To independently and transiently silence *Asy1, SPO11-1, DMC1, PHS1*, and *RAFL* (wheat homolog of the rice *Raftin1 like,* LOC_Os09g30320) genes in *Triticum aestivum* L. a virus-induced gene silencing (VIGS) approach was undertaken and carried out in the following steps: i) PCR-based cloning of selected genes from the 'Chinese Spring' genome. ii) For all VIGS experiments the barley streak mosaic virus (BSMV) based vectors (pBSMV α42, pBSMV β42.sp1, and pSL038-1) were used. The BSMV-based VIGS system was earlier demonstrated to trigger a high level of gene suppression in wheat (Bennypaul et al. 2012; Bhullar et al. 2014; Desjardins et al. 2020; Raz et al. 2021). The target gene fragments were cloned into the pSL038-1 to develop VIGS vectors. Subsequently, the three BSMV vectors - pBSMV α42, pBSMV β42.sp1, and pSL038-1 (with a gene fragment) were linearized as described in Bennypaul et al. (2012). An empty pSL038-1 vector (without a gene fragment) was used as a control in these experiments. iii) For plant infiltration, infectious RNAs were transcribed from the three linearized plasmids (pBSMV α42, pBSMV β42.sp1, and pSL038-1) using the mMessage mMachine T7 *in vitro* transcription kit (Ambion, USA) following the manufacturer's recommendations. Before infiltration, equal volumes of transcribed RNAs were combined with the FES buffer (abrasive agent used for inoculation). Subsequently, wheat plants at the boot stage were inoculated by rubbing. iv) After infection, the recombinant virus produces double-stranded RNA in the host cell, which triggers the cell's inherent defense machinery to degrade the viral and the corresponding host mRNAs parallelly. The meiotic phenotypes of inoculated and control plants were studies subsequently following

Table 1. List of essential wheat meiotic genes, their chromosomal locations, and silencing phenotypes (N/A = not available; ? = the *Ph1* candidates identified in earlier studies; [1] univalents, bivalents, multivalents (trivalents and quadrivalents) and heteromorphic bivalents (Li et al. 2007); [2] univalents (Barakate et al. 2014); and [3] meiotic defects in chromatin compaction, axis formation, and the presence of chromosome fragmentation (Lambing et al. 2020).

Gene	Chromosome	Silencing phenotype in wheat meiocytes
Asy1	5A, 5B, 5D	Multivalents
DMC1	5A, 5B, 5D	Univalents
RAD51	7A, 7B, 7D	N/A[1]
PHS1	7A, 7B, 7D	Micronuclei
Zip1	2A, 2B, 2D	N/A[2]
SPO11-1	5A, 5B, 5D	Univalents
SPO11-2	7A, 7B, 7D	Univalents
Rec8	1A, 1B, 1D	N/A[3]
CDC2-4/Cdk2 (*Ph1*?)	5B	No obvious phenotype
Zip4/hyp3 (*Ph1*?)	5B	Multivalents
RAFL/c-Ph1 (*Ph1*?)	5B	Multivalents
MSH7 (*Ph2*)	3D	Multivalents
MSH4	2A, 2B, 2D	Univalents
MSH5	1A, 1B, 1D	Univalents
MSH2	N/A	Decrease (40%) in number of chiasmata per nucleus and univalents
FANCM	N/A	Decrease in number of chiasmata per nucleus and univalents

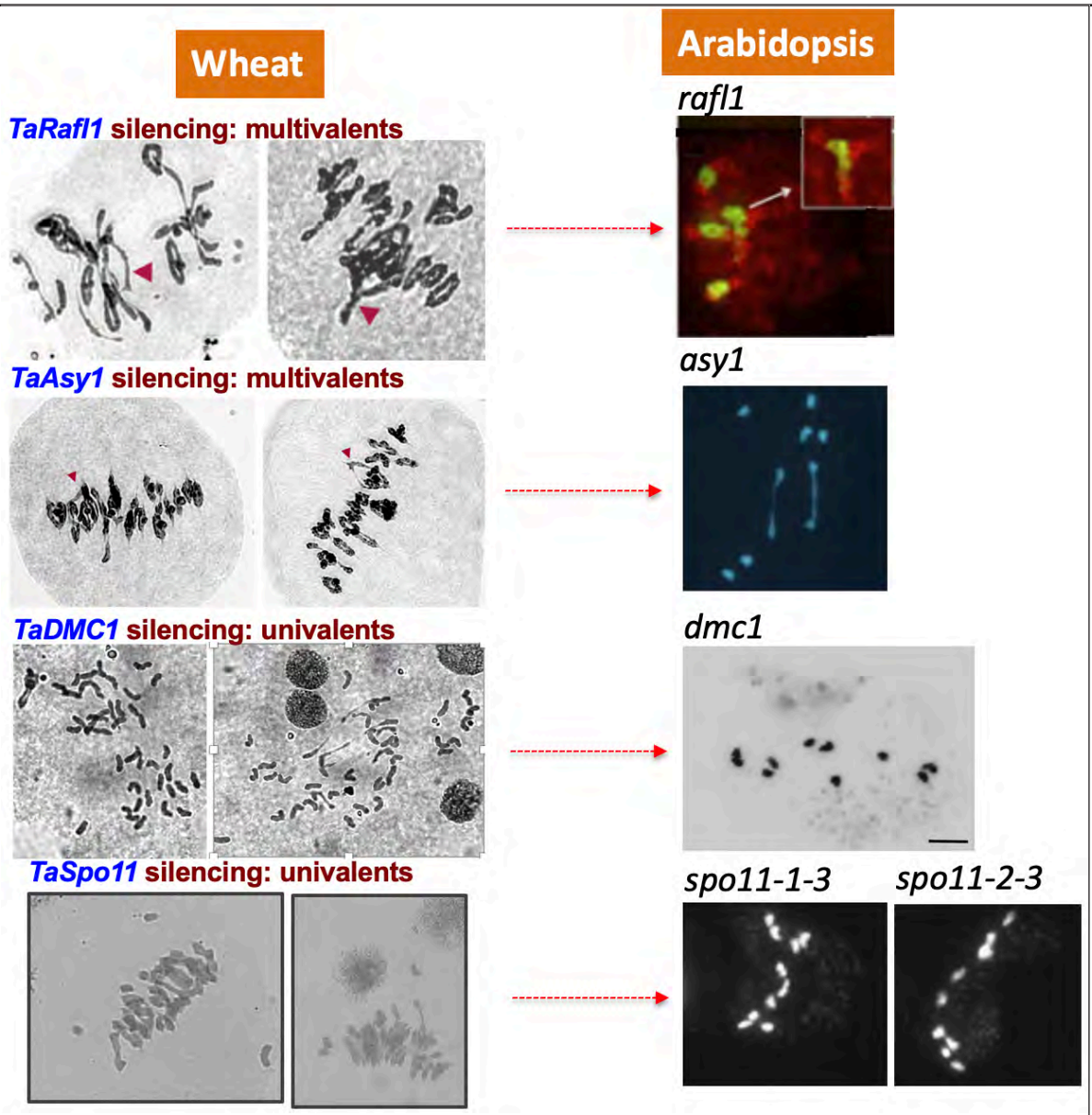

Fig. 1. Chromosome spreads of meiotic metaphase I pollen mother cells showing silenced phenotypes of the major wheat meiotic genes – *RAFL*, *Asy1*, *DMC1*, and *SPO11-1* and their corresponding silencing phenotypes in Arabidopsis (*RAFL* – Bhullar et al. 2014; *Asy1* – Sanchez-Moran et al. 2007; *DMC1* – Da Ines et al. 2013; *SPO11* – Stacey et al. 2006; Grelon et al. 2001).

Bennypaul et al. (2012).

Meiotic phenotypes of the recombinant BSMV inoculated plants. VIGS of the essential meiotic gene *DMC1* (Disrupted meiotic cDNA 1) showed an average of 30 univalents and six bivalents compared to the control where only bivalents were observed (Table 1, Fig. 1, p. 90). This result corresponded with the known function of the *DMC1* gene in the repair of double-stranded breaks at the meiotic prophase I (Bennypaul et al. 2012). Similarly, the VIGS of the wheat *SPO11-1* gene resulted in the production of univalent in ~21% of the analyzed cells (Fig. 1, Table 1 (p. 89)). The results corresponded with the earlier observations in *Arabidopsis* (Grelon et al. 2001) and wheat (Benyahya et al. 2020). VIGS of the wheat *Asy1* gene showed the formation of multivalents (Fig. 1, Table 1 (p. 89)). The result is consistent with what was observed for RNA interference lines of this gene in bread wheat (Boden et al. 2009). When VIGS was performed on the wheat *RAFL* gene, it showed a phenotype (quadrivalents or higher-order pairing) similar to the *Ph1* mutant (Bhullar et al. 2014). VIGS silencing of *PHS1* showed 21 bivalents with a laggard chromosome segment in 95% of the analyzed cells compared with only 21 bivalents in control (Fig. 2, p. 91). Micronuclei formation during

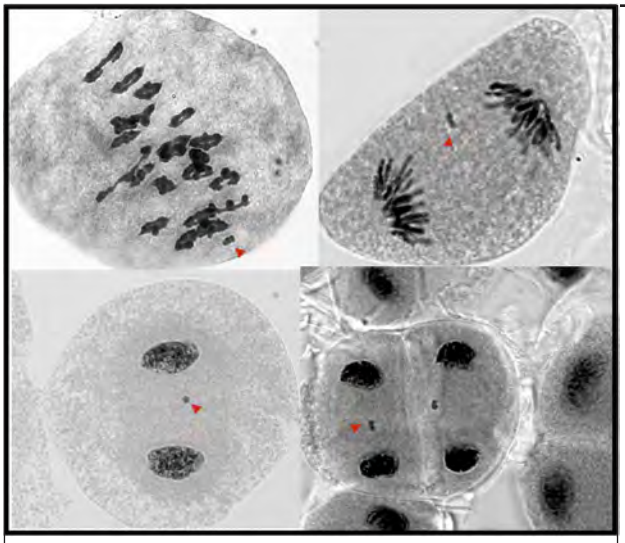

Fig. 2. Chromosome spreads of meiotic metaphase I pollen mother cells from *PHS1* silenced plants. Notice the chromosome fragment and micronuclei marked by the arrowhead.

anaphase and telophase during equational and reductional meiotic divisions was also observed (Fig. 2, p. 91).

Silencing some of these meiotic genes produced similar phenotypes in different plants, whereas the phenotypes differed for some genes, such as the *PHS1* silencing in corn resulted in multivalents and heteromorphic bivalents (Pawlowski et al. 2004). In contrast, in wheat, it resulted in chromosome fragmentation and the production of micronuclei. However, the phenotype (centromere clustering) of silencing *PHS1* and *RAFL* genes resembled in *Arabidopsis* (Ronceret et al. 2009; Bhullar et al. 2014), which might hint towards *RAFL*'s role in transporting ASY1, DMC1, ZIP1, and/or ZIP4 from cytoplasm to nucleus like PHS1's role in transporting RAD50 (Ronceret et al. 2009).

A few applications of this knowledge about the molecular functions of the meiotic genes could be: Controlling recombination, i.e., manipulating the frequency and distribution of the cross overs, clonal seeds production, haploids/doubled haploids production, and induction of homoeologous recombination to facilitate alien introgression.

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SOUTH DAKOTA

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South Dakota Agricultural Experiment Station releases a new hard red winter wheat cultivar SD Andes for production in South Dakota and the region.

Sunish Sehgal

SD Andes is a hard red winter wheat cultivar developed and released by the South Dakota Agricultural Experiment Station in autumn 2020. SD Andes was derived using doubled-haploid technology from the cross 'Striker / SD03184-4' and released primarily for its superior adaption to rainfed wheat production systems in South Dakota and adjacent wheat-producing states. SD Andes is a semidwarf wheat (*RhtB1b*) and is expected to offer the producers a higher-yielding winter wheat cultivar with excellent straw strength and good stripe rust resistance. SD Andes could be a good replacement for late-maturity cultivars such as Redfield and Ideal and others such as Oahe and Overland.

In the last three years, SD Andes has been evaluated in 41 environments in South Dakota. When compared over 11 South Dakota CPT location-years in eastern South Dakota, SD Andes ranked second overall and yielded (70.9 bu/ac) higher than Oahe (70.2 bu/ac), Ideal (69.4.0 bu/ac), Redfield (68.3 bu/ac), Draper (68.2 bu/ac), and Overland (65.4 bu/ac), but lower than Winner (71.3 bu/ac). In 19 South Dakota CPT location-years in central South Dakota, SD Andes yielded (75.7 bu/ac) higher than Overland (75.6 bu/ac), Oahe (75.1 bu/ac), and Redfield (74.1 bu/ac), but lower than Winner (79.2 bu/ac). In 11 South Dakota CPT location-years in western South Dakota SD Andes yielded (63.5 bu/ac) higher than Ideal (63.0 bu/ac), Draper (62.2 bu/ac), Oahe (61.7 bu/ac), Winner (61.3 bu/ac), Redfield (60.6 bu/ac), and

Overland (57.6 bu/ac) but lower than Keldin (65.0 bu/ac). Full data is available at https://extension.sdstate.edu/sites/default/files/2020-08/S-0002-2020-01-WW-Regional_Summary.pdf.

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New Small Grains Breeder at Virginia Tech.

Following the 2020 harvest season, Dr. Nicholas Santantonio began his transition as the new lead of the small grains breeding program at Virginia Tech. Dr. Santantonio hopes to continue on Dr. Griffey's legacy, while incorporating new technologies into the program, including genomic selection, high-throughput phenotyping, and a digital infrastructure in hopes of accelerating cultivar development and release.

2020 wheat production in the Commonwealth of Virginia.

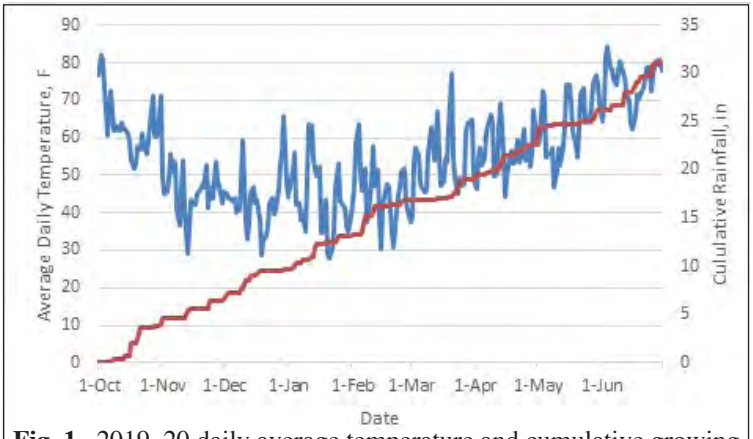

Fig. 1. 2019–20 daily average temperature and cumulative growing season precipitation for Virginia.

Growing season (Fig. 1). Early autumn 2019 was unseasonably warm and dry in most of the Commonwealth, delaying planting in some areas. Rain in mid to late October mitigated the dry conditions but also slowed planting. By 25 October, 58% of intended acres were planted, increasing to 71% by 3 November, which was more than a 20% increase over 2018–19. In December over 90% of the state reported adequate moisture and 69% of wheat was reported to be in good condition. January and February were relatively warm and wet resulting in muddy fields. Reports held that 78% of wheat was in good or excellent condition. March brought more rain and cooler than normal temperatures with 80% of wheat acres in good or excellent condition. By mid-April, wheat condition continued to be very good with 3% of the crop headed, compared with 11% on this date last year. Cooler weather continued through the month with only 13% of the crop headed by 20 April. Some areas experienced frost. On 6 May, 51% of the wheat crop had headed, compared with the 5-year average of 55%. Over 80% of the crop continued to be rated good or excellent. Frost damage and moisture stress caused the percentage of the wheat crop rated good to decline to 66% by mid-May. A late frost event on the weekend of 9 May caused significant damage in some fields, resulting in near total loss, though this was not wide-

spread. By 20 May, 91% of wheat had headed. Wheat harvest began in early June with 11% of the crop harvested by 10 June. Some areas experienced rain but harvest increased to 20% of acres by 17 June. By 1 July, 73% of wheat acres were harvested, 7% greater than the 5-year average.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service, Virginia farmers planted 220,000 acres (89,100 hectares) of wheat in 2019 of which 130,000 acres (52,650 hectares) were harvested for grain. Wheat yields averaged around 60 bu/acre (4,031 kg/ha). In total 7.8 x 10^6 bushels (212,472 metric tons) of wheat were produced in Virginia in 2019–20.

Disease incidence and severity. Disease pressure was fairly light across the Commonwealth of Virginia in 2020. Diseases were rated on a scale of 0 (no disease)–9 (severe disease). Leaf rust (*Puccinia triticina*) was rated at two locations within the Official Variety Trial. The overall mean for leaf rust across both locations was 1.3 with the leaf rust check; Massey received a 7. Powdery mildew (*Blumeria graminis*) was rated at the Eastern Virginia AREC. An overall mean of less than 1 was observed, with ratings ranging from 0–5.

State cultivar tests. The Virginia 2019–20 soft red winter wheat Official Variety trial included 130 entries. Wheat trials were planted in seven-inch rows at Blackstone, Orange, Holland, Painter, and Shenandoah Valley. They were planted in six-inch rows at Blacksburg and Warsaw. The no-till locations (Holland and Shenandoah Valley) were planted at 48 seed/f^2. All other locations were planted at 44 seed/f^2. Selecting the best wheat cultivars is challenging but becomes easier with adequate information on performance over multiple environments. Past seasons across Virginia have provided the opportunity to evaluate day length sensitivity, spring freeze damage, glume blotch, scab (Fusarium head blight), and general plant health. Many newer wheat cultivars and lines performed well in all environments tested. The future for wheat cultivars adapted to Virginia conditions is very positive.

Newly released cultivars. Four soft red winter wheat cultivars, including **Croplan 8118** (VA16W-202), **SSI30-06** (DH-12SRW057-006), **DH12SRW057-006**, and **13VTK429-3** were released by the Virginia Agricultural Experiment Station.

Table 1. Virginia Wheat Yield Contest results.

Yield rank	Wheat class	Grower	Farm	County	Yield (bu/ac)	Yield (kg/ha)
1	SRW	Philip Haynie II	Haynie Farms	Northumberland	121.6	8,170
2	SRW	PJ Haynie	Haynie Farms	Northumberland	119.8	8,049
3	SRW	Justin Welch	Welch Farms	Northumberland	118.9	7,989
1	HRW	Katie Myer	Laurel Springs Grains	Richmond County	88.7	5,960
2	HRW	Josh Long	Brann and Long Farms	Montgomery	82.7	5,557
3	HRW	Dan Brann	Brann and Long Farms	Montgomery	70.4	4,730

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

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

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Craig F. Morris, Douglas A. Engle, Alecia Kiszonas, Mary Baldridge, Gail Peden, William Kelley, Shelle Lenssen, Eric Wegner, Janet Luna, Stacey Sykes, Robin Saam, Eden Stout, Kelly Leonard, Susan Conrad, Yvonne Thompson, Meriem Auon, Sintayehu Daba, Katrina Johnson, Megan Russo, Daniel Zborowski, and Judene Mclane.

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, super soft wheat, grain flavor, and Falling Number.

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