ANNUAL WHEAT NEWSLETTER

Volume 66

Contribution no. 21-044-B from the Kansas Agricultural Experiment Station,
Kansas State University, Manhattan.

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Volume 66

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I. SPECIAL REPORTS

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

Providing a full-genome, sequence-based tool box for wheat improvement.

Following the publication of the reference sequence of the bread wheat genome, IWGSC RefSeq v1.0, in the journal *Science* in August 2018, the International Wheat Genome Sequencing Consortium (IWGSC) continued its efforts to lay a foundation to accelerate wheat improvement and, by empowering all aspects of basic and applied wheat science, increase profitability throughout the industry.

The IWGSC has now moved into Phase II and focuses its efforts on these activities:

1–**IWGSC–Arbor Biosciences Collaboration** for the development of tools for the community: exome array, promotor capture panel, etc.;
2–**IWGSC Diversity Project** to characterize the breadth of worldwide wheat diversity by *de novo* sequencing and assembly of at least eight landraces at high quality to obtain ancient wheat haplotypes and sequence multiple landraces and elite cultivars at lower quality to capture modern genetic diversity, including alien introgressions;
3–**IWGSC Gold Standard** reference sequence: gap filling and integration of manual and functional annotation to IWGSC RefSeq v1.0 and subsequent versions;
4–**IWGSC Toolbox**: continued development of user-friendly, integrated databases and tools to benefit public breeders and industry partners.

The IWGSC has an ongoing **collaboration with Arbor Biosciences** to provide tools for the community. In October 2019, *myBaits®* Expert Wheat Exome capture panel, designed using IWGSC RefSeq v1.0, was released. The panel utilizes over two x 10^6 probes to cover 200 megabases of high-confidence exons in the genome and is compatible with both hexaploid and tetraploid cultivars of wheat. The IWGSC and Arbor Biosciences are now working on the design of a promoter capture that will be available soon. Plans also are underway for Arbor Biosciences to develop add-on modules for the exome panel. These will include new manual and functional annotations of IWGSC RefSeq v1.0, the updated and annotated RefSeq v2.1, expected later this year, and genome-wide SNPs.

In the IWGSC **Wheat Diversity 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 v1.0 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. Recent pilot studies and reports from the barley and polyploid sequencing projects are guiding the development of the strategy for tackling the IWGSC wheat diversity project.

An **improved version** of the reference wheat genome, IWGSC RefSeqv 2.0, has been available under the Toronto protocol at the IWGSC data repository hosted by URGI-INRA since July 2019. Additional improvements and corrections and integration of targeted annotation of IWGSC RefSeq v2.0 as well as the manual and functional annotations contributed by the community for RefSeq v1.0 are currently being made. An updated and annotated RefSeq v2.1 is expected to be available to the community later this year.

The IWGSC has decided to scale down its activities to develop integrated **databases**, as new open-source platforms, such as Sherlock, have been released.

In early 2020, the IWGSC started a **webinar series** to showcase research results, tools, and resources in order to connect widely with the wheat community beyond major scientific meetings. All webinars are free to attend and are posted subsequently on the IWGSC YouTube channel [https://www.youtube.com/c/internationalwheatgenomesequencingconsortium].

Data access.

All IWGSC RefSeq v1.0 and associated resources are publicly available at the IWGSC data repository at URGI–INRA Versailles, France. The data are also available at Ensembl Plants, Graingenes and WheatIS.

The IWGSC RefSeq v2.0 assembly is available for download and BLAST under the terms of the Toronto agreement at URGI [https://wheat-urgi.versailles.inra.fr/].

Reference.

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

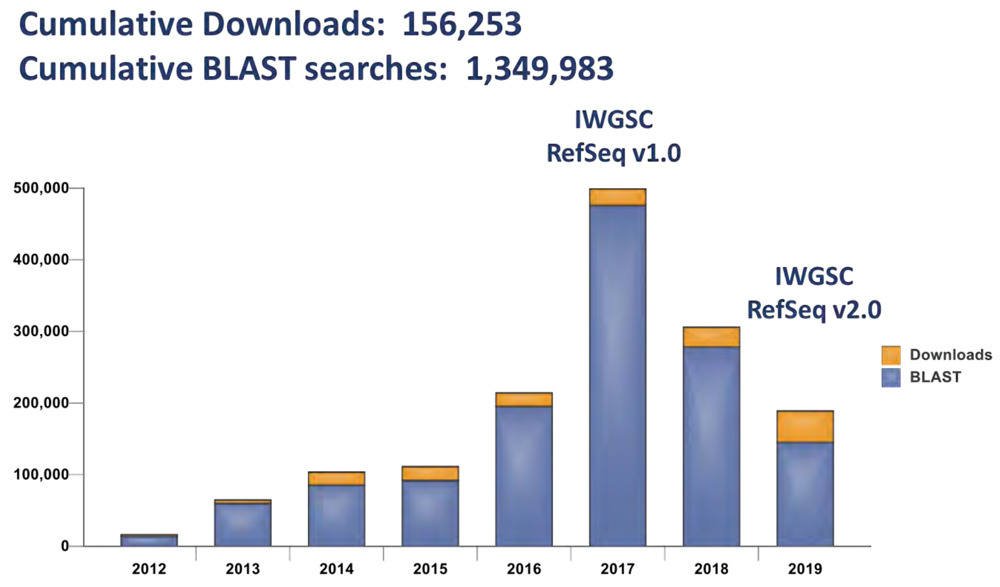

Fig 1. Cumulative downloads and BLAST searches at the IWGSC data repository from 2012 to 2019.

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.

III. CONTRIBUTIONS

ITEMS FROM AUSTRALIA

PLANT BREEDING INSTITUTE — UNIVERSITY OF SYDNEY
School of Life and Environmental Sciences, , Cobbitty, NSW 2570, Australia.

Wheat rust research in Australia – with a focus on the University of Sydney.

Peng Zhang and Robert F. Park.

Wheat is the most important crop in Australia, which is consumed both domestically and export to other countries. Australian wheat is well-known for its high quality and protein content. In recent years, wheat with different attributes have been exported to other countries for special purposes, such as making yellow alkaline noodle in Japan and China, and Japanese udon noodle and biscuit using soft wheat.

Increasing yield per se is not an easy task. However, we could indirectly achieve the yield increase by reducing the losses due to pests and diseases, which can account for 21.5% of the global wheat production (Savary et al. 2019). The three rust diseases (leaf rust, stem rust, stripe rust) are among the most damaging foliar diseases in wheat growing areas worldwide. Year 2020 marks 100 years of rust research at the University of Sydney. In 1921, Professor Walter Waterhouse performed the first race analysis.

It is thought that leaf rust and stem rust urediniospores may have survived on the hay brought from the UK with European settlers. Therefore, these two rusts have been causing serious yield damage since European settlement. Some of the early successful wheat cultivars, bred by the famous Australian wheat breeder William Farrer, were actually early maturing, rather than resistant to rusts, so that they could escape the damages caused by rusts later in the season.

Rust can be controlled by cultural practice and fungicide but fungicide does not provide complete control in highly susceptible cultivars, it also needs to be applied at the right timing. Using resistant cultivars is the most environmentally friendly and economic means to control rust, especially for countries like Australia where the average yield is low (1–1.5 t/ha). Researchers realized very early that in order to be able to manage the rust diseases and breed for resistant cultivars, pathogenicity surveys are critical so that we know which pathotypes are prevalent in the field and which resistance genes are effective. Based on the results from pathogenicity surveys, we provide support to wheat breeders, and also provide timely and regularly updated information on the rust responses of all Australian wheat cultivars to growers through active and regular extension activities. There is an arms race between the rust pathogens and resistance breeding. In order to stay at least one step ahead in the race, we have to know our enemy (the rusts) and what is available up to our sleeves for us to utilise. Australia is one of the very few countries in which breeders/researchers know which rust pathotypes are out there, which rust resistance genes are in the wheat materials, and which genes remain effective in which parts of the country.

Australia has a unique geographical advantage because it is isolated from the rest of the world's wheat-producing areas, except New Zealand. But the prevailing west to east wind direction makes air-borne rust spore movement from Australia to New Zealand more frequent than the other way. Historically, most of the variability in the rust pathogens was generated by mutation. Alternate hosts of wheat rust pathogens, for the sexual cycle on which recombination can occur, do not exist in Australia. Wellings (2007) was able to trace the pathways how different pathotypes of the wheat stripe rust pathogen gained virulence to resistance genes via single-step mutation, and Park et al. (1995) did the same for the wheat leaf rust pathogen and the wheat stem rust pathogen (Park 2007) in surveys since 1988. These surveys have provided the basis for rust resistance breeding efforts in wheat (Park 2008, 2015). In recent decades, mainly because of the significant increase in international travel, quite a few new pathotypes detected in Australia have come from foreign incursions. The two having significant impact were the stripe rust incursions in 1979 from France and in 2002 from

North America. The former was especially damaging, considering that before the 1979 incursion there was no stripe rust in Australia. Our pathogenicity surveys have indicated that the intercontinental movement of rusts is increasing.

After the 1973 stem rust epidemic in Australia, which caused a huge loss of AUD$100–200 x 10^6 at the time, a nationally co-ordinated centralized program National Cereal Rust Control Program (NCRCP) was founded with matching funds from Commonwealth Government and levy from farmers to tackle this serious "social" disease because rusts are airborne, pathogenically variable and sporadic in occurrence. The NCRCP later changed to become the Australian Cereal Rust Control Program (ACRCP), with the University of Sydney as the lead organization and also involving CSIRO, the University of Adelaide, and CIMMYT with funding support from the Grains Research and Development Corporation (GRDC), Australia. In Australia, genetic resistance to rust diseases in wheat alone was estimated to save the industry AUD$1 x 10^9 per annum (Murray and Brennan 2009) and the cost to benefit ratio was 1:21. Since the beginning of the program, one of the most important mandates is to ensure the outputs from our research are translated to the field to help all farmers.

Our R&D includes, but is not limited to, the following aspects: pathogenicity surveys, genetic analysis of the resistance, discovery and characterization of new genes conferring resistance, and germplasm screening, enhancement and deployment. Scientists work collaboratively in all these areas. Monitoring variability in rust pathogen populations is fundamental to all genetic approaches to rust control. We have been extensively involved in resistance gene discovery, and marker development for marker-assisted breeding and cloning. For stripe rust alone, some 19 rust resistance genes have been characterized and designated since 2012. Huge mutational and genetic populations for many wheat resistance genes have been generated, which are available for gene cloning. Gene cloning is crucial for developing perfect markers for high-throughput, marker-assisted breeding and gene pyramiding, discovering new resistance genes to be used in agriculture, providing new insights into gene functions, and allowing cloning of corresponding avirulence effectors so that the mechanism of host-pathogen interaction can be better understood to enable us to design new approach to control diseases.

Our group is one of the world leaders working on rust pathogenomics (Chen et al. 2017), which improves our capability in global surveillance of rusts and allows us to unravel the molecular basis of host: pathogen interactions. We have high throughput rust phenotyping facilities for seeding (greenhouse) and adult-plant (field) testing. Over the past three years, we used selected wheat rust pathotypes to conduct some 56,000 seedling rust tests and more than 165,000 adult plant field rust tests on breeding lines.

References.

Chen J, Upadhyaya NM, Ortiz D, Sperschneider J, Li F, Bouton C, et al. 2017. Loss of *AvrSr50* by somatic exchange in stem rust leads to virulence for *Sr50* resistance in wheat. Science **358**:1607-1610

Murray GM and Brennan JP. 2009. The current and potential costs from diseases of wheat in Australia. GRDC Rep 1-70.

Park RF. 2007. Stem rust of wheat in Australia. Aust J Agric Res **58**:558-566.

Park RF. 2008. Breeding cereal for rust resistance in Australia. Plant Path **57**:591–602.

Park RF. 2015. Long term surveys of pathogen populations underpin sustained control of the rust diseases of wheat in Australia. J Royal Soc New South Wales **148**:15-27.

Park RF, Burdon JJ, and McIntosh RA. 1995. Studies on the origin, spread, and evolution of an important group of *Puccinia recondita* f. sp. *tritici* pathotypes in Australasia. Eur J Plant Path **101**:613-622.

Savary S, Willocquet L, Pethybridge SJ, Esker P, McRoberts N, and Nelson A. 2019. The global burden of pathogens and pests on major food crops. Nature Ecol Evol **3**:430-439.

Wellings CR. 2007. *Puccinia striiformis* in Australia: a review of the incursion, evolution, and adaptation of stripe rust in the period 1979-2006. Aust J Agric Res **58**:567-575.

Publications.

Dinh H, Singh D, Periyannan S, Park R, and Pourkheirandish M. 2020. Molecular genetics of leaf rust resistance in wheat and barley. Theor Appl Genet **133**:2035-2050.

Gao L, Babiker EM, Nava IC, Nirmala J, Bedo Z, Lang L, et al. 2019. Temperature-sensitive wheat stem rust resistance gene *Sr15* is effective against *Puccinia graminis* f. sp. *tritici* race TTKSK. Plant Path **68**:143-151.

Gessese M, Bariana H, Wong D, Hayden M, and Bansal U. 2019. Molecular mapping of stripe rust resistance gene *Yr81* in a common wheat landrace Aus27430. Plant Dis **103**:1166-1171

Hiebert CW, Moscou MJ, Hewitt T, Steuernagel B, Hernández-Pinzón I, Green P, et al. 2020. Stem rust resistance in wheat is suppressed by a subunit of the mediator complex. Nature Comm **11**:1123.

Joukhadar R, Hollaway G, Shi F, Kant S, Forrest K, Wong D, et al. 2020. Genome-wide association reveals a complex architecture for rust resistance in 2300 worldwide bread wheat accessions screened under various Australian conditions. Theor Appl Genet **133**:2695-2712.

Kandiah P, Bariana H, Qureshi N, Wong D, Hayden M, and Bansal U. 2019. dentification of a new source of stripe rust resistance *Yr82* in wheat. Theor Appl Genet **132**:3169-3176.

Kankwatsa P, Park R, and Singh D. 2019. African wheat germplasm: a valuable resource for resistance to rust diseases. Plant Path **68**:1308-1319.

Li J, Chen Q, Zhang P, Lang T, Hoxha S, Li G, and Yang Z. 2019. Comparative FISH and molecular identification of new stripe rust resistant wheat-*Thinopyrum intermedium* ssp. *trichophorum* introgression lines. Crop J **7**:819-829.

Li J, Dundas I, Dong C, Li G, Trethowan R, Yang Z, Hoxha S, and Zhang P. 2020. Identification and characterization of a new stripe rust resistance gene *Yr83* on rye chromosome 6R in wheat. Theor Appl Genet **133**:1095-1107.

Lodhi S, Bariana H, Randhawa M, Gul Alvina, John P, and Bansal U. 2019. Identification of recombinants carrying stripe rust resistance gene *Yr57* and adult plant stem rust resistance gene *Sr2* through marker assisted selection. Plant Breed **138**:148-153 .

Mago R, Zhang P, Xia X, Zhang J, Hoxha S, Lagudah E, Graner A, and Dundas I. 2019 Transfer of stem rust resistance gene *SrB* from *Thinopyrum ponticum* into wheat and development of a closely linked PCR-based marker. Theor Appl Genet **132**:371-382.

Narang D, Kaur S, Steuernagel B, Ghosh S, Bansal U, Li J, Zhang P, et al. 2020. Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat *Aegilops peregrina*. Sci Rep **10**:7573.

Nsabiyera V, Baranwal D, Qureshi N, Kay P, Forrest K, Valarik M, Dolezel J, Hayden M, Bariana H, and Bansal U. 2020. Fine mapping of *Lr49* using 90K SNP chip array and flow-sorted chromosome sequencing in wheat. Front Plant Sci 10:1787.

Randhawa MS, Bains NS, Sohu VS, Chhuneja P, Trethowan RM, Bariana HS, and Bansal U. 2019. Marker assisted transfer of stripe rust and stem rust resistance genes unto four wheat cultivars. Agronomy **9**:497

Singh AK, Zhang P, Dong C, Li J, Singh S, Trethowan RM, and Sharp PJ. 2020. Development and molecular cytogenetic characterization of *Thinopyrum bessarabicum* introgression lines in hexaploid and tetraploid wheats. Theor Appl Genet **133**:2117-2130.

Singh AK, Zhang P, Dong C, Li J, Trethowan R, and Sharp P. 2019. Molecular cytogenetic characterization of stem rust and stripe rust resistance in wheat- *Thinopyrum bessarabicum* derived doubled haploid lines. Mol Breed **39**:125.

Visser B, Meyer M, Park R, Gilligan C, Burgin L, Hort M, Hodson D, and Pretorius Z. 2019. Microsatellite analysis and urediniospore dispersal simulations support the movement of *Puccinia graminis* f. sp. *tritici* from southern Africa to Australia. Phytopathology **109**:133-144.

Wang A, Dong C, Park R, and Roberts T. 2019. Carotenoid complement of rust spores: Variation among species and pathotype. Phytochemistry **161**:139-148.

Wu J, Dong C, Song L, and Park R. 2020. Long-read-based *de novo* genome assembly and comparative genomics of the wheat leaf rust pathogen *Puccinia triticina* identifies candidates for three avirulence genes. Front Genet **11**:521.

Zhang J, Zhang P, Dodds P, and Lagudah E. 2020. How target-sequence enrichment and sequencing (TEnSeq) pipelines have catalyzed resistance gene cloning in the wheat-rust pathosystem. Front Plant Sci **11**:678.

Zhang J, Zhang P, Hewitt T, Li J, Dundas I, Schnippenkoetter W, Hoxha S, Chen C, Park RF, and Lagudah E. 2019. A strategy for identifying markers linked with stem rust resistance in wheat harbouring an alien chromosome introgression from a non-sequenced genome. Theor Appl Genet **132**:125-135.

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 Rio Grande do Sul state, Brazil, 2018.

Ricardo Lima de Castro, Eduardo Caierão, João Leonardo Fernandes Pires, Aloisio Alcantara Vilarinho, 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), which aims to support the indications of cultivars. This work has the objective to evaluate wheat cultivar grain yield performance of the STWC-RS in 2018. The grain yield performance of 30 wheat cultivars (Ametista, BRS 327, BRS Belajoia, BRS Marcante, BRS Reponte, CD 1303, CD 1705, Esporão, FPS Amplitude, FPS Certero, Inova, LG Cromo, LG Fortaleza, LG Oro, LG Supra, ORS 1401, ORS 1402, ORS 1403, ORS 1405, ORS Madrepérola, ORS Vintecinco, TBIO Alpaca, TBIO Audaz, TBIO Iguaçu, TBIO Noble, TBIO Sintonia, TBIO Sinuelo, TBIO Sonic, TBIO Sossego, and TBIO Toruk) was studied in 12 environments (Coxilha, Cruz Alta, Passo Fundo–season 1, Passo Fundo–season 2, Vacaria–season 1, Vacaria–season 2, Augusto Pestana, Eldorado do Sul, Ijuí, Santo Augusto, São Borja, and Três de Maio), in the state of Rio Grande do Sul (RS) in 2018. The experiments were carried out in a randomized block design with three or four repetitions. Each plot consisted of five 5-m rows with 0.2-m spacing between rows and a plant density of ~330 plants/m^2. Grain yield data (kg/ha) 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). The 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, proposed by Carneiro (1988). In this analysis, the ideal cultivar was considered as the cultivar with a high grain yield, a high stability, a 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 2018 was 4,184 kg/ha. The experiment conducted in Coxilha had the highest average wheat grain yield of 5,814 kg/ha. The maximum wheat grain yield was 6,781 kg/ha in Coxilha (cultivar TBIO Sinuelo). Cultivars TBIO Audaz, CD 1705, ORS 1402, ORS Vintecinco, and ORS 1405 had adaptability and stability in favorable environments (environments with an average wheat grain yield higher than that of the general average). Culivars ORS 1402, TBIO Sossego, ORS Vintecinco, CD 1303, and LG Supra had adaptability and stability in unfavorable environments (environments with an average wheat grain yield lower than that of the general average). In general, averaged over all environments, ORS 1402 (4,602 kg/ha), TBIO Audaz (4,611 kg/ha), ORS Vintecinco (4,415 kg/ha), TBIO Sossego (4,428 kg/ha), and CD 1705 (4,436 kg/ha) came closest to the ideal cultivar.

Reference.

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

Wheat crop in the state of Rio Grande do Sul, Brazil, 2018.

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

Rio Grande do Sul is one of the main wheat-producing states in Brazil. Our objective was to analyze the wheat crop in RS in 2018. In 2018, RS harvested 709,558 ha of wheat (34.2% of the total area harvested in Brazil), producing 1,750,700 tons of wheat (32.3% of the Brazilian production), with an average of grain yield of 2,467 kg/ha (157 kg/ha below the Brazilian average of 2,624 kg/ha). Among the geographical mesoregions of Rio Grande do Sul state (Fig. 1), the RS Northwest mesoregion harvested the largest wheat area at 581,134 ha (81.9% of the cropped area in the state) and had the largest production, 1,378,427 tons of wheat grain (78.7% of state production) (Table 1). However, the average of wheat grain yield obtained in this mesoregion was the third lowest of the state: 2,372 kg ha^{-1} (95 kg ha^{-1} below the state average) - Table 1. The RS Northeast mesoregion harvested 36,734 ha of wheat (5.2 % of the cropped area in the state), produced 130,757 tons of wheat grain (7.5 % of state production) and had the highest average of wheat grain yield of the state: 3,560 kg ha^{-1} (1,093 kg ha^{-1} above the state average) - Table 1. The wheat crop in Rio Grande do Sul state, in 2018, had some unfavorable weather conditions, notably (i) lots of rain at the beginning of the crop growing period, resulting in high incidence of soil-borne wheat mosaic virus (SBWMV); and (ii) excessive rainfall in spring, resulting in high incidence of *Fusarium* head blight, the most important wheat disease in Rio Grande do Sul state. Comparing the wheat crop data with the results of the State Test of Wheat Cultivars in Rio Grande do Sul state (STWC-RS), in 2018, it was observed that the average of wheat grain yield of commercial crops was 1,717 kg ha^{-1} below the average of STWC-RS (4,184 kg ha^{-1}).

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 2018 (Source: IBGE. 2020).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	581,134	81.9	1,378,427	78.7	2,372
RS Northeast	36,734	5.2	130,757	7.5	3,560
RS Western Center	34,327	4.8	93,255	5.3	2,717
RS Eastern Center	7,670	1.1	16,322	0.9	2,128
Porto Alegre Metropolitan	1,730	0.2	4,211	0.2	2,434
RS Southwest	42,850	6.0	115,819	6.6	2,703
RS Southeast	5,113	0.7	11,909	0.9	2,329
Rio Grande do Sul State	709,558	100.0	1,750,700	100.0	2,467

Reference.

IBGE. 2020. Produção Agrícola Municipal. Available at: https://www.ibge.gov.br/estatisticas/economicas/agricultura-e-pecuaria/9117-producao-agricola-municipal-culturas-temporarias-e-permanentes.html?=&t=resultados. Acessed 28 March, 2020. Note: Banco de dados agregados de estudos e pesquisas realizados pelo IBGE [In Spanish].

BRS Reponte – high grain yield and wide adaptation wheat cultivar.

Pedro Luiz Scheeren, Eduardo Caierão, Márcio Só e Silva, Ricardo Lima de Castro, Luiz Eichelberger, Martha Zavariz de Miranda, Eliana Maria Guarienti, Alfredo do Nascimento Jr, Flávio Martins Santana, Leila Maria Costamilan, João Leonardo Fernandes Pieres, Maria Imaculada Pontes Moreira Lima, Douglas Lau, Gilberto Cunha, and Sírio Wieholter; Manoel Carlos Bassoi (Embrapa Soja, C.P. 231, 86.001-970 Londrina, Paraná, Brazil); and Vanderlei da Rosa Caetano (Embrapa Clima Temperado, C.P. 403, 96.010-971 Pelotas, Rio Grande do Sul, Brazil).

In wheat breeding, several strategies are applied to improve grain yield. Annually, a great number of cultivars of different origins are crossed. The plants derived from these segregating populations are exposed to the most diverse possible stresses to develop new cultivars with maximum technical and economic efficiency and generate improvements to maximize the economic-environmental sustainability of plantations, while maintaining or increasing the yield potential.

Simultaneously, the cultivar should be highly adaptable to the representative environments of the different wheat-producing regions of the country. BRS Reponte was selected under strong selection pressure, in contrasting environments, over several segregating generations on the experimental fields of Embrapa Wheat (wet area) and Embrapa Soybean (dry area), which probably resulted in the high-grain yield potential and wide adaptation to the different Brazilian wheat-growing regions. Our objective was to describe the yield performance, main agronomic traits, and the profile of processing and industrial quality for the end use of the Embrapa wheat cultivar BRS Reponte.

BRS Reponte was derived from the cross 'PF 980229/3/PF 93232/COOK*4/VPM 1//PF 940374', made in the winter of 2000 in a greenhouse of Embrapa Wheat (CNPT), in Passo Fundo, RS. The initial prehybridization involved an F_1 of 'PF 93232/COOK*4/VPM 1 (=LR 37 SR 38 YR 17=COOK *4/VPM 1)' with line PF 940374 (derived from EMB 27/KLEIN H 3609 b 1111). In the winter of 2001, the F_1 population resulting from the cross was grown in pots for seed multiplication in a greenhouse of Embrapa Wheat and bulk-harvested. In the winter of 2002, seeds were planted as segregating F_2 populations at the experimental station of Embrapa Soybean (CNPSo), in the District of Warta, in Londrina, Paraná. In the summer of 2002–03, seeds of a plant selected in the F_2 generation (22W) were sown in a greenhouse of Embrapa Wheat for multiplication and bulk-harvested (999F). In the winter of 2003, seeds of these plants were multiplied in the greenhouse in the F_3 generation (denominated 999F) and planted as segregating F_4 populations and cultivated again at Embrapa Soybean. A plant, designated 21W, was selected. From 2004 to 2007, all other generations were grown at Embrapa Wheat, in Passo Fundo, RS. Thus, in 2004, seeds of the plant selected in Londrina (21W) were grown in the plantation called Segregating F_5 - Passo Fundo and bulk-harvested (6500F). In the segregating F_6 generation, the plants were bulk-harvested again (6599F). In the F_7 generation, three plants were selected in the field by the genealogical method, i.e., after selection for grain traits, one of the plants was selected and named 3F. The F_8 seeds resulting from this plant were sown at commercial plant density in so-called Observation Plots (or OPs) in 2007. At this point, in 2008, the line with pedigree F68150-22W- 999F-21W-6500F-6599F-3F-0F, was named PF 070759. Also in 2008, the line was evaluated in the Preliminary Wheat Line Trial - 1st Year. In 2009, PF 070759 was tested in the Preliminary Wheat Line Trial - 2nd Year under the responsibility of Embrapa Wheat. Outstanding characteristics for resistance to fungal diseases in general and a good visual appearance of the grain, aside from excellent grain yield potential, were recorded.

The wheat cultivar BRS Reponte, derived from line PF 070759, passed through all experimenal stages until release. In 2010, 2011, and 2012, BRS Reponte was evaluated in a VCU trial to determine the value of cultivation and use. All tests were arranged in a randomized complete block design with three replications (fungicide and insecticide treatments of seeds and shoot). Each experimental unit, consisting of one genotype, was sown in five 5-m rows at a 0.2-m row spacing covering a total area of 5 m^2. All cultural treatments were applied according to the technical instructions of the Brazilian Wheat and Triticale Research Commission of 2009, 2010, and 2011. Prior to sowing, seeds for the tests were treated with triadimenol + imidacloprid. The trials were in the states of Rio Grande do Sul, Santa Catarina, and southern Paraná, in the wheat adaptation regions 1, cold/wet/high, and 2, moderately hot/humid/low. In the state of Rio Grande do Sul, experiments were in the counties of Vacaria (28°30'44", Latossolo Alumínico), Passo Fundo (28°15'46", Latossolo Vermelho Distroférrico), São Borja (28°39'38", Nitossolo Vermelho Distroférrico Latossólico), Três de Maio

Table 2. Grain yield (kg/ha) of BRS Reponte and the control cultivars BRS 327 and Quartzo. Means followed by the same letter are not significantly different according to the Scott–Knott method at a probability of 5%. % = percentage in relation to the mean of the two best control cultivars. Evaluation locations in 2010: L1 = Passo Fundo (June), L2 = Passo Fundo (July), L3 = São Borja 1st season, L4 = São Borja 2nd season, L5 = Três de Maio 1st season, L6 = Três de Maio 2nd season, L7 = Vacaria, L8 = Victor Graeff, L9 = Abelardo Luz, and L10 = Canoinhas. Locations in 2011: L1 = Passo Fundo (June), L2 = Passo Fundo (July), L3 = São Borja 1st season, L4 = São Borja 2nd season, L5 = Três de Maio, L6 = Vacaria, L7 = Victor Graeff, L8 = Canoinhas, L9 = Chapecó, L10 = Guarapuava, and L11 = Ponta Grossa. Locations in 2012: L1 = Cruz Alta, L2 = Passo Fundo (June), L3 = Passo Fundo (July), L4 = Santo Augusto, L5 = São Borja, L6 = São Luiz Gonzaga, L7 = Três de Maio, L8 = Vacaria, L9 = Chapecó, L10 = Guarapuava, and L11 = Ponta Grossa.

	2010		2011		2012		Mean	
Genotype	**kg/ha**	**%**	**kg/ha**	**%**	**kg/ha**	**%**	**kg/ha**	**%**
BRS Reponte	5,554 a	107	5,582 a	116	4,770 a	102	5,302 a	109
BRS 327 (control)	5,029 b	97	4,908 b	102	4,629 a	99	4,855 b	99
Quartzo (control)	5,340 a	103	4,709 b	98	4,701 a	101	4,917 b	101
Mean of control cultivars	5.185	100	4.809	100	4.665	100	4.886	100

(27°46’24:, Latossolo Vermelho Distroférrico), and Victor Graeff (28°15’46”, Latossolo Vermelho Distroférrico); in Santa Catarina in Abelardo Luz (26°33’53”, Latossolo Vermelho), Canoinhas (26°10’38”, Latossolo Bruno Aluminoférrico), and Chapecó (27°05’47”, Latossolo Vermelho Distroférrico); and in Paraná in Guarapuava (25°25’36”, Latossolo Bruno Ácrico Húmico) and Ponta Grossa (25°05’42”, Latossolo Vermelho Distroférrico).

During the VCU trial, BRS Reponte was compared with the control cultivars BRS 327 and Quartzo, which have high yield potential in the tested growing season(s) or throughout the experimental period and are representative of a high percentage of wheat-producing areas of southern Brazil. In overall performance for variable grain yield, the relative percentage of BRS Reponte compared with the mean of the two controls for each year, showed a production of 107% (2012), 116% (2013), and 102% (2014), and mean of 109%, in relation those of the controls, over the three years of evaluation (Table 2, p. 9). The highest grain yield (7,578 kg/ha) was produced in Ponta Grossa in 2010. According the Scott-Knott Mean Comparation Test, the cultivar BRS Reponte was equal to or superior to Quartzo and BRS 327 in each year of evaluation and in the mean of the years. In 2013, 2014, and 2015, complementary trials of distinctness, uniformity, and stability (DUS) were used to meet the requirements of MAPA for the process of cultivar protection. In 2016, BRS Reponte participated as a new cultivar in the ECCT, a state trial of wheat cultivars in Rio Grande do Sul. These evaluations were in the counties of Augusto Pestana, Coxilha, Cruz Alta, Eldorado do Sul, Ijuí, Não-Me-Toque, Passo Fundo, Santo Augusto, São Borja, Sertão, Três de Maio, and Vacaria. All cultural practices were applied according to the technical information of the Brazilian Wheat and Triticale Research Commission of 2016. In wheat breeding and adaptation region 1, BRS Reponte ranked first, with a mean yield of 6,633 kg/ha, corresponding to a relative percentage of 108% of the two best controls of the test. In wheat breeding and adaptation region 2, the cultivar ranked second, with a mean yield of 5,479 kg/ha and a relative percentage of 102% compared to the two best controls of the trial. Statewide, BRS Reponte produced a mean yield of 6,138 kg/ha, corresponding to a relative percentage of 106% of the two best controls (Table 3). With the exception of Region RS2, cultivar BRS Reponte belonged to group a by the Scott-Knott mean comparison test.

Table 3. Grain yield (kg/ha), rank, and relative yield percentage of cultivar BRS Reponte in relation to the mean of the two best controls (Ametista and TBIO Sinuelo) in the State Trial of Wheat Cultivars of Rio Grande do Sul in 2016, in the Mediterranean wheat breeding and adaptation regions 1 and 2, Passo Fundo, 2020. Means followed by the same letter in the table lines are not significantly different according to the Scott–Knott method at 5% probability.

	RS 1		**RS 2**		**RS Geral**	
Cultivar	**kg/ha**	**%**	**kg/ha**	**%**	**kg/ha**	**%**
BRS Reponte	6,633 a	108	5,479 b	103	6,138 a	106
Quartzo	6,170 b	101	5,832 a	110	6,025 a	104
TBIO Itaipu	6,358 b	104	5,380 b	101	5,939 a	103
ORS Vintecinco	6,349 b	104	5,211 b	98	5,861 a	102
TBIO Sinuelo	6,222 b	102	5,277 b	99	5,817 a	101
TBIO Toruk	6,209 b	101	5,178 c	98	5,767 a	100
TBIO Sossego	5,818 c	95	5,416 b	102	5,646 b	98
TBIO Iguaçu	5,877 c	96	5,337 b	101	5,645 b	98
LG Oro	5,820 c	95	5,375 b	101	5,629 b	98
BRS Marcante	5,945 c	97	5,188 c	98	5,620 b	97
BRS 327	6,038 b	99	5,006 c	94	5,596 b	97
CD 1104	5,846 c	96	5,258 b	99	5,594 b	97
Campeiro	5,874 c	96	5,172 c	97	5,573 b	97
Ametista	5,874 c	96	5,125 c	97	5,553 b	96
Jadeíte	5,749 c	94	5,286 b	100	5,551 b	96
TBIO Mestre	5,628 c	92	5,439 b	102	5,547 b	96
TBIO Noble	5,907 c	97	4,985 c	94	5,512 b	95
Topázio	5,603 c	92	5,131 c	97	5,401 c	94
Marfim	5,809 c	95	4,825 d	91	5,388 c	93
BRS Parrudo	5,798 c	95	4,831 d	91	5,384 c	93
CD 1805	5,537 d	90	5,076 c	96	5,339 c	93
TBIO Pioneiro	5,765 c	94	4,760 d	90	5,334 c	92
ORS 1401	5,561 d	91	4,933 d	93	5,292 c	92
LG Prisma	5,490 d	90	4,775 d	90	5,184 d	90
TBIO Sintonia	5,586 d	91	4,621 d	87	5,172 d	90
TBIO Tibagi	5,789 c	95	4,304 e	81	5,153 d	89
Esporão	5,511 d	90	4,534 e	85	5,092 d	88
Mean 2T	6,118	100	5,309	100	5,772	100
Overall mean	5,838		5,052		5,501	

BRS Reponte is a medium-sized cultivar (mean height 87 cm in Passo Fundo, RS) with an early cycle (an average 75 days-to-heading and 132 days-to-maturity in Passo Fundo). In the plant growth phase, the cultivar is moderately susceptible to lodging and moderately blight and frost-resistant. In terms of biotic stresses, BRS Reponte is moderately susceptible to wheat mosaic virus and yellow dwarf barley virus; characterized by resistance to powdery mildew (*Blumeria graminis*) and moderate resistance to Fusarium head blight (*Fusarium graminearum*); moderately susceptible to tan spot of wheat (*Pyrenophora tritici-repentis* (Died.) Drechsler) and to leaf rust on adult plants (*Puccinia triticina*). For preharvest sprouting, the reaction is moderately resistant. In terms of end use quality, cultivar BRS Reponte was classified as bread wheat in the Homogeneous Wheat Region 2 of Rio Grande do Sul and Santa Catarina and as domestic wheat in the Homogeneous Wheat Breeding and Adaptation Region 1 of Rio Grande do Sul, Santa Catarina, and Paraná, according to the Normative Instruction No. 38, of November 30, 2010, since, respectively, 72% and 68% of the samples were classified in the respective classes.

BRS Reponte grain samples from the Homogeneous Wheat Breeding and Adaptation Region 1 of Rio Grande do Sul, Santa Catarina, and Paraná, analyzed between 2012 and 2014 in the Laboratory of Grain Quality of Embrapa Wheat, the mean gluten strength (W) was 251 x 10^{-4} J with a mean elasticity index (Ie) 45.2% (Table 4). In samples from the Homogeneous Wheat Breeding and Adaptation Region 2 of Rio Grande do Sul and Santa Catarina analyzed in the same period, the mean gluten strength (W) for BRS Parrudo was 310 x 10^{-4} J with a mean elasticity index (Ie) 50.9%. The preliminary end-use quality classification of bread wheat suggests the use of this cultivar for bread, pasta, and cracker production and as a domestic wheat, suggests flour production for domestic use, confectionery, and other products.

Table 4. Industrial and processing quality traits of cultivar BRS Reponte in the Wheat Adaptation Regions 1 and 2 of Brazil, from 2010 to 2012; Passo Fundo, 2020. For the tenacity/extensibility ratio, P = tenacity or resistance to extension and L = dough extensibility or average abscissa at bubble rupture (mm). Representative locations of region 1 are Passo Fundo, Rio Grande do Sul (RS); Vacaria (RS); Victor Graeff (RS); Canoinhas, Santa Catarina (SC); Ponta Grossa, Paraná (PR), and Guarapuava (PR). Representative locations of Region 2 are São Borja (RS), Três de Maio (RS), Chapecó (SC), and Abelardo Luz (SC).

Traits	Mean of Region 1	Mean of Region 2	Overall mean or sum
Number of samples/region	25	25	50
Mean of falling number	350	338	344
Mean of gluten strength (x10^{-4} Joules)	310	251	230
Mean of luminosity (0 = black, 100 = white (Minolta))	92.7	92.2	92.6
Mean of color b (+ = yellow hues, – = blue hues (Minolta))	10.4	10.0	10.2
Mean of tenacity/extensibility ratio (P/L)	0.9	0.9	0.9
Mean of elasticity index (%)	45.2	50.9	48.0

The flag leaf of cultivar BRS Reponte is on a predominantly upright stem with light-colored auricles. The shape of the highest node on the stem is wide. The predominantly pyramidal shaped ear of the cultivar is awned, light colored and bears longish red grains. BRS Reponte is registered (#32066) and protected (# 20160199) by the Ministry of Agriculture, Livestock and Food Supply (MAPA). Embrapa Wheat is responsible for the production of genetic seed of the cultivar and Embrapa Products and Market (SPM) for production of basic seed. The first batch of basic seed was released for sale in 2017, because of a delay in the protection enforcement due to technical constraints of the DUS (Distinguishability, Uniformity and Stability) tests of the cultivar by MAPA.

References.

Comissão Brasileira de Pesquisa de Trigo e Triticale. 2011. Indicações Técnicas para Trigo e Triticale – Safra 2012. Embrapa Agropecuária Oeste, Dourados. 204 pp [In Spanish].

Comissão Brasileira de Pesquisa de Trigo e Triticale. 2012. Indicações Técnicas para Trigo e Triticale – Safra 2013. Instituto Agronômico do Paraná (Iapar), Londrina, PR. 220 pp [In Spanish].

Comissão Brasileira de Pesquisa de Trigo e Triticale. 2013. Indicações Técnicas para Trigo e Triticale – Safra 2014. Fundação Meridional, Londrina, PR. 235 pp [In Spanish].

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TaAPO-A1, an ortholog of rice ABERRANT PANICLE ORGANIZATION 1, is associated with total spikelet number per spike in elite European hexaploid winter wheat cultivars.

We dissected the genetic basis of total spikelet number (TSN) along with other traits, viz. spike length (SL) and flowering time (FT) in a panel of 518 elite European winter wheat varieties. Genome-wide association studies (GWAS) based on 39,908 SNP markers revealed highly significant quantitative trait loci (QTL) for TSN on chromosomes 2D, 7A, and 7B, for SL on 5A, and FT on 2D, with 2D-QTL being the functional marker for the gene *Ppd-D1*. The physical region of the 7A-QTL for TSN revealed the presence of a wheat ortholog (*TaAPO-A1*) to *APO1* – a rice gene that positively controls the spikelet number on the panicles. Interspecific analyses of the *TaAPO-A1* orthologs showed that it is a highly conserved gene important for floral development and present in a wide range of terrestrial plants. Intraspecific studies of the *TaAPO-A1* across wheat genotypes revealed a polymorphism in the conserved F-box domain, defining two haplotypes. A KASP maker developed on the polymorphic site showed a highly significant association of *TaAPO-A1* with TSN, explaining 23.2% of the total genotypic variance. Also, the *TaAPO-A1* alleles showed weak but significant differences for SL and grain yield. Our results demonstrate the importance of wheat sequence resources to identify candidate genes for important traits based on genetic analyses.

Genetic control of spikelet sterility and yield-related traits in winter wheat.

Grain yield improvement in wheat requires a deep genetic understanding of grain yield-related traits (e.g., spikelet fertility and sterility), which is imperative need for covering the global food demand. In this study, we detected ample natural variation with moderate to high heritability values in 22 agronomic traits collected over 8 years of field experiments from ancient hexaploid wheat accessions. A GWAS using 15K SNPs with Best linear unbiased estimates for traits over the years was applied to reveal the genetic factor in the studied traits. Many QTL associated with agronomic traits were detected. The GWAS output was supported via other biostatistical and bioinformatics analyses to detect the most causative SNPs and then putative candidate genes underlying the agronomic traits. Six SNPs co-located physically within the genes encoding enzymes, hormone response, metal ion transport, and response to oxidative stress, have been identified. Metal ion transport and *Gibberellin 2-oxidases* (*GA2oxs*) genes showed strong involvement in controlling spikelet sterility, which had not been reported yet in wheat. These genes were highly expressed in yield components. Applying genome-wide prediction outputs revealed moderate to high values that encourage the implementation of the traits to accelerate breeding of yield improvement by making an early prediction. These findings demonstrate the usefulness of ancient wheat accessions as a valuable resource for yield-boosting.

Genetic dissection of grain architecture-related traits in a winter wheat population.

The future productivity of wheat as the most grown crop worldwide is the utmost importance for global food security. Thousand-kernel weight (TKW) is closely associated with kernel size traits, such as kernel length, kernel width, and kernel diameter ratio in wheat. Kernel size traits usually contribute to grain yield by affecting the TKW and also can be associated with milling and processing of wheat. Discovering the natural variation of the genetic architecture of complex traits and detect QTL as well as identifying candidate genes associated with traits is our main aim. Therefore, grain architecture-related traits and TKW were measured for 3 years from each of 261 worldwide winter wheat accessions. Significant differences ($P < 0.001$) among years, genotypes, and their interaction were detected. A GWAS was performed using the 15K Infinium SNP array that consisted of 17,093 valid SNPs after quality control. FARM-CPU model using (GAPIT) in R was applied in order to to avoid any false negative and control for the false positive associations by preventing model overfitting. We found many QTL, including 79 highly associated SNPs across 13 chromosomes, of which eight multi-traits associated SNPs. The identified candidates genes showed strong involvment in controlling at least two or more grain architecture traits. These findings offer valuable results for pyramiding novel genetic regions conferring proper grain characteristics and providing further insights for understanding the genetics of grain yield.

Impact of foliar diseases on wheat fruiting efficiency.

Several estimations indicate that current genetic gains in wheat will not be enough to satisfy the increased demand of this cereal. Thus, identifying physiological traits that remain stable in the presence of biotic stresses to increase wheat yield potential is fundamental. Foliar diseases are one of the main biotic factors limiting wheat yield. Wheat yield can be analyzed in terms of two principal components, the number of grains per unit area and their average weight, being variations more associated to the grain number. Grain number can be considered the product of the spike dry weight and the number of grains set per unit of spike dry weight, i.e., fruiting efficiency (FE), which indicates the efficiency with which resources allocated to the spikes at anthesis are used to set grains. For the last 50 years, improvements in wheat yield were obtained by increasing the number of grains per unit area, althrough a higher biomass partition to the spike and FE could be a suitable trait for selection to increase the grain number. Furthermore, FE might constitute a possible attribute of wheat tolerance, as there could exist genotypes that maintain a high FE in the presence of diseases, which could keep the yield stable in such conditions. Nevertheless, before implementing FE as a selection criterion for increasing yield in breeding programs, it is necessary to consider whether it may cause important trade-offs with other yield components, such as grain weight. The present work aims to (i) assess the effect of foliar diseases on FE and (ii) determine the relationships and possible presence of trade-offs or associations between FE, grain weight, and heading date, given the variability of the genotypes used. Experiments were at the Julio Hirschhorn Experimental Station, National University of La Plata, Argentina, using a split-plot design. The main plots were the fungicide treatments, with or without fungicide. The subplots were a collection of 110 spring wheat genotypes previously mapped provided by IPK, Gatersleben, Germany. Disease severity (%) was obtained by visual estimation of the percentage of leaf area affected by foliar diseases at three growth stages (GS), shoot development (GS31), anthesis (GS60), and early dough grain (GS80), and the ABCPE was estimated. The number of grains per spike, spike dry weight at maturity, and date of heading was assessed and FE calculated. Data were analyzed using ANOVA and a correlation analysis between TKW and FE was made for each genotype. Significant differences were observed for severity within genotypes, treatments, and the interaction of 'genotypes × treatments' at GS60 and GS80. At GS31, severity showed significant differences only among genotypes. The genotypes were mostly affected by leaf rust (*Puccinia triticina*) and tan spot (*Pyrenophora tritici-repentis*). The FE was significantly different among genotypes. The fungicide treatments and the 'genotypes × treatments' interaction did not show significant differences for this trait. Nevertheless, there where genotypes that did not show a decrease in FE in the presence of foliar diseases, suggesting that FE could be a component of wheat tolerance. We found no correlation between FE and TKW, supporting the idea that there is not a competitive partial compensation (trade-off) between them and offers evidence that FE could be improved without altering TKW within this set of genotypes. Moreover, there were no associations between the number of grains per spike, FE, and heading date. In contrast, TKW and heading date did show associations. This work will continue with the identification of QTL for FE and associated traits.

Broadening the genetics bases of wheat breeding lines using crosses with landraces to overcome biotic and abiotic stresses.

This project, started in 2011, aimed to develop new plant materials suitable to tolerate biotic and abiotic stresses. These materials mainly received from genebank of Germany (IPK-Gaterslebnen), Czech Republic, and ICARDA and originated from Iran, Afghanistan, Pakistan, India, Nepal, Turkey, Iraq, Syria, Azerbaijan, and Tajikistan. In addition, many modern cultivars from all over the world were included. Then these materials were evaluated based on several agronomic traits at field experiments on 6 consecutive years. Simultaneously, part of this collection was tested for drought and salinity under PEG and hydroponic cultures in the lab, respectively. Some of lines were tested using allele-specific markers for breadmaking quality and vernalization genes. After the first two years of evaluation, many crosses were made to generate segregating populations. In order to broaden the genetic bases of the new wheat breeding lines, the crosses were made using landraces as at least one of the parents. Crosses between the accessions were continued in the following years. Currently, segregating populations include 20 in the F_6 generation (each having 1,000–5,000 individuals), 40 in the F_4 generation, 90 in the F_3 generation, 100 in the F_2 generation, 50 in the F_2 generation derived from double crosses, and 100 in the F_1 generation. In 2019, among the F_6 populations, 900 lines were selected based on a primary evaluation and this year are being tested agin. Next year, the F_6 populations will be evaluated in field experiments for drought and salinity stresses. Above all, our wheat collection harbors more than 2,300 accessions and we plan to increase the number of the accessions to 4,000. Meanwhile, two panels of accessions, each including 184 accessions, were selected for a GWAS for different traits. Finally, this project is open for international collaboration to release new drought, salinity, and disease stress-tolerant cultivars in the future.

Viability and storability of short-lived wheat pollen.

Wheat sheds tricellular pollen at maturity, which rapidly loses (within one hour) the ability to germinate under ambient conditions. To gain a comprehensive overview of processes contributing to viability loss, identifying viable pollen is required. Therefore, the present study aims to evaluate and improve pollen viability tests and identify parameters affecting the viability and storability of pollen.

The analysis of pollen tube growth on 112 liquid and 45 solid artificial media revealed that a solid medium with 594 mM raffinose, 0.81 mM H_3BO_3, and 2.04 mM $CaCl_2$ at pH5.8, showed the highest pollen germination. Partly or complete substitution of raffinose by other sugars, such as sucrose, maltose, or sorbitol, reduced the *in vitro* germination of the pollen, assuming a higher metabolic efficiency or antioxidant activity of raffinose. *In vitro* pollen germination varied between 26 lines ($P < 0.001$); between winter (15.3 ± 8.5%) and spring types (30.2 ± 13.3%), and was highest for the spring wheat TRI 2443 (50.1 ± 20.0%). Alexander staining failed to discriminate between viable, fresh pollen and inviable pollen inactivated by ambient storage for >60 min. The viability of fresh wheat pollen, assessed by fluorescein diacetate (FDA) staining and impedance flow (IF) cytometry using the Ampha Z32, was 79.2 ± 4.2% and 88.1 ± 2.7%, respectively. When inviable, stored pollen was additionally tested, it correlated at an r = 0.54 ($P < 0.05$) and r = 0.67 ($P < 0.001$) with *in vitro* germination, respectively. Although wheat pollen beneficially developed on medium containing raffinose, fresh pollen contained only minor amounts. Sucrose was the most abundant sugar, followed by glucose and fructose. After storage for one hour at ambient and cold conditions, the content of the soluble sugars increased by two- to three-fold, assuming that sugars are actively mobilized during pollen storage.

In conclusion, wheat pollen shows a high metabolic activity after shedding, which may lead to rapid viability loss. Pollen viability can be analysed by FDA staining and IF cytometry. These tests may overestimate pollen tube growth. Artificial media for *in vitro* pollen germination require specific adaptations. On adapted media, pollen tube growth can be exactly analyzed. However, as the exact viability of a larger pollen batch can be elusive, a combination of pollen viability tests may provide reasonable indications of the ability of pollen to germinate and grow.

A SNP-based GWAS analysis of seed longevity.

Seed longevity varies among different species and could be influenced by several environmental factors during seed formation, harvest, and storage. Genetic analysis of seed has been carried out in several crop species using various marker systems and populations. We reanalyzed two association mapping panels (a winter wheat (WW) and spring wheat (SW) collection) genotyped with high-quality SNP marker system to look for potential novel loci linked to longevity, search for possible candidate genes, and obtain a better understanding of the mechanisms in seed deterioration in wheat. Association analysis of WW revealed a total of 16 associations on chromosomes 1A, 2A (10 associations), 2D, 6B (three associations), and 7A linked to longevity. Likewise, a total of 56 associations were uncovered in SW, observed on chromosomes 1A, 1B (10 associations), 2A (two associations), 2B (six associations), 2D, 3A (two associations), 3B, 4A (two associations), 4B (16 associations), 5B (nine associations), 7A (three associations), 7B (two associations), and 7D. The associations discovered could be confined to 24 QTL based on the marker proximities to each other. Among them, four QTL were observed in WW, 18 QTL in SW, and two QTL were common to both WW and SW. The loci were distributed on chromosomes 1A (two QTL), 1B, 2A (four), 2B (two), 2D, 3A, 3B, 4A (two), 4B (two), 5B (three), 6A, 7A (two), 7B, and 7D. Of these, 11 QTL were reported earlier. The rest of the 13 QTL on chromosomes 2A (two), 2B, 3A, 4A, 4B, 5B (two), 6A, 7A (two), 7B, and 7D, are potentially novel. The new QTL in this study highlight the importance of proper genome coverage to identify most of the related loci influencing the trait of interest.

A BLAST analysis revealed a total of 37 genes probably involved in seed longevity, which potentially can be targeted for advanced molecular research towards seed longevity in wheat. Common candidate genes to other studies are *stem rust resistance protein Rpg1* and *NBS-LRR resistance-like protein FAR1-related sequence 6-like protein*. In SW, we also calculated that with the pyramiding of favorable alleles, an increase of up to 12.79% in longevity could be witnessed, which confirms that seed longevity is a polygenic trait.

In conclusion, our analysis discovered 13 potentially novel loci for seed longevity using SNP whole-genome mapping in two different association mapping populations. These novel loci were unnoticed in previous reports. Furthermore, this highlights the importance of dense genetic maps covering otherwise uncovered genome parts to detect novel loci for seed longevity. Moreover, because more and more populations are being characterized with SNPs, the results of this investigation will help genebank curators and plant breeders to decide about regenerating their germplasm.

The effects of growth retardants on 1,000-kernel weight and plant height in winter wheat.

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Abstract. The effects of growth retardants interfering with the gibberellic acid (GA) metabolism on plant height are well documented. We were interested to additionally study the effects of growth retardants on grain size in wheat lines where plant height and grain size depended on the genotype. In nearly isogenic wheat lines containing the dwarfing gene *Rht12* as well as in wheat lines containing the QTL for grain size *QTgw.ipk-7D,* the effects of three growth retardants Regalis, Cycocel, and Topflor on the expression of plant height and grain size were measured as 1,000-kernel weight (TKW) were investigated. Plant height was mainly reduced by Regalis and Cycocel preanthesis treatments. A reduction of grain size was caused by a Regalis postanthesis treatment in most lines, whereas in several cases, a preanthesis application of growth retardants led to an increase in grain size. In control blocks, a correlation between grain size and plant height was observed, which remained stable in most treatments, except the Regalis preanthesis treatment. Our results support the conclusion that GAs play a role in the expression of grain size, and that interference in GA metabolism can interfere with grain development.

Introduction. The starting point of the current study were two sets of wheat lines where a positive correlation of grain size and plant height were observed based on the genotype. The first set of lines include introgression lines of the winter wheat cultivar Prinz with an introgression of a synthetic wheat on chromosome 7D, which leads to increased TKW and, secondary, an increase in plant height (Röder et al. 2008). The second set of lines is a collection of nearly isogenic lines carrying the GA-sensitive dwarfing gene *Rht12*. The effect of the allelic status of *Rht12*/*rht12* on TKW was described earlier (Worland et al. 1994) and also was confirmed in the current study. Because the genetic dissection of these wheat lines did not allow us to distinguish if the simultaneous effects on plant height and TKW were caused by the pleiotropic action of a single gene or by the action of two closely linked genes, we were interested to investigate if both effects could functionally be dissected by the application of growth retardants.

A number of chemical compounds were described to interfere with gibberellin biosynthesis at various stages of the metabolic pathway and many of these compounds are applied in agriculture as growth retardants with effects on plant height and architecture (for review see Rademacher 2000). Although the role of GA on the expression of plant height is well documented (Schwechheimer and Willige 2009), several reports also describe regulatory effects of GA in embryogenesis and seed development (Holdsworth et al. 2008). The decrease of bioactive GAs led to dwarf phenotypes and decreased grain size in transgenic wheat plants (Appleford et al. 2007).

The effects of the growth retardant chlormequat (CCC) on plant height and yield in GA-insensitive wheats were examined by Gale and Youssefian (1984). Isogenic lines carrying *Rht-B1b* (*Rht1*) and *Rht-D1b* (*Rht2*) were almost unaffected by the chemical. However, investigating GA-insensitive ‘tall dwarfs’, Börner and Meinel (1993) found a positive effect of CCC on yield resulting from shortening the plant. The authors concluded that even in the case of GA-insensitive wheats, a plant height optimum may be beneficial.

The goal of this investigation was to study the effects of three growth retardants on the expression of plant height and grain size in dependence of the genotype of the plant.

Materials and methods. In the first experiment, lines derived from the winter wheat cultivar Prinz were investigated. The Prinz-derived lines are described in Röder et al. (2008). They comprise homozygous BC$_4$F$_3$ lines with and without an introgression of the synthetic wheat W-7984 (lab designation M6) on chromosome 7D in the genetic background of the cultivar Prinz. The presence of the introgression was determined by the allelic state of the microsatellite marker *Xgwm1002-7D,* which explains a major portion of the phenotypic variance of TKW and plant height in these lines. When the introgression is present, the plants have a higher TKW and are taller than the control lines without introgression or the original Prinz cultivar. In these experiments, each treatment block has two replicates (10 plants each) of Prinz, two BC$_4$F$_3$ lines without the introgression, and four BC$_4$F$_3$ lines with the introgression were included. Each line was represented with 10 plants in each treatment block.

The focus of the second experiment was on introgression lines carrying the dwarfing gene *Rht12*. This material was obtained from A.J. Worland, John Innes Centre, Norwich, UK. The *Rht12* gene was introgressed in various genetic backgrounds from a mutant of the winter wheat Karcag 522 (Viglási 1968). Specifically, the following pairs of lines were investigated: AJ/AB 23-1 (Mercia, *Rht12*) and AJ/AB 24-1 (Mercia, *rht12*); AJ/AB 25-1 (Mercia, *Rht12*) and AJ/AB 26-1 (Mercia, *rht12*); AJ/AB 27-1 (Bezostoya, *Rht12*) and AJ/AB 28-1 (Bezostoya, *rht12*); AJ/AB 29-1 (Bezostoya, *Rht12*) and AJ/AB 30-1 (Bezostoya, *rht12*); AJ/AB 43-1 (Huntsman, *Rht12*) and AJ/AB 44-1 (Huntsman, *rht12*); and AJ/AB 45-1 (Huntsman, *Rht12*) and AJ/AB 46-1 (Huntsman, *rht12*). The *Rht12* gene was originally mapped on the distal end of the chromosome arm 5AS (Korzun et al. 1997). We mapped the gene again in 223 F$_2$-plants of the cross 'AJ/AB 23-1 × AJ/AB 24-1'. The *Rht12* gene was closely linked to the locus for awn inhibitor *B1* and mapped in the interval of microsatellite markers *Xgwm995* and *Xwmc524* (Fig. 1).

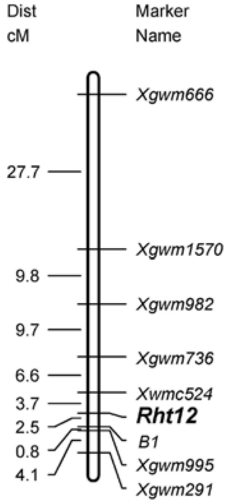

Fig. 1. Genetic map of chromosome arm 5AL containing the dwarfing gene *Rht12* and the awn inhibitor *B1*.

The experiment consisted of 10 treatment blocks each containing all wheat lines that were tested. Each wheat line was represented with one row of 10 plants in each treatment block. The spacing of the rows was 15 cm. Four blocks represented untreated control blocks. Each of the remaining blocks was tested with one of the following growth retardants: Regalis (BASF, Germany; applied concentration 0.15%), Cycocel (Feinchemie Schwebda GmbH, Germany; applied concentration 0.2%), and Topflor (Spiess-Urania Chemicals GmbH, Germany; applied concentration 0.05%). For each growth retardant, one preanthesis treatment (22 May, 2008) and one postanthesis treatment (9 June, 2008) was applied. The average flowering time was 29 May, 2008. The preanthesis treatment was applied before ear emergence, the postanthesis treatment ~10 days after flowering. Plant height was measured from soil to the tip of the plant, excluding awns, in five plants per row. From each plant, the main spike was harvested and TKW determined by calculating grain weight per spike/grain number/spike.

Table 1. Two-way ANOVA in cultivar Prinz-derived lines.

Source of variation	Degrees of freedom	Sum of squares	Mean squares	F-value	P-value
PLANT HEIGHT					
Treatment	9	8,644	960	57.1	<0.001
Genotype	2	1,883	941	56.1	<0.001
Treatment × Genotype	18	839	46	2.8	<0.001
Residual	360	6,043	16	—	—
Total	389	19,297	49	—	—
1,000-KERNEL WEIGHT					
Treatment	9	3,229	358	29.6	<0.001
Genotype	2	1,632	816	67.3	<0.001
Treatment × Genotype	18	687	38	3.1	<0.001
Residual	766	9,282	12	—	—
Total	795	15,198	19	—	—

The statistical analysis was based on five measurements for plant height and 10 measurements for TKW for each line/treatment combination. The ANOVA and t-test analysis was conducted with the program SigmaPlot 11.0. The program tested automatically for normality of the phenotypic distribution and for equality of variance. In cases where these tests failed, a

Table 2. Effects of growth retardants on plant height in Prinz-derived lines; absolute plant height is given in cm. The control is a mean of four replications. ^{2} Application of a Mann-Whitney rank sum test. *, **, *** significant treatment compared to control at *P<0.5*, *P<0.01*, *or P<0.001*, respectively. ↑ increasing or ↓ decreasing effect compared to control.

Line	Genetic background	Control	Regalis (preanthesis)	Regalis (postanthesis)	Cycocel (preanthesis)	Cycocel (postanthesis)	Topflor (preanthesis)	Topflor (postanthesis)
Prinz	*Xgwm1002-Prinz*	70.8	56.4***^{2}↓	73.2	63.4***^{2}↓	70.3	68.9*^{2}↓	70.4
BC_4F_3-lines without introgression (2 lines)	*Xgwm1002-Prinz*	68.1	54.9***^{2}↓	70.5	63.3***^{2}↓	69.4	67.9	69.4
BC_4F_3-lines with introgression (4 lines)	*Xgwm1002-M6*	74.5	54.4***^{2}↓	74.6	69.7***^{2}↓	72.2*↓	74.0	72.2

Table 3. Effects of growth retardants on 1,000-kernel weight in Prinz-derived lines; calculated weight is given in grams. The control is a mean of four replications. ^{2} Application of a Mann-Whitney rank sum test. *, **, *** significant treatment compared to control at *P<0.5*, *P<0.01*, *or P<0.001*, respectively. ↑ increasing or ↓ decreasing effect compared to control.

Line	Genetic background	Control	Regalis (preanthesis)	Regalis (postanthesis)	Cycocel (preanthesis)	Cycocel (postanthesis)	Topflor (preanthesis)	Topflor (postanthesis)
Prinz	*Xgwm1002-Prinz*	62.3	62.1	53.2***↓	61.7	58.8***↓	63.5	61.0*^{2}↓
BC_4F_3-lines without introgression (2 lines)	*Xgwm1002-Prinz*	60.1	60.4	56.5***↓	60.6	59.9	62.9***^{2}↑	59.8
BC_4F_3-lines with introgression (4 lines)	*Xgwm1002-M6*	63.5	64.6	59.2***↓	66.1***↑	61.9*↓	66.0***^{2}↑	61.0**^{2}↓

Mann-Whitney rank sum test was performed alternatively to a t-test.

Results. Three groups of lines (genotypes) were tested comprising the winter wheat cultivar Prinz, four BC_4F_3 lines with genomic introgression on chromosome 7D and two BC_4F_3 lines without genomic introgression on chromosome 7D. Ten treatment blocks were performed, of which four blocks represented untreated control blocks. A two-way ANOVA analysis indicated that for plant height treatment as well as genotype and the interaction of both were siginificant with $P < 0.001$ (Table 1, p. 16). Treatment and genotype showed similar F-values of 57.1 and 56.1, respectively. All three variants, treatment, genotype, and interaction, also were significant for TKW. Here, the most variance was found in the genotype with an F-value of 67.3 compared to 29.6 for treatment.

The treatments comprised the application of three growth retardants Regalis, Cycocel, and Topflor; each was tested in a preanthesis and a postanthesis spraying. For plant height, the most significant effect was detected in the Regalis preanthesis treatment, which reduced the plant height to between 72.9% and 80.6% compared to the untreated controls (Table 2). Significant effects with $P < 0.001$ in a t-test also were observed for the Cycocel preanthesis treatment, which reduced plant height from 89.6% to 93.5% compared to the untreated controls. All other treatments were not significant or showed only spurious effects in single cases.

In the controls, the BC_4F_3 lines with an introgression were significantly taller ($P<0.001$ in a Mann-Whitney rank sum test) than the BC_4F_3 lines without an introgression and the Prinz lines. The same pattern of genotypic-based differences in plant height was also observed in the Cycocel preanthesis treatment, whereas in the Regalis preanthesis treatment no genotype-based significant differences in plant height were found (Fig. 2, p. 18).

Considering TKW, the most severe treatment effects were observed for the postanthesis Regalis treatment, which led to a reduction of 85.4% to 94.0% compared to that of the untreated controls ($P<0.001$ in a t-test). Less significant tendencies towards the reduction of TKW also were observed in the Cycocel postanthesis and Topflor postanthesis treatments in specific genotypes (Table 3). On the other hand, Cycocel preanthesis and Topflor preanthesis treatments resulted in increased TKW for the BC_4F_3 lines with an introgression. The genotype-based differences in TKW between BC_4F_3 lines without and with introgression were significant at *P<0.001* in all cases except the Cycocel postanthesis and the Topflor postanthesis treatments (Fig. 3).

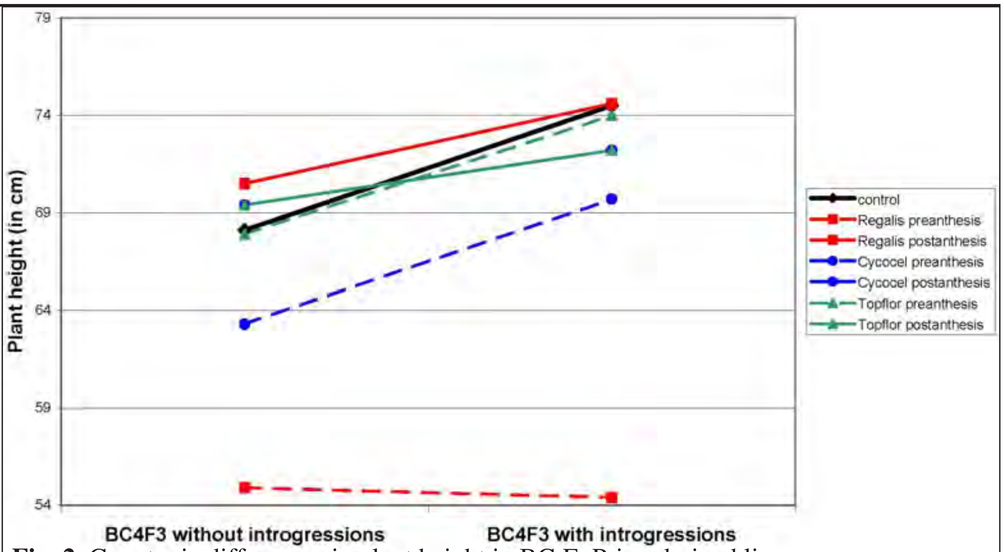

Fig. 2. Genotypic differences in plant height in BC_4F_3 Prinz-derived lines.

The correlation coefficients between plant height and TKW ranged from 0.25 to 0.78 in the four control blocks, with an average of 0.54 over all control blocks. The correlation coefficients dramatically decreased and inverted into negative correlations for the Regalis preanthesis and the Cycocel postanthesis treatments. The disturbance of correlation in the Regalis preanthesis treatment is mainly caused by effects on plant height (Table 4, p. 19).

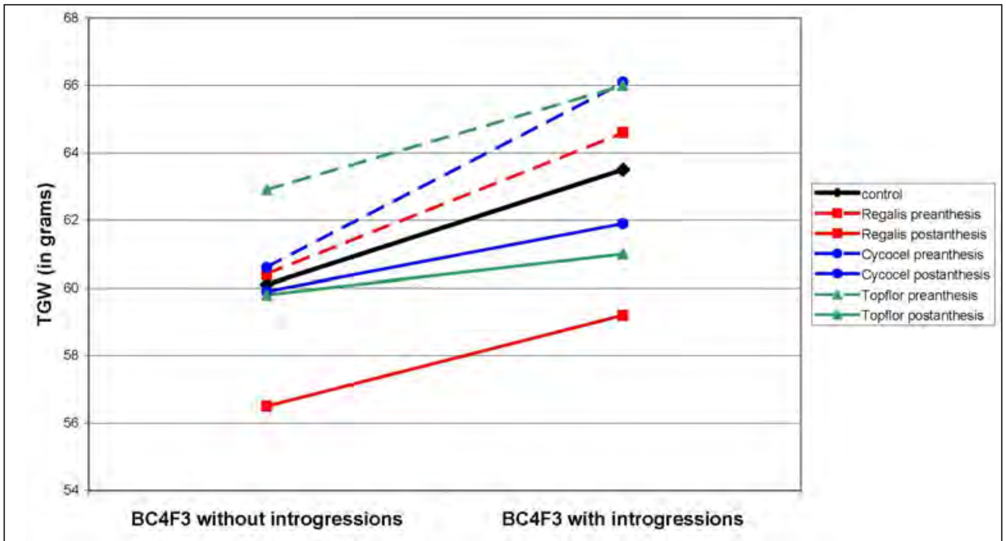

Fig. 3. Genotypic differences in 1,000-kernel weight in BC_4F_3 Prinz-derived lines.

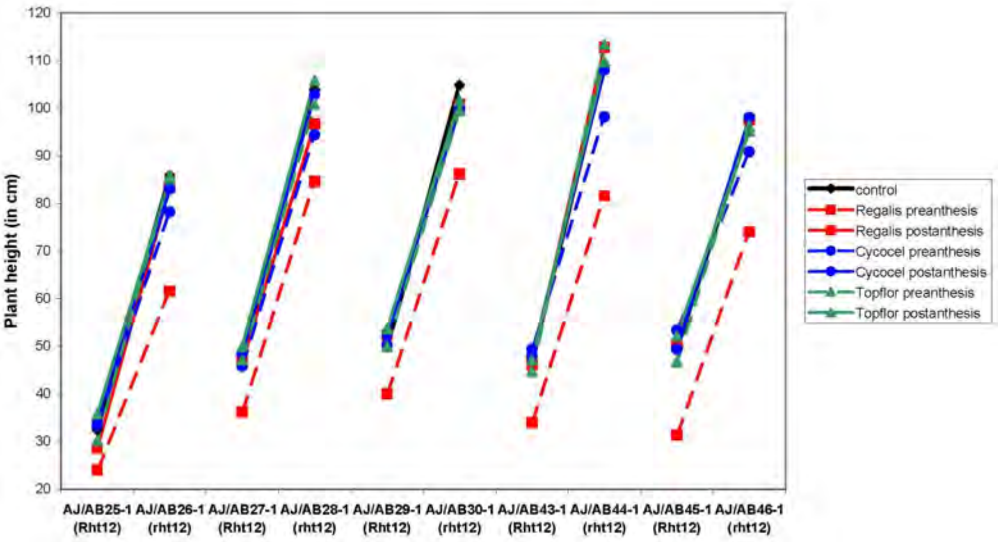

Fig. 4. Genotypic differences in plant height in the *Rht12* near-isogenic lines.

The effects of growth retardants were studied in five pairs of nearly isogenic introgression lines with and without the dwarfing gene *Rht12* representing three different genetic backgrounds. The experiment comprised four untreated control blocks and six treatment blocks as described for the 'Prinz'-derived lines. In a two-way ANOVA analysis, treatment as well as genotypes showed significant variation for plant height and for TKW with most variance residing in the genotype component (Table 5). The analysis of interaction failed because the test for normality was not passed.

Table 4. Correlation coefficients between plant height and 1,000-kernel weight.

Treatment	Prinz-derived lines	*Rht12*/*rht12* lines
Control 1	0.35	0.79
Control 2	0.40	0.92
Control 3	0.78	0.89
Control 4	0.25	0.84
Control all	0.54	0.83
Regalis preanthesis	–0.19	0.51
Regalis postanthesis	0.22	0.83
Cycocel preanthesis	0.94	0.91
Cycocel postanthesis	–0.16	0.85
Topflor preanthesis	0.66	0.80
Topflor postanthesis	0.18	0.82

The presence of the dwarfing gene *Rht12* led to a severe reduction of plant height in the controls ranging from 38% in the Mercia genetic background to 51% in the Huntsman lines (Table 6) related to those in the respective lines without the gene. This genotypic effect also was observed in all treatment blocks (Fig. 4, p. 18). The Regalis preanthesis treatment resulted in a significant ($P<0.001$ in a t-test) reduction of plant height in all lines compared to the respective controls. The Cycocel preanthesis treatment was only moderately effective in all lines without the *Rht12* gene, whereas all other treatments were without effect.

Table 5. Two-way ANOVA in in *Rht12*/*rht12* near-isogenic lines.

Source of variation	Degrees of freedom	Sum of squares	Mean squares	F-value	P-value
Plant height					
Treatment	9	13,520	1,502	62	<0.001
Genotype	9	346,574	38,508	1,586	<0.001
Residual	456	11,067	24	—	—
Total	474	371,483	783	—	—
1,000-kernel weight					
Treatment	9	2,313	257	13	<0.001
Genotype	9	24,891	2,765	140	<0.001
Residual	962	18,994	20	—	—
Total	980	45,994	47	—	—

For TKW, the presence of the dwarfing gene *Rht12* led to a reduction ranging from 75% in the Mercia genetic background to 90% in the Huntsman lines, compared to those in the respective lines without the gene (Table 6, p. 20). The effects of the growth-retardant treatments did not result in a clear cut picture, because the increase as well as decrease of TKW was observed in various lines and treatments compared to the control (Table 7, p. 20). Similar to the results observed for the Prinz-derived lines, the Regalis postanthesis treatment resulted in a significant reduction of TKW in several lines. All three preanthesis treatments had increasing effects for several lines, whereas for other lines, a decrease of TKW was observed. However, in all treatments, the genotypic effect of *Rht12* basically reduced TKW compared to those in the respective lines without *Rht12* (Fig. 5).

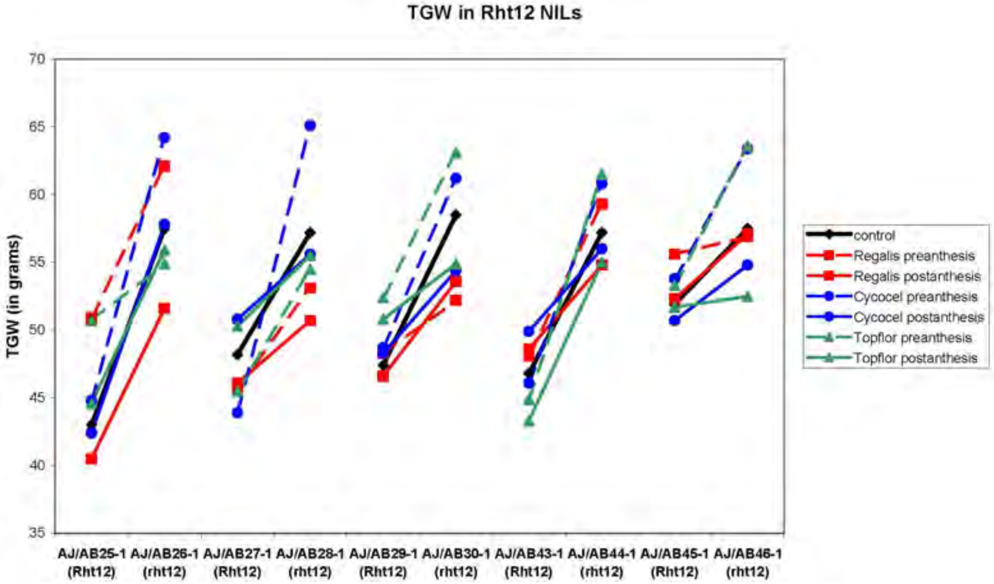

Fig. 5. Genotypic differences in 1,000-kernel weight in the *Rht12* near-isogenic lines.

In the four untreated control blocks, a high and positive correlation between TKW and plant height was observed, ranging from 0.79 to 0.92. A similar range of correlation was also found in the treatment blocks, except in Regalis preanthesis, where the correlation was reduced to 0.51 (Table 4, p. 19).

Table 6. Effects of growth retardants on plant height in *Rht12*/*rht12* lines; absolute plant height is given in cm. [1] Mean of 4 replications. [2] Application of a Mann-Whitney rank sum test. *, **, *** significant treatment compared to control at *P<0.5*, *P<0.01*, and *P<0.001*. ↑ increasing or ↓ decreasing effect compared to control.

Line	Genetic background	Control[1]	Regalis (preanthesis)	Regalis (postanthesis)	Cycocel (preanthesis)	Cycocel (postanthesis)	Topflor (preanthesis)	Topflor (postanthesis)
AJ/AB 25-1	Mercia (*Rht12*)	32.5	24.0*** ↓	28.6*↓	33.4	34.6	30.2	35.8
AJ/AB 26-1	Mercia (*rht12*)	85.8	61.6*** ↓	83.4	78.2**↓	83.0	85.8	85.2
AJ/AB 27-1	Bezostoya (*Rht12*)	48.5	36.2*** ↓	46.6	45.8	48.4	47.2	50.0
AJ/AB 28-1	Bezostoya (*rht12*)	103.9	84.6*** ↓	96.7	94.4**↓	102.8	100.8	105.8
AJ/AB 29-1	Bezostoya (*Rht12*)	49.8	40.0*** ↓	52.4	50.2	52.4	50.0	53.7
AJ/AB 30-1	Bezostoya (*rht12*)	104.8	86.2***[2]↓	100.8	99.4*↓	99.8	99.6*↓	101.6
AJ/AB 43-1	Huntsman (*Rht12*)	46.9	34.0*** ↓	46.2	49.4	48.0	44.8	47.2
AJ/AB 44-1	Huntsman (*rht12*)	109.0	81.6***[2]↓	112.8	98.2**[2]↓	108.0	113.4	109.8
AJ/AB 45-1	Huntsman (*Rht12*)	49.5	31.4*** ↓	50.0	53.4*↑	49.4	46.8	52.2
AJ/AB 46-1	Huntsman (*rht12*)	96.9	74.0*** ↓	97.6	90.8**↓	98.0	96.2	95.2

Table 7. Effects of growth retardants on 1,000-kernel weight in *Rht12*/*rht12* lines; calculated weight is given in grams. [1] Mean of 4 replications. [2] Application of a Mann-Whitney rank sum test. *, **, *** significant treatment compared to control at *P<0.5*, *P<0.01*, and *P<0.001*. ↑ increasing or ↓ decreasing effect compared to control.

Line	Genetic background	Control[1]	Regalis (preanthesis)	Regalis (postanthesis)	Cycocel (preanthesis)	Cycocel (postanthesis)	Topflor (preanthesis)	Topflor (postanthesis)
AJ/AB 25-1	Mercia (*Rht12*)	43.0	50.9*** ↑	40.5	44.8	42.4	50.7*[2] ↑	44.6
AJ/AB 26-1	Mercia (*rht12*)	57.5	62.1***[2] ↑	51.6***[2] ↓	64.2*** ↑	57.8	54.9*[2] ↓	55.9
AJ/AB 27-1	Bezostoya (*Rht12*)	48.2	45.7*[2] ↓	46.1 *[2] ↓	43.9***[2] ↓	50.8	45.5**[2] ↓	50.3
AJ/AB 28-1	Bezostoya (*rht12*)	57.5	53.1***[2] ↓	50.7***[2] ↓	65.1***[2] ↑	55.6	54.5	55.5
AJ/AB 29-1	Bezostoya (*Rht12*)	47.4	48.3	46.6	48.7	48.3	52.4**[2] ↑	50.8**[2] ↑
AJ/AB 30-1	Bezostoya (*rht12*)	58.5	52.2***[2]↓	53.6***[2] ↓	61.2** ↑	54.4*** ↓	63.1**[2] ↑	54.9**[2] ↓
AJ/AB 43-1	Huntsman (*Rht12*)	46.8	48.1	48.6	46.1	49.9	44.9	43.3
AJ/AB 44-1	Huntsman (*rht12*)	57.2	59.3	54.8	60.8* ↑	56.0	61.5** ↑	55.0
AJ/AB 45-1	Huntsman (*Rht12*)	51.9	55.6	52.3	53.8	50.7	53.3	51.7
AJ/AB 46-1	Huntsman (*rht12*)	57.5	56.9	57.1	63.4***[2] ↑	54.8*[2] ↓	63.6***[2] ↑	52.5*** ↓

Discussion. The most severe effects were observed with a Regalis treatment, which led to a significant reduction of plant height in a preanthesis application in all lines (Tables 2, p. 17, and 6) and to a significant reduction of grain size in a postanthesis application in all Prinz-derived lines and in *Rht12*-derived lines in a Mercia and Bezostoya background (Tables 3, p. 17, and 7). In the presence of *Rht12*, a significant effect on TKW was observed in only one case. According to manufacturer's information (https://www.agro.basf.co.za/en/Products/Overview/Regalis%C2%AE.html), Regalis is a prohexadion with a structural similarity to 2-oxoglutaric acid. Regalis interferes with the formation of active gibberellins by blocking the action of GA_{20}-3β-hydroxylase, a late step in GA-synthesis. Besides these effects, Regalis also blocks the formation of ethylene by inhibiting the ACC oxidase that catalyzes the oxidation of 1-aminocyclopropane carboxylic acid (ACC) to ethylene with ascorbic acid as a cofactor. This effect of prohexadion is based on its structural similarity to ascorbic acid.

The Cycocel preanthesis treatment affected plant height in all Prinz-derived lines and in the cultivars Mercia, Bezostoya, and Huntsman, however, it was without effect in the presence of the *Rht12* gene (Tables 2, p. 17, and 6, p. 20). In several of the cultivars with reducing effect on plant height, the Cycocel preanthesis treatment exerted an increasing effect on TKW (Tables 3, p. 17, and 7, p. 20). In a postanthesis treatment, Cycocel had a decreasing effect on TKW in few lines, but no clear cut pattern emerged (Tables 3, p. 17, and 7, p. 20). Cycocel is based on the action of chlormequat chloride which is an inhibitor of *ent*-kaurene synthase involved in the early steps of GA-biosynthesis (Rademacher 2000).

In our hands, Topflor was without effect on plant height, whereas for TKW both decreasing and increasing effects were observed. The increasing effects dominated in the preanthesis treatment (Tables 3, p. 17, and 7, p. 20). Topflor contains flurprimidol, a N-containing heterocycle, which blocks cytochrome P450-dependent monooxygenases, thereby inhibiting oxidation of *ent*-kaurene into *ent*-kaurenoic acid (Rademacher 2000).

Genotype-dependent differences in plant height and TKW were maintained in all treatments, only the Regalis preanthesis treatment led to a neutralization of the genotype-dependent effects in plant height in the Prinz-derived lines. In the *Rht12*-lines, generally a high correlation between TKW and genotype was observed; this correlation was lower in the control blocks of the Prinz-derived lines and no correlation was observed for some of the treatment blocks (Table 4, p. 19). A possible reason is that in the Prinz-derived lines, absolute differences in plant height are much smaller than in the *Rht12*-lines.

In a previous report, the chromosomal location of several gibberellin metabolic pathway genes from barley and wheat were established (Spielmeyer et al. 2004). Here, three loci for *ent*-kaurenoic acid oxidase (*KAO*) genes were reported on wheat chromosomes 7AS, 4AL, and 7DS, making *KAO* a potential candidate for the plant height QTL on chromosome 7DS in the Prinz-derived lines. The GA-responsive *dwarf3* mutant in maize is encoded by *ent*-kaurenoic acid oxidase, a member of the CYP88A subfamily cytochrome P450 enzymes (Helliwelll et al. 2001). By refined linkage mapping, the chromosomal locations of the *KAO*-loci in wheat were confirmed, but due to its mapping position, *KAO* could be excluded as candidate for the QTL in the Prinz-derived lines (Khlestkina et al. 2010).

The strong effects of Regalis in the *Rht12* lines may point to the action of a GA_{20}-oxidase. The semidwarf gene *sd-1*, an important gene in the Green Revolution of rice, is proposed to be caused by a defective GA_{20}-oxidase (Spielmeyer et al. 2002). Three homoeologues of the GA_{20}-oxidase gene *TaGA20ox1* were functionally characterized and mapped to wheat chromosomes 5BL, 5DL, and 4AL (Appleford et al. 2006). On the other hand, Korzun et al. (1997) mapped *Rht12* on the distal end of chromosome arm 5AL in the region of the T5AL/4AL translocation. We confirmed the mapping of Korzun et al. (1997) on chromosome arm 5AL, although in our case, *Rht12* mapped 4.9 cM proximal to marker *Xgwm291* (Fig. 1, p. 13), whereas in Korzun et al. mapped *Rht12* 5.4 cM distal to *Xgwm291*. In any case, no mapped GA-oxidase gene has been reported for chromosome 5AL (Spielmeyer et al. 2004).

Conclusion. Our data support the evidence that blocking GA-synthesis has effects on plant height as well as on grain development and that genotypic effects remain strong even in treatment blocks.

References.

Appleford NEJ, Evans DJ, Lenton JR, Gaskin P, Croker SJ, Devos KM, Phillips AL, and Hedden P. 2006. Function and transcript analysis of gibberellin-biosynthetic enzymes in wheat. Planta **223**:568-582.

Appleford NEJ, Wilkinson MD, Ma Q, Evans DJ, Stone MC, Pearce SP, Powers SJ, Thomas SG, Jones HD, Phillips AL, Hedden P, and Lenton JR. 2007. Decreased shoot stature and grain alpha-amylase activity following ectopic expression of a gibberellin 2-oxidase gene in transgenic wheat. J Exp Bot **58**:3213-3226.

Börner A and Meinel A. 1993. The effects of the growth retardant chlormequat (CCC) on plant height and yield in GA insensitive wheats. Plant Breed **110**:255-258.

Gale MD and Youssefian S. 1984. Pleiotropic effects of the Norin 10 dwarfing genes *Rht1* and *Rht2*, and interactions in response to chlormequat. *In:* Proc 6th Internat Wheat Genet Symp, Kyoto, Japan. pp. 271-277.

Helliwell CA, Chandler PM, Poole A, Dennis ES, and Peacock WJ. 2001. The CYP88A cytochrome P450, ent-kaurenoic acid oxidase, catalyzes three steps of the gibberellin biosynthesis pathway. Proc Natl Acad Sci **98**:2065-2070.

Holdsworth MJ, Bentsink L, and Soppe WJJ. 2008. Molecular networks regulating Arabidopsis seed maturation, after-ripening, dormancy and germination. New Phytol **179**:33-54.

Khlestkina EK, Kumar U, and Röder MS. 2010. Ent-kaurenoic acid oxidase genes in wheat. Mol Breed **25**:251-258.

Korzun V, Röder M, Worland AJ, and Börner A. 1997. Intrachromosomal mapping of the dwarfing (*Rht12*) and vernalisation response (*Vrn1*) genes in wheat by using RFLP and microsatellite markers. Plant Breed *116*:227-232.

Rademacher W. 2000. Growth Retardants: effects on gibberellin biosynthesis and other metabolic pathways. Ann Rev Plant Physiol Plant Mol Biol **51**:501-531.

Röder MS, Huang XQ, and Börner A. 2008. Fine mapping of the region on wheat chromosome 7D controlling grain weight. Funct Integr Genomics **8**:79-86.

Schwechheimer C, and Willige BC. 2009. Shedding light on gibberellic acid signaling. Curr Opin Plant Biol **12**:57-62.

Spielmeyer W, Ellis MH, and Chandler PM. 2002. Semidwarf (*sd-1*), "green revolution" rice, contains a defective gibberellin 20-oxidase gene. Proc Natl Acad Sci USA **99**:9043-9048.

Spielmeyer W, Ellis M, Robertson M, Ali S, Lenton JR, and Chandler PM. 2004. Isolation of gibberellin metabolic pathway genes from barley and comparative mapping in barley, wheat and rice. Theor Appl Genet **109**:847-855.

Viglási P. 1968. Short-strawed mutants of Karcag 522 winter wheat induced by gamma rays. Acta Agron Acad Sci Hung **17**:205-214.

Worland AJ, Sayers EJ, and Börner A. 1994. The genetics and breeding potential of *Rht12*, a dominant dwarfing gene in wheat. Plant Breed **113**:187-196.

Publications.

Alomari DZ, Eggert K, von Wirén N, Polley A, Plieske J, Ganal MW, Pillen K, and Röder MS. 2019. Whole-genome association mapping and genomic prediction for iron concentration in wheat grains. Internat J Mol Sci **20**:76.

Börner A and Ciucă M. 2019. Proc 17th Internat EWAC Conf, 3–8 June, 2018, Bucharest, Romania. 141 pp.

Börner A and Khlestkina EK. 2019. *Ex-situ* genebanks – seed treasure chambers for the future. Rus J Genet **55**:1299-1305.

Börner A, Lohwasser U, Khlestkina EK, Pshenichnikova TA, Osipova SV, Misheva S, and Simon M.R. 2019. Examples of successful collaboration (2015-2018). *In:* Proc 17th Internat EWAC Conf (Börner A and Ciucă M, Eds), 3-8 June, 2018, Bucharest, Romania. pp. 2-10.

Chesnokov YV, Kanash EV, Mirskaya GV, Kocherina NV, Rusakov DV, Lohwasser U, and Börner A. 2019. QTL mapping of diffuse reflectance indices of leaves in hexaploid bread wheat (*Triticum aestivum* L.). Rus J Plant Physiol **66**:77-86.

Chu J, Zhao Y, Beier S, Schulthess A, Stein N, Philipp N, Röder MS, and Reif JC. 2020. Suitability of single-nucleotide polymorphism arrays versus genotyping-by-sequencing for genebank genomics in wheat. Front Plant Sci **11**:42.

Dawit W, Badebo A, Hunde B, Kassa D, and Röder MS. 2019. Haplotype analysis of Ethiopian bread wheat (*Triticum aestivum*) cultivars and elite lines for yellow rust resistance genes using linked molecular markers. Afr J Biotech **18**:37-57.

Dudziak K, Zapalska M, Börner A, Szczerba H, Kowalczyk K, and Nowak M. 2019. Analysis of wheat gene expression related to the oxidative stress response and signal transduction under short-term osmotic stress. Sci Rep **9**:2743.

Dudziak K, Bulak P, Zapalska M, Börner A, Szczerba H, Leśniowska-Nowak J, and Nowak M. 2019. Using intervarietal substitution lines for the identification of wheat chromosomes involved in early responses to water-deficit stress. PLoS One **14**:e0221849.

Gerard GS, Alqudah A, Lohwasser U, Börner A, and Simón MR. 2019. Uncovering the genetic architecture of fruiting efficiency in bread wheat: a viable alternative to increase yield potential. Crop Sci **59**:1853-1869.

Impe D, Reitz J, Köpnick C, Rolletschek H, Börner A, Senula A, and Nagel M. 2020. Assessment of pollen viability for wheat. Front. Plant Sci **10**:1588.

Kumar U, Kumar S, Prasad R, Röder MS, Kumar S, Chand R, Mishra VK, Joshi AK. 2019. Genetic gain on resistance to spot blotch of wheat by developing lines with near immunity. Crop Breed Genet Genom **1**:e190017.

Mourad AMI, Alomari DZ, Alqudah AM, Sallam A, and Salem KFM. 2019. Recent advances in wheat (*Triticum* spp.) breeding. *In:* Advances in Plant Breeding Strategies: Cereals: Vol. 5 [Al-Khayri JM, Jain SM, and Johnson DV, Eds). Springer International Publishing. pp. 559-593.

Muqaddasi QH, Jayakodi M, Börner A, and Röder MS. 2019. Identification of consistent QTL with large effect on anther extrusion in doubled haploid populations developed from spring wheat accessions in German Federal *ex situ* Genebank. Theor Appl Genet **132**:3035-3045.

Muqaddasi QH, Reif JC, Röder MS, Basnet BR, and Dreisigacker S. 2019. Genetic mapping reveals large-effect QTL for anther extrusion in CIMMYT spring wheat. Agronomy **9**:407.

Muqaddasi QH, Brassac J, Koppolu R, Plieske J, Ganal MW, and Röder MS. 2019. *TaAPO-A1*, an ortholog of rice *ABERRANT PANICLE ORGANIZATION 1*, is associated with total spikelet number per spike in elite European hexaploid winter wheat (*Triticum aestivum* L.) varieties. Sci Rep **9**:13853.

Muqaddasi QH, Zhao Y, Rodemann B, Plieske J, Ganal MW, and Röder MS. 2019. Genome-wide association mapping and prediction of adult stage *Septoria tritici* blotch infection in European winter wheat via high-density marker arrays. Plant Genome **12**:180029.

Nagel M, Seal CE, Colville L, Rodenstein A, Un S, Richter J, Pritchard HW, Börner A, and Kranner I. 2019. Wheat seed ageing viewed through the cellular redox environment and changes in pH. Free Radic Res **53**:641-654.

Philipp N, Weise S, Oppermann M, Börner A, Keilwagen J, Kilian B, Arend D, Zhao Y, Graner A, Reif JC, and Schulthess AW. 2019. Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. Sci Data **6**:137.

Pshenichnikova TA, Doroshkov AV, Simonov AV, Yudina MA, Afonnikov DA, Permyakova MD, Permyakov A V, Osipova SV, and Börner A. 2019. Leaf hairiness in wheat: genetic, evolutional and physiological aspects. *In:* Proc 17th Internat EWAC Conf (Börner A and Ciucă M, Eds), 3-8 June, 2018, Bucharest, Romania. pp. 32-38.

Pshenichnikova TA, Osipova SV, Permyakova MD, Permyakov AV, Shishparenok AA, Rudikovskaya EG, Doroshkov AV, Verchoturov VV, Kovaleva NM, Chistyakova AK, Leonova IN, Lohwasser U, and Börner A. 2019. Genetic dissection of drought tolerance by analysis of a recombinant chromosome substitution double haploid mapping population of bread wheat for 2A chromosome. *In:* Proc 17th Internat EWAC Conf (Börner A and Ciucă M, Eds), 3-8 June, 2018, Bucharest, Romania. pp. 50-55.

Rehman Arif MA and Börner A. 2019. Mapping of QTL associated with seed longevity in durum wheat (*Triticum durum* Desf.). J Appl Genet **60**:33-36.

Sallam A, Alqudah AM, Dawood MFA, Baenziger PS, and Börner A. 2019. Drought stress tolerance in wheat and barley: advances in physiology, breeding and genetics research. Internat J Mol Sci **20**:3137.

Schierenbeck M, Fleitas MC, and Simón MR. 2019. Nitrogen fertilization and fungicide mixtures in wheat: how do they affect the severity, yield and dynamics of nitrogen under leaf rust infections? Eur J Plant Pathol **155**:1061-1075.

Rehman Arif MA and Börner A. 2020. An SNP Based GWAS analysis of seed longevity in wheat. Cer Res Commun. In press.

Rehman Arif MA, Attaria F, Shokat S, Akram S, Waheed MQ, Anjuman Arif A, and Börner A. 2020. Mapping of QTLs associated with yield and yield related traits in durum wheat (*Triticum durum* Desf.) under irrigated and drought conditions. Internat J Mol Sci **21**:2372.

Schreiber M, Himmelbach A, Börner A, and Mascher M. 2019. Genetic diversity and relationship of domesticated rye and its wild relatives as revealed through genotyping-by-sequencing. Evol Appl **12**:66-77.

Tarawneh RA, Szira F, Monostori I, Behrens A, Alqudah AM, Thumm S, Lohwasser U, Röder MS, Börner A, and Nagel M. 2019. Genetic analysis of drought response of wheat following either chemical desiccation or the use of a rain-out shelter. J Appl Genet **60**:137-146.

Uranga JP, Schierenbeck M, Perelló AE, Lohwasser U, Börner A, and Simón MR. 2020. Localization of QTL for resistance to *Pyrenophora teres f. maculata*, a new wheat pathogen. Euphytica **216**:56.

Wiebach J, Nagel M, Börner A, Altmann T, and Riewe D. 2020. Age-dependent loss of seed viability is associated with increased lipid oxidation and hydrolysis. Plant Cell Environ **43**:303-314.

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Current research activities.

Induced mutations for yellow (stripe) rust resistance in background of elite cultivars of the North Western Plains Zone of India.

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North Western Plain Zone (NWPZ) is a major wheat-producing zone in India with around 10 x 10^6 ha land under cultivation that contributes to nearly 50% of Indian wheat production. Wheat production in the NWPZ 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. Due to the rapid emergence of new virulent pathotypes in this zone, most of the wheat cultivars become susceptible to prevalent races of yellow rust. Breeding for yellow rust resistance by conventional approachs leads unwanted variability in genetic architecture of the high-yielding cultivars. Hence, in such a scenario, to achieve enhanced resistance to yellow rust, a mutation-breeding approach was initiated in the popular bread wheat cultivar DBW-88. Healthy seeds were irradiated with gamma rays and the M_1 grown at Trombay in 2014–15. Subsequently, the M_2 was screened under artificial epidemic conditions for yellow rust at IIWBR, Karnal. Selected resistant mutants were confirmed in the M_3 generation and then carried forward for stability in subsequent mutant generations. Mutant lines in the M_6 and M_7 generations were screened for yellow rust resistance at Karnal. Mutant lines showed resistance to stripe rust in artificial field epidemic conditions (immune to 5MS) compared to the parent DBW-88 (60-80S). Resistant lines (M_8) were evaluated for agronomic and yield traits in the *rabi* 2019–20 season; six lines were found to be promising in yield and yellow rust resistance. Two high-yielding lines will be promoted to the station trial in *rabi* 2020–21. These lines provide an additional germplasm resource for resistance to yellow rust and can be used directly after yield trials or can be used as donor(s) in other high-yielding backgrounds.

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

Mutation-induced, improved plant types in elite *Sharbati* wheat cultivars of the Central zone of India.

G. Vishwakarma, A.S. Shitre, 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).

The Central Zone (CZ) of India is well known for high-quality wheat production, which is liked by consumers and also fetches a premium price to the farmers. The *Sharbati* wheat cultivars of the CZ are highly popular among farmers and consumers due to their excellent *chapatti*-making quality. Wheat cultivars HI-1500 (Amrita) and HI-1531 (Harshita) are two popular high yielding *Sharbati* wheats of the CZ due to their good yield, resistance to stem and leaf rust, and tolerance to drought and heat stress. However, the plant type of these cultivars is tall and, hence, suffers from lodging during strong winds, heavy irrigation and unseasonal rain, or hailstorms, leading to considerable losses to the farmers. Mutation breeding was utilized to improve the plant type of these cultivars, while keeping background similar to the parent for easy acceptance by the farmers. Gamma ray-treated M_1 seeds were raised at Trombay, Mumbai, and the M_2 generation subsequently was grown and screened for desired trait at the IARI Regional Station, Indore (CZ). Putative mutants with improved plant type, such as reduced height, increased tillering, and early maturity, were identified. These mutants were advanced to a stable mutant generation (M_3 to M_5) at Indore. Currently, these mutants are being evaluated for their agronomic performance and phenotypic characterization of parents and mutants at Indore. Promising lines with improved plant type and higher yield will be advanced for multi-location testing in CZ in *rabi* 2020–21.

Improvement of wheat cultivar C-306 for maturity and rust resistance using mutation and molecular breeding approaches.

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Wheat cultivar C-306 is known for its excellent *chapatti*-making quality and is a landmark cultivar in India. Although released for CZ of India, C-306 is grown in many other zones. The cultivar was released in 1969 and is still popular among farmers and consumers, primarily due to its excellent *chapatti*-making quality. As is the case with many old cultivars, C-306 suffers from two major drawbacks, a semi-late maturity making it susceptible to terminal heat stress in the short wheat-growing season of the CZ, and susceptibility to leaf and stem rust, a prevalent problem in the CZ of India. In view of the popularity and demand for C-306 in the flour-making industry and by farmers, induced mutation breeding for improving C-306 was initiated at Nuclear Agriculture & Biotechnology Division, BARC, and an early maturing (20–25 days) mutant was developed. The early maturing mutant of C-306 was suitable for cultivation in the CZ of India as it escapes the terminal heat stress during grain-filling. To further improve rust resistance in the mutant, the rust resistance gene *Sr24*/*Lr24* was introduced from a NIL of C-306 (HW-2004) using marker-assisted breeding. An improved C-306 with early maturity and rust resistance was developed. Currently, the F_6 generation of these improved lines is being evaluated at multiple locations in the CZ for maturity, rust resistance, and yield performance. Lines with early maturity, rust resistance, and improved yield may be suitable for cultivation in the CZ of India.

Radiation-induced mutation breeding for developing spot blotch resistance in popular varieties of North Eastern Plains Zone of India.

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The North Eastern Plain Zone (NEPZ) of India is a very important wheat-growing zone with almost 30% of total area under wheat production in India. Due to various constraints in wheat production, the average productivity in the NEPZ is low compared to the national average. One of the most important constraint in this zone is the foliar disease spot blotch caused by *Bipolaris sorokiniana* (*Helminthosporium sativum*). Spot blotch accounts for a 20-40% yield loss and severely affects end-use quality of grain. Genetic sources of spot blotch resistance are mainly quantitative in nature and, hence, are difficult to introgress in to new wheat cultivars. To improve spot blotch resistance in high-yielding and popular cultivars of the NEPZ, mutation breeding was initiated. Cultivar HI-1563 was irradiated using gamma rays and the M_1 was raised at ARS, Niphad. The M_2 was planted in plant-to-row progeny and screened for spot blotch resistance in artificial epidemic conditions at UBKV, Coochbehar, a natural hot-spot for spot blotch. Putative spot blotch-resistant mutants were identified during *rabi* 2019–20 and will be subjected to further confirmation and testing in the M_3 generation in the ensuing *rabi* 2020–21 season. These putative mutants hold promise to be used as direct or indirect sources for resistance to spot blotch in the NEPZ.

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

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Induced mutagenesis is an important tool for crop improvement in plant breeding. Over the years, induced mutagenesis has led to many success stories for improvement in both biotic and abiotic stresses in plants. Globally, the most common mutagens used for induced mutagenesis are physical mutagens and, in particular, gamma rays originating from isotopic sources, such as ^{60}Co or ^{137}Cs. However, over the years, ion-beam mutagenesis also has demonstrated to be useful in induced-mutation breeding. Many novel mutants are reported to be developed using ion sources. Ion beams, compared to gamma rays, are particle in nature and have a very different mechanism of interaction with genetic material; as a result they have very a high linear energy transfer and cause a different spectrum of mutations. We optimized irradiation of Indian wheat using H^+ ion beams using the Pelletron LINAC accelerator facility at TIFR, Mumbai, India. H^+ ion beam energy, seed geometry, and the spread of the ion beam for irradiation were optimized. A radio-sensitivity test with two wheat cultivars was made and compared with gamma rays, which showed the higher lethality and growth reduction properties of H^+ ions. Currently, the radiobiological effectiveness of a proton beam is being studied at the cytogenetic and DNA damage level to compare it with gamma rays and other ion beams. Optimization of ion-beam mutagenesis will open a new mutagenesis approach in important crops for their improvement for various target traits.

Genetic improvement of wheat for yield and quality traits.

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Genetic improvement for yield and yield-related traits. Yield improvement is always a primary objective in any crop improvement program. Crop improvement for other traits, such as nutritional quality and disease resistant, also requires yield equal to or more than the check cultivars. Several intervarietal crosses were made during last 4 years for improvement in yield and yield-related traits. To combine the traits from various backgrounds and suitability to diverse climatic conditions of India, genotypes having better yield and suitability in the different climatic zones of India were involved in a crossing program. One improved genotype, TAW 33, developed at our center, showed the highest grain hardness index over 2 years. Quality testing was at IIWBR, Karnal, which is the central coordinating authority for wheat improvement program. TAW 33 is being tested for second year performance in the Maharashtra State Level Varietal Trial. Another genotype, TAW 159, is being tested in multi-location trials for yield under late-sown conditions. Recombinant progenies in the F_3, F_4, and F_5 generations are being advanced to the next generations. We are growing 153 stable and improved lines in a rod row trial at ARS, Niphad, Nasik. These lines will be tested for rust reaction and resistant lines will be advanced to yield trials.

Genetic improvement for quality; profiling wheat genotypes for polyphenol oxidase activity. Wheat is consumed in different forms, such as chapatti, noodles, bread, biscuits, pasta, pan bread, flat bread, cake, and rolls. The color of the wheat product is an important quality parameter. Polyphenol oxidase (PPO) is an enzyme located in bran layer of the wheat kernel. The enzymatic activity of PPO is responsible for the discoloration of dough and, ultimately, the end-product. We selected 120 genotypes, which include released cultivars and stable advanced lines, based on their stability, improved agronomical traits, and yield. An enzymatic assay, using L-DOPA as substrate, showed wide variation among the genotypes for PPO activity. The PPO activity measured after 30 min ranged from 6.40 to 121.20 au/min/g in the 2016–17 season and 9.53 to 124.31 au/min/g in 2017–18. Activity measured after 90 min ranged from 4.69 to 71.52 au/min/g in 2016–17 and 1.35 to 106.16 au/min/g for 2017–18. During 2016–17, the lowest PPO activity measured after 30 min was for genotypes AKDW2997-16, AKDW4791 AKDW4750, NIAW2302, NIAW1415, and AKDW4791; and after 90 min for genotypes AKDW2997-16, NIAW2348, AKDW4750, and NIAW1279. The highest PPO activity measured after 30 min was recorded for genotypes NIAW560, RAJ3766 LOK 1, HS490, RAJ 4266, and NIAW560; and after 90 min in LOK 1, RAJ3766, FLW 1, and NIAW1045. During 2017–18, the lowest PPO activity after 30 min was in genotypes AKDW4791, AKDW4832, NIAW1994, AKDW4750, NIAW1415, and AKDW4832; and after 90 min interval for AKDW4791, AKDW4750, NIAW1279, and LBPY2010-11. The highest activity at 30 mins was in genotypes RAJ3766, FLW6, NIAW560, DWR9507, PBW452; and at 90 min in FLW6, NIAW560, RAJ3766, DBW14, and DWR9507. Further work is in progress.

Publications.

Vishwakarma, Sanyal, Saini, Sahu, Singh Patel RR, Sharma D, Tiwari R, and Das BK. 2019. GLADS: a gel-less approach for detection of STMS markers in wheat and rice. Plos One **14**(11): e0224572 https://doi.org/10.1371/journal.pone.0224572.

Vishwakarma G, Sanyal RP, Shirte AS, Gadekar DA, Saini A, and Das BK. 2019. Validation and marker assisted selection of stem rust resistance gene *Sr2* in Indian wheat using gel-based and gel-free methods. J Crop Sci Biotech **22**(4):309-315.

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Genetic and epigenetic studies for a variety of traits in wheat in genomics era.

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During 2019–20, we continued to work on several projects.

1. The study of the genetics of a number of traits: tolerance to abiotic stresses, including heat, drought, preharvest sprouting; tolerance to biotic stresses involving resistance to nematodes, leaf rust, and spot blotch; other agronomic traits including grain morphology, N-use efficiency, and biofortification (including grain Fe and grain Zn). QTL interval mapping and genome-wide association studies (GWAS) were mainly used for the study of genetics of these traits. The studies also included meta-QTL analysis for several traits including drought tolerance, resistance to leaf rust, and the biofortification traits of grain Fe and grain Zn.
2. Marker-assisted selection for introgressing individual genes for tolerance to heat and drought, and pyramiding of genes for grain protein content and resistance to the three rusts
3. In silico identification of useful genes in wheat using corresponding orthologues from rice.
4. Transcriptome analysis for leaf rust resistance due to adult plant leaf rust resistance gene *Lr*48.
5. Epigenetic studies for resistance against leaf rust due to seedling or the all-stage resistance gene *Lr28* and the adult-plant resistance gene *Lr48*. These studies involved the analysis of DNA methylation, histone modifications, and ncRNA (including miRNAs and lncRNAs).

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

To study the genetics of tolerance to abiotic stresses, we have collaborative projects, one each for heat tolerance (funded by BIRAC, DBT, India), drought tolerance (funded by DBT, India), and preharvest-sprouting tolerance (funded by Department of Science and Technology, Government of India). Our objective is to study the genetics of heat and drought tolerance and preharvest-sprouting tolerance to develop prebreeding material with improved tolerance to these abiotic stresses.

QTL analysis for heat tolerance. High ambient temperature is known to affect 40% of the wheat-growing area in the world. According to an estimate, every 1°C rise in temperature above the optimal temperature of 26°C leads to a 3–4% decrease in grain yield in wheat. In India, the wheat crop suffers mainly from terminal heat stress, sometimes due to late sowing (December/January). A sudden rise in temperature during anthesis causes significant reduction in grain number (due to sterility) and grain weight. Therefore, knowledge of the genetic control of heat tolerance is essential for breeding high-yielding, heat-tolerant, and climate-resilient wheat genotypes.

In view of the above, we have undertaken the following studies. First, a DH population consisting of 177 lines was developed (at WSU, USA) from a cross between the heat-tolerant cultivar Giza168 and the heat-sensitive cultivar PBW343. The DH population, along with the two parents, has already been evaluated for 18 traits, including yield and yield-components. For this purpose, the crop was raised using three planting dates (timely, late, and very late) at two different locations (Meerut and Lucknow) for two consecutive years (crop seasons 2017–18 and 2018–19), comprising a total of 12 environments. During the third year (2019–20), the DH populations are being evaluated at the three planting dates at the Meerut location only, eventually providing data for 18 traits for QTL analysis involving 15 environments (2 locations x 3 sowing dates x 2 years; third year sowing dates at only the Meerut location). The data collected during the crop seasons 2017–18 and 2018–19 suggested a significant decline in the mean performance of all the traits of the DH population under late and very late sown conditions. The SNP genotyping data of the DH population, generated through GBS (outsourced to Gene shifters, LLC, Pullman, WA, USA), is being used to construct a SNP-based genetic map and for QTL identification.

In another collaborative study involving CCS University, Meerut, University of Adelaide, Australia, and CIMMYT, Mexico, QTL analysis for grain yield and phenology was conducted using a DH population derived from the cross 'Excalibur/Kukri' (earlier developed by Peter Langridge and his group at Adelaide, Australia). The DH population was phenotyped extensively in 32 field experiments across climatic zones in Australia, India, and Mexico, where the wheat crop experiences drought and heat stress. A total of 128 QTL were identified for four traits: grain yield, 1,000-kernel weight (TKW), days-to-heading, and grain-filling duration. These QTL included 24 for yield and 27 for TKW, showing a significant Q x E interaction. A set of 14 small, main-effect QTL for yield across environments also were identified. One of these main-effect QTL, *QYld.aww-1B.2* for grain yield, was fine-mapped to a 2.9-cM genomic region corresponding to 2.2 Mbp, which contained 39 predicted genes.

Meta-QTL analysis for drought tolerance. In the past, a large number QTL have been reported for different traits under drought in wheat, but major QTL with high precision and closely associated markers were not available. In view of this, we retrieved ~374 mapped QTL from 14 studies that were conducted earlier involving 43 drought-responsive traits in different mapping populations. The analysis was conducted using the software BioMercator V4.2. For final analysis, only 56 of the 374 QTL were retained by the software, due to inadequate information for the remaining QTL. A consensus map consisting of 5,680 markers (SSRs, RFLP, and DArT) was prepared using two reference maps available in the GrainGenes database. The 56 QTL were projected onto this consensus map leading to identify 13 MQTL (MQTL1 to MQTL13) on six different chromosomes (1D, 3B, 5A, 6D, 7A, and 7D). An individual MQTL corresponded to two (for MQTL8) to 23 (MQTL11) original QTL for different traits. The confidence intervals for each of the 13 MQTL ranged from 2.07 cM to 19.46 cM, which is narrower than those of the original QTL, suggesting greater precision in the mapping of MQTL. Also, due to the use of a dense consensus map, the markers very closely associated with MQTL could be identified. The MQTL identified during this study may be utilized in MAS more effectively, while breeding for drought tolerance.

We also identified >100 candidate genes underlying the above 13 MQTL. The proteins encoded by these candidate genes belonged to the following categories: glycosyl-hydrolase family of drought tolerance, glycosyl-hydrolase family, protein kinase, proteins with zinc finger, WRKY gene family, cytochrome P450, DREB transcription factor, aquaporin gene family, and proline dehydrogenase. We plan to validate these candidate genes through a study of their expression in seedlings of drought-tolerant and drought-sensitive wheat cultivars grown under moisture stress.

GWAS for heat stress tolerance. The genetic architecture of 11 heat stress responsive traits was examined in an association mapping panel (273 diverse wheat genotypes) using three different software for GWAS (GAPIT, SUPER, and FarmCPU). The data also was used for genomic prediction using rrBLUP. For this purpose, phenotypic data were recorded on eight agronomic and three physiological traits at Meerut (Uttar Pradesh) and Powerkheda (Madhya Pradesh) under timely sown (TS) and late-sown (LS) conditions. Genotype data involved 17,937 SNP markers (genotyping work was outsourced to Kilian Andrzej of DArT Pvt Ltd in Australia and funded by CIMMYT, Mexico). Terminal heat stress generated by LS conditions, reduced grain yield by 48% at Meerut and 42% at Powerkheda.

During GWAS, under LS conditions, SUPER captured maximum number of marker–trait associations (MTAs) ($P<0.001$) followed by FarmCPU and GAPIT (167 at Meerut and 178 at Powerkheda using SUPER; 147 at Meerut and 156 at Powerkheda using FarmCPU; 124 at Meerut and 129 at Powerkheda using GAPIT). The MTAs ($P<0.01$) were converted to QTL based on LD decay information (LD decay=3.0 cM), leading to identification of 118 (34+46+38) QTL at Meerut and 140 (33+66+41) QTL at Powerkheda for different traits. These QTL also included stable and pleiotropic QTL. Candidate genes for some of the important MTAs under LS condition also were identified. These candidate genes differed for different traits and included genes that encoded the following (beside others): (i) proteins containing LRR (leucine rich repeats) domain (for grain filling duration under LS), (ii) calcium ion binding proteins (for 1000-grain weight under LS), (iii) bi-directional SWEET transporter for SPAD chlorophyll content, (iv) thioredoxin, cytP450 (for days to heading), and (v) alpha/beta hydrolase and lipid transfer protein (for grain yield).

Genomic prediction (GP) analysis revealed moderate (>0.4) to low (<0.4) prediction accuracies for the different traits at both the locations. Moderate GP accuracies at Powerkheda were observed for days-to-anthesis (LS and TS), days-to-maturity (only TS), and grain yield per plot (TS). Similarly, at Meerut, moderate GP accuracies were estimated for days-to-heading (LS and TS), grain yield per plot (TS and LS), days-to-anthesis and maturity (only LS), canopy temperature depression (only TS), and plant height (only LS).

Overall, the study revealed a complex genetic architecture for different traits related to tolerance to heat stress in wheat. The MTAs identified under LS conditions may prove useful for molecular breeding leading to development of heat tolerant wheat cultivars.

Studies on AGPase genes in relation to heat tolerance. AGPase is a rate-limiting enzyme in starch synthesis and responds to heat stress. The enzyme is encoded by a family of 11 genes (identified by us earlier through an *in silico* study), which are being subjected to a detailed study for the analysis of genetic variability and allele mining, so that genotypes with heat-stable AGPase and the corresponding heat stable alleles may be identified.

SNPs for 11 genes for AGPase were mined using the available genome sequences of ~65 wheat genotypes including Chinese Spring. Although sequence polymorphism for all the 11 AGPase genes (except AGPaseLS on 5A) was available, maximum polymorphism (based on number of SNPs) was recorded for the *AGPaseLS* gene on chromosome 5B. SNPs in the *AGPaseLS* gene on chromosome 1B (detected in >50% genotypes) are being validated in a set of 75 genotypes (46 heat tolerant and 29 heat sensitive) using a KASP assay.

Quantitative real-time PCR expression analysis is planned for all 11 AGPase genes in a heat-tolerant (Giza168) and a heat-sensitive (PBW343) cultivar. Data is being collected for three different post-anthesis grain development stages to understand the dynamics of the expression of these genes as influenced by heat stress at different grain developmental stages. Our preliminary results indicate that majority (7) of the 11 genes are expressed at 10 to 15 DAA.

Quantification of the effect of heat stress on pollen germination, seed set, and grain filling. In a collaborative study with CCS University, Meerut, and two institutions in the USA (Kansas State University, Manhattan, and Washington State University, Pullman), a set of 28 diverse, spring wheat genotypes were exposed to heat stress (34/16°C day/night temperatures) for 10 days during flowering and for 30 days during grain filling to quantify genetic variability in pollen germination, photosynthesis, and yield under controlled-environment conditions. Pollen grains collected immediately at anthesis (between 0530 and 0630 h) were incubated on liquid *in vitro* pollen germination media. Averaged across wheat genotypes, a significant reduction in pollen germination (39.9%, $P < 0.001$) was recorded from plants exposed to heat stress. Heat stress for 10 days during flowering induced significant reduction in seed number (15.4 and 23.0%) and seed weight (32.3 and 34.6%) on main and primary spikes, respectively, compared with the control. Heat stress during grain filling had a more pronounced impact on seed weight in the main spikes (16 and 22%) and seed number in primary spikes (2.7 and 9.3%). Genotypes KSG025 and KSG1214, with higher seed number, seed weight, and harvest index and appreciable pollen germination under heat stress, were identified as candidate donors for simultaneously enhancing flowering and post-flowering heat tolerance in spring wheat.

GWAS for preharvest sprouting tolerance (PHST). Off-season rains at the time of grain ripening trigger physiological changes and influence the internal composition of the wheat grain that results in deterioration of edible parts (i.e., starch), changes in nutritional quality and a decline in grain yield. This problem typically involves cause and effect relationship between seed dormancy and germination (sprouting). Dormancy generally develops during seed maturation and is conserved in the mature seeds; this is influenced by environmental and genetic factors. Seeds exhibit variation in seed dormancy during maturity, and its deficiency leads to the sprouting grains within spikes. This phenomenon is called preharvest sprouting, which occurs in many wheat-producing states of India, although northern and eastern parts are more prone to PHS.

Studies on genetics of PHST have been in progress in our laboratory for almost two decades. The present study involved the use of a Spring Wheat Reference Set (SWRS) comprised of 190 genotypes. Phenotypic data on PHST was recorded at Meerut over two crop seasons (2017–18 and 2018–19) using the following parameters/traits: (i) PHS using intact spikes (scale 1–9, where 1 = PHS tolerant and 9 = PHS susceptible), (ii) Hagberg falling number (FN; time in seconds), and (iii) grain color (GC; scale 1–5, where 1 = white, 2 = dark white, 3 = amber, 4 = light red, and 5 = dark red). In addition, data were recorded on days-to-heading (DTH), days-to-anthesis (DTA), and days-to-maturity (DTM). Descriptive statistics revealed a high variability for PHS (CV = 33.7%), FN (CV = 37.7%), and GC (GC = 40.8%) compared to phenology traits such as DTA, DTM, and DTH for which the CV values were low (3–6% only). Violin plots showed almost normal distribution for all the six traits. 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 GC.

Association mapping will identify marker loci associated with PHS tolerance, FN, and GC utilizing phenotypic data and 17,000 SNP markers (also used for heat tolernace). For this purpose, the genotypic data was subjected to a population structure analysis. Further analysis involving principal component analysis, kinship analysis, and identification of significant MTAs using GAPIT is in progress. This study will allow us to identify important MTAs and the underlying candidate genes for improvement of PHS tolerance in wheat.

Genetics of tolerance to biotic stresses.

GWAS for resistance to cereal cyst and root lesion nematodes. Cereal cyst nematode (*Heterodera avenae*) and root lesion nematode (*Pratylenchus thornei*) are among the most important plant parasitic nematode species reported worldwide. These nematodes cause significant yield loses in wheat. GWAS and QTL interval mapping studies were used to study the genetics of resistance against *H. avenae*. For GWAS, ~200 exotic genotypes (obtained from Marion Röder, IPK, Gatersleben, Germany) and ~160 indigenous wheat genotypes (obtained from NBPGR, New Delhi) were screened for resistance to *H. avenae* under controlled conditions for two years with a minimum of five replicates of each genotype. ANOVA showed significant phenotypic variation for number of cysts in the roots and in the soil. SNP genotyping data generated using SNP arrays was provided by Marion Röder for 200 exotic genotypes and S. Sharma (NBPGR, New Delhi) for ~160 indigenous genotypes.

The phenotypic and genotypic data will be used to find significant MTAs, which should prove useful for identification of candidate genes and development of diagnostic markers for future wheat breeding. GWAS results will also be supplemented with the results of QTL analysis. For this purpose, the novel ITMI mapping population is being screened for resistance to *H. avenae* (seed and SNP genotyping data of the population were procured from Marion Röder. Currently, statistical analysis will examine the variation for resistance to *H. avenae* in the DH population.

In a separate study, ~160 indigenous wheat genotypes also were screened for resistance to *P. thornei* under controlled conditions. Nematode counts ranged from 144 to 13,896 per plant. Further genetic studies for resistance against this nematode are in progress.

GWAS for resistance to spot blotch using SNPs and haplotype data. A GWAS for spot blotch is being conducted using 303 SWRS genotypes and 13,968 SNP markers (genotyping data used for heat tolerance). Phenotypic data on the 303 genotypes was recorded for two years at two locations (BHU, Varanasi, UP, and Borlaug Institute for South Asia (BISA) Farm Pusa, Samastipur, Bihar) on the following three traits: (i) AUDPC (area under disease progress curve), which involved the use of disease severity at three different growth stages (GS), i.e., GS 63 (beginning of anthesis), GS 69 (on completion of anthesis), and GS 77 (late milk stage); (ii) the incubation period (recorded from the time of inoculation to first appearance of visible symptoms); and (iii) lesion number per leaf.

Using this data, GWAS has two different approaches: (i) using SNP data involving the software TASSEL, GAPIT, FarmCPU, and SUPER, and (ii) using haplotype data based on SNPs. In the latter approach, the SNP tags were mapped with a reference genome to obtain genomic coordinates, and haplotype blocks were prepared within 1-Mb intervals totalling 6,060 haplotype blocks. In each haplotype block, haplotypes were developed based on unique combinations of SNP alleles. The haplotype data is being used for GWAS to find haplotypes associated with resistance to spot blotch.

Genetics of some other traits.

GWAS for grain morphology. Grain morphology traits are important agronomic characteristics with a significant market value. Data for six morphological traits, such as grain area size, grain width, grain length-width ratio, grain perimeter length, grain length, and factor form density were recorded for two years on 225 diverse spring wheat genotypes belong to the SWRS collection. Currently, phenotypic data is being analyzed. The available 17,937 SNP markers (obtained through outsourcing to Kilian Andrzej in Australia and funded by CIMMYT, Mexico) and the phenotypic data will be utilized for GWAS for identification of MTAs for different grain morphology traits.

Interval mapping for nitrogen-use efficiency (NUE). Nitrogen (N) is one of the essential macro-nutrients for plant growth and development. Excessive use of N fertilizers in commercial wheat cultivation is believed to cause environmental degradation. Therefore, development of genotypes with improved NUE that may give high yield with low or optimum input of N is an important objective in wheat breeding programs. In order to achieve this objective, we examined the genetic variability for NUE and its two component traits, N-uptake efficiency (NUpE) and N-utilization efficiency (NUtE).

A set of 21 Indian wheat cultivars was evaluated under three levels of soil N (60, 120, and 180 kg/ha) in a split-plot design over two years at IIFSR, Modipuram, Meerut. The results suggested significant differences for NUE and its two components, although these traits declined with increasing levels of N. The decline was more prominent in NUE relative to NUpE and NUtE. ANOVA suggested significant variation for two of the three traits (NUE and NUtE). Interactions also were largely significant with some exceptions. Cultivars showing high NUE included HD2967, HUW468, and PBW343, and cultivars showing low NUE included C306 and K65 (the two old and tall cultivars).

For interval mapping, an RIL mapping population developed using the cross 'HUW468 (semidwarf with high NUE) / C306 (tall with low NUE)', and the genotypic data was made available by VK Mishra (BHU, Varanasi, India). This mapping population and the genotypic data is being used to study the genetic architecture of NUE and its component traits in order to identify molecular markers associated with NUE. These markers should prove useful for MAS in a breeding program aimed towards development of high yielding wheat genotypes with relatively higher NUE.

Genetics of biofortification for grain iron and zinc. Iron (Fe) and zinc (Zn) are two important micronutrients that are essential for maintenance of human health. For human populations in developing countries, biofortification of crops through breeding is a cost-effective and sustainable strategy to solve Fe and Zn malnutrition. Consumption of Fe and Zn biofortified staple cereals, such as wheat, may help ameliorate malnutrition in humans. Genetic studies on Fe and Zn content in wheat are being undertaken in our laboratory through support provided under a flagship multi-institutional project funded by DBT, Govt. of India, under the leadership of the National Agri-Biotechnology Institute (NABI, Mohali, Punjab, India).

GWAS for grain Fe and Zn content. GWAS will use a set of 288 wheat genotypes belonging to the Watkins collection (made available by Parveen Chhuneja, PAU, Ludhiana, India) and a diverse collection of indigenous wheat genotypes, with an objective to identify genomic region(s) associated with grain Fe and Zn content. The genomic region(s)/genes identified using GWAS will be deployed in breeding programs through MAS. For this purpose, phenotypic data on grain Fe and Zn content on wheat genotypes will be recorded at two different locations under timely sown conditions over two years.

Pyramiding of Fe/Zn genes from alien species. In the past, under a DBT project on biofortification, H.S. Dhaliwal and his group at Akal University, Baru Sahib, Himachal Pradesh, utilized the alien species *Ae. kotschyi* (containing high Fe and Zn) for developing wheat material with improved Fe and Zn. Six introgression lines with improved Fe and Zn, in the background of cultivar PBW343, were made available for the current project and are being utilized for pyramiding of genes in PBW343. Using these introgression lines, eight crosses were already attempted. Foreground MAS will be carried out in F_2 progenies of each of the eight crosses to identify homozygous plants for all the genes.

Meta-QTL analysis for grain Fe and Zn. Meta-QTL analysis for grain Fe and Zn traits of already reported QTL is being performed to identify more robust markers associated with genes for grain Fe and Zn. This will allow us to identify QTL with narrow intervals and closely linked markers. The MQTLs and associated markers will then be used for MAS leading to improvement of grain Fe and Zn content.

Candidate genes for grain Fe/Zn using co-expression network. Significant SNPs obtained from GWAS for Fe (7 SNPs) and Zn (6) content in wheat were used to find candidate genes associated with these SNPs with the help of a co-expression network analysis. In this study, genes found in 50-kb flanking regions of associated SNPs were extracted. Co-expression network was prepared from 850 RNA-seq expression data obtained from IWGSC. Genes co-expressed (obtained from co-expression network) and genes in the flanking regions of associated SNPs were collectively considered as candidate genes. In this manner, five genes for grain Fe content and two genes for grain Zn content were identified. Later, functional annotation of these genes was performed and a gene encoding calcium-binding protein (with EF-hand motif) was identified as candidate gene for one of the SNPs associated with Fe.

Transcriptomic studies involving Lr48.

In a collaborative study involving CCS University, Meerut, ICAR-IARI, New Delhi, and ICAR-IIWBR, Regional Station, Flowerdale, Shimla, a genome-wide transcriptome analysis was undertaken in the leaf-rust resistant bread wheat line CSP44 carrying the adult-plant resistance (APR) gene *Lr*48. Two pre-adult plant (P-AP) susceptible stages (S48 and S96) and two APR stages (R48 and R96) were used for RNA-seq (sequencing outsourced to SciGenom, Kochi, Kera-a, India by ICAR-IARI, New Delhi). At the susceptible P-AP stage (during S48 to S96), expression increased in 2,062 genes and declined in 130 genes; 1,775 of 2,062 differentially expressed genes (DEGs) also exhibited high expression during early incompatible stage R48. A comparison of S96 with R96 showed that the expression of 80 genes was enhanced and that of the 208 genes that declined at the AP stage. At the APR stage (during R48 to R96), expression of 25 genes increased and that of 126 genes declined. Apparently, the resistance during late-adult stage (R96) is caused by regulation of the expression of relatively fewer genes, although at P-AP stage (S48 to S96), an increase in expression of large number of genes was witnessed; expression of majority of these genes also kept on increasing during AP stage at R48 also. Altogether, the study suggested that APR may mimic some kind of systemic acquired resistance. The host specific DEGs belonged to 10 different classes, including genes involved in defence, transport, epigenetics, photosynthesis, and genes encoding some transcription factors. The pathogen-specific DEGs (including three genes encoding known biotrophic effectors) seem to help the pathogen in infection/growth through large-scale, stage-specific, enhanced expression of the host's genes. A putative candidate gene for *Lr48,* containing protein kinase domain (its ortholog in rice encoding OsWAK8), was identified.

Marker-assisted selection.

Marker-assisted selection has been an important component of research in our laboratory, which follows genetic studies in most cases. The activity involves introgression of desirable traits using DNA-based markers that are either developed in our own laboratory through interval mapping and GWAS or are collected from published literature. This leads to development of advanced prebreeding lines to be used in developing cultivars with improved traits. Wherever necessary, MAS also is used for pyramiding of genes for more than one trait.

MAS for drought tolerance. In order to develop drought-tolerant, high-yielding Indian wheat cultivars, MABC (marker-assisted backcrossing) was used to transfer an important drought insensitive QTL (*Qyld.csdh.7AL*) into three high-yielding but drought-sensitive Indian wheat cultivars HD2967, DBW88, and WB2. The advanced lines developed in this exercise, are being raised simultaneously at the Research Farm of Ch. Charan Singh University, Meerut, India, for seed multiplication and at IIWBR, Karnal, for screening for resistance to rusts under high disease pressure in field conditions. The selected improved progenies will be evaluated in field trials during the 2020–21 crop season.

MAS for heat tolerance. We are attempting to transfer desirable alleles of 10 QTL reported for six different heat-response traits from the heat-tolerant Egyptian cutivar Giza168 in to the background of the Indian wheat PBW343 using MABC. In BC_2F_1, plants that were phenotypically similar to the recipient parent and carried 3–8 QTL were selected in 2018–19 and were backcrossed again. Foreground selection followed by phenotypic selection will be made in the BC_3F_1 population during the current crop season (2019–20) to identify plants containing a combination of maximum number of desirable QTL and also having high phenotypic similarity with the recipient parent. Selected plants will be selfed to obtain BC_3F_2 progenies, when plants carrying combination of QTL in homozygous condition in 2020–21 will be identified.

MAS for pyramiding of genes/QTL for grain quality and rust resistance. A project on improving quality traits, including grain protein content (GPC), has been underway in our laboratory for almost two decades. We identified a number of markers associated with quality traits. Advanced lines with high GPC in the background of PBW343 (once a superior high-yielding, disease resistant cultivar) were developed through MAS. However, during the development of these lines, the recipient parent PBW343 became susceptible to different rusts, due to the evolution of new races of the pathogen. Therefore, an effort is now being made to pyramid rust resistance genes in these advanced lines.

Genes/QTL for a number of traits, including grain quality and resistance against the three rusts (leaf, stem, and stripe), were pyramided in the background of the elite Indian wheat PBW343. Two improved lines, PBW343 Unnat (*Yr70/Lr76+Lr37/Yr17/Sr38*) and PBW343-DCH5 (*Gpc-B1/Yr36+QPhs.ccsu-3A.1+QGw.ccsu-1A.3+Lr24/Sr24+Glu-A1-1/Glu-A1-2*) each in the background of PBW343 were crossed. These two lines were developed using MAS at PAU, Ludhiana, and CCSU, Meerut, respectively. In F_3 generation, several plants with all the desirable traits, were selected on the basis of DNA markers (except the glutenin genes). For the selection of lines carrying two tightly linked *Glu-A1* genes (*Glu-A1-1* and *Glu-A1-2*), foreground selection using SDS–PAGE analysis was exercised in seed harvested from the F_4 lines derived from the F_3. A number of F_4 lines were found to be positive for two HMW-glutenin genes and were homozygous for all the 10 to 12 genes/QTL. The advanced lines were further used for screening and rust-resistant lines were selected. Phenotypic evaluation of MAS-derived lines, along with parental genotypes and check cultivar, at two locations (Meerut and Ludhiana) identified 12 lines that had significantly higher GPC (0.7–2.1%) without any grain yield penalty and four lines with significantly higher yield with no penalty for GPC. The 16 lines that had either higher grain yield or higher GPC and were also resistant to three rusts constitute valuable material for wheat improvement.

In a separate study, MAS will pyramid QTL/genes for improved grain quality (grain protein content and pre-harvest sprouting tolerance) and resistance to all the three rusts using the cultivars HD2967 and Lok1 developed using MAS. Three lines were used: (i) HD2967 (*Gpc-B1/Yr36 + Lr24*); (ii) HD2967 (*Lr19/Sr25 + Yr10 + Lr34*, provided by Dr. Vinod, ICAR-IARI, New Delhi); and (iii) Lok1 (*Gpc-B1/Yr36+ Lr24 + Qphs.dpivic.4A.2*). We attempted 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 the F_2, F_3, and F_4 generations derived from these crosses. F_5 progenies carrying pyramided genes are being raised simultaneously at the Research Farm of CCS University, Meerut, for seed multiplication, and at IIWBR, Karnal, for screening for rust resistance under high disease pressure in field conditions. The desirable progenies will be evaluated in field trial during 2020–21.

In silico identification and characterization of wheat genes.

In silico identification of wheat genes, which have been sequenced and characterized in other crops (e.g., rice) also is an important activity in our laboratory, and several genes and gene families were identified and characterized using this approach. Results of only two such studies will be described here, which were conducted in 2019–20. Results of previous, similar studies are described (Ann Wheat Newslet **65**:25-26).

SET domain family genes. SET domain genes (SDGs) play an important role in histone lysine methylation (H3Kme) and thereby indirectly regulate expression of many genes associated with chromatin remodeling. SDGs belonging to the SET domain gene family have been thoroughly characterized in several diploid species. However, in allohexaploid bread wheat, structural and functional characterization of SDGs was done in our laboratory for the first time. In this study, we identified a total of 130 TaSDGs (representing 117 unique genes excluding duplications) distributed on all the 21 wheat chromosomes using the latest version of the whole-genome sequence of wheat. Following are some important features of TaSDGs: (i) 26 duplications (13 pairs of genes) were detected and involved in the expansion of the TaSDG family; (ii) a number of cis-elements and TFBS (transcription factor binding sites) were identified in the promoter regions of TaSDGs indicating their response to hormonal treatments and biotic/abiotic stresses; (iii) 96 of these TaSDGs carried 196 SSRs (simple sequence repeats); (iv) 25 TaSDGs carried 42 transposable elements; (v) 27 TaSDGs had targets for 18 different miRNAs, and (vi) 49 TaSDGs contained 122 lncRNAs.

Based on domain organization and phylogenetic analysis, 130 TaSDG proteins were classified into six classes (I–V and VII). The molecular functions of these SDGs were mostly restricted to zinc ion binding, histone-lysine N-methyltransferase activity, and protein binding. *In silico* expression analysis indicated the following features: (i) relatively higher expression (FPKM >20) of eight of the 130 TaSDGs in different tissues, and (ii) downregulation of 30 TaSDGs under heat, drought, and heat + drought stress at the seedling stage. qRT-PCR analysis also studied the expression of 11 representative TaSDGs at the seedling stage under abiotic (heat and drought) and biotic (leaf rust) stresses in contrasting genotypes. In general, TaSDGs were down-regulated under abiotic stresses, suggesting their possible role in negative regulation of genes involved in heat and drought stress tolerance. Contrary to this, under biotic stress involving leaf rust, the differentially expressed genes showed upregulation in resistant a NIL (HD2329 + *Lr28*) and downregulation in a susceptible cultivar (HD2329), suggesting a role of these TaSDGs in suppression of genes imparting leaf rust resistance.

***Thermo-tolerance 1* gene.** Grain production in all crops is under serious threat due to different abiotic and biotic stresses, and wheat crop is no exception. High ambient temperature reduces vegetative growth and development in wheat thereby significantly limiting grain production. At the tissue level, processes such as repair of the misfolded toxic proteins and elimination of cytotoxic denatured proteins are used to protect plant cells from severe heat stress. We observed that proteasome-mediated elimination of unfolded/misfolded toxic proteins is more effective than recovering their catalytic activities by the function of heat shock proteins (HSPs).

Recently, the gene *Thermo-tolerance 1* (TT1*)* was characterized in African rice (*Oryza glaberrima*; accession ID KR05475). The *OgTT1* gene encodes a α2 subunit of 26S proteasome, which is involved in the degradation of ubiquitinated proteins that were denatured/misfolded due to heat stress, thus responding to high temperatures. We identified orthologs of this gene not only in wheat, but also in its progenitors (*T. urartu*, *Ae. tauschii*, *T. turgidum subsps. dicoccoides* and *turgidum*). Full-length cDNA sequences of *OgTT1* gene were retrieved from the NCBI database; tBLASTx and BlastP analysis was conducted using Ensembl Plants (http://plants.ensembl.org/index.html) to identify true orthologs of this gene in wheat and its progenitor species. The gene was found to be present on chromosomes of homoeologous groups 2 and 3. The shortest gene belonged to *T. turgidum* subsp. *turgidum* 3B (4,223 bp) and longest to *T. urartu_08515* (7,064 bp; A genome). This difference in the gene size was largely due to differences in the size of UTRs and the introns. The gene had 11 exons in each of 10 species (except the longest gene of *T. urartu_09515*, which had 13 exons). All the three types of intron phases (0, 1, and 2) were found in the genes of different species. Promoter analysis allowed identification of cis-regulatory elements in the 1 kb upstream of the start codon. These elements are presumably involved in regulation of gene expression in response to abiotic stresses (HSE and TCA), hormones (GARE for gibberellic acid, and ABRE for abscisic acid), endosperm development (GCN4 and Skn1), and light (ACE, G box, I box, Sp1, GA, GAG, and GT1).

Expression of *TT1* genes in wheat was examined using microarray data. The analysis indicated that the level of expression of *TT1* genes was highest in root, stem, and spike/endosperm tissues during anthesis and grain development. In the developing grain, the expression of *TT1* located on 2A/3A was higher than that of on 2D, and that *TT1* on 2B/3B was significantly higher than the expression of *TT1* on 3D.

Further work is needed to confirm the chromosomal locations of the TT1 gene copies using nulli-tetrasomic lines of Chinese Spring. Validation through expression analysis using qRT-PCR and allelic variation of TT1 genes under heat stress is also planned.

Epigenetic regulation of leaf rust resistance.

Rusts in wheat are among the most devastating diseases. Among the three rusts, leaf rust alone causes huge yield losses. Epigenetic studies involving leaf rust were initiated in our laboratory, mainly in 2016–17 through a multi-institutional project funded by ICAR-NASF, New Delhi. Collaborating institutions included ICAR–IARI, New Delhi, and the ICAR–IIWBR Regional Station, Shimla. Epigenetic modifications due to seedling resistance (also called all-stage resistance (ASR)) gene *Lr28* and the APR gene *Lr48* were examined using a pair of NILs for *Lr28* and the cultivar CSP44, which carries the APR gene *Lr48*.

The initial studies involving *Lr28* and *Lr48* involved transcriptomics to find differentially expressed genes (due to *Lr28*/*Lr48*) following leaf rust infection. The results of transcriptomics were published earlier. Subsequently, we initiated epigenetic studies (involving DNA methylation, histone modifications and ncRNA). During 2019–20, we mainly conducted DNA methylation following MeDIP for *Lr48* and bisulphite sequencing (BiS-seq) for *Lr28* (MeDIP work on *Lr28* is already published; see list of publications). In this report we briefly describe the following work: (i) DNA methylation studies involving *Lr48* using MeDIP, (ii) genome-wide DNA methylation using BiS-seq involving *Lr28*, and (iii) ncRNAs (including miRNA and lncRNA) involving *Lr28*.

DNA methylation due to *Lr28* using BiS-seq. Continuing our earlier studies, the dynamics of DNA methylation was examined in wheat–leaf rust pathosystem utilizing genome-wide BiS-seq of the susceptible wheat HD2329 and its resistant NIL (HD2329 +*Lr28*) at 0 hbi (hours before infection) and 96 hai (hours after infection). BiS-seq was carried out for the following four treatments though outsourcing to Nucleome Informatics Pvt. Ltd., Hyderabad: (i) susceptible HD2329 at 0hbi (S0), (ii) susceptible HD2329 at 96 hai (S96), (iii) resistant NIL HD2329+*Lr28* at 0hbi (R0), and (iv) resistant NIL HD2329+*Lr28* at 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 in CHH context than in the CG and CHG contexts.

Genomic distribution of DMRs suggested that they were localized in intergenic regions, promoters, TTSs (transcription termination sites), and intron and exon regions in decreasing order. More hypomethylated DMGs than hypermethylated DMGs were found in S96 (compared to S0) and in R0 (compared to S0). The reverse was true for R96 (compared to S96 and R0) for all the three contexts. This pattern of DNA methylation suggests that the level of methylation changed with passage of time (0 hbi to 96 hai) and also differed between the susceptible cultivar and its resistant NIL due to presence of *Lr28*. Our observations also suggested that there could be suppression of genes due to hypomethylated DMRs in the promoter and TTS regions and to hypermethylation in introns and exons (gene body). Some of the important proteins encoded by DMGs included PR1, PR4, PR5, TIR-NBS-LRR, NBS-LRR, CC-NBS-LRR, WAK, WRKY, RLK, and RLP, which have a role in leaf rust resistance. These results improved our understanding of the molecular mechanism of plant immunity involving DNA methylation as an important component of epigenetic control of gene expression due to leaf rust resistance *Lr28*.

DNA methylation due to *Lr48* using MeDIP. A genome-wide DNA methylation analysis (using MeDIP) was undertaken in a leaf-rust resistant bread wheat line CSP44 with APR gene *Lr48* (this work was mainly undertaken by Neelu Jain and her cororkers at ICAR-IARI). For this purpose, DNA was isolated from leaf tissues both at the P-AP susceptible and APR stage. Samples were collected at 0 hbi (S0 and R0) and 96 hai (S96 and R96) and were subjected to MeDIP sequencing (outsourced to SciGenom, Kochi, Kerala, India).

A total of 52,872 DMRs were identified in all the four treatment pairs (S0 vs S96, S0 vs R0, R0 vs R96, and S96 vs R96). However, when the 0 hbi and 96 hai treatments were compared in each of S and R stages, a greater number of hypomethylated DMRs (1,920 in S and 11,119 in R) than hypermethylated DMRs (1,068 in S and 9,506 in R) were observed in both the S96 and R96 (relative to S0 and R0). A majority of the DMRs were present in the intergenic regions followed by gene bodies (including exons and introns), promoters, and regulatory regions (including 5' and 3'UTRs). The differentially methylated genes (DMGs) for S96 included those coding for glycerol-3-phosphate acyltransferase, photosystem II CP47 reaction centre protein, methionine S methyltransferase, and serine threonine protein kinase. Similarly, proteins encoded by DMGs in R96 included ATP-dependent clp protease, cyt b 559, peroxidase, NADH-ubiquinone oxidoreductase, phosphate transporter 13, and 50S ribosomal protein. Overall, the DMGs at both S and R stages were involved in carbohydrate degradation, phospholipid metabolism, protein ubiquitination and protein biosynthesis, energy metabolism, and lipid metabolism.

A comparison of MeDIP data with RNA-seq data revealed that only 27 DMGs in R96 (relative to R0) and onr DMG in S96 (relative to S0) matched with RNA-seq data. The expression of these genes (as revealed by RNA-seq data) was apparently regulated by differential DNA methylation. These results also indicate that the expression of only a small proportion of genes was influenced by DNA methylation, suggesting a possible role of several other genetic and/or epigenetic factors in regulating *Lr48* mediated APR to leaf rust in wheat.

Role of noncoding RNA (ncRNA) in *Lr28*-meditated leaf rust resistance. We earlier examined the role of miRNA (using smRNA-seq data) and lncRNA (using SAGE libraries) in *Lr28*-mediated leaf rust resistance. Continuing these efforts and collaborating with ICAR–IARI, we identified additional miRNAs and lncRNAs using RNA-seq data of the leaf rust susceptible cultivar HD2329 (S) and its resistant NIL HD2329+*Lr28* (R) at 0hbi (S0 and R0) and 96 hai (S96 and R96).

To identify miRNAs and lncRNAs, RNA-seq data was used (RNA-seq work was outsourced to SciGenom, Kochi, Kerala, India by ICAR-IARI, New Delhi). A total of 50 miRNAs were identified in both the R and S lines. Only 16 of these miRNAs were differentially expressed between the S and R lines. Of these 16 miRNAs, 11 miRNAs were upregulated and only one was downregulated in the R96 (relative to S96). Four miRNAs were upregulated in R96 (relative to R0). Expression of the 10 miRNAs (out of 11) upregulating in R96 also was confirmed by qRT-PCR analyses.

A total of 1,194 target genes also were identified for 50 miRNAs with complete or partial complementarity using psRNATarget server. The differentially expressed miRNAs targeted important genes, which included disease-response genes encoding the proteins serine/threonine protein kinase, keto-acyl synthase, peroxidase, pentatricopeptide repeat containing protein, transporters, and transcription factors.

A total of 1,178 lncRNAs also were predicted from the same data that was also used to identify miRNAs; 22 lncRNAs were found to be differentially expressed. One of these lncRNA c43470 is a precursor for two miRNAs, miR1132 and miR1436. Three lncRNA also were found to be target mimics for three miRNAs (miR1439, miR5169, and miR1127). To validate these target mimics, qRT-PCR was performed on the three miRNA, their five target genes, and three lncRNA as target mimics. As expected, the relative expression pattern of three lncRNA (c32751, c88698, and c37688) that were found to be target mimics was in contrast to the expression pattern for the three miRNA (miR1127, miR1439, and miR5169).

Publications.

Batra R, Gautam T, Pal S, Chaturvedi D, Rakhi, Jan I, Balyan HS, and Gupta PK. 2020. Identification and characterisation of SET domain gene family in bread wheat. Sci Rep (under review).

Bheemanahalli R, Sunoj VSJ, Saripalli G, Vara Prasad PV, Balyan HS, Gupta PK, Grant N, Gill KS, and Krishna Jagadish SV. 2019. Quantifying the impact of heat stress on pollen germination, seed-set and grain-filling in spring wheat. Crop Sci **59**:684-696 [doi: 10.2135/cropsci2018.05.02920].

Gahlaut V, Jaiswal V, Singh S, Balyan HS, and Gupta PK. 2019. Multi-locus genome wide association mapping for yield and its contributing traits in hexaploid wheat under different water regimes. Sci Rep [https://doi.org/10.1038/s41598-019-55520-0].

Gautam T and Gupta PK. 2020. Sequence variation in genes encoding miRNAs/targets and other related approaches for possible use in crop improvement. Plant Breed **139**:28-41.

Gautam T, Amardeep, Saripalli G, Rakhi, Kumar A, Gahlaut V, Gadekar DA, Oak M, Sharma, PK, Balyan HS, and Gupta PK. 2020. Introgression of a drought insensitive grain yield QTL for improvement of four Indian bread wheat cultivars using marker assisted breeding without background selection. J Plant Biochem Biotechnol [https://doi.org/10.1007/s13562-020-00553].

Gautam T, Dhillon GS, Saripalli G, Rakhi, Pratap V, P, Kaur S, Chhuneja P, Sharma PK, Balyan HS, and Gupta PK. 2020. Marker-assisted pyramiding of genes/QTL for grain quality and rust resistance in wheat (*Triticum aestivum* L.). Mol Breed (revised manuscript under review).

Gupta PK, Balyan HS, Gahlaut V, Saripalli G, Pal B, Basnet B, and Joshi AK. 2019. Hybrid wheat: past, present and future. Theor Appl Genet **132**:2463–2483

Gupta PK, Balyan HS, Sharma S, and Kumar R. 2020. Genetics of yield, abiotic stress tolerance and biofortification in wheat (*Triticum aestivum* L.). Theor Appl Genet (in press).

Gupta PK. 2020. How does cell machinery sense and deal with hypoxia? The 2019 Nobel Prize in Medicine. Proc Natl Acad Sci India Sect B Biol Sci 90 [Doi.org/10.1007/s40011-020-01182-2].

Jain N, Rani S, Sharma C, Sinha N, Singh A, Sharma JB, Prasad P, Saripalli G, Sharma PK, Balyan HS, Gupta PK, and Prabhu KV. 2020. Large-scale stage-specific regulation of gene expression during host-pathogen interaction in CSP44 bread wheat carrying AP gene *Lr*48. Funct Plant Biol [doi: 10.1071/FP18336].

Nawathe S, Yadav PS, Chand R, Mishra VK, Vasistha NK, Meher PK, Joshi AK, and Gupta PK. 2020. ToxA-Tsn1 interaction for spot blotch susceptibility in Indian wheats: an example of inverse gene-for-gene relationship. Plant Dis **104**:71-81.

Prasad P, Savadi S, Bhardwaj SC, and Gupta PK. 2020. The progress of leaf rust research in wheat. Fungal Biol [Doi.org/10.1016/j.funbio.2020.02.013].

Saripalli G, Kalpana S, Gautam T, Kumar S, Raghuvanshi S, Prasad P, Jain N, Sharma PK, Balyan HS, and Gupta PK. 2020. Genome-wide analysis of H3K4me3 and H3K27me3 modifications due to *Lr28* for leaf rust resistance in bread wheat (*Triticum aestivum*). Plant Mol Bio (revised manuscript under review).

Saripalli G, Sharma C, Gautam T, Singh K, Jain N, Prasad P, Roy JK, Sharma JB, Sharma PK, Prabhu KV, Balyan HS, and Gupta PK. 2020. Complex relationship of DNA methylation with gene expression during wheat-leaf rust interaction in a pair of NILs differing for *Lr28*. Mol Bio Rep **47**:1339-1360.

Savadi S, Prasad P, Sharma K, Rathore R, Bhardwaj SC, Gangwar OP2 , Khan H , Kumar S, Jain N, and Gupta PK. 2020. Development of novel transcriptome based SSR markers in *Puccinia triticina* and their potential application in genetic studies. Tropical Plant Pathol (in press).

Tura H, Edwards J, Gahlaut V, Garcia M, Sznajder B, Baumann U, Shahnnia F, Reynolds M, Langridge P, Balyan HS, Gupta PK, Schnurbusch T, and Fleury D. 2019. QTL analysis and fine mapping of a QTL for yield-related traits in wheat grown in dry and hot environments. Theor Appl Genet **133**:239–257

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Frontline demonstration of improved wheat production technologies: impact on yield gain and economic returns at the farmers' field.

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Introduction. Wheat is the second most staple food in India, and the commodity has witnessed rapid strides in production, especially after the introduction of high-yielding cultivars during the Green Revolution. Technological innovations and interventions in the form of semidwarf cultivars led to a major quantum jump in crop output (Sharma et al. 2014; Ramadas et al. 2019). Frontline demonstration (FLD), an adaptive research on improved cultivars and technologies, be-

Table 1. Particulars of the Frontline Demonstration (FLD) coverage on wheat during 2018–19.

	**Wheat growing zone**	**Number of FLDs conducted**	**Area covered (acres)**	**Number of farmers covered**
	Northern Hills Zone (NHZ) Hilly areas of Jammu and Kashmir (except Jammu, Samba, and Kathua districts), Himachal Pradesh (except Paonta Valley and Una district), Uttarakhand (excluding Tarai region), Sikkim, and hills of West Bengal and North Eastern states	138	138.00	229
	North Eastern Plains Zone (NEPZ) Eastern Uttar Pradesh, Bihar, Jharkhand, West Bengal (excluding hills), Odisha, Assam, and Plains of North Eastern states (except Sikkim)	453	455.34	498
	North Western Plains Zone (NWPZ) Punjab, Haryana, Western Uttar Pradesh (except Jhansi division), Rajasthan (except Kota & Udaipur divisions), Delhi, Tarai region of Uttarakhand, Una district and Paonta Valley of Himachal Pradesh, Jammu, Samba and Kathua districts of Jammu and Kashmir and Chandigarh	403	403.00	382
	Central Zone (CZ) Madhya Pradesh, Chhattisgarh, Gujarat, Kota and Udaipur divisions of Rajasthan and Jhansi and Chitrakoot divisions of Uttar Pradesh	282	284.00	258
	Peninsular Zone (PZ) Maharashtra, Karnataka, Andhra Pradesh, Goa, plains and Nilgiri & Palani hills of Tamil Nadu	223	223.00	195
	INDIA	1,499	1,503.34	1,562

ing demonstrated by the National Agricultural Research System (NARS) at selected farmers' fields, is more popular owing to its potential benefits among stakeholders. FLD has a significant role in crop acreage expansion through improved technology percolation, yield enhancement, and profitability. FLDs in wheat was started during 1993–94 and, since then, wheat production and protection technologies have been promoted aggressively across wheat-growing zones (Singh et al. 2019). Under this program, extension personnel act as catalysts, change agents who set up learning situations (demonstrations) for the farmers and use them for transfer of technology. In this context, we analysed the impact of wheat FLDs on yield and profitability at the farmers' field.

Data and methods. The present study sourced data from different cooperating centres of FLDs for 2018–19. During the 2018–19 wheat crop season, 1,499 demonstrations were conducted through 83 cooperating centers. The technologies, such as improved wheat (*T. aestivum* and *T. turgidum* subsps. *durum* and *dicoccum*) cultivars with a complete package of practices, rotavator, zero tillage/happy seeder, and bio-fertilizers were demonstrated in 1,562 randomly selected farmers' fields of five wheat-growing zones covering 1,503.34 acres (ICAR–IIWBR 2019) (Table 1, p. 37). Data on different parameters, such as yield, sale price, and costs, were recorded from the FLD beneficiaries. Conventional analyses, percentage, benefit:cost ratio (B:C ratio), and cost of production per unit of output were used to analyze the impact at the farmers' field.

Results and discussion. Wheat FLDs were organized and distributed across India primarily cultivated under three broad conditions, timely sown irrigated, late sown irrigated, and timely sown restricted irrigation/rainfed. Demonstrations were organized for all the three wheat species; bread wheat, grown on more than 96% of the total wheat area; durum, and dicoccum, which occupies around 4% of the area (Singh et al. 2019). Yield level, gain, and economic returns for 1,562 farmers' fields are given in Table 2. Across zones, the demonstrated cultivars and technologies have shown yield superiority over the check (Tiwari et al. 2014; Soni et al. 2017), ranging from 7.99% in the NWPZ to 20.21% in the NEPZ. The northeastern region of India has been the focus for the second Green Revolution in wheat (contributes 22% of production on a holding 27% of area) owing to its prospects and, hence, immense scope exists for increasing the production level and income of the farmers (Singh et al. 2017). The yield gain due to improved cultivars over the check was highest in the NEPZ (20.21%), followed by the NHZ (19.00%), PZ (15.28%), CZ (12.01%), and NWPZ (07.99%). Yield gaps arise due to the difference in management by the farmers, i.e., the package of practices followed by the farmers (Ramdas et al. 2012; Sendhil et al.2014). Concerted efforts are needed to bridge the yield, technology, and knowledge gaps (Tiwari et al., 2014).

Table 2. Yield level, gain, and economic returns in farmers' fields (n = 1,562). Yield gain significant at 1% probability. 1 US dollar was equivalent to 71 Indian Rupees in 2019.

	Yield level (kg/ha)		Yield gain		Profit (Rupee/ha)		B:C Ratio		Cost of Production (Rupee/kg)	
Zone	FLD	Check	kg/ha	%	FLD	Check	FLD	Check	FLD	Check
NHZ	3,326	2,795	531	19.00	54,772	41,752	2.72	2.36	9.75	11.34
NEPZ	3,789	3,152	637	20.21	48,660	34,816	2.48	2.04	9.11	11.22
NWPZ	5,227	4,840	387	7.99	89,276	80,779	4.06	3.76	5.66	6.14
CZ	4,804	4,289	515	12.01	70,181	58,463	3.08	2.76	7.44	8.21
PZ	3,376	2,928	448	15.28	53,983	40,470	3.03	2.59	8.22	9.15
INDIA	4,104	3,601	503	13.97	64,592	52,680	3.07	2.70	7.89	9.13

On an average, wheat cultivars or technologies demonstrated at farmers' fields under the FLD program gave 3.07 per Rupee of investment in comparison to the check cultivar (2.70 Rupees). A significant difference in B:C ratio was noticed between the FLD and check plots across zones and, in the case of FLDs, ranged from 4.06 Rupee (NWPZ) to 2.48 (NEPZ), indicating the scope for wheat improvement technology adoption. The profit per hectare in FLDs was highest in NWPZ (~89,276 rupees), followed by the CZ and NHZ. Among the wheat-growing zones, the cost of production was lowest in the NWPZ, 5.66 Rupee/kg, due to higher productivity in the NWPZ states of Punjab and Haryana (Ramdas et al. 2012), followed by less operational costs (ICAR–IIWBR 2019). Clearly, FLDs in wheat resulted in economic gains (Joshi et al. 2014; Sharma et al. 2016; Verma et al. 2016; Singh 2017).

Conclusions. Yield gaps arise due to differences in the package of practices adopted by the farmers and, hence, FLDs are conducted to bridge the existing yield, technology, and knowledge gaps. Overall, this analysis indicated yield gain and profitability at the farmers' field, establishing that FLDs carry successful technologies from lab to land. The difference in profit earned from wheat cultivation is subject to farm–farmer–region-specific conditions and varies from case to case. This study recommends adoption of improved cultivars and technologies under a recommended package of practices (region-specific) for increasing wheat productivity, cost reduction resulting in enhanced economic returns, and the welfare of the farmers.

References.

ICAR-IIWBR. 2019. Progress report of AICRP on wheat and barley 2018-19. Social Sciences (Singh S, Kumar A, Sendhil R, and Singh GP, Eds). ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. 41 pp [https://doi.org/10.13140/RG.2.2.19887.89763].

Joshi NS, Bariya MK, and BB Kunjadia. 2014. Yield gap analysis through front line demonstrations in wheat crop. Internat J Sci Res Pub **4**(9):1-3.

Ramadas S, Kumar TK and GP Singh. 2019. Wheat production in India: trends and prospects. *In:* Global Wheat Production. Intech Open [https://doi.org/10.5772/intechopen.86341].

Ramdas S, Singh R, and Sharma I. 2012. Exploring the performance of wheat production in India. J Wheat Res **4**(2):37-44.

Sendhil R, Singh R, Ramasundaram P, Kumar A, Singh S, and Sharma I. 2014. Yield gap in wheat: approach, quantification and resetting research priorities in India. J Wheat Res **6**(2):138-149

Sharma I, Sendhil R, Gupta OP, and Singh R. 2014. Status of wheat in India. *In:* Wheat Recent Trends on Production Strategies of Wheat in India, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur and ICAR-IIWBR. pp.1-13.

Sharma V, Kumar V, Sharma SC, and Singh S. 2016. Productivity enhancement and popularization of improved production technologies in wheat through frontline demonstrations. J Appl Nat Sci **8**(1):423-428 [https://doi.org/10.31018/jans.v8i1.810].

Singh GP, Sendhil R, and Chatrath R. 2017. Doubling farmers' income in north-eastern region of India by 2022: a roadmap for wheat producers. *In:* Souvenir released during the 56th All India Wheat & Barley Research Workers' Meet, BHU, Varanasi, 2017.

Singh S, Kumar A, Sendhil R, Singh R, Singh M, Chand R, and Singh GP. 2019. Impact of wheat frontline demonstrations in India: a decade of experience. ICAR–Indian Institute of Wheat and Barley Research, Karnal. ISBN:978-93-5382-920-9.

Singh SB. 2017. Impact of frontline demonstrations on yield of wheat (*Triticum aestivum*) under rain fed condition in Uttarakhand. Internat J Sci Environ Tech **6**(1):779-786.

Soni A, Kawdeti K, Awasthi MK, Nema RK, and Tiwari YK. 2017. Yield gap analysis through demonstration in wheat crop under tribal area of Jabalpur, India. Agric Sci Digest **37**:157-159 [https://doi.org/10.18805/asd.v37i2.7994].

Tiwari BK, Sharma A, Sahare KV, Tripathi PN, and Singh RR. 2014. Yield gap analysis of wheat through front line demonstration under limited irrigation conditions. Plant Arch **14**(1):495-498.

Verma AK, Jeengar KL, Ram J, and Naager KC, 2016. Popularization of high yielding varieties of wheat (*Triticum aestivum* L.) in Jhalawar district of Rajasthan state through Frontline Demonstrations. J Wheat Res **8**(1):39-44.

Publications.

Balaganesh G, Makarabbi G, and Sendhil R. 2019. Tracking the performance of wheat production in Uttar Pradesh. Ind J Econ Dev **15**(2):216-224 [https://doi.org/10.5958/2322-0430.2019.00026.X].

ICAR–IIWBR. 2019. Progress Report of AICRP on Wheat and Barley 2018-19. Social Sciences (Singh S, Kumar A, Sendhil R, and Singh GP, Eds). ICAR–Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. 41 pp [https://doi.org/10.13140/RG.2.2.19887.89763].

Kumar A, Gupta A, Singh S, Singh C, Sendhil R, Singh M, Chand R, and Singh GP. 2020. Improved wheat varieties for various production zones and production conditions. Extension Folder 78. ICAR–Indian Institute of Wheat and Barley Research, Karnal.

Mamrutha HM, Rinki K, Sendhil R, Renu M, Prasad SVS, Biradar S, Mavi GS, Dhar T, Bahadur R, Bhagwan JH, Prakash S, Singh H, Shukla RS, Srivastava M, Singh C, Gosavi AB, Salunke VS, Dhyani VC, and Singh GP. 2020. Developing stress intensity index and prioritizing hotspot locations for screening wheat genotypes under climate change scenario. Ecol Indicators 118C:106714 [https://doi.org/10.1016/j.ecolind.2020.106714].

Meena RP, Venkatesh K, Sendhil R, Rinki, Sharma RK, Tripathi SC, and Singh GP. 2019. Identification of water use efficient wheat genotypes with high yield for regions of depleting water resources in India. Agric Water Manag 223 [https://doi.org/10.1016/j.agwat.2019.105709].

Ramadas S, Kumar TK, and Singh GP. 2019. Wheat production in India: trends and prospects. *In:* Global wheat production. Intech Open [https://doi.org/10.5772/intechopen.86341].

Sendhil R and Sharma AK. 2020. A comparative economics of seed vis-à-vis grain production in wheat. *In:* Entrepreneurship development in seed production of Rabi crops (Mishra CN, Sharma AK, Jasrotia P, Kumar S, Singh SK, and Singh GP, Eds). ICAR–Indian Institute of Wheat and Barley Research, Karnal. pp. 165-168.

Sendhil R, Arti, Lal, Gururaj BM, A Jamaludheen A, Chaudhary U, and Rathore R. 2019. Price synamics and extent of integration in Indian wholesale and retail wheat markets. J Agric Sci Tech **21**(3):517-530 [https://jast.modares.ac.ir/article-23-13660-en.html].

Sendhil R, Kumar A, Singh S, and Singh GP. 2019. Wheat production technologies and food security: the nexus and prospects. *In:* Ascertaining food security through livelihood enriching interventions: challenges and opportunities (Pouchepparadjou A, Umamaheswari L, and Devi S, Eds). pp. 7-15.

Sendhil R, Kumar A, Singh S, Singh M, Pandey JK, and Singh GP. 2019. Technical efficiency in wheat production: insights from farm households in Bihar. Ann Wheat Newslet **65**:27-28.

Sendhil R, V Sangeetha, P Ramasundaram, Kumar A, and Singh S. 2020. Biofortification for enhancing nutritional outcomes and policy imperatives. *In:* Wheat and barley grain biofortification (Gupta OP, Vandey P, Narwal S, Sharma P, Ram S, and Singh GP, Eds). Woodhead Publishing, Elsevier. ISBN 9780128184448 [https://doi.org/10.1016/B978-0-12-818444-8.00013-4].

Singh C, Gupta A, Gupta V, Kumar P, Sendhil R, Tyagi BS, Singh G, Chatrath R, and Singh GP. 2019. Genotype × environment interaction analysis of the multi-environment wheat trials in India using AMMI and GGE Biplot approach. Crop Breed Appl Biotech **19**:309-318 [http://dx.doi.org/10.1590/1984-70332019v19n3a43].

Singh C, Gupta A, Kumar P, Sendhil R, Gopalareddy K, Gupta V, Singh SK, Sharma AK, Tyagi BS, Singh G, Chatrath R, and Singh GP. 2020. Multi-environment analysis of grain yield in a diverse set of bread wheat genotypes. J Cereal Res **12**(1):29-39.

Singh GP, Sendhil R, and Gopalareddy K. 2019. Maximization of national wheat productivity: challenges and opportunities. *In:* Current trends in wheat and barley research and development (Sai Prasad SV, Mishra AN, and Singh GP, Eds). ICN:218/2019.

Singh GP, Sendhil R, and Jasrotia P. 2019. AICRP on wheat and barley salient achievements and future directions. Ind J Fertilizers **15**(4):80-90.

Singh S, Kumar A, Sendhil R, Singh R, Singh M, Chand R, and Singh GP. 2019. Impact of wheat frontline demonstrations in India: a decade of experience. ICAR-Indian Institute of Wheat and Barley Research, Karnal. ISBN: 978-93-5382-920-9.

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Effect of interspecific competition between Triticum turgidum subsp. durum and Convolvulus arvensis in an organic production system in the Yaqui Valley, Sonora, Mexico.

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Abstract. Weed control is considered the main obstacle for high crop productivity in organic agriculture. In most cases, losses caused by weeds exceed those of any other category of agricultural pests. The effect of interspecific competition between the durum wheat cultivar CIRNO C2008 and field bindweed was evaluated during the 2019–20 autumn–winter crop season in a commercial field with a cooperating farmer in block 1010 of the Yaqui Valley, Sonora, Mexico. Sowing date was 16 December, 2019, using 175 kg/ha of seed in beds 500 m long with three rows and 80 cm apart. Treatments were wheat in a bindweed-free area of the field and wheat in a highly infested area. *C. arvensis* was not controlled during the growing season. To determine wheat grain field, three replications (0.8/m^2 each) per treatment were harvested. The average wheat dry biomass obtained in the treatments without *C. arvensis* competition was 9.441 t/ha, whereas it was 0.987 with interspecific competition; grain yield was 4.720 and 0.493 t/ha, respectively. The average *C. arvensis* dry biomass obtained was 6.395 t/ha. These results indicate that without an efficient organic method for control of *C. arvensis*, the organic wheat production will probably not be economically feasible in this region of northwest Mexico.

Introduction. Currently, there is an increasing demand for technologies that promote environmental sustainability, society-oriented development, and long-term management of natural resources (Leff 2002). 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). In agroecology, inter- and intraspecific competition in a community is a process that initiates given the lack of resources. Intraspecific competition between plants of the same crop and interspecific competition between crop plants and weeds occur simultaneously in agriculture. Competitive interactions between two plants can have negative effects on the growth rate, survival, reproduction, or performance of one or both plants (Tilman 1988). In monocultures, as the population increases, the average production per plant decreases, due to an increase in competition for the resources necessary for growth (Willey and Heath 1969). The effect of this competition is reflected in growth reduction of individuals who are in a more unfavorable competitive situation. Although the word competition suggests that the negative effect is due to the depletion of some limiting resources, plants can have negative effects on each other through allelopathy (Weiner 1993). In organic agriculture, weed control is considered the main obstacle for high crop productivity. In most cases, losses caused by weeds exceed those of any other category of agricultural pests. Under conditions of water stress, weeds can reduce crop yield by more than 50% through competition for moisture alone (Abouziena and Haggag 2016). Damage caused by weeds to the crop can be defined as the loss of yield depending on the density of weeds. Other parameters used are the initial, final, and accumulated biomass, and the abundance and relative frequency of weeds. The threshold for the economic damage is understood to be that situation of weeding, in which the cost of applying a control treatment equals the benefit of the measure adopted. The annual loss caused by weeds in agriculture in developing countries has been estimated in 125 x 10^6 tons of food, enough to feed 250 x 10^6 people (Parker and Fryer 1975, cited by Labrada et al. 1996).

In the Yaqui Valley, Sonora, Mexico, *Convolvulus arvensis*, is a species that dramatically affects wheat yield under conventional production systems. However, in organic production systems where herbicides cannot be used, the problem is even more serious. *Convolvulus arvensis* is a perennial weed that spreads rapidly, producing up to 25 or more stems in one season that can reach up to 3 m in length. The root system is deep, extensive, and can go up to 3 m or more. The plant also forms underground rhizomes, ranging in length from a few centimeters to over a meter. The roots have a high regenerative capacity, which is why even after deep tillage weed plants reappear on the soil surface. The plant also produces seed that can remain in the soil for 20 years or more. The fragments of roots and rhizomes also are means of propagation of the weed, so the cultivation or tillage tasks that divide and distribute these underground parts can help to increase infestations (Timmons 1949, cited by Labrada et al. 1996). Assuming that the intraspecific competition between plants of the cultivated species is constant, it is possible to analyze the effect of a monospecific infestation on the yield of the crop. Yield losses caused by weeds can be predicted by empirical or mechanistic models. Empirical models are based on relationships between independent variables, such as weed density or cover, growth rate, weed emergence time in relation to that of the crop, and crop yield as a dependent variable. Mechanistic models are based on processes such as light interception, photosynthesis, and partitioning of dry matter between different parts of competing plants (cultivation and weeds). These models have limited practical use, but are good tools for deriving empirical models (Sattin and Berti 2004). The objective of this evaluation 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 interspecific competition between durum wheat cultivar CIRNO C2008 (Figueroa-López et al. 2010) and field bindweed (*C. arvensis*) was evaluated during the 2019–20 autumn–winter crop season in a clay soil field with a cooperating farmer located in block 1010 of the Yaqui Valley, Sonora, Mexico, at 27°20'28.80" N latitude and 109°55'57.52" W longitude, 36 masl. This region has a warm climate (BW (h)) and extreme heat according to Koppen's classification, modified by Garcia (1988). Sowing date was 16 December, 2019, using 175 kg/ha of seed in beds 500 m long with three rows and 80 cm apart. For agronomic management, INIFAP's technical recommendations were followed by the cooperating farmer (application of 10 t/ha of poultry manure, soil preparation with a harrow, mechanical cultivation, and two manual weedings of species other than *C. arvensis*, one presowing and three complementary irrigations, and the use of beneficial insects for pest control) (Cortes and Ortiz 2018). No control of *C. arvensis* was made during the growth season. To determine wheat grain field and biomass, three replications (0.8/m^2 each) per treatment were harvested. The biomass obtained in the treatment with interspecific competition was separated into weed and wheat biomass, then dried for 48 h in a stove with continued air circulation at 65°C. Grain yield was calculated based in previous studies published by Quiñones et al. (2019) and Sañudo et al. (2019).

Table 1. Grain yield and biomass production of durum wheat cultivar CIRNO C2008 and *Convolvulus arvensis* under an organic production system in the Yaqui, Valley, Sonora, Mexico, during the 2019–20 crop season.

Variable	Replications			Average
	I	II	III	
GRAIN YIELD (T/HA)				
Wheat control	4.987	4.275	4.900	4.720
Wheat with *C. arvensis*	0.433	0.654	0.393	0.493
BIOMASS (T/HA)				
Wheat control	9.975	8.550	9.800	9.441
Wheat with *C. arvensis*	0.866	1.309	0.786	0.987
C. arvensis	6.550	5.450	7.187	6.395

Results and discussion. Average wheat grain yield was 4.720 t/ha (range 4.275–4.900) in the treatment without *C. arvensis* competition and 0.493 (range 0.393–0.654) with the weed (Table 1). Therefore, yield loss was 4.227 t/ha in this particular area of the field where the evaluation was carried out. The average wheat dry biomass obtained in the treatment without *C. arvensis* competition was 9.441 t/ha, whereas only 0.987 t/ha with interspecific competition, a difference of 8.454 t/ha. The range of dry biomass obtained of *C. arvensis* was 5.450 to 7.187 t/ha· with an average of 6.395. Plots with the highest *C. arvensis* biomass production showed the lowest wheat yield; the third replication showed 7.187 t/ha of *C. arvensis* biomass and 0.393 t/ha of wheat grain yield, whereas the first replication showed 6.550 t/ha of *C. arvensis* biomass and 0.433 t/ha of wheat grain yield (Table 1). The infestation level of *C. arvensis* in the evaluation site is shown (Fig. 1, p. 43), and the aspect of the control treatment where wheat developed without the presence of the weed (Fig. 2, p. 43). An increase the seeding rate of a particular crop could be a possible solution to the interspecific competition with a weed. Walsh (2019) explored the impact that crop density might have on the biomass and seed production of four weed species found in Australian wheat. He reported that when wheat was sown at the commercially recommended density of 120 plants/m^2, the biomass of *Lolium rigidum*, *Raphanus raphanistrum*, *Bromus diandrus*, and *Avena fatua* was reduced by 69, 73, 72, and 49%, respectively, compared to weeds grown in the absence of wheat. Weed seed production was reduced by 78% (*L. rigidum*), 78% (*R. raphanistrum*), 77% (*B. diandrus*), and 50% (*A. fatua*). When wheat was sown more densely (400 plants/m^2), there were additional reductions in both weed biomass (19% (*L. rigidum*), 13% (*R. raphanistrum*), 20% (*B. diandrus*), and 39% (*A. fatua*)) and seed production (12% (*L. rigidum*), 13% (*R. raphanistrum*), 17% (*B. diandrus*), and 45% (*A. fatua*)). Wheat grain yields remained the same. The results of the evaluation indicate that without an efficient organic method for control of *C. arvensis*, organic wheat production will probably not be economically feasible in this region of northwest Mexico.

Fig. 1. Interspecific competition between the durum wheat cultivar CIRNO C2008 and *Convolvulus arvensis* in a commercial field in the Yaqui Valley, Sonora, Mexico, during the 2019–20 crop season.

Fig. 2. Area of a commerical field where the durum wheat cultivar CIRNO C2008 developed without the presence of *Convolvulus arvensis* in the Yaqui Valley, Sonora, Mexico, during the 2019–20 crop season.

Conclusions. The interspecific 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.

References.

Abouziena HF and Haggag WM. 2016. Weed control in clean agriculture: A review. Métodos Alternativos de Controle não Químicos de Plantas Daninhas: Uma Revisão. Planta Daninha, Viçosa-MG **34**(2):377-392.

Cortes-Jimenez JM and Ortiz-Avalos AA. 2018. Agricultura orgánica: resultados de investigación y transferencia de tecnología en el sur de Sonora. Libro técnico No. 8. Campo Experimental Norman E. Borlaug. INIFAP. Cd. Obregón, Sonora. México. 180 p (In Spanish).

Figueroa-López P, Félix-Fuentes JL, Fuentes-Dávila G, Valenzuela-Herrera V, Chávez-Villalba G, and Mendoza-Lugo JA. 2010. CIRNO C2008, nueva variedad de trigo cristalino con alto rendimiento potencial para el estado de Sonora. Revista Mexicana de Ciencias Agrícolas **1**(5):745-749 (In Spanish).

García E. 1988. Modificaciones al sistema de classificación climática de Köppen. Instituto de Geografía de la Universidad Nacional Autónoma de México. Serie Libros número 6. México, D.F. 90 p (In Spanish).

Labrada R, Caseley JC, and Parker C. 1996. Manejo de Malezas para Países en Desarrollo. Estudio FAO Producción y Protección Vegetal 120. Roma, Italia [http://www.fao.org/3/t1147s00.htm#Contents].

Leff E. 2002. Ética, vida, sustentabilidad. Pensamiento Ambiental Latinoamericano. Programa de las Naciones Unidas para el Medio Ambiente Red de Formación Ambiental para América Latina y el Caribe, México D.F. 332 p (In Spanish).

Quiñones RCA, Sañudo LPA, Cortés JJM, and Ortiz AAA. 2019. Componentes de rendimiento de trigo de la variedad CENEB ORO 2017, con manejo orgánico en el Valle del Yaqui. Memoria de la XXXI Semana Internacional de Agronomía de la Facultad de Agricultura y Zootecnia. Universidad Juárez del estado de Durango. Gómez Palacio, Durango, México. pp. 965-969 (In Spanish)

Restrepo MJ, Angel SDI, and Prager M. 2000. Agroecología. Centro para el Desarrollo Agropecuario y Forestal, Inc. (CEDAF), Santo Domingo, República Dominicana. 134 p (In Spanish).

Sañudo LPA, Quiñones RCA, Ortiz AAA, and Cortés JJM. 2019. Componentes de rendimiento en la variedad de trigo (*Triticum durum* L.) CIRNO C2008, con manejo orgánico en el Valle del Yaqui. Memoria de la XXXI Semana Internacional de Agronomía de la Facultad de Agricultura y Zootecnia. Universidad Juárez del estado de Durango. Gómez Palacio, Durango, México. pp. 506-510 (In Spanish).

Sattin M and Berti A. 2004. Manejo de malezas para países en desarrollo. Addendum I *(*Labrada R Ed). Estudio FAO Producción y Protección Vegetal 120 Add. 1. Roma [http://www.fao.org/3/y5031s00.htm#Contents] (In Spanish).

Tilman D. 1988. Plant strategies and the dynamics and structure of plant communities. Monographs in Population Biology 26. Princeton University Press. 360 pp [https://books.google.com.mx/books princeton?hl=en&q=&vid=ISBN9780691084893].

Walsh JM. 2019. Enhanced wheat competition effects on the growth, seed production, and seed retention of major weeds of Australian cropping systems. Weed Sci Soc Amer **67**(6):657-665.

Weiner J. 1993. Competition among plants. Treballs de la SCB. Department of Biology. Swarthmore College. Swarthmore, Pennsylvania 19081. USA. Vol. **44**:99-109.

Willey RWand Heath SB. 1969. The quantitative relationship between plant population and crop yield. Adv Agron **21**:281-321.

Phenotypic and molecular characterization of bread wheat cultivar Borlaug 100

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Abstract. Phenotypic and molecular characterization was performed on the bread wheat cultivar Borlaug 100, based on the visual analysis following the UPOV guidelines, and by evaluating 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), by the extraction of DNA, PCR, and electrophoresis. Borlaug 100 has an average height of 92 cm, 78 days-to-heading, and 116 days-to-physiological maturity. Plant growth habit is intermediate and shows a very high frequency of recurved flag leaves. Ear glaucosity is medium, and awns are distributed the entire length and are white. Grain color is white. The presence of *Sr22*, which is effective against Ug99, was detected, as well as *Sr24*, which is linked to the resistance to most races of stem rust, among them Ug99 (TTKSK). The mutation *pina-D1b*, which is also related to the texture of the endosperm (grain hardiness), also was detected.

Introduction. Before the 1990s, bread wheat was the dominant class in northwest Mexico. In the state of Sonora, bread wheat occupied more than 50% of the area dedicated to wheat from the agricultural season 1983–84 to 1993–94. However, many wheat producers decided to grow durum wheat, because the Mexican government implemented domestic quarantine No. 16, which limited the cultivation of bread wheat in fields where Karnal bunt was detected at levels greater than 2% infected grains (SARH 1987). Other important factors were that durum wheat showed greater grain yield than bread wheat, and during that period of time, did not have problems with leaf rust. In addition, there were opportunities for export of durum wheat (Figueroa-López et al. 2010). From 2011 to 2019, Mexico has imported on average 4.4 x 10^6 tons of bread wheat, primarily from the the USA (60.1%), Canada (18.7%), Russia (17.4%), Ukraine (3.1%), and Argentina (0.7%) (CIMA 2019). The Mexican government has implemented a program of economic incentives for the cultivation of bread wheat in order to minimize imports as much as possible (SADER 2019), but there also is a need for the production of outstanding bread wheat cultivars with characteristics such as high yield potential, resistance to diseases, and quality. Disease resistance and quality are closely related to climatic conditions and agronomic management. Therefore, exploring efficient strategies that improve the productivity of a crop supported with biotechnological procedures (Pazmiño Ibarra 2012) is important. Strategies such as tissue culture and molecular biology (Levitus et al. 2010), will optimize available resources to speed up breeding (Morillo et al. 2014), and will allow us to predict its development in the future. However, characterizing the new materials from which genotypes with desired traits will become cultivars for commercial cultivation is necessary.

Materials and methods. The experimental work was carried out during the 2018–19 and 2019–20 crop seasons at the Norman E. Borlaug Experimental Station, which belongs to The National Institute for Forestry, Agriculture, and Livestock Research, located in block 910 of the Yaqui Valley, Sonora, Mexico at 27°20'28.80" N and 109°55'57.52" W, 36 masl. This region has a warm climate (BW (h)) and extreme heat according to Koppen's classification, modified by Garcia (1988). The sowing date was 15 December in both seasons, with a seed density of 100 kg/ha in five beds 88 m long with two rows. Beds were 80 cm apart. Fertilization consisted of 180 kg/ha of urea and 60 kg of monoammonium

Table 2. functional markers used for molecular characterization of the bread wheat cultivar Borlaug 100.

Trait	Locus	Marker	Heredity	Primer sequence (5’ 3’)	Allele	Fragment size	Chromosome	Reference
Stem rust	*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	*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	*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
Reduction in plant height	*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

phosphate (11-52). After the irrigation for seed germination, four complementary irrigations were applied in both seasons. The bread wheat cultivar Borlaug 100 (Fig. 3) (Camacho-Casas et al., 2017) released by the wheat breeding program of INIFAP. This cultivar was obtained by the cross 'ROELFS07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/TUKURU//FRET2' and selections were made by The Global Wheat Program of the International Maize and Wheat Improvement Center. Phenotypic characterization was based on visual analysis and following UPOV guidelines (1994). Molecular characterization consisted in identifying the presence of genes *Lr34*, *Sr2*, *Sr22*, *Sr24*, *Sr25*/*Lr19*, *Sr26*, *Sr35*, *Sr39*, *Pin-a, Pin-b*, *Rht-D1*, and *Rht-B1*, and the T1BL·1RS translocation (Table 2, p. 45). Sampling of the plant material was by manually cutting the nerves of young leaves and selecting areas free of necrosis or lesions that might be present. Samples were stored in 1.5-mL tubes at -20°C and later at -85 °C previous to lyophilization. DNA extraction was based on the method of Saghai-Maroof (1984) followed by PCR and electrophoresis. The sequences used are described (Table 2, p. 45).

Fig. 3. Bread wheat cultivar Borlaug 100.

Results. Phenotypic characterization (Table 3) was based on the descriptors of The *International Union* for the Protection of New Varieties of *Plants* (UPOV). Borlaug 100 has an average height of 92 cm, 78 days-to-heading, and 116 days- to-physiological maturity. Plant growth habit is intermediate and with a very high frequency of recurved flag leaves. Spike glaucosity is medium, and awns are distributed the whole length and are a white color. Grain color is white. As a result of the molecular characterization, the presence of the *Sr22* gene, which is linked to the long arm of chromosome 7A (Khan et al. 2005) was detected. Three linked markers, CFA2019, CFA2123, and BARC121, were used to determine the haplotype of *Sr22*, and CFA2123 was used for the identification because it is the closest (Miranda et al.,2007). The presence of *Sr22* has been observed to be effective against Ug99, however, it has a negative effect on grain yield. Therefore, *Sr22* has been deployed in a limited number of lines and cultivars (Olson et al. 2010). *Sr24* (localized in chromosome 3DL) also was found in Borlaug 100. This gene is widely used in commercial wheat cultivars around the world and offers resistance to most races of stem rust, including the virulent race Ug99 (TTKSK).

Table 3. Phenotypic characterization of the bread wheat cultivar Borlaug 100.

Structure	Characteristic	Description
Coleoptile	Anthocyanin coloration	absent or very weak
Flag leaf	Anthrocyanin coloration of auricles	absent or very weak
	Glaucosness of sheath	strong
Culm	Glaucosness of neck	strong
	Pith in cross section	thin
Spike	Distribution of awns	entire length
	Awn length at the tip of the ear	medium
	Density	medium
	Glaucosness	medium
	Color	white
	Lenth excluding awns	medium
Grain	Color	white
	Shape	semi-elliptical
Plant	Growth habit	intermediate
	Frequency with recurved flag leaf	very high
	Height	medium
	Seasonal type	spring type

Results of the analysis of gene *PINA* (*Pina-D1a* and *Pina-D1b*) allowed the detection of the mutation *pina-D1b*, which is related to the texture of the endosperm (hardiness of the grain). This trait determines its final potential uses. Grains with hard texture require more milling energy than those with soft texture in order to reduce the endosperm into flour and, during this milling process, a greater number of starch granules are physically damaged. Because damaged starch granules absorb more water than the undamaged, flour from hard wheat is preferred for making bread with yeast, whereas flour from soft wheat is selected for making cookies and cakes. The texture of the endosperm is controlled mainly by the hardiness locus (*Ha*) in the short arm of chromosome 5D. *Ha* is simple inherited trait and, eventhough the main locus is known as hardiness, softness is in fact the dominant trait.

The presence of the *Rht-B1* gene in materials of wheat is lightly higher (Youssefian et al. 1992). Pearce et al. (2011) indicate that when dwarf genes *Rht-B1* and *Rht-D1* were analyzed as determinants of height in current wheat cultivars, it was concluded that the group that averaged the shortest height was not the one with mutations *B1bD1b* (double dwarf), but mutations *B1aD1b* (4 cm shorter than the average) and the tallest was *B1bD1a*.

Conclusions. the bread wheat cultivar Borlaug 100 has outstanding characteristics, which may be useful as basis for the incorporation of heritable traits to new wheat materials. These traits vary from resistance to disease, high industrial quality, and good agronomic stand.

References.

Camacho-Casas MA, Chávez-Villalba G, Fuentes-Dávila G, Figueroa-López P, Huerta-Espino J, Villaseñor-Mir HE, Félix-Fuentes JL, and Ortíz-Monasterio JI. 2017. Borlaug 100, variedad de trigo harinero para el noroeste de México. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Norman E. Borlaug. Folleto Técnico No. 100. Cd. Obregón, Sonora, México. 32 p. ISBN 978-607-37-0718-3 [In Spanish].

Centro de Información de Mercados Agroalimentarios (CIMA). 2019. Importaciones y exportaciones de trigo. https://www.cima.aserca.gob.mx/work/models/cima/pdf/ ci_ie/2019/Importaciones_exportaciones_trigo_300419.pdf. Accessed on 30 May, 2020 [In Spanish].

Ellis M, Spielmeyer W, Gale K, Rebetzke G, and Richards R. 2002. "Perfect" markers for the *Rht-B1b* and *Rht-D1b* dwarfing genes in wheat. Theoretical and Applied Genetics **105**(6-7):1038-1042.

Figueroa-López, P, Félix-Fuentes JL, Fuentes-Dávila G, Valenzuela-Herrera V, Chávez-Villalba G, and Mendoza-Lugo JA. 2010. Evaluating grain yield in ten genotypes of durum wheat at different sowing dates and irrigation conditions at the Yaqui Valley Experimental Station, Sonora, Mexico. Ann Wheat Newslet **56**:127-130.

García E. 1988. Modificaciones al sistema de classificación climática de Köppen. Instituto de Geografía de la Universidad Nacional Autónoma de México. Serie Libros número 6. México, D.F. 90 p [In Spanish].

Gautier MF, Aleman ME, Guirao A, Marion D, and Joudrier P. 1994. *Triticum aestivum* puroindolines, two basic cystine-richseedproteins: cDNA sequence analysis and developmental gene expression. Plant Mol Biol **25**(1):43-57.

Giroux MJ and Morris CF. 1997. A glycine to serine change in puroindoline b is associated with wheat grain hardness and low levels of starch-surface friabilin. Theor Appl Genet **95**(5-6):857-864.

Gold J, Harder D, Townley-Smith F, Aung T, and Procunier J. 1999. Development of a molecular marker for rust resistance genes *Sr39* and *Lr35* in wheat breeding lines. Electr J Biotech **2**:1-2.

International Union for the Protection of New Varieties of Plants (UPOV). 1994. Guidelines for the conduct of test for distinctness, homogeneity and stability of wheat (*Triticum aestivum* L. emend, Fiori et Paol.) http://www.upov.int/index_en.html.

Khan RR, Bariana HS, Dholakia BB, Naik SV, Lagu MD, Rathjen AJ, and Gupta VS. 2005. Molecular mapping of stem and leaf rust resistance in wheat. Theor Appl Genet **111**(5):846-850.

Lagudah ES, McFadden H, Singh RP, Huerta-Espino J, Bariana HS, and Spielmeyer W. 2006. Molecular genetic characterization of the *Lr34*/**Yr18** slow rusting resistance gene region in wheat. Theor Appl Genet **114**(1):21-30.

Levitus G, Echenique V, Rubinstein C, Hopp E, and Mroginski L. 2010. Biotecnología y Mejoramiento Vegetal II. INTA, Argentina. 648 p [In Spanish].

Mago R, Bariana HS, Dundas IS, Spielmeyer W, Lawrence GJ, Pryor AJ, and Ellis JG. 2005. Development of PCR markers for the selection of wheat stem rust resistance genes *Sr24* and *Sr26* in diverse wheat germplasm. Theor Appl Genet **111**(3):496-504.

Mago R, Brown-Guedira G, Dreisigacker S, Breen J, Jin Y, Singh R, and Spielmeyer W. 2011. Anaccurate DNA marker assay for stem rust resistance gene *Sr2* in wheat. Theor Appl Genet **122**(4):735-744.

Miranda LM, Perugini L, Srnić G, Brown-Guedira G, Marshall D, Leath S, and Murphy JP. 2007. Genetic mapping of a *Triticum monococcum*-derived powdery mildew resistance gene in common wheat. Crop Sci **47**(6):2323-2329.

Morillo E, Márquez Carrillo ME, and Falconí E. 2014. Caracterización molecular de 297 genotipos de trigo (*Triticum aestivum* L.) provenientes del centro internacional de mejoramiento de maíz y trigo e inferencia de su estructura genética (Tesis de grado. Universidad de las Fuerzas Armadas. Quito, Ecuador. 65 p [In Spanish].

Olson EL, Brown-Guedira G, Marshall DS, Jin Y, Mergoum M, Lowe I, and Dubcovsky J. 2010. Genotyping of US wheat germplasm for presence of stem rust resistance genes *Sr24*, *Sr36*, and *Sr1RSA*. Crop Sci **50**(2):668-675.

Pazmiño I. V. 2012. Evaluación de la respuesta del germoplasma de trigo (*Triticum aestivum* L.) del INIAP a la aplicación de dos métodos biotecnológicos para la obtención y selección de plantas resistentes a roya amarilla (Bachelor's thesis, SANGOLQUÍ/ESPE/2012) [In Spanish].

Pearce S, Saville R, Vaughan SP, Chandler PM, Wilhelm EP, Sparks CA, and Thomas SG. 2011. Molecular characterization of *Rht-1* dwarfing genes in hexaploid wheat. Plant Physiol **157**(4):1820-1831.

Prins R, Groenewald JZ, Marais GF, Snape JW, and Koebner RMD. 2001. AFLP and STS tagging of *Lr19*, a gene conferring resistance to leaf rust in wheat. Theor Appl Gene **103**(4):618-624.

Saghai-Maroof MA, Soliman KM, Jorgensen RA, and Allard RWL. 1984. Ribosomal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics. Proc Natl Acad Sci USA **81**(24):8014-8018.

Secretaría de Agricultura y Desarrollo Rural (SADER). 2019. Disminuye Agricultura importaciones de trigo y arroz, y anula la de leche en polvo, con el Programa Precios de Garantía. https://www.gob.mx/segalmex/articulos/disminuye-agricultura-importaciones-de-trigo-y-arroz-y-anula-la-de-leche-en-polvo-con-el-programa-precios-de-garantia. Accessed on 30 May, 2020.

Secretaría de Agricultura y Recursos Hidráulicos (SARH). 1987. Cuarentena interior No. 16 contra el Carbón Parcial del trigo.. Diario Oficial, (jueves) 12 March, 1987, México [In Spanish].

Weng Y, Azhaguvel P, Devkota RN, and Rudd JC. 2007. PCR-based markers for detection of different sources of 1AL.1RS and 1BL.1RS wheat-rye translocations in wheat background. Plant Breed **126**(5):482-486.

Youssefian S, Kirby EJM, and Gale MD. 1992. Pleiotropic effects of the GA-insensitive *Rht* dwarfing genes in wheat. 2. Effects on leaf, stem, ear and floret growth. Field Crops Res **28**(3):191-210.

Zhang W, Olson E, Saintenac C, Rouse M, Abate Z, Jin Y, Akhunov E, Pumphrey M, and Dubcovsky J. 2010. Genetic maps of stem rust resistance gene *Sr35* in diploid and hexaploid wheat. Crop Sci **50**(6):2464-2474.

Validation of bread wheat cultivars Borlaug 100 and Onavas F2009 in semicommercial plots in southern Sonora during the 2018–19 crop season.

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Abstract. Validation of bread wheat cultivars Borlaug 100 and Onavas F2009 was in semicommercial plots with cooperating farmers in Navojoa and Bácum counties in southern Sonora, Mexico, during the 2018–19 crop season. Seed density was 200 and 180 kg/ha in Navojoa and Bácum counties, respectively, and sowing was on 21 and 28 December, 2018, respectively. Plots consisted of 12 500-m beds with two rows spaced 80 cm apart. The variables evaluated were grain yield, test weight, 1,000-kernel weight (TKW), biomass/m^2, spikes/m^2, spike weight/m^2, spike length, grain length, and plant height. Borlaug 100 had an average grain yield of 7.106 t/ha in New Bacame, whereas Onavas F2009 yielded 6.899; yields in Campo 77 were 7.118 and 6.973 t/ha, respectively. No statistical differences were detected for test weight, TKW, biomass/m^2, spikes/m^2, spike length, and grain length. Statistical differences were detected in spike weight/m^2 in New Bacame; Borlaug 100 had a higher weight than Onavas F2009, with an average of 1.03 kg/m^2, whereas Onavas F2009 registered 0.91 kg/m^2. In contrast, in Campo 77, Onavas F2009 had an average of 1.31 kg/m^2, whereas Borlaug 100 had 0.80 kg/m^2. In New Bacame, a significant statistical difference in plant height between cultivars was noted, Onavas F2009 (109 cm) was 7 cm taller than Borlaug 100; in Campo 77, there was no height difference between the cultivars.

Introduction. Southern Sonora, Mexico, is characterized for being one of the main regions for wheat production in the country, where 221,000 ha were sown during the 2018-19 crop season (SIAP 2018), and durum wheat continues to predominate. However, during the last two crop seasons, the federal government has implemented economic incentives to cultivation of bread wheat (SADER 2019), so the area has increased, and farmers have demanded new bread wheat cultivars. Therefore, breeding programs have focused on generating bread wheat genotypes with resistance to diseases, better industrial quality, higher grain yield potential, because these factors determine the release of an experimental wheat line as a commercial cultivar. The establishment of validation wheat plots is an important tool to evaluate the behavior of experimental candidate lines for release, as well as for recently released cultivars by The National Institute for Forestry, Agriculture, and Livestock Research. The purpose of this activity is to provide information to the farmers, which is generated in their own fields under their own management practices. Our objective was to evaluate two commercial, bread wheat cultivars at two locations in the Yaqui Valley in semicommercial plots for grain yield, test weight, TKW, biomass/m^2, spikes/m^2, spike weight/m^2, spike length, grain length, and plant height.

Fig. 4. Some phenotypic features of bread wheat cultivar Borlaug 100.

Fig. 5. Some phenotypic features of bread wheat cultivar Onavas F2009.

Materials and methods. This work was at two sites during the 2018–19 crop season in semicommercial plots located in New Bacame, Navojoa County (27°09'30" N and 109°35'27" W, 49 masl), with a seed density of 200 kg/ha and sown on 21 December, 2018; and in Campo 77, Bácum County (27°22'35.32"N and 110°06'07.71" W, 16 masl), with a seed density of 180 kg/ha and sown on 28 December, 2018. Plots consisted of 12 500-m beds with two rows spaced 80 cm apart with three replications. The bread wheat cultivars tested were Borlaug 100 (Fig. 4) (Camacho-Casas et al. 2017) obtained from the cross 'ROELFS07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/TUKURU//FRET2' and Onavas F2009 (Fig. 5) (Figueroa-López et al. 2012) obtained from the cross 'KAMBARA1*2/ BRAMBLING'. Variables evaluated were grain yield, test weight, TKW, biomass/m^2, spikes/m^2, spike weight/m^2, spike length, grain length, and plant height. The maximum temperature was recorded in both locations during the crop season. Statistical analysis was performed using the SAS program for Windows 9.0.

Results and discussion. A statistical difference was obtained in grain yield in New Bacame, where cultivar Borlaug 100 had an average of 7.106 t/ha, whereas Onavas F2009 yielded 6.899 t/ha. The average yield of Borlaug 100 was 500 kg below the average obtained in validation plots during three crop seasons in a total of 11 semicommercial plots, previous to its release as commercial cultivar (Camacho-Casas et al. 2017); Onavas F2009 had the same average yield as shown in validation plots in two crop season and in a total of five semicommercial plots (Figueroa-López et al. 2012). In Campo 77, no statistical differences were detected, but grain yield was slightly higher than that in New Bacame for both cultivars (7.118 and 6.973 t/ha, respectively). Félix-Valencia et al. (2009) indicate that for optimum development, wheat plants require a state of climatic comfort from seed germination to maturity. In terms of yield potential, optimum conditions of air temperature during the night provide a stage of rest for the crop while the daily temperature stimulates growth. Rawson and Macpherson (2001) indicate that as temperature rises, physiological development increases; however, growth (size increase) decreases (Fig. 6, p. 50). Sowing date is an important factor, because the crop might suffer during heading and grain filling(Noriega et al. 2019). Félix-Valencia et al. (2009) reported that late sowing, from 16–31 December, renders grain yields with a 7–13% reduction. No statistical differences were detected for test weight; however, it was slightly higher in Borlaug 100 (80.8–82.3) with an average of 81.5, whereas Onavas F2009 (79.2–81.8) averaged of 80.7. No statistical differences between cultivars at either location were observed in TKW but, similar to test weight, the average was higher in Borlaug 100 (54.2 g) than that of Onavas F2009 (53.1 g). Biomass/m^2 also had the same pattern, 1.31 kg for Borlaug 100 and 1.29 kg for Onavas F2009. Although there were no statistical differences in spikes/m^2, the average number of spikes (264) was lower in Campo 77 than in New Bacame, where the average number was 41 more spikes/m^2. Statistical differences were detected in spike weight/m^2. In New Bacame, Borlaug 100 registered a higher weight (0.86–1.10 kg/m^2; average 1.03 kg/m^2) than Onavas F2009 (0.82–1.00 kg/m^2; average 0.91 kg/m^2). In contrast, in Campo 77, Onavas F2009 had a range of 1.19 to 1.5 kg/m^2 with an average of 1.31 kg/m^2, whereas Borlaug 100 had a range of 0.76 to 0.86 kg/m^2 with an average of 0.80 kg/m^2. The overall average of both cultivars in New Bacame was 0.97 kg/m^2 and 1.05 kg/m^2 in Campo 77. The average spike length of Onavas F2009 was 11.3 cm, 0.73 cm longer than that of Borlaug 100; however, there were no statistical differences between this variable in both locations. Similarly, there were no statistical differences in grain length; however, grain produced by Borlaug 100 was longer than that of Onavas F2009 at both locations. The overall average of Borlaug 100 was 0.74 cm and was 0.72 cm for Onavas F2009. In New Bacame, there was a significant statistical difference in plant height between cultivars. Onavas F2009 (109 cm) was 7 cm taller than Borlaug 100. In Campo 77, there was no difference between cultivars. Borlaug 100 registered a height of 95 cm previous to its release, which could have been the average of four seasons with four sowing dates, and with four and two complementary irrigations (Camacho-Casas et al. 2017).

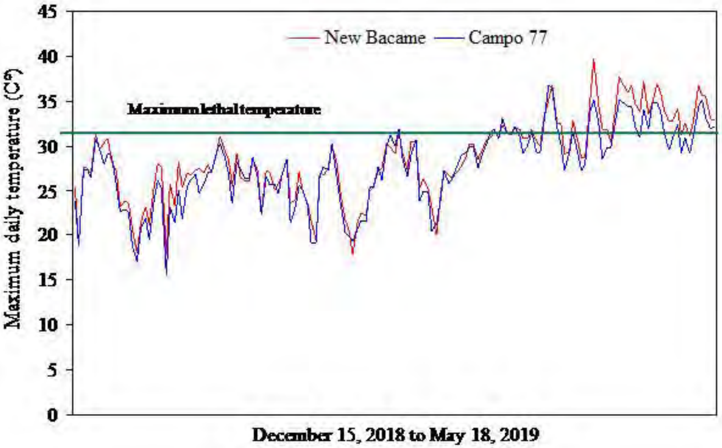

Fig. 6. Maximum daily temperature in New Bacame, Navojoa County (red), and in Campo 77, Bácum County (blue), in the state of Sonora, Mexico, during the 2018–19 growing season.

Conclusions. The bread wheat cultivar Borlaug 100 has outstanding characteristics that may be useful as basis for the incorporation of heritable traits to new wheat material. One of these traits is grain yield, where in semicommercial fields with cooperating farmers from southern Sonora, it produced an average of 7.1 t/ha. With economic incentives from the federal government in an attempt to reduce bread wheat imports, the area grown with bread wheat, and specifically with cultivar Borlaug 100 in southern Sonora, may surpass its 77,214 ha during the 2019–20 crop season.

References.

Camacho-Casas MA, Chávez-Villalba G, Fuentes-Dávila G, Figueroa-López P, Huerta-Espino J, Villaseñor-Mir HE, Félix-Fuentes JL, and Ortíz-Monasterio JI. 2017. Borlaugh 100, variedad de trigo harinero para el noroeste de México. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Norman E. Borlaug. Folleto Técnico No. 100. Cd. Obregón, Sonora, México. 32 p. ISBN 978-607-37-0718-3 (In Spanish).

Félix Valencia P, Ortíz Enríquez JE, Fuentes Dávila G, Quintana Quiróz JG, and Grageda Grageda J. 2009. Horas frío en relación al rendimiento de trigo: áreas de producción del estado de Sonora. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Valle del Yaqui. Folleto Técnico No. 63. Cd. Obregón, Sonora, México. 40 p. ISBN 978-607-425-159-3 (In Spanish).

Figueroa-López P, Fuentes-Dávila G, Valenzuela-Herrera V, Chávez-Villalba G, Félix-Fuentes JL y Mendoza-Lugo JA. 2012. Ónavas F2009, variedad de trigo harinero para el noroeste de México. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Norman E. Borlaug. Folleto Técnico No. 86. Cd. Obregón, Sonora, México. 26 p. ISBN 978-607-425-777-9 (In Spanish).

Noriega-Carmona MA, Cervantes-Ortiz F, Solís-Moya E, Rangel-Lucio JA, Rodríguez-Pérez G, Mendoza-Elos M, and García-Rodríguez JG. 2019. Efecto de la fecha de siembra sobre la calidad de semilla de trigo en el Bajío, México. Revista Fitotecnia Mexicana 42(4):375-384 (In Spanish).

Rawson HM, and Macpherson H. G. 2001. Trigo regado: manejo del cultivo. Organización de las naciones unidas y la alimentación. Roma. 112 p (In Spanish).

Servicio de Información Agroalimentaria y Pesquera (SIAP). 2018. Anuarios dinámicos http://www.siap.sagarpa.gob.mx. Consulted on 10 March, 2018 (In Spanish).

Secretaría de Agricultura y Desarrollo Rural (SADER). 2019. Disminuye Agricultura importaciones de trigo y arroz, y anula la de leche en polvo, con el Programa Precios de Garantía. https://www.gob.mx/segalmex/articulos/disminuye-agricultura-importaciones-de-trigo-y-arroz-y-anula-la-de-leche-en-polvo-con-el-programa-precios-de-garantia, Consulted on 30 May, 2020.

Wheat production with high grain protein content in southern Sonora Mexico.

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Abstract. An inverse engineering process was carried out to determine the management of the fertilization applied by durum wheat farmers who obtained high grain protein content. The Tablex Miller Company provided protein content data of shipments during the summer of 2017. Ten wheat farmers who obtained more than 12% protein were interviewed in order to ascertain grain yield, rate, timing, source, and application method of fertilizer. During the 2017–18 and 2018–19 crop seasons, a follow up was conducted with five of the ten farmers. According to the information provided and the results of production, 100% of the farmers applied nitrogen before sowing, at sowing, and during complementary irrigations. Achieving 7.0 t/ha is feasible with a protein content greater than 12.10%, which provides an additional $112/ha.

Introduction. In the state of Sonora, Mexico, the annual average area established with wheat during the years 2008 to 2019 was 287,856 ha with a maximum of 322,935 and a minimum of 223,437 ha. During the same period, the average grain yield was 6.28 t/ha for a production of 1,793,735 ton. In 2019, the wheat area harvested was 260,536 ha, out of which 151,267 ha were from the District of Rural Development (DDR) 148-Cajeme and 90,289 ha from the DDR-149-Navojoa, for a total of 241,556 ha for this region of the state (SIAP 2020). Of the total wheat established in this region, the average of the last three crop seasons, 77% corresponds to durum wheat and 23% to bread wheat (CESAVE-SON 2020). Durum wheat produced in the state of Sonora has three main avenues for marketing: balanced animal feed, industry, and export. This region contributes with 42% of the total wheat export from Mexico. However, the conditions to access for the export market need to comply with a specific quality; that if not fulfilled, is penalized on the economic value, implicating important monetary losses (Garza and Bringas 2016). Therefore, farmers must select wheat cultivars that comply with the requirements of the target market and the regional strategies for disease management (primarily Karnal bunt). In both cases, it is important that the wheat cultivar used has a high yield potential and satisfies the quality standards established by the market (Cortés et al. 2011). During the last few decades, valuing of the intangible attributes of agricultural products has been highlighted, which gained importance based on frequent ethical considerations by consumers. The tendency for demand of differentiated products and quality is growing, and in many instances seals and brands transmit and guarranty the existence of those attributes (Riveros and Wienke 2014). In southern Sonora, economic incentives (bonus) of $7 to $30 per ton are granted if the grain protein content has a range of 11.5 to 11.69% or is ≥14%. With an average grain yield of 7.0 t/ha, this bonus represents an additional income of $48/ha at $7/t and $205.7 at $30/t when 14% of protein content is achieved. In general, wheats with a high protein content have low grain yields and vice versa. High-yielding wheats that present a protein content lower than 11.5%, also have problems with yellow berry. Our objective was to evaluate the feasibility to obtain a high-yielding durum wheat with high protein content under the conditions of southern Sonora.

Materials and methods. During the summer of 2017, an inverse engineering process was used to manage the fertilization applied by wheat farmers who obtained high protein content. The Tablex Miller Company provided data for protein content in shipments. Ten wheat farmers, who obtained more than 12% protein, were interviewed to ascertain the grain yield, rate, timing, source, and fertilizer application method. Once the modules of high protein content were located and after soil preparation, soil samples were collected from each one at 0–30 cm depth in September 2017. Samples were taken to the Soil and Plant Nutrition Laboratory at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, for physio-chemical analysis and consequently for fertilization recommendation for the following wheat season. Results were subjected to a descriptive statistical analysis in Excel. During the 2017–18 and 2018–19 crop seasons, a follow-up was made in five of the ten fields with high protein content in 2017. Those fields with the highest protein content were selected based on the wheat–wheat rotation history and ease od access to the field. Data for yield and protein were taken from the average of the reports provided by the reception center to the farmer. The grain sample collected from each vehicle in the reception center was approximately 2 kg.

Results and discusion. Inverse-engineering studies analyze available products in the market to learn their details. A finished product is minutely analyzed to understand the reasoning of each detail of construction or function (Ramos 2013). The results of the physio-chemical analysis of the soil samples are shown (Table 4, p. 52). Values for electric conductivity, percent of interchangeable sodium, and hydraulic conductivity indicated no problems with salinity, sodicity, or compaction. The concentration of the microelements iron and manganese was adequate but deficient for copper and zinc. However, in the case of wheat, no reports for the response to the application of these microelements are known (Cortés et al. 2015), and so their application was not suggested. With respect to the exchangeable bases, such as calcium, magnesium, and potassium, they were in a high concentration The level of organic matter was classified as low, moderately alkaline for the pH according to the classification of the official Mexican norm (NOM-021-RECNAT-2000), which establishes specifications for soil fertility, salinity, classification, studies, sampling, and analysis (DOF 2002). For nitrogen and phosphorus, recommendations were made individually for each module, depending on their availability in the soil and the expected grain yield. Phosphorus was suggested to be applied before sowing for a greater wheat yield (Cortés et al. 2017). A divided nitrogen application was recommended; except in the case of organic fertilizer use, application before sowing was recommended. The availability of nitrogen in the soil before the presowing irrigation defines the amount to apply during the crop season. Nitrogen availability depends on sampling depth, the previous crop and yield, the fertilizer applied, amount of rainfall registered during the summer, use of organic fertilizers, organic matter content, and soil texture. A soil analysis indicates the amount of available nitrogen and the soil characteristics that promote greater leaching or volatilization of the fertilizer applied (Cortés and Ortiz 2020).

Table 4. Statistical variables of physio-chemical characteristics of soil samples taken at a depth of 0–30 cm from durum wheat fields with high protein content in the Yaqui Valley, Sonora, Mexico, in 2017.

Variable	Mean	Physio-chemical variable		Standard deviation
		Minimum	Maximum	
Phosphorus ppm	21.5	2.40	47.7	12.4
Nitric nitrogen (kg/ha)	85.5	21.0	138.0	36.9
Organic matter (%)	1.34	0.63	2.05	0.47
Calcium carbonate (%)	6.65	4.95	9.57	1.61
Hydraulic conductivity (cm/h)	6.62	2.82	10.44	2.47
pH in $CaCl_2$	7.67	7.26	7.84	0.17
Electric conductivity (dS/m)	1.37	0.60	2.89	0.66
Total salts (ppm)	879	384	1,847	424
Relation of sodium absorption	3.55	1.86	7.96	1.85
Interchangeable sodium (%)	3.77	1.46	9.49	2.44
Copper (ppm)	0.63	0.42	0.85	0.13
Iron (ppm)	2.59	1.73	3.43	0.54
Manganese (ppm)	4.20	2.50	5.62	1.23
Zinc (ppm)	0.44	0.18	0.83	0.22
Calcium meq (100/g)	34.6	18.0	43.6	8.03
Magnesium meq (100/g)	6.60	5.76	7.79	0.68
Sodium meq (100/g)	2.71	2.30	3.29	0.34
Potassium meq (100/g)	0.90	0.59	1.24	0.22
Sand (%)	36.6	10.8	50.0	11.2
Silt (%)	21.4	12.0	49.3	10.7

Table 5. Fertilization, grain yield, protein, economic bonus, number of irrigations, and fractioning of nitrogen in durum wheat fields with high protein content during the 2016–17 crop season. [1] 10 t/ha of chicken manure applied, [2] sprinkler irrigation, [3] presowing, [4] number of irrigations, and [5] 1,000 L from worm humus leach distributed in all irrigations.

Field	Fertilization (N–P–K–S–Zn)	Grain yield (ton/ha)	Protein (%)	Bonus (in USD$)	Number of irrigations	Fractioning of nitrogen
1	350–108–0–0–0	7.90	12.04	16	3	P [3]; 2 I [4]
2	323–62–0–0–0	7.80	12.25	16	3	P; 2 I
3	300–52–0–0–0	7.00	12.70	16	3	P; 2 I
4	335–40–0–15–1.5	8.20	12.23	16	3	P; 3 I
5	363–50–0–15–1.5	7.80	12.17	16	3	P; 2 I
6	97–26–0–0–0	5.20	12.98	16	10 [2]	P; humus [5]
7	327–38–0–0–0	4.90	12.97	16	2	P; 2 I
8 [1]	340–0–0–0–0	6.00	12.50	16	3	P; 2 I
9	345–60–0–15–1.5	6.56	12.70	16	4	P; 2 I
10	227–26–0–0–0	6.00	13.14	19	3	P; 3 I
Mean		**6.74**	**12.57**			

Interviews with farmers describe the fertilization established during the crop seasons 2016–17 (Table 5), 2017–18 (Table 6, p. 53), and 2018–19 (Table 7, p. 53). Similarly, grain yield is reported as well as the protein content, the economic bonus in dollars, and the number of irrigations and fractioning of nitrogen. During the 2016-17 crop season, based on the interviews with farmers, we observed that 80% applied 300 units or more of nitrogen. The maximum quantity of nitrogen applied was 363 units and the minimum was 97. The field with the lowest rate of nitrogen was irrigated with sprinklers, and with a total of 10 complementary irrigations during the crop season in which 100 L/ha of worm humus leach was applied at each irrigation. However, Ortiz and Cortés (2017) indicated that the nutritional input of the worm humus leach is very low compared to other types of manures, therefore, the low yield reported in this field is attributed to low fertilization. In field number 7, more than 300 units of nitrogen were applied; however, it had only two complementary irrigations. In an evaluation in the Yaqui Valley, Sonora, the interaction of nitrogen rate with the number of irrigations and its effect on grain yield and protein content was studied. The highest yield was linked to the highest fertilization with four complementary irrigations. The lowest yield was correlated with the highest fertilization and two complementary irrigations, however, this interaction reported the highest protein content (Cortés and Ortiz 2020). During the 2017–18 and 2018–19 crop seasons, the highest protein content in the field with the lowest rate of nitrogen applied was observed; 10 t/ha of chicken manure were applied in this field, which provided 150 units of additional nitrogen. Different manures, such as chicken manure, can be classified as slow-release nitrogenous fertilizers because they provide nitrogen during the entire season making it feasible to obtain high yield and high protein content in wheat (Cortés et al. 2008). In general, in all seasons, we observed that 100% of the farmers applied nitrogen during the first and second complementary irrigations. In the first two seasons, two farmers applied nitrogen until the third complementary irrigation. The amount of phosphorus applied varied; one had no application of phosphorus. In this plot, chicken manure was applied for two seasons in a row; the maximum amount applied was 200 kg/ha of monoammonium phosphate during 2016–17. Fractional application of nitrogen is fundamental in order to obtain wheat with high protein content, the exceptions being when organic fertilizers with gradual release, when chemical fertilizers with urease inhibitors, or with controlled release are applied (Cortés and Ortiz 2020).

Table 6. Fertilization, grain yield, protein, economic bonus, number of irrigations, and fractioning of nitrogen in durum wheat fields with high protein content during the 2017–18 crop season. [1] 10 t/ha of chicken manure applied, [2] presowing, and [3] number of irrigations.

Field	Fertilization (N–P–K–S–Zn)	Grain yield (ton/ha)	Protein (%)	Bonus (in USD$)	Number of irrigations	Fractioning of nitrogen
1	405–40–0–10–1.5	7.13	11.69	7	3	P[2]; 3 I[3]
2	374–60–0–15–1.5	8.10	12.90	16	4	P; 3 I
3	312–78–0–0–0	8.60	11.50	7	3	P; 2 I
4[1]	240–0–0–0–0	7.00	13.14	19	3	P; 1 I
5	335–78–0–0–0	7.80	12.10	16	3	P; 2 I
Mean		**7.72**	**12.26**			

Table 7. Fertilization, grain yield, protein, economic bonus, number of irrigations, and fractioning of nitrogen in durum wheat fields with high protein content during the 2018–19 crop season. [1] 10 t/ha of chicken manure applied, [2] presowing, and [3] number of irrigations.

Field	Fertilization (N–P–K)	Grain yield (ton/ha)	Protein (%)	Bonus (in USD$)	Number of irrigations	Fractioning of nitrogen
1	345–0–0	9.91	12.09	13	3	P[2]; 2 I[3]
2	315–0–0	10.77	11.94	13	4	P; 2 I
3	309–100–0	7.66	11.84	10	3	P; 2 I
4[1]	280–0–0	8.70	12.55	16	3	P; 2 I
5	10 ton of compost	8.65	12.31	16	3	P
Mean		**9.12**	**12.15**			

Conclusion. Obtaining 7.0 t/ha of durum wheat grain yield under the conditions of southern Sonora is feasible when the protein percentage is greater than 12.10%, which renders an additional income of $112.0/ ha for high protein content.

References.

Comité Estatal de Sanidad Vegetal del Estado de Sonora (CESAVESON). 2020. Permisos de siembra. Available at: https://cesaveson.com/index.php/home/permisos. Consulted on 10 April, 2020 (In Spanish).

Cortés JJM, Valenzuela SC, and Uribe MHR. 2008. Memoria sobre uso de abonos orgánicos en la agricultura. Centro de Investigación Regional del Noroeste-INIFAP. Campo Experimental Valle del Yaqui. April 2008. Cd. Obregón, Sonora, México. 70 p (In Spanish).

Cortés JJM, Fuentes DG, Ortiz EJE, Tamayo ELM, Cortez ME, Ortiz AAA, Félix VP, and Armenta CI. 2011. Agronomía del trigo en el sur de Sonora. Libro Técnico Núm. 6. Campo Experimental Norman E. Borlaug. INIFAP. Cd. Obregón, Sonora. 238 p (In Spanish).

Cortés JJM and Ortiz AAA. 2020. Manejo de la fertilización para obtener trigo con alto contenido de proteína. Folleto Técnico No. 108. Centro de Investigación Regional del Noroeste-CENEB-INIFAP. March 2020. Cd. Obregón, Sonora. 60 p (In Spanish).

Cortés JJJ, Ortiz AAA, and Zazueta EG. 2015. Uso de microelementos en la agricultura. Publicación especial No. 22. Centro de investigación regional del Noroeste-INIFAP. Campo experimental Norman E. Borlaug. March 2015. pp. 60-63 (In Spanish).

Cortés JJM, Ortiz AAA, and Zazueta EG. 2017. Respuesta del trigo a fuentes y dosis de fósforo en el Valle del Yaqui, Sonora. Memorias del XX Congreso Internacional de Ciencias Agrícolas. 26-27 October, 2017. Mexicali, Baja California. pp. 252-258 (In Spanish).

Diario Oficial de la Federación (DOF). 2002. Norma oficial mexicana, que establece las especificaciones de fertilidad, salinidad y clasificación de suelos. Estudios, muestreo y análisis. NOM-021-RECNAT-2000. 67 p (In Spanish).

Garza LMC and Bringas CT. 2016. Definición del mercado de trigo cristalino en el Valle del Yaqui, México. Economía, teoría y práctica. No 44. pp. 193-215. Available at: http://www.scielo.org.mx/scielo.php?script=sci_arttext&pid=S0188-33802016000100193&lng=es&nrm=iso Consulted on 11 July, 2019.

Ortiz AAA y Cortés JJM. 2017. Lixiviado de humus de lombriz en la producción de trigo orgánico en el Valle del Yaqui, Sonora. Memorias del XIV simposio internacional y IX congreso nacional de agricultura sostenible. 25-30 September, 2017. Ciudad Obregón, Sonora, México. pp. 171-176 (In Spanish).

Ramos ADA. 2013. Uso de la ingeniería inversa como metodología de enseñanza en la formación para la innovación. World Engineering Education Forum. Cartagena de Indias, Colombia. 7 p (In Spanish).

Riveros H y Wienke H. 2014. Valor agregado en los productos de origen agropecuario: aspectos conceptuales y operativos. Instituto Interamericano de Cooperación para la Agricultura (IICA). San José Costa Rica. 44 p. (In Spanish).

Servicio de Información Agroalimentaria y Pesquera (SIAP). 2020. Avance de siembras y cosechas. Resumen nacional por estado. Trigo grano. Ciclo otoño-invierno. Riego + temporal. Available at: https://nube.siap.gob.mx/cierreagricola/ Consulted on 10 April, 2020 (In Spanish).

Durum wheat grain yield components under organic production in the Yaqui Valley, Sonora, Mexico.

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Abstract. Organic management of crops is incipient in southern Sonora, Mexico, but there is infrastructure, market, and interest by farmers. Our objective was to evaluate wheat yield components of wheat cultivars CENEB Oro C2017 and CIRNO C2008 in a plot with organic certification at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Mexico, during the 2018–19 growing season. Sowing was on 14 December, 2018, in beds with two 110-m rows. The soil was prepared by three rounds of disc harrowing. Two rates of chicken manure were applied, 10 t/ha and 7.5 t/ha. Bio Crack and Fubagro were applied 45 and 65 days after sowing for green aphid and rust control, respectively. Weeds were controlled by hand scarification between rows. There was one presowing and three complementary irrigations during the season. The experimental design was a randomized complete block split plot with six replications and a mean comparison by Tukey's test (0.05). Harvest was manually with a hand sickle. Variables evaluated were grain yield, 100-kernel weight, biomass/m^2, number of grains/spike, grain/m^2, and number of spikes/m^2. Statistical differences between cultivars for all variables were evaluated. With the exception of 100-kernel weight and grains/spike, differences were detected for fertilization rates. CENEB Oro C2017 produced a higher average grain yield (7.6 t/ha) than that of CIRNO C2008 (6.5 t/ha) at both fertilization rates. Maximum grain yield of CENEB Oro C2017 was 8.1 t/ha and 6.9 t/ha for CIRNO C2008. With the exception of the 100-kernel weight, the yield components were greater for CENEB Oro C2017 than for CIRNO C2008, and they were statistically different. Biomass/m^2 was the variable that related most with grain yield in both cultivars.

Introduction. The Mexican state of Sonora is the main wheat producer with an average area of 289,077 ha and grain yield of 6.26 t/ha per crop season during the last 10 years. In southern Sonora, 90% of the wheat is grown in the counties of Cajeme, Navojoa, Benito Juárez, Etchojoa, Huatabampo, Bacúm, San Ignacio Río Muerto, Empalme, and Guaymas, and the average grain yield over the last 10 years was 6.18 t/ha (SIAP 2020). Organic management of agricultural crops is still incipient in the region, but there is infrastructure, market, and the interest by the farmers to implement certified organic agriculture. The debate about this topic has already begun, as in other parts of the world, where many reports indicate that organic production renders lower yields than conventional agriculture (Bilsborrow et al. 2013; Kumar et al. 2014; Bacenetti et al. 2016). These reports attribute the low production to the use of organic fertilizers with little availability of nitrogen or that this element is not immediately available in the sources of nitrogen used. However, comparative studies on maize, under conventional and organic management, have reported yields of 6.6 and 11.3 t/ha, respectively (Vidal et al. 2016). The cost of an organic production system is reported to be a 3.5% cost reduction and a gross income of 71% over that income reported by conventional management (Vidal et al. 2016). In any agricultural regions, the most important criteria for choosing a crop are based on potential yield and economic revenue. Several studies on certified organic production in the Yaqui Valley, Sonora, Mexico, indicate that a certified organic production system is similar to those under conventional production (Cortes and Ortiz 2017). However, wheat yield components under an organic production system has not been studied. Our objective was to evaluate wheat yield components of two commercial durum wheat cultivars in a plot with organic certification.

Materials and methods. The evaluation was during the autumn–winter 2018–19 crop season at the Norman E. Borlaug Experimental Station in block 970 in the Yaqui Valley, Sonora, Mexico, in a plot with organic certification (AGRICERT MEXICO–SENASICA 2019; BIOAGRICERT 2019a, b). Durum wheat commercial cultivars CENEB Oro C2017 (Chávez-Villalba et al. 2018) and CIRNO C2008 (check cultivar) (Figueroa-López et al. 2010) were sown on 14 December, 2018, in beds with two rows. The experimental plot consisted of 12 beds 110 m long separated by 80 cm. The soil was prepared by three rounds of disc harrowing in order to incorporate into the soil debris of the previous crop. Two treatments, with different rates of chicken manure, T_1= 10 t/ha and T_2= 7.5 t/ha, were incorporated by disc harrowing. For phytosanitary management, two applications were made for control of the green aphid (*Schizaphis graminum*) with Bio Crack, a product based on garlic (*Allium sativum*) and chamomile (*Matricaria chamomilla*), and with Fubagro, a product based on creosote bush (*Larrea tridentate*) and cluster pine (*Pinus pinaster*) for control of rusts. Both products have a registration by the OMRI (Organic Materials Review Institute, https://www.omri.org/). Two liters of commercial product per ha were applied 45 and 65 days after sowing. Weeds were controlled by scarification between rows and twice by hand. One presowing irrigation and three complementary irrigations were made during the crop season. The experimental design was a randomized complete block split plot with six 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 done 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. Microsoft Excel was used to obtain the relationship between yield components. With the data from both durum wheat cultivars, graphs were constructed to establish the relationship between yield components and wheat yield.

Results and discussion. Significant statistical differences were detected between durum wheat cultivars for all the variables evaluated and the rates of fertilization, with the exception of 100-kernel weight and grains/spike (Table 8). Cultivar CENEB Oro C2017 produced a higher average grain yield (7.6 t/ha) than CIRNO C2008 (6.5 t/ha), statistically different at both fertilization rates (Table 9, p. 56). There was a greater difference in grain yield (1.192) between cultivars when the high fertilization rate was applied than with the low rate (1.042). The grain yield produced by each cultivar was higher when 10 t/ha of chicken manure was applied than with 7.5 t/ha. The difference for CIRNO C2008 was 0.9 t and 1.050 t for CENEB Oro C2017. The grain yield produced by both cultivars under certified organic agriculture is similar to that reported for conventional wheat at the regional and national level of 6.41 t/ha and 6.08 t/ha, respectively (SIAP 2020). With the exception of the 100-kernel weight, the rest of the yield components were higher in CENEB Oro C2017 than in CIRNO C2008 and were statistically different. CIRNO C2008 had 15.0% greater weight than that of CENEB Oro C2017. PIEAES 2020 reported a difference of up to 23%. CIRNO C2008 produces larger grains than those of CENEB Oro C2017 (Fig. 7) and, therefore, a great 100-kernel weight. The difference in the other yield components was 10.3 for biomass/m^2, 19.2 for grains/spike, 27.6 for grains/m^2, and 12.1% for spikes/m^2. A combined average grain

Fig. 7. Grain produced by durum wheat cultivars CENEB Oro C2017 and CIRNO C2008.

Table 8. Analysis of variance of yield components and grain yield of durum wheat cultivars CIRNO C2008 and CENEB Oro C2017 with two rates of organic fertilizer (chicken manure), during the 2018–19 crop season in the Yaqui Valley, Sonora Mexico (* = statistically significant at Tukey 0.05).

Source of variation	Grain yield (t/ha)	100-kernel weight (g)	Biomass/m^2 (kg)	Grains/spike	Grains/m^2	Spikes/m^2
Replications	8.60	1.45	8.50	6.00	6.94	0.42
Cultivar (A)	28.09*	74.99*	6.61*	25.33*	63.19*	11.66*
Fertilization (B)	21.42*	2.26	9.88*	1.23	17.53*	35.55*
A*B	0.13	0.01	1.04	0.88	0.60	3.07

yield of 7.571 t/ha for both cultivars with the high rate of organic fertilizer was greater than that obtained with the low rate of fertilizer (6.596 kg/ha) and statistically different. The grain yield difference between the rates applied was 975 kg/ha. A high fertilizer rate also had greater numbers and was statistically different for biomass/m^2 (11.1), grains/m^2 (15.5), and spikes/m^2 (20.3%). The correlation of grain yield with biomass/m^2 had a value of 0.9, followed by number of grains/m^2 at 0.8, spikes/m^2 at 0.6, and number of grains/spike at 0.5 (Fig. 8). These results coincide with those of Sanduño et al. (2019), Quiñonez et al. (2019), Valdés et al. (2017), and López (2011).

Table 9. Mean comparison of yield components and grain yield of durum wheat cultivars CIRNO C2008 and CENEB Oro C2017 with two rates of organic fertilizer (chicken manure), during the 2018–19 crop season in the Yaqui Valley, Sonora Mexico (numbers in columns with the same letter are not statistically different at Tukey 0.05).

Cultivar / fertilizer	Grain yield (t/ha)	100-kernel weight (g)	Biomass/m^2 (kg)	Grains/spike	Grains/m^2	Spikes/m^2
CIRNO C2008						
10.0 t/ha	6.975	5.524	1.509	42	12,676	300
7.5 t/ha	6.075	5.664	1.370	43	10,758	253
Average	6.525 b	5.594 a	1.439 b	42 b	11,717 b	276 b
CENEB Oro C2017						
10.0 t/ha	8.167	4.675	1.715	50	17,585	357
7.5 t/ha	7.117	4.829	1.494	54	14,792	272
Average	7.642 a	4.752 b	1.604 a	52 a	16,189 a	314 a
CV (%)	**7.2**	**4.6**	**6.5**	**10.1**	**9.8**	**9.2**
Average of both cultivars						
10.0 t/ha	7.571 a	5.096 a	1.612 a	45 a	15,131 a	329 a
7.5 t/ha	6.596 b	5.247 a	1.432 b	48 a	12,775 b	262 b

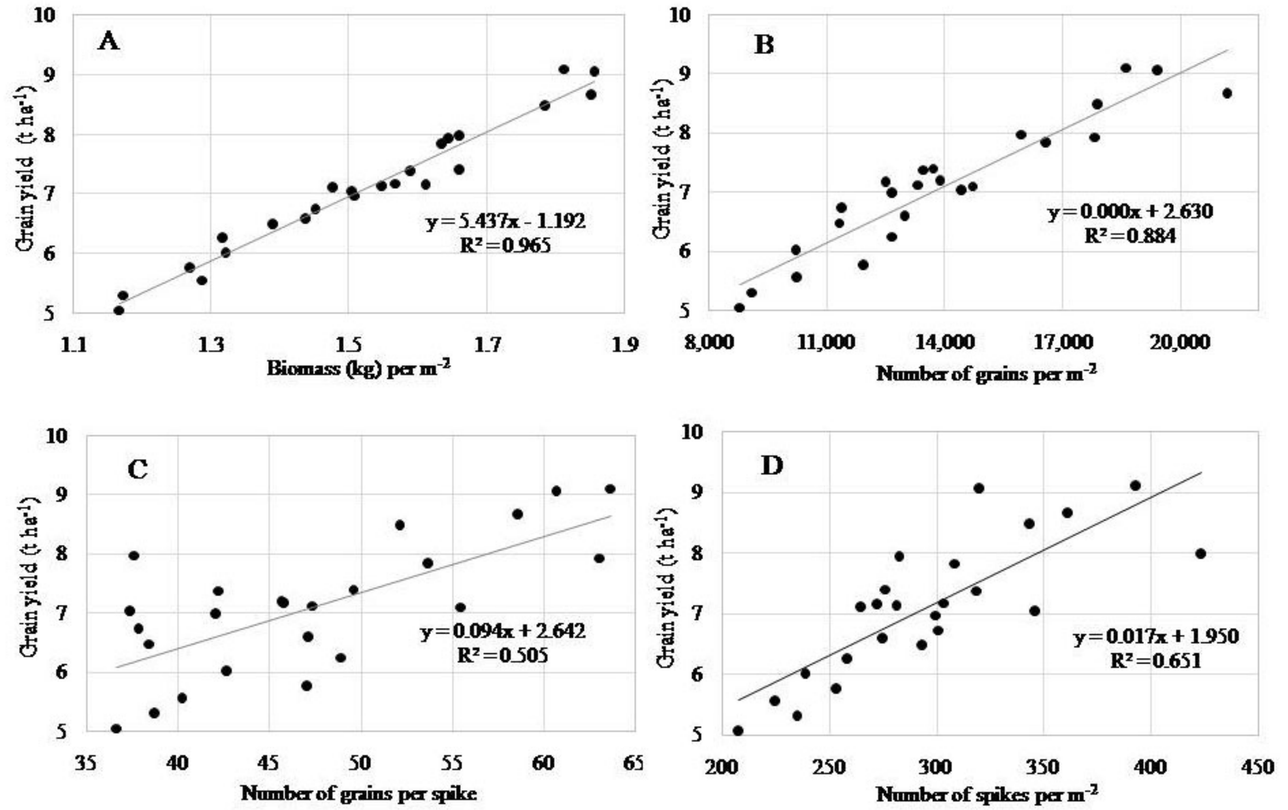

Fig. 8. Relationship between grain yield and yield components of durum wheat; A. biomass/m^2; B. number of grains/m^2; C. number of grains/spike; and D. number of spikes/m^2.

Conclusions. The grain yield produced by durum wheat cultivars CENEB Oro C2017 and CIRNO C2008 under certified organic agriculture is similar to that reported for conventional wheat at the regional and national level. Under organic agriculture, the maximum grain yield produced by cultivar CENEB Oro C2017 was 8.1 t/ha with a rate of 10 t/ha of chicken manure. CIRNO C2008 reached 6.9 t/ha with the same rate of organic fertilizer. Biomass/m^2 is the component that is most related with grain yield in both durum wheat cultivars CENEB Oro C2017 and CIRNO C2008.

References.

AGRICERT MEXICO – SENASICA (Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria). 2019. Organic Certificate. Number OMK80KCC. Control code IS SENASICA-OCO-16-005-K80K.

Bacenetti J, Fusi A, Negri M, Bocchi S, and Fiala M. 2016. Organic production systems: Sustainability assessment of rice in Italy. Agric Eco Environ **225**:33-44. doi:10.1016/j.agee.2016.03.046

BIOAGRICERT. 2019a. Product certifícate of organic operation according to BAC Equivalent Organic Standard (reg. 834/07 art. 33.3). Number EUK80KCC. Control code MX BIO 132 K80K.

BIOAGRICERT. 2019b. Conformity Certificate. Organic operation is certified to the USDA National Organic Program Regulation 7 CFR part. 205. Number NPK80KCC. Control code MX BIO 132 K80K.

Bilsborrow P, Cooper J, Tétard JC, Srednicka TD, Baraski M, Eyer M, Schmidt C, Shotton P, Volakakis N, Cakmak I, Ozturk L, Leifert C, and Wilcockson S. 2013. The effect of organic and conventional management on the yield and quality of wheat grown in a long-term field trial. Eur J Agron **51**:71-80.

Chávez-Villalba, G., Camacho-Casas, M., Ammar, K., Alvarado-Padilla, J., Fuentes-Dávila, G. y Borbon-Gracia, A. 2018. CENEB Oro C2017: nueva variedad de trigo duro para el noroeste de México. Revista Mexicana de Ciencias Agrícolas **9**(7):1560-1563 https://doi.org/https://doi.org/10.29312/remexca.v9i7.1679.

Cortés JJM and Ortiz AAA. 2017. Agricultura orgánica: una nueva revolución verde para el Valle del Yaqui, Sonora. XIV Simposio Internacional y IX Congreso Nacional de Agricultura Sostenible, Cd. Obregón, Sonora, México. pp. 252-261 (In Spanish).

Figueroa-López P, Félix-Fuentes JL, Fuentes-Dávila G, Valenzuela-Herrera V, Chávez-Villalba G, and Mendoza-Lugo JA. 2010. CIRNO C2008, nueva variedad de trigo cristalino con alto rendimiento potencial para el estado de Sonora. Revista Mexicana de Ciencias Agrícolas **1**(5):745-749 (In Spanish).

Kumar S, Bauddh K, Barman SC, and Patrap SR. 2014. Amendments of microbial biofertilizers and organic substances reduces requirement of urea and DAP with enhanced nutrient availability and productivity of wheat (*Triticum aestivum* L.). Ecol Eng **71**:432-437.

López CC. 2011. Variación en rendimiento de grano, biomasa y número de granos en cebada bajo tres condiciones de humedad del suelo. Trop Subtrop Agroeco **14**:907-918 (In Spanish).

Patronato para la Investigación y Experimentación Agrícola del Estado de Sonora (PIEAES, A.C.). 2019. Trigos cristalinos. http://www.pieaes.org.mx/variedades.html. Consulted on 12 April, 2020 (In Spanish).

Quiñonez RCA, Sañudo LPA, Cortés JJM, and Ortiz AAA. 2019. Componentes de rendimiento de trigo de la variedad CENEB ORO 2017, con manejo orgánico en el Valle del Yaqui. XXXI Semana internacional de Agronomía. Gómez Palacio, Durango, México. pp. 965-969 (In Spanish).

Sanduño LPA, Quiñonez RCA, Ortiz AAA, and Cortés JJM. 2019. Componentes de rendimiento en la variedad de trigo (*Triticum durum* L.) CIRNO C2008, con manejo orgánico en el Valle del Yaqui. XXXI Semana internacional de Agronomía, Gómez Palacio, Durango, México. pp. 506-510 (In Spanish).

Servicio de Información Agroalimentaria y Pesquera (SIAP). 2020. Avance de siembras y cosechas. Resumen nacional por estado. Trigo grano. Ciclo otoño-invierno. Riego + temporal. https://nube.siap.gob.mx/cierreagricola/. Consulted on 10 April, 2020 (In Spanish).

Valdés VC, Estrada CG, Martínez RCG, and Domínguez LA. 2017. Rendimiento de grano en trigo modificado por cambios en la fuente durante el llenado de grano. Revista Mexicana de Ciencias Agrícolas **8**(1):79-90 (In Spanish).

Vidal MV, Camarena OE, and Coutiño EB. 2016. Manejo agronómico integral-orgánico y su impacto en la producción y productividad del maíz de riego en Nayarit. IV Foro Internacional de Agricultura Orgánica. Nuevo Vallarta, Nayarit, México. pp. 319-323 (In Spanish).

Evaluation of advanced bread wheat lines for Karnal bunt resistance in the field during the 2014–15 crop season.

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Abstract. We evaluated 1,203 advanced bread wheat for resistance to Karnal bunt during the 2014–15 crop season. Sowing dates were 19 and 29 November, 2014, using 8 g of seed for a 0.7-m row in a bed with two rows. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage, in five heads/line. Harvesting was done manually, and the percentage of infection was determined by counting healthy and infected grains. The percent infection of the advanced lines at the first date was 0–83.5% with an average of 28.1% and 0–74.7% at the second sowing date with an average of 21.4%. The average percent infection was 0–70.3% with a mean of 24.7%. The only line that did not show infected grains was 'BAVIS/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92'. Twelve lines fell into the 0.1–2.5% infection category, 33 within 2.6–5.0%, 78 within 5.1–10.0%, 720 within 10.1–30.0%, and 359 had more than 30% infection. Lines with the highest percent infection were 'TACUPETOF2001/SAUAL//BLOUK#1/3/SAUAL/YANAC//SAUAL with 83.5, VEE/MJI//2* TUI/3/PASTOR/4/BERKUT/6/2*OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI' at 83.0 and 'WBLL1/KUKUNA//TACUPETOF2001/3/UP2338*2/VIVITSI/4/HUW234+LR34/PRINIA*2//KIRITATI' at 80.3%, all sown on 19 November, 2014. The average of the three highest levels of infection of the susceptible check was 98.6%.

Introduction. Karnal bunt of wheat caused by *Tilletia indica* occurs on bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). This disease was first identified in India (Mitra 1931) and later in Mexico (Duran 1972), Pakistan (Munjal 1975), Nepal (Singh et al. 1989), Brazil, (Da Luz et al. 1993), the United States (APHIS 1996), Iran (Torarbi et al. 1996), the Republic of South Africa (Crous et al. 2001), and apparently in Afghanistan (CIMMYT 2011). In general, the fungus partially affects some grains in a plant (Bedi et al. 1949) (Fig. 9) and, in some occasions, they are totally destroyed. Although the fungus may penetrate the embryo, it does not necessarily cause damage (Mitra 1935; Chona et al. 1961). Partially infected grain may give rise to healthy plants, although it is reported that the percentage of germination decreases depending on the level of seed infection (Rai and Singh 1978; Singh 1980; Bansal et al. 1984), and that severely affected seed lose viability or show abnormal germination (Rai and Singh 1978). Fuentes-Dávila et al. (2013) indicate that seed with the greatest infection, but with the embryo intact, produce the greatest number of tillers. Control of this pathogen is difficult because teliospores are resistant to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1985, 1988). Chemical control can be accomplished by applying fungicides during flowering (Salazar-Huerta et al. 1997; Fuentes-Dávila et al. 2005, 2016, 2018); however, this measure is not feasible when quarantines do not allow tolerance levels for seed production (SARH 1987). The use of resistant wheat cultivars is the best control method, and it also would reduce the possibilities of introduction of the disease into Karnal bunt-free areas. Since the 1940s, several species of *Triticum* have been evaluated for resistance to Karnal bunt (Bedi et al. 1949; Singh et al. 1986; 1988). Bread wheat is most affected by the disease; under artificial inoculation some lines may show more than 50% infected grain (Fuentes-Dávila et al. 1992; 1993). Therefore, continued evaluation of new advanced lines and wheat cultivars is necessary. Our objective was to evaluate the reaction of 1,203 advanced bread wheat lines for resistance to *T. indica* in the field.

Fig. 9. Segment of a wheat spike with dark areas indicating the presence of infected grains with *Tilletia indica*. The grain shows a characteristic small lesion at the base caused by the pathogen.

Materials and methods. We evaluated 1,203 advanced bread wheat lines for resistance to Karnal bunt during the autumn–winter 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico, located in block 910 in the Yaqui Valley, Sonora, México (27°22'04.64" N and 109°55'28.00" W, 37 masl) with warm climate (BW (h)) and extreme heat according to Koppen's classification modified by García (1988). Sowing dates were 19 and 29 November, 2014, using 8 g of seed for a 0.7-m row in a bed with two rows in a clay soil with pH 7.8. For agronomic management, INIFAP's technical recommendations were followed (Figueroa-López et al. 2011). Inoculum was prepared by isolating teliospores from infected grains, followed by centrifugation in a 0.5% sodium hypochlorite solution, and plating on 2% water-agar Petri plates. After teliospore germination, fungal colonies were transferred and multiplied on potato-dextrose-agar. Inoculations were by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage in five heads from each line (Fig. 10). High relative humidity in the experimental area was provided by an automatic mist spray-irrigation system (Fig. 11) five times a day for 20 min each time. To avoid bird damage, an anti-bird net system was installed in the area used for evaluation of the wheat lines. Harvest was done manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. Evaluated lines originated from the collaborative project between the Global Wheat Program of the International Maize and Wheat Improvement Center (CIMMYT) and the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP).

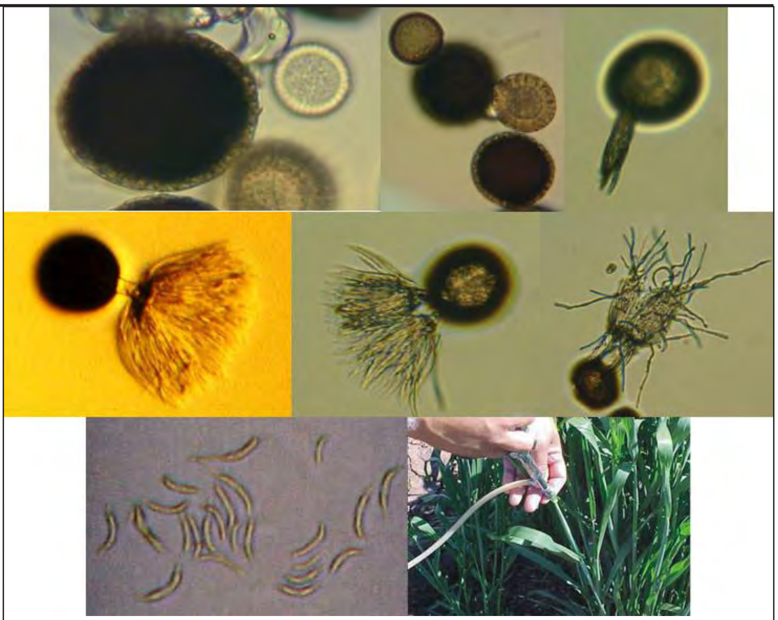

Fig. 10. Teliospores and teliospore germination (top), production of primary and secondary sporidia (middle), and inoculation by injection during the boot stage of the wheat plant (bottom right).

Results. The range of percent infection of the advanced lines at the first sowing date was 0–83.5% with an average of 28.1%, and 0–74.7% at the second sowing date, with an average of 21.4%. The average range for percent infection was 0–70.3% with an average of 24.7%. Overall (average of the two dates), one line did not show infected grains, 12 fell into the 0.1–2.5% infection category (five lines had less than 2.5% infection at both dates, Table 10, p. 60), 33 within 2.6–5.0%, 78 within 5.1–10.0%, 720 within 10.1–30.0%, and 359 with more than 30.0% infection (Fig. 12, p. 60). The average of the three highest percentage of infection of the susceptible check KB-SUS 1 was 98.6%. Besides the five lines that in both dates consistently showed a percentage of infection below 2.5%, there were 17 that consistently showed a percentage of infection below 5.0% at both dates. Lines with less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). The line that did not show infected grains was 'BAVIS/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE. SQUARROSA(224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92'. The highest were lines 'TACUPETO F2001/SAUAL//BLOUK #1/3/SAUAL/YANAC//SAUAL' with 83.5%, 'VEE/MJI//2*TUI/3/PASTOR/4/BERKUT/6/2*OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI' with 83.0%, and 'WBLL1/KUKUNA//TACUPETOF2001/3/UP2338*2/ VIVITSI/4/HUW234+LR34/PRINIA*2//KIRITATI' with 80.3%, all at the first sowing date. In the group of advanced bread wheat lines evaluated during the 2014–15 crop season, 46 are worth

Fig. 11. Mist-irrigation system and anti-bird ne system in the area used to evaluate advanced bread wheat lines for resistance to *Tilletia indica*.

evaluating in the following season in order to verify their resistance shown to *T. indica*. These lines may be prospects for commercial release, or at least be used as progenitors in breeding programs.

Table 10. Advanced bread wheat lines with less than 2.5% infection with *Tilletia indica,* at two sowing dates after artificial field inoculation, during the 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico.

Entry	Pedigree and selection history	Range of infection	Average
131	WBLL1/FRET2//PASTOR/4/WEAVER//VEE/PJN/3/MILAN/5/PICAFLOR #1 CMSS10Y00364S-099Y-099M-099NJ-099NJ-20WGY-0B	1.9–2.4	2.15
467	SAUAL*2/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA(TAUS 4/WEAVER/5/2*PASTOR/7/PBW343*2/KUKUNA*2//FRTL/PIFED CMSS10B00424S-099M-099NJ-099NJ-26WGY-0B	0.5–1.5	0.99
527	BAJ #1//RL6077/AOC-YR/6/YAR/AE.SQUARROSA (783)/4/GOV/AZ//MUS/3/ SARA/5/MYNA/VUL//JUN CMSS10B00777T-099TOPY-099M-099NJ-099NJ-11WGY-0B	1.3–1.5	1.41
716	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/WAXWING/SRTU//WAXWING/KIRITATI CMSS10B01023T-099TOPY-099M-099NJ-099NJ-23WGY-0B	0.6–0.9	0.80
963	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ/4/PARUS/PASTOR CMSA10M00466S-050ZTM-0SY-30M-0WGY	0.5–0.8	0.65

Conclusions. The range of the average percent infection of 1,203 advanced bread wheat lines evaluated for resistance to Karnal bunt during the autumn–winter 2014–15 crop season, was 0.0–70.3% with an average of 24.7%. One line did not show any infected grain at both dates. Five lines consistently showed a percentage of infection below 2.5% at both sowing dates and 17 were below 5.0%. Lines with the highest percentage of infection were 'TACUPETOF2001/SAUAL//BLOUK#1/3/SAUAL/YANAC//SAUAL' with 83.5%, 'VEE/MJI//2*TUI/3/PASTOR/4/BERKUT/6/2*OASIS/5*BORL95/5/CNDO/R143//ENTE/ MEXI75/3/AE.SQ/4/2*OCI' at 83.0%, and 'WBLL1/ KUKUNA//TACUPETOF2001/3/UP2338 *2/VIVITSI/4/HUW234+LR34/PRINIA*2//KIRITATI' with 80.3%, all at the first swoing date. The average of the three highest levels of infection of the susceptible check was 98.6%.

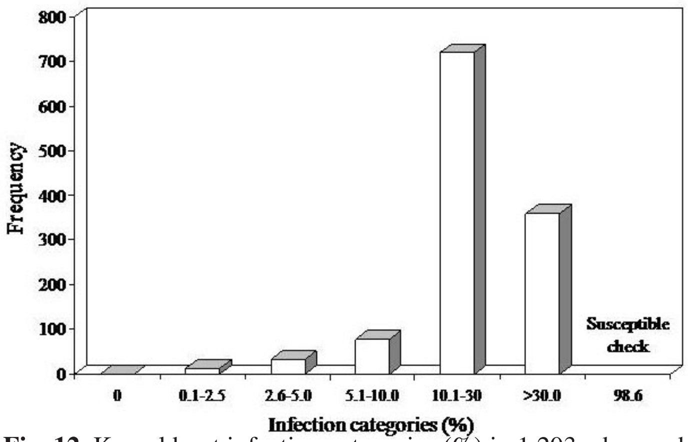

Fig. 12. Karnal bunt infection categories (%) in 1,203 advanced bread wheat lines artificially inoculated in the field at two sowing dates during the 2014–15 crop season at the Norman E. Borlaug Experimental Station in the Yaqui Valley, Sonora, Mexico. The average of the three highest scores of infection of the susceptible check was 98.6%.

References.

Agarwal VK, Verma HS, and Khetarpal RK. 1977. Occurrence of partial bunt on triticale. Plant Prot Bull **25**:210-211.

APHIS. 1996. Karnal bunt: situation report update (March 29). USDA-APHIS, Plant Protection and Quarantine (http://www.aphis.usda.gov/oa/bunt).

Bansal R, Singh DV, and Joshi LM. 1984. Effect of Karnal bunt pathogen [*Neovossia indica* (Mitra) Mundkur] on weight and viability of wheat seed. Ind J Agric Sci **54**:663-666.

Bedi SKS, Sikka MR, and Mundkur BB. 1949. Transmission of wheat bunt due to *Neovossia indica* (Mitra) Mundkur. Ind Phytopat **2**:20-26.

Chona BL, Munjal RL, and Adlakha KL. 1961. A method for screening wheat plants for resistance to *Neovossia indica*. Ind Phytopat **14**:99-101.

CIMMYT. 2011. Training to beat Karnal bunt in Afghanistan. http://blog.cimmyt.org/tag/karnal-bunt/. Accessed 1 March, 2014.

Crous PW, Van Jaarsveld AB, Castlebury LA, Carris LM, Frederick RD, and Pretorius ZA. 2001. Karnal bunt of wheat newly reported from the African continent. Plant Dis **85**:561.

Durán R. 1972. Further aspects of teliospore germination in North American smut fungi. II. Can J Bot **50**:2569-2573.

Da Luz WC, Mendes MAS, Ferreira MASV, and Urben AF. 1993. *Tilletia indica* on wheat in the south of the state of Rio Grande do Sul, Brazil and measures for eradication. Fitopatologia Brasileira **18**:S329.

Figueroa-López P, Fuentes-Dávila G, Cortés-Jiménez JM, Tamayo-Esquer LM, Félix-Valencia P, Ortiz-Enríquez E, Armenta-Cárdenas I, Valenzuela-Herrera V, Chávez-Villalba G, and Félix-Fuentes JL. 2011. Guía para producir trigo en el sur de Sonora. Folleto para productores No. 39. INIFAP-CIRNO, Campo Experimental Norman E. Borlaug. Cd. Obregón, Sonora, México. 63 p (In Spanish).

Fuentes-Davila G, and Rajaram S. 1994. Sources of resistance to *Tilletia indica* in wheat. Crop Prot **13**(1):20-24.

Fuentes-Davila G, Rajaram S, Pfeiffer WH, and Abdalla O. 1992. Results of artificial inoculation of the 4th Karnal Bunt Screening Nursery (KBSN). Ann Wheat Newslet **38**:157-162.

Fuentes-Davila G, Rajaram S, Pfeiffer WH, Abdalla O, Van-Ginkel M, Mujeeb-Kazi A, and Rodríguez-Ramos R. 1993. Resultados de inoculaciones artificiales del 5o. vivero de selección para resistencia a *Tilletia indica* Mitra. Revista Mexicana de Micología **9**:57-65 (In Spanish).

Fuentes-Dávila G, Tapia-Ramos E, Toledo-Martínez JA, and Figueroa-López P. 2005. Evaluación de efectividad biológica de folicur 250 EW (Tebuconazol) para el control del carbón parcial (*Tilletia indica*) del trigo (*Triticum aestivum*), en el valle del Yaqui, Sonora, México, durante el ciclo de cultivo 2003-2004. Resúmenes, XIII Congreso Latinoamericano de Fitopatología, III Taller de la Asociación Argentina de Fitopatólogos. 19–22 April, 2005, Villa Carlos Paz, Córdoba, Argentina. Resumen HC-29, p. 271 (In Spanish).

Fuentes-Dávila G, Félix-Valencia P, Ayón-Ibarra CA, Figueroa-López P, Camacho-Casas MA, Félix-Fuentes JL, Chávez-Villalba G, and Rosas-Jáuregui IA. 2016. Biological effectiveness of several fungicides for control of karnal bunt (*Tilletia indica*) of wheat, in the field. Ann Wheat Newslet **62**:28-31.

Fuentes-Dávila G, Figueroa-López P, Cortés-Jiménez JM, Félix-Valencia P, Camacho-Casas MA, Chávez-Villalba G, Félix-Fuentes JL, and Ortiz-Ávalos AA. 2013. Effect of the level of wheat seed infection with karnal bunt, on germination and tiller production. Ann Wheat Newslet **59**:45-48.

Fuentes-Dávila G, Rosas-Jáuregui IA, Ayón-Ibarra CA, Álvarez-Amado KD, Félix-Valencia P, and Félix-Fuentes JL. 2018. Biological effectiveness of Opus, Folicur, Juwel, and Bemistop for control of Karnal bunt (*Tilletia indica*) of wheat in the field. Ann Wheat Newslet **64**:30-33.

García E. 1988. Modificaciones al sistema de classificación climática de Köppen. Instituto de Geografía de la Universidad Nacional Autónoma de México. Serie Libros número 6. México, D.F. 90 p. (In Spanish).

Krishna A and Singh RA. 1982. Effect of physical factors and chemicals on the teliospore germination of Neovossia indica. Ind Phytopath **35**(3):448-455.

Mitra M. 1931. A new bunt of wheat in India. Ann Appl Biol **18**:178-179.

Mitra M. 1935. Stinking smut (bunt) of wheat with a special reference to *Tilletia indica* Mitra. Ind J Agric Sci **5**:1-24.

Munjal RL. 1975. Status of Karnal bunt (*Neovossia indica*) of wheat in Northern India during 1968-1969 and 1969-1970. Ind J Mycol Plant Path **5**(2):185-187.

Rai RC and Singh AA. 1978. A note on the viability of wheat seeds infected with Karnal bunt. Seed Res **6**:188-190.

Salazar-Huerta FJ, Figueroa-Lopez P, Smilanick, JL, and Fuentes-Davila G. 1997. Evaluation of foliar fungicides for control of Karnal bunt of wheat during 1986-1989 in northwestern Mexico. Revista Mexicana de Fitopatología **15**:73-80.

SARH. 1987. Cuarentena interior No. 16 contra el Carbón Parcial del trigo. Secretaría de Agricultura y Recursos Hidráulicos. Diario Oficial, (jueves) 12 March, 1987, México (In Spanish).

Singh DV. 1980. A note on the effect of Karnal bunt infection on the vigour of wheat seed. Seed Res **8**:81-82.

Singh DV, Agarwal R, Shrestha KJ, Thapa RB, and Dubin HJ. 1989. First report of *Tilletia indica* on wheat in Nepal. Plant Dis **73**:273.

Singh DV, Joshi LM, and Srivastava KD. 1986. Varietal suceptibility and spread of Karnal Bunt of wheat in India. Rachis **5**:40-42.

Singh A, Singh KP, and Tewari AN. 1988. Salient findings of Karnal bunt research at Pantnagar. Department of Plant Pathology, G.B. Pant University of Agriculture and Technology, Pantnagar **263**:145.

Smilanick JL, Hoffmann JA, and Royer MH. 1985. Effect of temperature, pH, light, and desiccation on teliospore germination of *Tilletia indica*. Phytopath **75**:1428-1431.

Smilanick JL, Hoffmann JA, Secrest LR, and Wiese K. 1988. Evaluation of chemical and physical treatment to prevent germination of *Tilletia indica* teliospores. Plant Dis **72**:46-51.

Torarbi M, Mardoukhi V, and Jalaiani N. 1996. First report on the occurrence of partial bunt on wheat in the southern parts of Iran. Seed and Plant **12**:8-9.

Zhang Z, Lange L, and Mathur SB. 1984. Teliospore survival and plant quarantine significance of *Tilletia indica* (causal agent of Karnal bunt) particularly in relation to China. Eur Plant Prot Bull **14**:119-128.

Prevailing temperatures, cold and heat units in the Yaqui Valley during the 2017–18 and 2018–19 wheat seasons.

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Abstract. Because temperature is the weather factor that greatly affects the development of the wheat plant, we analyzed the temperatures that prevailed in the Yaqui Valley during the 2017–18 and 2018–19 wheat seasons. Temperature data were obtained from the automated meteorological station network in Sonora comprising 21 stations in the Valley. The data were collected on a 10-min frequency, every hour, and daily, and consisted of approximately 12,000 records from the autumn–winter 2017–18 and 2018–19 crop seaseon, which ranges from 15 November to 30 April. The average of each weather station was calculated, taking into consideration the maximum and minimum temperature, the cold units, and the heat units for each season. Data were captured in Excel with the daily-hourly records from all stations. The average hourly temperature was calculated, so that we could determine if cold or heat units occurred on given day in the Valley. From the same database, we calculated the cold and heat units for each weather station, so that differences of microclimates within the Valley could be detected. During the 2017–18 wheat season, the temperature ranged from 3.1°C to 36.9°C with an average of 18.3°C, 341 cold units, and a total of 190 heat units were recorded. In 2018–19, the temperature ranged from 1.0°C to 34.2°C with an average of 17.1°C, 469 cold units, and 127 heat units. With the exception of blocks 1730 and 2918, which only had information for 2018–19, most of the other stations had a similar pattern of occurrence of cold units. For example, blocks that recorded the highest number of cold units, more than 400 in 2017–18 and more than 500 in 2018–19 were 111, 609, 1213, 1418, 2010, and Estación Corral.

Introduction. In the state of Sonora, Mexico, the annual average area established with wheat between 2008 and 2019 was 287,856 ha with a maximum of 322,935 and a minimum of 223,437 ha. During the same period, the average grain yield was 6.28 t/ha for a production of 1,793,735 ton. In 2019, the wheat area harvested was 260,536 ha, out of which 151,267 ha were from the District of Rural Development (DDR) 148-Cajeme (Yaqui Valley) and 90,289 ha from DDR-149-Navojoa, for a total of 241,556 ha for this region of the state (SIAP 2020). Of the total wheat established in this region, the average for the last three crop seasons, 77% was durum wheat and 23% was bread wheat (CESAVESON 2020).

The Yaqui Valley is an agricultural region in Northwest Mexico (27°N, 110°W) with agro-climatic conditions similar to that of 40% of developing world wheat production (Pingali and Rajaram 1999). The Valley covers the area between the Sierra Madre Mountains to the east and the Gulf of California to the west (Fig. 13). The region produces some of the highest wheat yields in the world and is one of the country's most productive breadbaskets (Naylor et al. 2001), resulting from a combination of irrigation, high fertilizer rates, and modern cultivars (Matson et al. 1998). The climate in the Yaqui Valley is semi-arid, with an average annual precipitation of 317 mm falling mainly between June and September. The wheat growing season (November–April) is characteristically dry, and farmers typically apply 4–5 irrigations throughout the crop season. Most of the soils in the region are vertisols with an organic matter content below 1%, whereas the coastal and river areas are characterized by aridisols with slightly higher organic matter (Lobell et al. 2002). Because of its geographic position, the state of Sonora shows a south to north gradient of extreme temperature and occurrence of precipitation, which characterizes it as dry and warm most of the year. Oscillation of the temperature during the autumn and winter months is from –1° a 31ºC and from 20º to 42ºC during the summer months. So, for agriculture, temperature is the weather factor most related to wheat annual productivity (Félix-Valencia et al. 2009), which also could cause adverse effects (Félix-Valencia et al. 2012).

Fig. 13. Location of weather stations in the Yaqui Valley, Sonora, Mexico.

Wheat cultivars in the state of Sonora show a favorable expression in grain yield when the occurrence of cold units is well distributed during the crop season. The response varies based on the geographic location and the dominant effect of the annual climatic phenomenon known as *La Niña* and *El Niño* or cold, neutral, or warm temperature, and that is historically related to the annual variations of the average wheat grain yields in each District of irrigation (Félix-Valencia et al. 2008). Temperature databases are useful for explaining in great part the behavior of a particular crop during the different phenological stages and for the implementation of agronomic adjustments (Félix-Valencia et al. 2012). Several methodologies value the importance of air temperature in order to explain the phenological behavior of crops, using thermal sums (cold and heat units) as bioclimatic indexes, which allow us to establish the relationship between development of the plant in extreme climatic periods. This simplistic methodology of thermal sums (Confalone and Navarro 1999) can explain the variability of plant development up to 98% (Arnold 1959). The development of the temperature sensor, as we know it today, took several centuries and a variety of people were involved, among them scientists and laymen, including Claudius Galeno, Robert Hooke, Gay-Lussac, Galileo Galiei, Santorio Santorio, Daniel Gabriel Fahrenheit, Thomas Johann Seebeck, Humprey Davey, C.H. Meyers, William Herschel, Samuel Langley, Anders Celsius, William Thomson (Omega Engineering Inc. 2020). The influence that atmospheric time and climate have upon the anthropogenic activities have made necessary the continuous measurement of meteorological variables, such as temperature, relative humidity, barometric pressure, wind speed, and precipitation (CESAVESON 2014). The effort to measure temperature reflects the importance not only of recording meteorological variables, but also on consistent periods of time for their analysis. The technological progress has used automated registration of data with orderly storage which promotes harmonization and also allows the comparison of data from different regions. In the state of Sonora, Mexico, 65% of the economic revenues come from the agricultural subsector. Therefore, to have all the necessary tools to take care of this subsector and to look after the adequate development of the agriculture in the state is of primary importance. Since 2014, the State Committee for Plant Health (CESAVESON) took over the state automated weather net system under the name REMAS (Red Estatal de Estaciones Automatizada de Sonora), which has the purpose to continue the development, management, and maintenance of the stations in order to guarantee plant health and facilitate the export of agricultural products produced in the state (CESAVESON-SIAFESON 2020). REMAS covers great part of the agricultural area in the state with 109 active weather stations; 20% are located in the District of Rural Development (DDR) 148-Cajeme (Yaqui Valley) and 12% in the DDR-149-Navojoa (Mayo Valley). Because temperature is the weather factor that greatly affects the development of the wheat plant, our objective was to analyze the temperatures (minimum, maximum, and number of cold units) that prevailed in the Yaqui Valley during the 2017–18 and 2018–19 wheat seasons.

Materials and methods. Temperature data were obtained from the automated meteorological station network in Sonora (REMAS 2019) comprising 21 stations in the Yaqui Valley (Fig. 13, p. 62). Data were collected daily on a 10-min frequency every hour. The data set consisted of approximately 12,000 records from the auatumn–winter 2017–18 and 2018–19 crop seasons, which covers from 15 November to 30 April. A cold unit was considered as one hour recorded by a given weather station with a temperature below 10°C, whereas a heat unit was considered as one hour recorded by a given weather station with a temperature above 30°C (Félix-Valencia et al. 2009). The average of each weather station was calculated, taking into consideration the maximum and minimum temperature, the cold units, and the heat units for each season. The daily-hourly records from all the stations were captured in Excel. The average hourly temperature was calculated, so that it could be determined if cold or heat units occurred on given day in the Valley. From the same database, we calculated the cold and heat units for each weather station, so that microclimate differences within the Valley could be detected. Graphics were built with the information obtained.

Results and discussion. ***Crop season 2017–18.*** During this crop season, the temperature ranged from 3.1°C to 36.9°C with an average of 18.3°C (Fig. 14). An average of 341 cold units were recorded in the Yaqui Valley (Fig. 15, p. 64). The occurrence of cold units began on week 4 (6–12 December). Weeks 11 (24–30 January) and 15 (21–27 February) had the highest number of cold units; a total of 57 each, followed by week 10 (17–23 January), 54 cold units (Fig. 16, p. 64). The weather stations with the highest number of cold units were block 2010, Estación Corral, and block 609 with 558, 532, and 526 cold units, respectively. Weather stations with the lowest number of cold units were block 720 and 1423 with 233 and

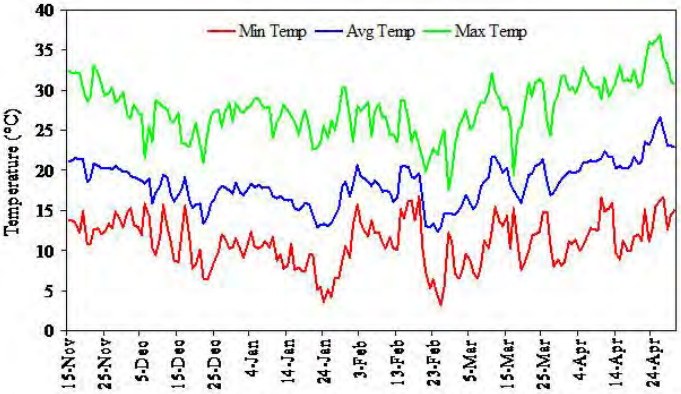

Fig. 14. Maximum,minimum, and average temperatures prevailing durng the autumn–winter 2017–18 wheat season in the Yaqui Valley, Sonora, Mexico.

196 cold units, respectively (Fig. 17). At the beginning of the season there were 20 heat units during the first week (15–21 November) and 12 during the second week (22–28 November). Other weeks with accumulated heat units were 17 (7–13 March) with four, 19 (21–27 March) with 12, and 20 (28 March to 3 April) with 11. A total of 190 heat units occurred during this crop season (Fig. 14, p. 63). Heat units might have an adverse effect on some phenological phases of the wheat plant, such as in seedling development and on the flower, so that ultimately they will affect grain yield.

Crop season 2018–19. During this crop season, the temperature ranged from 1.0°C to 34.2°C with an average of 17.1°C (Fig. 18, p. 65), 2.1, 2.7, and 1.2°C less than in the previous season. An average of 469 cold units were recorded in the Yaqui Valley (Fig. 15), 128 more than in season 2017–18. Week 7 (27 December to 2 January) had the highest number of cold units with a total of 75, followed by week 11 (24–30 January) with 62, and week 15 (21–27 February) with 58 (Fig. 16). During weeks 8 to 10 (3–23 January), there were hours with slightly higher temperatures (Figs. 16 and 18), therefore, there were fewer records of cold hours ranging from 21 to 29. A total of 127 heat units (>30°C) were 63 less than in season 2017–18, but their occurrence was detected until week 20 (28 March to 3 April). The weather station with the highest number of cold units was block 1730, followed by Estación Corral, and block 609, with 745, 653, and 624, respectively. Blocks 419 (325) and 1423 (274) had the lowest number of cold units (Fig. 17).

Cold units recorded by each weather station, with the exception of blocks 1730 and 2918 that had information only for 2018–19, had similar patterns (Fig. 17). For example, blocks that recorded the highest number of cold units, more than 400 in season 2017–18 and more than 500 in 2018–19 were 111, 609, 1213, 1418, 2010, and Estación Corral. This supports the idea that microclimates occur in both the Yaqui and Mayo Valleys. Through zoning, farmers would have a more precise weather and forecast information in order to implement better agronomic management of wheat in the region (Torres-Cruz et al. 2020). The difference in the average temperature between wheat seasons (1.2°C) most probably played an important role in the grain yield obtained in the Yaqui Valley, which was 6.7 t/ha in 2017–18 (Uniradio Noticias 2018) and 7.1 in 2018–19 (Diario del Yaqui 2019). High temperatures have a complex effect on crops, and the final result on yield and quality by thermal stress will strongly depend on the characteristics of such a stress (i.e., severity, duration, and/or in combination with other stresses), the crop (phenologic stage when it occurs and species/genotype), and the interaction with other environmental factors (Savin 2010). Wardalaw and Wrigley (1994) and Tewolde et al. (2006) calculated that yield reduction in winter cereals due to high temperatures during the grain-filling

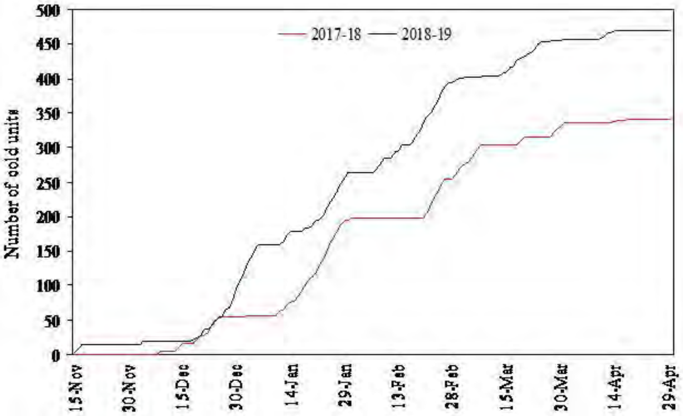

Fig. 15. Accumulated cold units from 15 November to 30 April during the autumn–winter 2017–18 and 2018–19 wheat seasons in the Yaqui Valley, Sonora, Mexico.

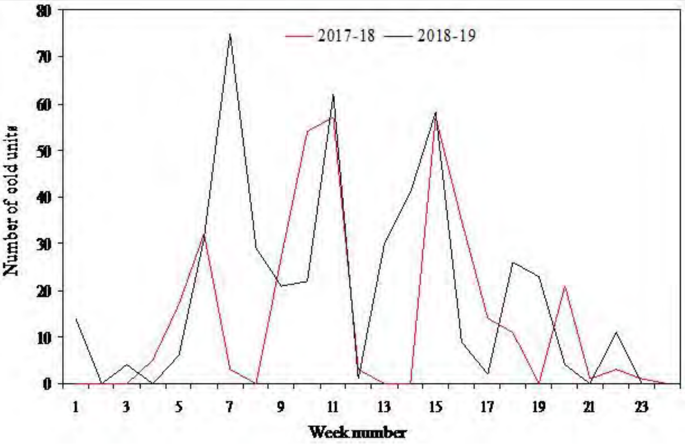

Fig. 16. Accumulated weekly cold units from 15 November to 30 April during the autumn–winter 2017–18 and 2018–19 wheat seasons in the Yaqui Valley, Sonora, Mexico.

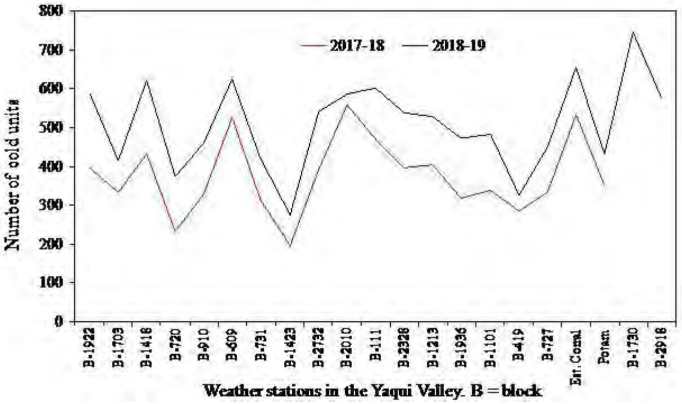

Fig. 17. Cold units in each weather station during the autumn–winter 2017–18 and 2018–19 wheat seasons in the Yaqui Valley, Sonora, Mexico.

period may reach 10–15%. The occurrence of such temperatures depends on factors such as sowing date and altitude, among others. As agricultural areas expand, crops in these new areas may experience stress levels, including thermally important ones. Even in traditional agricultural zones, increases in the occurrence of these thermal stresses are expected, understanding that a thermal stress is a temperature increase above a determined threshold for a period of time, enough to cause irreversible deleterious effects on development and growth of crops, in this way reducing their yield and or quality (Wahid et al. 2007).

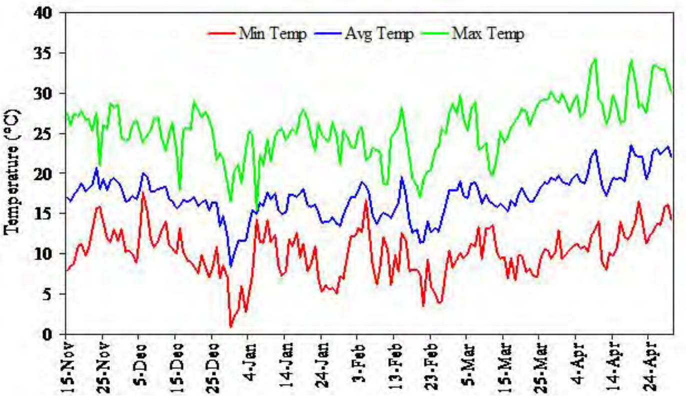

Fig. 18. Maximum,minimum, and average temperatures prevailing durng the autumn–winter 2018–19 wheat season in the Yaqui Valley, Sonora, Mexico.

Conclusions. During the 201718 wheat season, the temperature ranged from 3.1°C to 36.9°C with an average of 18.3°C and 341 cold units were recorded in the Yaqui Valley, Sonora, Mexico. In the 2018–19 season, the temperature ranged from 1.0°C to 34.2°C with an average of 17.1°C and 469 cold units. With the exception of blocks 1730 and 2918, which had information for only the 2018–19 season, most of the other stations had similar patterns of occurrence of cold units. For example, blocks that recorded the highest number of cold units, more than 400 in 2017–18 and more than 500 in 2018–19 were 111, 609, 1213, 1418, 2010, and Estación Corral. Heat units recorded were 190 for the 2017–18 wheat season and 127 for 2018–19.

References.

Arnold CY. 1959. The determination and significance of the base temperature in a linear heat unit system. Proc Amer Soc Hort Sci **74**:430.445.

Canfalone AE and Navarro DM. 1999. Comparación de modelos de tiempo térmico para maíz. Revista Brasileria de Agrometeorología, Santa María **7**(2):207-211 (In Spanish).

CESAVESON (Comité Estatal de Sanidad Vegetal de Sonora). 2014. SAGARHPA y CESAVE firman convenio para operar REMAS. http://cesaveson.com/index.php/home/nota/12. Consulted on 20 May, 2020 (In Spanish).

CESAVESON (Comité Estatal de Sanidad Vegetal del Estado de Sonora). 2020. Permisos de siembra. Available at: https://cesaveson.com/index.php/home/permisos. Consulted on April 10, 2020 (In Spanish).

CESAVESON-SIAFESON (Comité Estatal de Sanidad Vegetal del Estado de Sonora-Sistema de Alerta Fitosanitaria del Estado de Sonora). 2020. Red de Estaciones Meteorológicas Automáticas de Sonora. www.siafeson.com/remas. Consulted on 20 May, 2020 (In Spanish).

Diario del Yaqui. 2019. Supera el trigo rendimiento. https://diariodelyaqui.mx/index.php/2019/ 05/31/supera-trigo-rendimiento/. Consulted on 25 May, 2020 (In Spanish).

Félix-Valencia P, Leyva-Coronoa JC, Ortíz-Enríquez JE, Quintana-Quiróz JG, Grageda-Grageda J, and Jiménez-Ortega G. 2008. Comportamiento histórico y tendencia del clima en la zona agrícola y pecuaria del sur de Sonora, Expectativas ante un cambio climático. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Valle del Yaqui. Libro Técnico No. 4. Cd. Obregón, Sonora, México. 202 p. ISBN 978-607-425-109-8 (In Spanish).

Félix-Valencia P, Ortíz-Enríquez JE, Cabrera-Carbajal F, Chávez-Villalba G, Fuentes-Dávila G, and Figueroa-López P. 2012. Daños a la producción de trigo causado por heladas en el sur de Sonora. Diagnóstico del ciclo de trigo oi-2010-2011. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Norman E. Borlaug. Folleto Técnico No. 87. Cd. Obregón, Sonora, México. 70 p. ISBN 978-607-425-911-7 (In Spanish).

Félix-Valencia P, Ortíz-Enríquez JE, Fuentes-Dávila G, Quintana-Quiróz JG, and Grageda-Grageda J. 2009. Horas frío en relación al rendimiento de trigo: áreas de producción del estado de Sonora. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Valle del Yaqui. Folleto Técnico No. 63. Cd. Obregón, Sonora, México. 40 p. ISBN 978-607-425-159-3 (In Spanish).

Lobell DB, Ortiz-Monasterio JI, Addams CL, and Asner GP. 2002. Soil, climate, and management impacts on regional wheat productivity in Mexico from remote sensing. Agric Forest Meteorology **114**:31-43.

Matson PA, Naylor R, and Ortiz-Monasterio I. 1998. Integration of environmental, agronomic, and economic aspects of fertilizer management. Science **280**:112-114.

Naylor RL, Falcon WP, and Puente-Gonzalez A. 2001. Policy reforms and Mexican agriculture: views from the Yaqui Valley. CIMMYT, International Maize and Wheat Improvement Center, Economics Program Paper No. 01-01, CIMMYT, Mexico, D.F.

Omega Engineering Inc. 2020. A brief history of the temperature sensor. https://mx.omega.com/ technical-learning/historia-del-sensor-de-temperatura.html. Consulted on 20 May, 2020.

Pingali PL and Rajaram S. 1999. Global wheat research in a changing world: options and sustaining growth in wheat productivity. *In:* CIMMYT 1998–1999 World Wheat Facts and Trends (Pingali PL Ed). CIMMYT, Mexico, D.F.

REMAS (Red de Estaciones Metereológicas Automáticas de Sonora). 2019. Descargar datos. http://www.siafeson.com/remas/. Consulted on 15 May, 2019 (In Spanish).

Savin R. 2010. Estrés abiótico y calidad en cereales de invierno. *In:* Avances en ecofisiología de cultivos de granos (Miralles DJ, Aguirrezábal LN, Otegui ME, Kruk BC, and Izquierdo N, Eds). Editorial Facultad de Agronomía, UBA, Buenos Aires, Argentina, pp. 201-210 (In Spanish).

Servicio de Información Agroalimentaria y Pesquera (SIAP). 2020. Avance de siembras y cosechas. Resumen nacional por estado. Trigo grano. Ciclo otoño-invierno. Riego + temporal. Available at: https://nube.siap.gob.mx/cierreagricola/ Consulted on 10 April, 2020 (In Spanish).

Tewolde H, Fernandez CJ, and Erickson CA. 2006. Wheat cultivars adapted to post-heading high temperature stress. J Agron Crop Sci **192**:111-120.

Torres-Cruz MM, Castro-Quiroa LA, Fuentes-Dávila G, Borrego-Soto G, and Félix-Valencia P. 2020. Temperatura y humedad relativa para la determinación de zonas de influencia climatológica en los valles agrícolas del sur de Sonora, mediante la técnica de agrupamiento. Revista Internacional de Investigación e Innovación Tecnológica (submitted) (In Spanish).

Uniradio noticias. 2018. Finaliza cosecha de trigo con mejores rendimientos que el año pasado. https://www.uniradionoticias.com/noticias/cdobregon/527742/finaliza-cosecha-de-trigo-con-mejores-rendimientos-que-el-ano-pasado.html. Consulted on 25 May, 2020.

Wahid A, Gelani S, Ashraf M, and Foolad MR. 2007. Heat tolerance in plants: An overview. Environ Exper Bot **61**:199-223.

Wardlaw IF and Wrigley CW. 1994. Heat tolerance in temperate cereals: an overview. Aust J Plant Physiol **21**:695-703.

Organic wheat production in the Yaqui Valley, Sonora, Mexico.

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

Abstract. 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, rather than the use of inputs with adverse effects. In 2016, organic agriculture was practiced in 178 countries on 57.8 x 10^6 ha. Mexico is 13th in area dedicated to organic production with 673,968 ha and 3rd by number of producers with 210,000. In the Yaqui Valley, Sonora, until 2000, the available technology for wheat production only focused on the chemical control of pests and use of chemical fertilizers. Organic production of wheat is a technological innovation developed by the National Institute for Forestry, Agriculture, and Livestock Research at the Norman E. Borlaug Experimental Station (CENEB), with financial support by the farmers' association. During seven years, wheat was produced without any prohibited products by the Agricert Certification Agency. Sowing was in beds with 80 cm separation with two rows 30 cm apart, which facilitated mechanical weed control. Organic fertilization was with manure available in the Yaqui Valley from swine, cattle, and chickens, as well as compost. Four irrigations were applied during the crop seasons in which cultivars tolerant to leaf rust and Karnal bunt were planted. OMRI-listed products were used for control of pests and diseases. Grain yields obtained were similar and sometimes 10% higher than those obtained in the conventional production system, although chicken manure produced the best and most consistent results. A plot at CENEB was granted organic certification by AGRICERT MEXICO–SENASICA and BIOAGRICERT.

Organic agriculture. In September 2005, in Adelaide, Australia, the General Assembly of The International Federation of Organic Agriculture Movements (IFOAM), Organics International, passed a motion to establish a succinct definition of organic agriculture. After nearly three years of work by a designated task force, a definition reflecting the four principles of organic agriculture in a succinct way was adopted in Vignola, Italy, as follows:

> 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 principle of health, the principle of ecology, the principle of equity, and the principle of precaution (IFOAM 2005a).

A marked increase in organic production worldwide was reported by Willer and Yussefi (1999); 73 countries with organic agriculture in an area of 10.55 x 10^6 ha and, by the year 2016, practiced in 178 countries in an area of 57.8 x 10^6 ha. Countries with the most area in organic agriculture are Australia (27.1 x 10^6 ha), Argentina (3.0 x 10^6 ha), and China (2.3 x 10^6 ha). In this context, Mexico is 13th in position in area dedicated to organic production with 673,968 ha and 3rd by number of dedicated producers at 210,000. In addition to the certified organic area, in Mexico there are 1,202,306 ha dedicated to wild harvesting and 90,000 ha for organic beekeeping, where there is a total of 368,000 hives (Lernoud and Willer 2018). Statistics for organic agriculture area in Mexico started in 1996 with 21,265 ha, up to 673,968 ha registered in 2016 (Willer and Yuseffi 1999, 2001; Yuseffi and Willer 2000; Yuseffi 2003, 2004, 2005, 2006; Willer and Klicher 2009, 2010, 2011; Willer and Lernoud 2012, 2013; Lernoud and Willer 2015, 2016, 2017, 2018; Willer et al. 2014).

Conventional wheat production and the initiative for organic production in the Yaqui Valley. Every year, an average of 1,000,000 tons of wheat grain are produced in the Yaqui Valley, Sonora, which includes both *Triticum durum* and *T. aestivum*. The average grain yield of the last 13 years was 6.45 t/ha, with a range of 5.16 to 7.13. The highest average grain yield was obtained in the 2011–12 crop season, when 654 cold units were recorded in the region (Félix-Valencia et al. 2012), and the lowest in 2014–15, when the season was quite humid, warm, and an epidemic of spot blotch caused by *Bipolaris sorokiniana* broke out in the region. Until 2000, the available technology for wheat production in southern Sonora focused only on the chemical control of pests and diseases and the application of chemical fertilizers. From the 2000–01 crop season, a collaborative project was initiated between The National Institute for Forestry, Agriculture, and Livestock Research (INIFAP) and The Foundation for Agricultural Research and Experimentation in the State of Sonora (PIEAES) which is economically funded by several associations of farmers in the region, with the objectives to generate organic technology for wheat production and obtain organic certification for wheat production in the Yaqui Valley.

Progress. This technological innovation was developed by INIFAP at the Norman E. Borlaug Experimental Station located in block 910 of the Yaqui Valley, Sonora, México (27°22'04.64"N and 109°55'28.26"W, 37 masl) with a warm climate (BW (h)) and extreme heat according to Koppen's classification, modified by Garcia (1988). During seven years, wheat was produced without any banned products by the certification agency AGRICERT, which supervised the organic management of wheat. Tillage included disking, chisel plough, and cultivation. Every crop season, sowing dates were from 15 November to 15 December using 20–110 kg/ha of seed. Sowing was in beds with 80 cm separation with two rows 30 cm apart, which facilitated mechanical weed control. Organic fertilization was with manure, available in the Yaqui Valley from swine, cattle, and chickens, as well as compost. Four irrigations were applied during the crop season in which wheat cultivars tolerant to leaf rust and Karnal bunt were planted. For control of pests and diseases of wheat, OMRI (Organic Materials Review Institute, https://www.omri.org/)-listed products were used. From the first year of evaluation, some treatments with organic fertilization produced higher wheat yield than those with chemical fertilization. For example, chicken manure at 20 t/ha produced up to a 10% higher grain yield. With the application of chicken manure in the fifth year, all manure combinations produced a higher grain yield and protein content than those obtained with chemical fertilization. From this information, we determined the type of manure and the rate that optimized grain yield and quality. A great variety of organic insecticides are available to control pests that attack wheat in the Yaqui Valley, mainly based on neem (*Azadirachta indica*), pyrethrins, castor bean soap (*Ricinus communis*), garlic extracts (*Allium sativum*), and cinnamon (*Cinnamomun verum*). For the diseases, their control is still deficient, because the fungicides available are of contact type that must be applied two or three times. The best strategy is to use cultivars tolerant to the most common diseases. The Norman E. Borlaug Experimental Station in block 910 in the Yaqui Valley, Sonora, Mexico, was granted the organic certification in 2019 (AGRICERT MEXICO–SENASICA 2019; BIOAGRICERT 2019a, b).

Conclusions. Grain yield of wheat obtained under an organic system, is similar and sometimes up to 10% higher than that obtained with the conventional system used in the Yaqui Valley. Organic wheat production in the Valley offers great advantages over the conventional system traditionally used in this region, such as a less negative impact on the environment and a better public health.

References.

AGRICERT MEXICO – SENASICA (Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria). 2019. Organic Certificate. Number OMK80KCC. Control code IS SENASICA-OCO-16-005-K80K.

BIOAGRICERT. 2019a. Product certifícate of organic operation according to BAC Equivalent Organic Standard (reg. 834/07 art. 33.3). Number EUK80KCC. Control code MX BIO 132 K80K.

BIOAGRICERT. 2019b. Conformity Certificate. Organic operation is certified to the USDA National Organic Program

Regulation 7 CFR part. 205. Number NPK80KCC. Control code MX BIO 132 K80K.

Félix-Valencia P, Ortíz-Enríquez JE, Cabrera-Carbajal F, Chávez-Villalba G, Fuentes-Dávila G, and Figueroa-López P. 2012. Daños a la producción de trigo causado por heladas en el sur de Sonora. Diagnóstico del ciclo de trigo oi-2010-2011. INIFAP, Centro de Investigación Regional del Noroeste, Campo Experimental Norman E. Borlaug. Folleto Técnico No. 87. Cd. Obregón, Sonora, México. 70 p. ISBN 978-607-425-911-7 (In Spanish).

García E. 1988. Modificaciones al sistema de classificación climática de Köppen. Instituto de Geografía de la Universidad Nacional Autónoma de México. Serie Libros Número 6. México, D.F. 90 p (In Spanish).

International Federation of Organic Agriculture Movements (IFOAM). 2005a. Principles of organic agriculture. https://www.ifoam.bio/en/organic-landmarks/principles-organic-agriculture. Consulted on 25 April, 2020.

International Federation of Organic Agriculture Movements (IFOAM). 2005b. Normas de IFOAM para la producción y el procesamiento orgánicos. Versión 2005. Alemania, agosto 2017. 138 p. Available at: http://somexpro.org/wpcontent/uploads/2008/12/ifoam.pdf (In Spanish).

International Federation of Organic Agriculture Movements (IFOAM). 2008. Definition of organic agriculture. https://www.ifoam.bio/en/organic-landmarks/definition-organic-agriculture. Consulted on 25 April, 2020.

Lernoud J and Willer H. 2015. Current statistics on Organic Agriculture Worlwide: Organic Area, Producers, Market and Selected Crops. The World of Organic Agriculture. Statistics and Emerging Trends 2015. FiBL-IFOAM Report. Research Institute of Organic Agriculture (FiBL), Frick, and International Federation of Organic Agriculture Movements (IFOAM), Bonn. p. 37.

Lernoud J and Willer H. 2016. Current statistics on Organic Agriculture Worlwide: Organic Area, Producers, Market and Selected Crops. The World of Organic Agriculture. Statistics and Emerging Trends 2016. FiBL-IFOAM Report. Research Institute of Organic Agriculture (FiBL), Frick, and International Federation of Organic Agriculture Movements (IFOAM), Bonn. p. 40.

Lernoud J and Willer H. 2017. Current statistics on Organic Agriculture Worlwide: Area, Operators, and Market. The World of organic agriculture statistics and emerging trends 2017. Research Organics International, Bonn. pp. 23, 25, 30.

Lernoud J and Willer H. 2018. Current statistics on Organic Agriculture Worlwide: Area, Operators, and Market. The World of organic agriculture statistics and emerging trends 2017. Research Institute of Organic Agriculture (FiBL) Frick, and IFOAM – Organics International, Bonn. pp. 40, 47, 56, 61, 87, 280.

Willer H and Klicher L. 2009. Anexos. The World of Organic Agriculture. Statistics and Emerging Trends 2009. FiBL-IFOAM Report. IFOAM, Bonn and FiBL, Frick. p. 279.

Willer H and Klicher L. 2010. Anexos. The World of Organic Agriculture. Statistics and Emerging Trends 2010. FiBL-IFOAM Report. IFOAM, Bonn and FiBL, Frick. p. 217.

Willer H and Klicher L. 2011. Anexos. The World of Organic Agriculture. Statistics and Emerging Trends 2011. FiBL-IFOAM Report. IFOAM, Bonn and FiBL, Frick. p. 250.

Willer H and Lernoud J. 2012. Current statistics on Organic Agriculture Worlwide: About. The World of Organic Agriculture. Statistics and Emerging Trends 2012. FiBL-IFOAM Report. Research Institute of Organic Agriculture (FiBL), Frick, and International Federation of Organic Agriculture Movements (IFOAM), Bonn. p. 40.

Willer H and Lernoud J. 2013. Current statistics on Organic Agriculture Worlwide: Organic Area, Producers, Markets and Selected Crops. The World of Organic Agriculture. Statistics and Emerging Trends 2013. FiBL-IFOAM Report. Research Institute of Organic Agriculture (FiBL), Frick, and International Federation of Organic Agriculture Movements (IFOAM), Bonn. p. 42

Willer H, Lernoud J, and Schlatter B. 2014. Current statistics on Organic Agriculture Worlwide: Organic Area, Producers and Market. The World of Organic Agriculture. Statistics and Emerging Trends 2014. FiBL-IFOAM Report. Research Institute of Organic Agriculture (FiBL), Frick, and International Federation of Organic Agriculture Movements (IFOAM), Bonn. pp. 39, 283.

Willer H and Yussefi M. 1999. Organic Agriculture Worldwide. Statistics and Perspectives. Stiftung Ökologie and Landbau. Bad Dürkheim: SÖL, 2000. p. 23.

Willer H and Yussefi M. 2001. Organic Agriculture World-Wide. Statistics and Perspectives. Stiftung Ökologie and Landbau. Bad Dürkheim: SÖL, 2000. p. 23.

Yuseffi M. 2003. Development and State of Organic Agriculture Worldwide. The World of Organic Agriculture - Statistics and Future Prospects – 2003. Tholey-Theley: International Federation of Organic Agriculture Movements, 2003. p. 15.

Yuseffi M. 2004. Development and State of Organic Agriculture Worldwide. The World of Organic Agriculture - Statistics and Future Prospects – 2004. Tholey-Theley: International Federation of Organic Agriculture Movements, 2003. p. 15.

Yussefi M. 2005/2006. Organic Agriculture by Continent. The World of Organic Agriculture – Statistics and Emerging Trends-2004. p. 15.

Yussefi M and Willer, H. 2000. Organic Agriculture Worldwide. Statistics and Perspectives. Stiftung Ökologie and Landbau. Bad Dürkheim: SÖL, 2000. p. 17, 19.

ITEMS FROM THE RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE FOR THE SOUTH-EAST REGIONS (ARISER)

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The synthesis of new donors and sources of valuable traits in spring bread wheat: resistance to bio-and abiostressors, productivity and bread making quality.

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

Our goal is to produce a collection of new introgression lines of spring bread wheat resistant to leaf and stem rust. Using prebreeding studies will determine the adaptability of the introgression lines to abiotic and biotic stresses and their breeding value. In addition, we will determine the effect of intergeneous and interspecific exchanges on the quality of the end product of-flour and bread.

Under artificial and natural infection by leaf and stem rust pathogens, we evaluated resistance in the original near-isogenic lines with alien translocations and their combinations, as well as in a set of introgression lines with genes from various relatives of bread wheat. The effectiveness of the alien leaf rust genes *Lr9*, *Lr24*, *Lr28*, *Lr29*, *Lr41*, *Lr51*, *Lr57*, *Lr64*, *LrSatu,* and *LrSp*, transfers from durum wheat cultivars Saratovskaya 57, NICK, Zolotaya volna, and from *Thinopyrum elongatum* CI-7-57, *T. aestivum subsp. kiharae*. *T. turgidum* subsp. *dicoccoides*, *T. timopheevii* were detected. The effectiveness of the alien stem rust genes combinations, including the genes *Sr25*, *Sr31, Sr57, Sr38, Sr22, Sr35, SrSp, Sr6Agi,* and *SrSatu* were revealed. Changes in the population structure of *Puccinia triticina* in 2018 were observed. Differences in the composition of the 2018 *P. triticina* population by virulence/avirulence genes were in the different type of reactions to genes *Lr9, Lr19, Lr23, Lr24, Lr29,* and *Lr47*. Under drought conditions in 2019, grain productivity of the NILs slightly increased in those with the 6D (6Agi) substitution and *LrSatu*/*SrSatu* transfer. The positive influence on grain productivity was observed in introgressions of spring bread wheat lines 'Favorit/*T. persicum**2//Favorit (substitution of 6D(6Agi)' + *T. persicum* genetic material), 'Saratov29/*Th. elongatum* (CI-7-57)*5//Saratov29', 'Saratov74/*T. turgidum* subsp. *dicoccum* k7507//Saratov73/3/Saratov73', and 'Dobrynya/Zolotaya volna//Dobrynya 6Agi/3/ Dobrynya'. Lines L379 (Bel/3/Altar84/*Ae. tauschii* (224)//Pgo/4/S68) and L375 (L505/3/Croc/*Ae. tauschii* (205)//Weaver /4/ L505/5/L505) were distinguished from the set of spring bread wheat lines obtained from crosses of CIMMYT synthetics with Saratov-bred cultivars. L375 carries *Lr19*/*Sr25* + *Lr26*/*Sr31*+ *Lr41*, i.e., translocations T7DS-7DL-7Ae#1L + T1BL·1R#1S + T2DS–*Ae. tauschii*-2DL. These lines have good bread-making quality.

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The role of edaphic stress in the uptake of nitrogen by seedlings of the spring wheat cultivar Lisa.

N.V. Poukhalskaya and L.V. Osipova.

The germination of wheat grains in a medium containing aluminum ions was studied. Ten-day-old seedlings were cultivated in a medium containing labeled nitrogen using ammonium sulphate at a concentration of 0.3 g/L, an enrichment of 50%. We investigated the concentration of aluminum in the environment: 4, 8, 10, 24, 40, and 80 mg Al/L (aluminum sulfate).

Results. Germination in the spring wheat cultivar Lisa was extremely sensitive to the acidic reaction of the environment. Aluminum sulphate is a hydrolytically acidic salt, and concentration of Al^{3+} ions of 10, 24, 40, and 80 mg Al/L caused significant acidification of the solution (Fig. 1). As a result, we found that the wheat cultivar Lisa is highly sensitive to the acidic reaction of the environment; the seed had 95% germination, but root growth did not occur (Fig. 2). The initiation of root growth and elongation is delayed. The root system does not develop due to the inhibition of the growth processes. Aluminum is known to lead to a thickening of the root, root cells divide but the extension of the roots is inhibited. We determined this not only for adult, fully functioning roots, but also at the during germination.

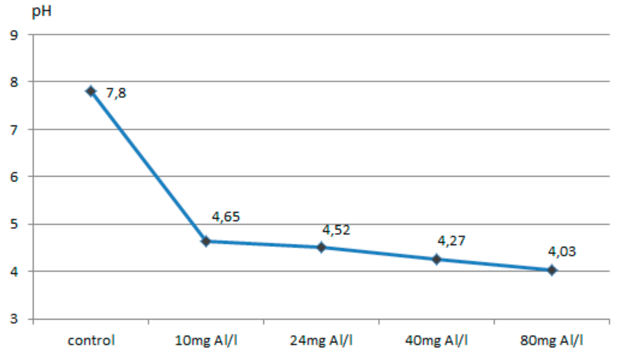

Fig. 1. The change in pH of a solution with increasing aluminun concentration.

The length of the root system of a 10-day-old seedling in the control variant was 3.59±1.3 cm. In variants at 10, 24, 40, and 80 mg Al/L, root length decreased, 0.45, 0.30, 0.27, and 0.15 cm, respectively. A tendency for a decrease in root length was observed, but the differences were not significant.

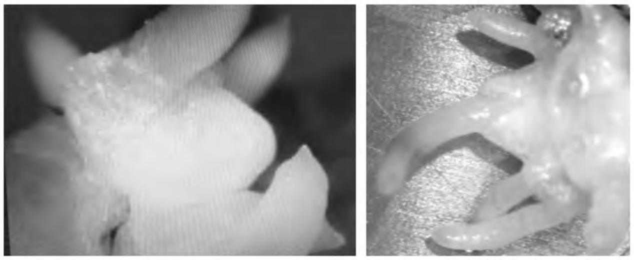

Fig. 2. Roots of a wheat seedling of the cultivar Liza in a solution 40 mg/L (left) and 24 mg/L Al (right).

We increased the pH to 5.8. Our attempts to change the pH value without changing the content of aluminum chloride activated root growth, which we associate with the possibility of activating the hormonal effect on cell growth. The control of the cell growth depends on auxins. Therefore, of interest was to separate the influence of the processes caused by the activation of hormonal influence and those of aluminum toxicity (Fig. 3).

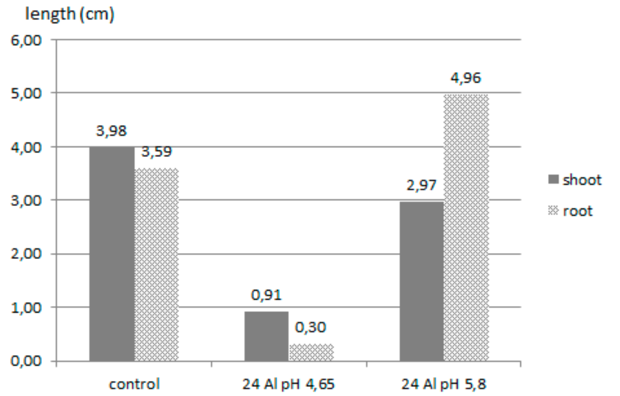

Fig. 3. Changes in seedling shoot and root lengths in solutions containing aluminum ions at pH 4.65 and 5.8. Root growth was observed eventhough the growth of the shoot was lagging.

Using the ^{15}N-labeled, the ability of a horse system to absorb NH_4^+ ions in the presence of aluminum in an acidic environment was investigated. We also studied the degree of nitrogen absorption recovery with an increase in pH to 5.8. We found that the absorption of ions decreases accordingly to a decrease in growth parameters (Fig. 4, p. 71).

The question of the change in absorption under the influence of both the acid reaction of the medium and the actual aluminum toxicity of solutions is being considered. With a decrease in pH, there is no significant difference in the effect of the concentration of aluminum ions on growth and absorption processes. Edaphic stress is of predominant importance in its physical parameters; the importance of variation in the concentrations of aluminum ions against the background of low pH values has not been established. No significant differences between the uptake of nitrogen by seedlings were identified. In some experiments, acidification of the medium with aluminum sulfate reduced the uptake of nitrogen by plants by 55.3–69.5%.

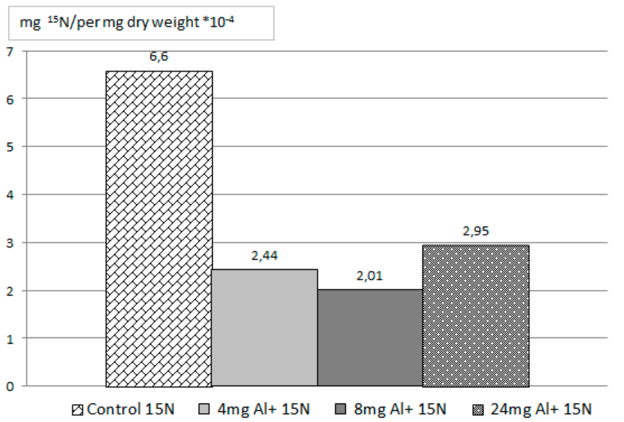

Fig. 4. The content of labeled nitrogen ^{15}N in wheat plants after 10 days of growth per mg dry weight*10^{-4}.

An analysis of the state of the root system of plants shows that cell growth is disrupted by stretching, which causes root thickening. This situation is characteristic of a violation of the auxin cell cycle control. Studying the influence of aluminum ions on nitrogen absorption by roots at pH 5–7 made it possible to establish that the intrinsic influence of aluminum ions is capable of reducing the absorption of nitrogen to 36% at 24mAl/L.

References.

Caasson SA and Keith L. 2003. Genes and signaling in root development// New Phytol **158**:11-38.
Dhillon KS, Yagodeen BA, and Vernichenko IV. 1984. Uptake and assimilation of nitrate and ammonium ions by tomato plants deficient in various micronutrients. Plant and Soil **1**:23.
Lutova LA, Egova TA, Dodueva IE, and Osipova MA. 2010. Plant developmental genetics: for biological specialties of universities. Sankt-Pet, 432 pp.
Poukhalskaya NV. 2018. The study of the effect of aluminum ions, potassium, and their combined effect on the growth of wheat plants in vegetation experiments. Ann Wheat Newslet **64**:35.
Poukhalskaya NV, Ziangirova YR, Davadov FD, and Pavlova NI. 2012. The role aluminum salts ($AlCl_3$, $Al(NO_3)_3$, and $Al_2(SO_4)_3$ in the formation of spring wheat resistance to aluminum toxicity. Ann Wheat Newslet **58**:212-213
Williams PH, Rowarth IS, and Tregurtha RJ. 2000. Recovery of ^{15}N-labeled fertilizer by perennial ryegraseed crop and subsequent wheat crop. Nut Cycl Agro Eco **64**:117-123.

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The dynamics of seed longevity in winter wheat.

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Introduction. The most common way to conserve plant genetic resources is to keep them at low temperature in the form of seeds dried to a certain moisture content. But even under optimal storage conditions, seeds gradually lose their germination capacity. The duration of preservation of seed viability depends on a number of external factors, including growing conditions, air humidity during ripening and collection of seed, seed ripeness, and damage by pathological microflora, and on their genetic characteristics. The ability of seeds to remain viable for a long time is an important factor in *ex situ* storage. In this regard, the issue of predicting the longevity of seed is important. For this purpose, a convenient method is the accelerated aging of seeds, which can provide information on their ability for long-term storage in a short time. According to the recommendations of the International Seed Testing Association (ISTA), accelerated aging stress test exposes seed for short periods to high temperature and high relative humidity. During the test, the seed absorbs moisture from the humid environment and the raised seed moisture content, along with the high temperature, causes rapid seed ageing (ISTA 2017). This is a harsh method that allows quick results within a few days. However, this method has several disadvantages. First, it is not clear at what stage of aging the seed is during the determination of germination;

second, it is not known what happens to the seed under such drastic impacts. In this work, a milder method of accelerated aging was used, which makes it possible to observe the dynamics of the process (Safina and Filipenko 2013). Using this method, we investigated a panel of 96 winter wheat accessions. GWAS analysis was applied at different stages of aging.

Materials and methods. The wheat panel investigated is described in detail by Kobiljski et al. (2002). Material originated from 21 countries on five continents. Details on molecular markers (DArT) used for genotyping of the panel are described by Neumann et al. (2011). The previously published method (Safina and Filipenko 2013) was used for accelerated aging. Before starting the experiments, the initial germination (GOST-12038-84 2011) and humidity (GOST 12041-82 2011) of the seed was determined. Then the seed was placed in glass jars with a volume of 50 ml (12 jars of each sample, 100 seed/jar), which were installed in a thermostat with a temperature of 37°C and a relative humidity of 100% and left open to moisten the seed. Humidity was created using a tray of water, preinstalled on the bottom shelf of the thermostat. When the seed reached the critical humidity (about 14.5% for wheat), the jars were sealed with corks and left in the thermostat for accelerated aging. Every seven days, seed germination was determined (two jars of each sample were taken for one determination). A GWAS analysis was performed as described by Neumann et al. (2011).

Results and discussion. The initial germination of most of the wheat samples studied ranged from 90 to 100%. Differences in the decrease in germination of the samples was observed already after 7 days of aging, and it did not depend on the initial germination. However, when the initial germination rate was below 85%, its decline was much faster than that of the others. Two samples with an initial germination of 80% had a germination rate below 50% after 14 days of aging (Fig. 1, Group 8). After 21 days, the germination about a quarter of the wheat seed samples had dropped to around or below 50%. The most explicit intraspecific variability in germination was found after 28 days. The range of values for the studied samples was from 0% to 90%. After 28 days of aging, around half of samples had a germination rate of less than 50%. The dynamics of reduced germination during accelerated aging is shown (Fig. 1). The samples were divided according to the rate of decrease in germination after 28 days into eight groups: Group 1: 81–90%; Group 2: 71–80%; Group 3: 61–70%; Group 4: 51–60%; Group 5: 41–50%; Group 6: 31–40%; Group 7: 21–30%; and Group 8: 0–20%. After 42 days of aging, 75% of the samples lost their germination completely. Thus, after 28 days of aging a high intraspecific variability in the rate of seed aging was found.

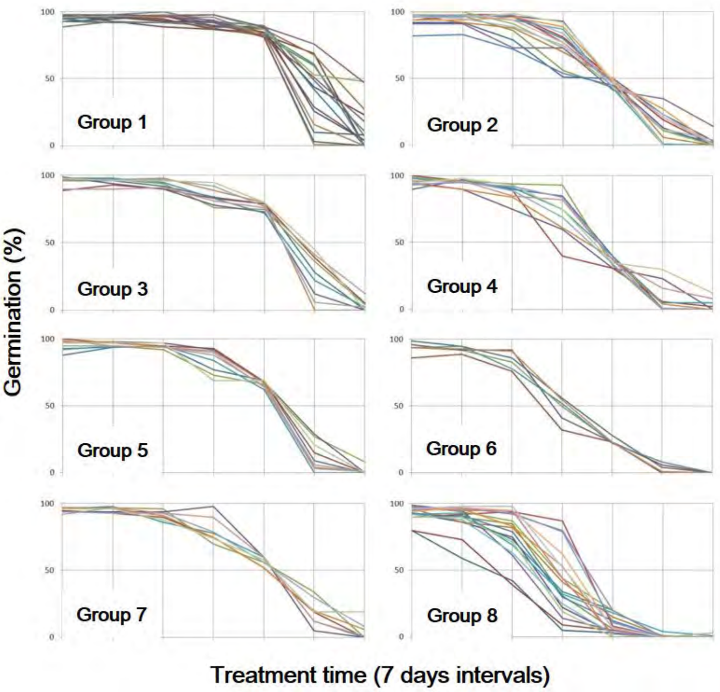

Fig. 1. Dynamics of the decrease in germination of wheat seed in the process of accelerated aging. The samples were divided according to the rate of decrease in germinatoin after 28 days into eight groups: Group 1: 81–90%; Group 2: 71–80%; Group 3: 61–70%; Group 4: 51–60%; Group 5: 41–50%; Group 6: 31–40%; Group 7: 21–30%; and Group 8: 0–20%.

GWAS analyses were performed at each time point of germination tests (Days 0, 7, 14, 21, 28, 35, and 42). Marker-trait associations (MTAs) at a significance level of $p<0.01$ and appearing with both models (GLM and MLM) used only were considered. For initial germination and germination after ageing, 8 and 29 MTAs, respectively, were identified on 12 different chromosomes (Table 1, p. 73). Most of the MTAs were treatment specific, i.e., appeared on a certain time point of analysis only. So, depending on the age of the seeds, different loci seems to be responsible. Five markers detected here are identical with those found by Rehman Arif et al. (2012) analyzing the same panel but at a temperature of 43 ± 0.5°C for 72 h. The five MTAs detected here were identified at five different time points.

Table 1. Markers associated with germination after accelerated aging investigated after days 0, 7, 14, 21, 28, 35, and 42. Red boxes indicate highly significant (*p<0.01*) MTAs appearing with both models (GLM and MLM). Red boxes marked with $$$$$ indicate MTAs also detected by Rehman Arif et al. (2012).

Marker	Locus	Chromosome	Day 0	Day 7	Day 14	Day 21	Day 28	Day 35	Day 42
wPt8682	31,70	1B		$$$$$$$		$$$$$$$			
wPt0413	49,20	1D		🟧					
wPt3114	68,33	2A	🟧	🟧					
wPt0330	8,02	2D					$$$$$$$		
wPt0619	5,23	2D						🟧	
wPt2781	4,53	2D						🟧	
wPt6574	8,72	2D						🟧	
wPt2938	17,18	3A	🟧						
wPt4077	20,23	3A							🟧
wPt4725	21,04	3A						🟧	
wPt0695e	54,73	3B			🟧				
wPt2377	53,51	3B					🟧		
wpt6239	44,89	3B				🟧	🟧		
wPt9432	44,03	3B							$$$$$$$
wPt9510	44,40	3B							🟧
wPt8657	182,62	4A	🟧	🟧	🟧				
wPt3991	111,88	4B						$$$$$$$	
wPt0605	58,20	5A					🟧		
wPt4131	34,67	5A							🟧
wPt1541	180,97	6B		🟧					
wPt2424	96,07	6B						🟧	
wPt4706	46,51	6B	🟧						
wPt8183	92,53	6B						$$$$$$$	
wPt3572	74,52	7A			🟧	🟧			
wPt1069	156,12	7B	🟧	🟧					
wPt1723	46,93	7B	🟧						
wPt5069	144,68	7B	🟧	🟧					
wPt6320	137,99	7B	🟧	🟧					
Σ			8	8	3	3	4	7	4

References.

GOST 12038-84. 2011. Crop seeds. Germination methods. Crop seeds. Methods of analysis. pp. 35-64.

GOST 12041-82. 2011. Crop seeds. Methods of analysis. pp. 107-114.

ISTA. 2017. International rules for seed testing. International Seed Testing Association. Bassersdorf. Switzerland.

Kobiljski B, Quarrie S, Dencic S, Kirby J, and Iveges M. 2002. Genetic diversity of the Novi Sad Wheat Core Collection revealed by microsatellites. Cell Mol Biol Lett **7**:685-694.

Neumann K, Kobiljski B, Dencic S, Varshney RK, and Börner A. 2011. Genome-wide association mapping: a case study in bread wheat (*Triticum aestivum* L.). Mol Breed **27**:37-58.

Rehman Arif MA, Nagel M, Neumann K, Kobiljski B, Lohwasser U, and Börner A. 2012. Genetic studies of seed longevity in hexaploid wheat using segregation and association mapping approaches. Euphytica **186**:1-13.

Safina GF and Filipenko GI. 2013. Longevity of seeds during storage and its prediction by accelerated aging works on applied botany, genetics and selection. St. Petersburg, Vavilov Institute of Research. T 174. pp. 123-130.

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Hybrid necrosis genes in Triticum aestivum subsp. spelta.

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Editors note: according to van Slageren (1994), the correct name for *T. spelta* is *T. aestivum* subsp. *spelta*. As in other cases in this and previous volumes, I am adhereing to van Slageren's suggested nomenclature.

Due to the absence of a wild ancestor of hexaploid wheat species, it remains unclear which subspecies of *Triticum aestivum* or *spelta* was primary. Most researchers assume that both subspecies originated in Western Asia outside the Fertile Crescent, with *spelta* as the primary and *aestivum* appearing later as a result of gene mutations (Pukhalskiy et al. 2019). In historical terms, with the development of world agriculture and grain exchange, domesticated species of tetraploid (*T. turgidum*) and hexaploid (subsps. *aestivum* and *compactum*) wheat gradually spread widely throughout Asia and Europe, which is confirmed by numerous archaeological studies (Zeven 1980). However, data supporting a secondary origin of spelt wheat cannot be neglected (Fljaksberger 1938; Helbaek 1952). Based on the archaeological excavations in some European regions, bread wheat and *T. turgidum* subsp. *dicoccum* were cultivated much earlier than spelt wheat. These data confirmed the hypothesis that bread wheat appeared before spelt wheat. The differences between Asian and European populations of *T. aestivum* subps. *spelta* at both morphological and genetic levels were shown (Perrino et al. 1996; Dorofeev et al. 1979). Studies of *T. aestivum* subps. *spelta* intraspecific variability by chromosome C-banding conducted in our laboratory revealed more diverse C-banding patterns in the Asian lines (var. kuckuckuckianum) compared with the European (var. europium) (Dedkova et al. 2004). At the same time, the results of chromosome 2A staining showed that the vast majority of European samples (91%) were of the *dicoccum* type and Asian spelt wheat samples (83%) belonged to the *aestivum* type. We suppose that this result confirms the secondary origin of the European spelt wheat. At the same time, a number of authors have shown that spelt wheat belonging to the Asian subspecies carry the hybrid necrosis gene *Ne1*, whereas the European samples have *Ne2* (Tsunewaki and Nakai 1973). To compare the cytogenetic analysis with the data on necrotic genotypes, we cytogenetically characterized the presence of *Ne1* and *Ne2* genes in the genotypes of spelt wheat. These samples of winter spelt wheat were obtained from the collection of the Vavilov Research Institute of Plant Industry, Russian Academy of Sciences. The genotypes of 28 spelt wheat samples were studied (Table 1, p. 75). The following winter wheat cultivars were used as testers: Co 725082, Felix, and Berthold (genotype $Ne1^{s}Ne1^{s}ne2ne2$) and Mironovskaya 808, Nemchinovskaya 52, and Yrsay (genotype $ne1ne1Ne2^{ms}Ne2^{ms}$). Allele strength was determined using the Hermsen criterion (1960, 1963).

Our results show that Asian spelt wheat differ from the European samples both in the hybrid necrosis genes and in the frequency of different genotypes (Table 1, p. 75). Asian spelt wheats carry the *Ne1* gene, whereas only the *Ne2* gene was detected in the European samples. The frequency of necrotic genotypes also differed. Thus, among the Asian spelt samples, noncarriers of hybrid necrosis genes (*ne1ne1ne2ne2*) prevail (85%); the *Ne1Ne1ne2ne2* genotypes comprising only 15%. These results are in good agreement with our data on *T. aestivum* subsp. *aestivum* necrotic genotypes in several countries of the Western Asia (Pukhalskiy et al. 2019). Among the European spelt wheat samples, the *ne1ne1Ne2Ne2* genotype prevails (80%), with noncarriers of hybrid necrosis genes comprising only 20%. On the whole, our results are consistent with those of Tsunewaki (1971) and convincingly confirm the hypothesis on the polyphyletic origin of *T. aestivum* subsp. *spelta*. The emergence of Asian spelt wheat resulted from spontaneous hybridization between *T. turgidum subsp. durum* and *Aegilops tauschii* in Iran, which later led to the appearance of hexaploid bread wheat. At the same time (time bounds are difficult to determine), the cultivation areas of emmer wheat increased in the direction of expanding wheat cultivation regions in Europe. The primary forms of bread wheat carrying the *Ne2* gene were imported to the same region. As a result of spontaneous hybridization between bread wheat and emmer wheat, speltoid forms bearing emmer wheat chromosomes that are not present in Asian spelt wheat appeared, as shown by data of differential staining of A-genome chromosomes. From bread wheat, European spelt inherited chromosomes of the B genome, both free of hybrid necrosis genes and carrying *Ne2*. The mutational processes that turned Asian spelt into bread wheat here marked the development of new forms of European bread wheat.

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Table 1. Necrotic genotypes of winter *Triticum aestivum subsp. spelta* samples (* haploid genotypes are shown).

Sample	Variety	Cultivar	Origin	Necrotic genotype*
Asian spelt wheat				
k-47010	*asialbispicatum, subbaktiaricum*	—	Iran	*ne1ne2*
k -52435	*schaartusicum*	—	Tajikistan	*ne1ne2*
k -52436	*schaartusicum*	—	Uzbekistan	*ne1ne2*
k -52437	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52438	*subbaktiaricum*	—	Tajikistan	$Ne1^{ms}ne2$
k -52439	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52442	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52443	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52444	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52445	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52448	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52445	*subsharkordii*	—	Tajikistan	*ne1ne2*
k -52448	*asialbispicatum*	—	Tajikistan	$Ne1^{ms}ne2$
k -52452	*subbaktiaricum*	—	Tajikistan	*ne1ne2*
k -52446	*subsharkordii*	—	Tajikistan	*ne1ne2*
European spelt wheat				
k -1723	*duhamelianum*	Spelz roter	Germany	*ne1ne2*
k -20764	*album*	—	Germany	*ne1ne2*
k -23552	*duhamelianum*	—	Austria	*ne1Ne2*
k -24696	*album*	Elsenegg Weisskorn	Switzerland	*ne1Ne2*
k -24699	*album*	Rufenach Weisskorn	Switzerland	*ne1Ne2*
k -24709	*duhamelianum*	Liestaler- Rotkorn	Switzerland	*ne1Ne2*
k -26340	*album*	Muri- Rotkorn	Switzerland	*ne1Ne2*
k -26343	*album*	Lenzburger Weisskorn	Switzerland	*ne1Ne2*
k -35665	*duhamelianum*	Steiners roter	Germany	$ne1Ne2^{s}$
k -40829	*duhamelianum*	Tirolen roter	Austria	*ne1Ne2*
k -40830	*duhamelianum*	Kopperhaus roter Spelz	Germany	*ne1Ne2*
k -40831	*album*	Kipperhaus weiser Spelz	Germany	*ne1Ne2*
k -45767	*viridarduini*	—	Czech Republic	*ne1ne2*
k -45766	*viridalbispicatum*	—	Czech Republic	*ne1Ne2*
k -45769	*duhamelianum*	Baulander Spelz	Germany	*ne1Ne2*

References.

Dedkova OS, Badaeva ED, Mitrofanova OP, Zelenin AV, and Pukhalskiy VA. 2004. Analysis of intraspecific divergence divergence of hexaploid wheat *Triticum spelta* L. by chromosome C-banding. Rus J Genet **40**(10):1111-1126.

Dorofeev VF, Filatenko AA, Migushova EF, et al. 1979. Cultivated flora of the USSR. 1. Wheat. L. Kolos. 346 pp.

Flyaksberger KA. 1938. Wheat. Sel'khoz M-L. 296 pp.

Helbaek H. 1952. Spelt (*Triticum spelta*) in Bronse Age Denmark. Akta archeogica. **23**:97-107.

Hermsen JGT. 1960. Quantitative in vestigations on progressive necrosis in wheat hybrids. Euphytica **1**:36-37.

Hermsen JGT. 1963. The genetic basis of hybrid necrosis in wheat. Genetica **12**:245-287.

Perrino P, Laghetti G, Antuono LF, et al. 1996. Ecogeographical distribution of hulled wheat species. *In:* Hulled Wheat. Proc 1st Internat Workshop Hulled Wheats. 21-22 July, 1995. Castelvecchio Pascoli, Tuskany (Italy)IPGRI. pp. 101-119.

Pukhalskiy VA, Zuev EV, Bilinskaya EN, and Kudryavtsev AM. 2019. Distribution of hybrid necrosis alleles in genotypes of aboriginal common wheat cultivars from Afghanistan, Palestine, and Transjordan. Rus J Genet **55**(8):904-911.

Tsunewaki K. 1971. Distribution of necrosis genes in wheat V. *Triticum macha, T. spelta* and *T. vavilovii*. Jap J Genet **46**(2):93-101.

Tsunewaki K and Nakai Y. 1973. Considerations on the origin and speciation of four groups of wheat from the distribution of necrosis and chlorosis genes. *In:* Proc 4th Internat Wheat Genet Symp (Sears LM and Sears ER, Eds). Missouri Agric Exp Sta, Columbia. pp. 123-129.
Zeven AC 1980. The spread of bread wheat over the old world since the neolithicum as indicated by its genotype for hybrid necrosis. J d'Agric Trad Bot Appl **XXVII**(I):19-53.

ITEMS FROM UKRAINE

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Influence of a presowing seed treatment with a extremely high frequency microwave field and plant growith regulators on plant density and yield of winter wheat.

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The article presents research on the impact of an ecologically safe presowing treatment with microwave irradiation technology and a winter wheat growth regulator. The interaction is between the agrometeorological conditions during the formation of grain yield in the southeastern part of the Forest-Steppe region of Ukraine.

An important step in the technology of growing crops is the presowing treatment of seed, primarily the disinfection of seed, mainly by chemicals that are directed against phytopathogens. According to Levchenko (2000), plant pest control measures cannot effect the yield potential, but they save what is grown under specific conditions. In recent decades, a purely physiological method, namely a low-power microwave treatment, has become widespread in presowing field crops. The theoretical basis for the technique has become the effect of the reaction of a living cell on the action of the microwave field (Gadzalo 2009; Shevchenko et al. 2007). The use of microwave technology provides a comprehensive solution to a number of problems in agricultural production, but most importantly helps to increase the yield and quality of grain. Kalinina et al. (2000) noted that the influence of the electromagnetic irradiation on the functioning of a biosystem is possible to control using electromagnetic waves. The results of experimental studies on winter wheat seed have detected the frequencies at which biological processes are activated. Analyzing the features of the microwave effect, assumptions of active substances in the grain were deduced. However, a process that begins without a moist environment between the seed treatment and sowing can lead to the death of the embryo and affect the process of the seed germination (Kendruk et al. 2001). Polevik et al. (2011) considered features of the presowing treatment of field crop seed with microwaves. They note that each crop requires a separate time for the treatment of seeds.

Plant growth regulators activate basic processes in plants, such as membrane processes, cell division, enzyme systems, and photosynthesis. The processes of respiration and nutrition help increase the biological activity of plants; reduce the content of nitrates, heavy metal ions, and radionuclides in products; and reduce the mutagenic effect of herbicides. The ecological effects of plant growth regulators on soil is caused by both a direct influence on microbial groups and by influence through the plant roots, where development increases by 15% under the plant growth regulators (Ponomarenko et al. 1992). Significant fluctuations in weather conditions, especially in recent decades, both by season and by the stage of vegetation, significantly affect the formation of crop yields and product quality. Kulbida and Adamenko (2008) showed that the greatest fluctuations in protein in the grain occur due to weather conditions (15%), soil (10%), cultivar (6%), fertilizers (5%), and agrotechnical measures (3.3%).

Methods and materials. Winter wheat productivity was accessed using a presowing treatment of seed with extremely high-frequency microwave field (EHF MF) irradiation and an additional treatment with a growth regulator in conjunction with agrometeorological conditions. An extremely high-frequency microwave seed irradiation used equipment of the Kharkiv National University of Radio Electronics at the range 2.5–3.4 GHz with energy consumption of 0.9 and 1.8 kW/kg of seed for 5–95 sec. Laboratory and field studies during 2011–13 were made with the winter wheat cultivar Astet in the Laboratory of Seed and Seed Science at V. Ya. Yuryev Plant Production Institute of National Academy of Agrarian Science. The presowing seed treatment after the irradiation was with the plant growth regulator Mars EL (0.2 L/t) and the seed fungicide Vitavax 200 FF (2.5 L/t).

Results and discussion. We tested different regimes of microwave irradiation for seed of the winter wheat cultivar Astet (0.9 and 1.8 kW/kg of seed). The most optimal regime for the treatment of winter wheat seed was 1.8 kW/kg of seed with an exposure of 15 sec, which provides the maximum seedling emergence and germination energy. The influence of the presowing treatment of winter wheat seed was combined with the analysis of meteorological conditions as an important factor of plant growth and development.

Seed of Astet was sowed at a rate of 4.5 x 10^6 braird seed/ha following a bare fallow. During 2010–13, sowing was at the optimal time for the Eastern Forest-Steppe Region in September (13 September, 2010; 16 September, 2011; and 9 September, 2013). The period between sowing and germination is described by an increased temperature regime. The average daily air temperature deviation from the long-term indicators was in the range 1.5 °C+3.5°C. Significant fluctuations in the amount of precipitation in September were observed from 178% of the normal in 2010 to 70–80 % of the normal in 2011 and 2012. The autumn period of the study is known to be more often arid and, therefore, the amount of precipitation and especially its intensity determines soil moisture as a major factor of the further growth and development of plants (Nesterec 2010). The peculiarities of the weather conditions during the sowing and germination stages and their influence on germination and the density of winter wheat were evaluated by a control without the presowing seed treatment.

A maximum plant density was 412 plants/m^2 and a seedling emergence of 91.6% were observed during the most favorable meteorological conditions of the autumn in 2010 and 2011 (Table 1). In 2012, 393 plants/m^2 and 87.3% were caused by increased temperature (deviation above the normal of +6.5°C) and a decrease in rainfall at sowing. At the same time, for 2010–12, the field germination rate of the control and in the treatment with the fungicide Vitavax 200 FF were practically the same (90.0-90.2%).

Table 1. Field germination rate for the winter wheat cultivar Astet depending on the presowing seed treatment, 2010–12 (EHF = extremely high frequency microwave field)

Seed treatment	Amount (plants/m^2)			Average	Field germination rate (%)			Average
	2010	2011	2012		2010	2011	2012	
1. Control (no treatment)	412	412	393	405	91.6	91.6	87.3	90.2
2. Vitavax, 200FF, 2.5 L/t	392	395	428	405	87.1	87.8	95.1	90.0
3. EHF 1.8 kW/kg, 15 sec	436	438	434	436	96,9	97.3	96.4	96.9
4. EHF 1.8 kW/kg, 15 sec + Mars EL	440	440	446	442	97.8	97.8	99.1	98.2
5. EHF 0.9 kW/kg, 45 sec	440	436	439	438	97.8	96.9	97.6	97.4
6. EHF 0.9 kW/kg, 45 sec + Mars EL	435	420	434	425	96.7	93.3	96.4	95.5
SSD $_{05}$	24.3	25.2	23.8	19.3	5.4	5.6	5.3	4.3

The presowing irradiation of seed with EHF MF at 1.8 kW/kg for 15 sec and 0.9 kW/kg for 45 sec resulted in an increase in germination by 6.9% and 7.4%, respectively. However, in the unfavorable climate of 2012, germination after treatment with Vitavax 200 FF exceeded that of the control by 7.8%. In the treatments with EHF MF and growth regulator Mars EL, germiantion was higher by 9.1-11.8%, indicating that, under adverse conditions, the effect of the presowing seed treatment on germination rate was more significant. Such a pattern allows us to conclude that the influence of a presowing seed treatment on winter wheat productivity is more effective under adverse weather conditions. In the treatment with EHF MF 1.8 kW/kg 15 sec + Mars EL, plant density was the highest in 2012 (446 plants/m^2) and field germination was 99.1%; the control had 393 plants/m^2 and 87.3%.

Plant density continues throughout the growing season and is accompanied by some dead plants until harvest. Plant density is influenced by many factors, in particular weather conditions, sowing time, seeding rates, and care of the crop, especially in the tillering-heading period (Petr et al. 1984). During tillering, stems of winter wheat form and determine the overall and productive tillering, significantly affecting the harvest. The duration of winter wheat autumn tillering largely depends on agrometeorological conditions (Vrkach 1984).

The coefficient of autumn tillering in the control treatment varied over the years according to germination rates. Maximum values of the coefficient of 3.6 were observed in 2010 and 2012 at air temperature and precipitation were normal or above normal. The minimum value for the tillering coefficient was 2.4 under conditions of insufficient humidity in 2011 and precipitation 60–70% of the normal.

Significant fluctuations in the plant density in the autumn by years, both in the control and in the irradiation variants testify to the unequal moisture supply between germination and termination of autumn vegetation. The maximum values of the tillage coefficient (3.6–4.1) and the number of tillers (1,393–1,687 tillers/m^2) were observed in the most humid autumn period in 2010. The minimum values of the tillage coefficient (2.4–2.6) and the number of tillers (980–1,028/m^2) were observed during the dry period of autumn tillering in 2011.

In certain EHF MF treatments, a change in plant density was observed over the years during the autumn booting stage but in a different pattern. The maximum values of the tillage coefficient and a number of stems were observed in 2012 were 3.7–4.2 and 1,559–1,709 tillers/m^2, respectively, and the minimum values were 1.9–2.2 and 756–909 tillers/m^2 in 2013. This distribution of tillering during the study period was facilitated by winter conditions and the condition of the plants at the beginning of spring vegetation. We found that an increase in the germination rate of winter wheat seed due to a presowing treatment with an EHF MF ensures a higher plant density throughout the entire growing season (Table 2). Thus, during autumn tillering after a seed treatment with EHF MF at 1.8 kW/kg for 15 sec or 0.9 kW/kg at 45

Table 2. Biometric indicators of winter wheat plants of the cultivar Astet depending on the presowing seed treatment with an extremely high frequency microwave field (EHF MF) and the plant growth regulators, 2010–13.

	Plant growth stage											
	Autumn tillering				**Boot**				**Grain filling**			
Treatment	**Number of plants/m^2**	**Number of tillers/m^2**	**Coefficient of tillering**	**Height (cm)**	**Number of plants/m^2**	**Number of tillers/m^2**	**Coefficient of tillering**	**Height (cm)**	**Number of plants/m^2**	**Number of tillers/m^2**	**Coefficient of tillering**	**Height (cm)**
1. Control (no treatment)	398	1,258	3.2	23.1	365	1,075	2.9	53.2	344	619	1.8	65.5
2. Vitavax 200 FF, 2.5 l/t	400	1,304	3.3	23.5	392	1,306	3.3	54.0	351	683	2.0	69.5
3. EHF 1.8 kW/kg, 15 sec	416	1,380	3.2	23.3	420	1,222	2.9	54.2	369	693	1.9	71.5
4. EHF 1.8 kW/kg, 15 sec + Mars EL	436	1,439	3.3	23.9	420	1,288	3.1	56.8	345	629	1.8	73.1
5. EHF 0.9 kW/kg, 45 sec	425	1,420	3.4	23.3	426	1,258	3.0	55.4	380	685	1.8	72.1
6. EHF 0.9 kW/kg, 45 sec + Mars EL	424	1,400	3.3	24.3	391	1,205	3.1	55.9	359	672	1.9	74.2
SSD$_{05}$	20.7	95.9	0.15	0.63	29.2	99.8	0.17	1.52	14.0	51.0	0.11	3.9

sec, the average plant density was 416 and 425 tillers/m^2, respectively, over the three years, a 4% and 7% increase over the control, respectively (Table 2, p. 78). In similar variants with additional pretreatment of seed with the plant growth regulator Mars EL, the plant density was 436 tillers/m^2 or 9.5% (1.8 kW/kg for 15 sec) and 424 tillers/m^2 or 6.5% (0.9 kW/kg at 45 sec) greater than that of the control (398 tillers/m^2 (SSD$_{05}$ = 20.7).

The plant density, i.e., the number of formed tillers, was calculated. We found that the coefficient of tillering for the control averaged 3.2 averaged over the three years. In most of the presowing seed treatments it was 3.3. The highest tillage coefficient (3.4) was observed in the EHF MF seed treatment at 0.9 kW/kg, 45 sec. As a result, the number of tillers/m^2 for the different EHF MF treatments for the three years on average exceeded the control indicators by 122 (1.8 kW/kg, 15 sec), 181 (1.8 kW/kg, 15 sec + Mars EL), 162 (0.9 kW/kg, 45 sec), and 142 (0.9 kW/kg, 45 sec + Mars EL) (SSD$_{05}$ = 95.9). The indicator of the seed treatments using Vitavax 200 FF was 76, 135, 116, and 96 tillers/m^2, respectively.

During the period of tillering–heading, the average daily air temperature varied within the norm, 17–22°C, and the amount of precipitation was 15–25 mm, during the interstage period from 7–19 days in 2013 and 2011. An important indicator for the formation of winter wheat yields is the length of the period from heading to full ripening. During the research period, the interstage period was from a minimum of 24 days in 2012 to a maximum of 36 days in 2011 and 2013 at an optimum temperature of 20–23°C. The uneven distribution of rainfall from 29 mm in 2012 to 207 mm (180% of the normal) in 2011 and their intensity caused a decrease in grain yield to 4.44 t/ha in 2011 compared to 6.63 t/ha in 2013 (Table 3).

Table 3. The crop capacity of winter wheat cultivar Astet depending on the presowing seed treatment (t/ha).

Seed treatment	Year			Average	+/– to control	Extra amount (%)
	2011	2012	2013			
Control (no treatment)	4.44	5.09	6.63	5.39	–	–
Vitavax 200 FF, 2.5 l/t (standard)	4.66	5.09	6.72	5.49	0.10	1.9
EHF 1.8 kW/kg, 15 sec.	4.73	5.21	6.79	5.58	0.19	**3.5**
EHF 1.8 kW/kg, 15 sec. + Mars EL, 0.2 l/t	4.88	5.18	6.82	5.63	0.24	**4.5**
EHF 0.9 kW/kg, 45 sec.	4.99	5.26	6.65	5.63	0.24	**4.5**
EHF 0.9 kW/kg, 45 sec.+ Mars EL, 0.2 l/t	4.64	5.09	6.69	5.47	0.08	1.5
SSD$_{05}$	0.22	0.12	0.11	0.18		

Presowing seed irradiations with an EHF MF at 1.8 kW/kg of seed and a 15 sec exposure and at 0.9 kW/kg of seed and a 45 sec exposure increased winter wheat yield on average by 0.19 or 3.5% in 2011 and 0.24 t/ha or 4.5% in 2013. Yield in the control treatment was 5.39 t/ha (SSD$_{05}$ = 0.18 t/ha) (Table 3). However, the effectiveness of this seed treatment varied significantly over the experimental years. For example, in 2011, when agrometeorological conditions were the least favorable for the growth and development of winter wheat, the yield was the lowest of all years. The positive effect of using EHF MF was the greatest, 7% and 12%, depending on the irradiation regime. Yields of the control treatment were 4.44 t/ha. The greatest effect of the seed treatment with Vitavax 200 FF at the recommended rate of 2.5 l/ha also was observed in 2011, 0.22 t/ha. The effectiveness of the additional EHF MF seed treatment and using the plant growth regulator Mars EL at a rate of 0.2 l/t depended on the irradiation regime and the conditions of the study year. Thus, on average for 2011–13, the winter wheat yield was 5.63 t/ha using EHF MF 1.8 kW/kg for 15 sec + Mars EL (0.2 L/t), whereas with EHF MF at 1.8 kW/kg and 15 sec + Mars EL was 5.58 t/ha. The differences in plant density for the individual years in the treatments with the seed irradiation indicate the influence of weather conditions on the plant growth starting with the restoration of spring vegetation.

Conclusions. An increase in the germination rate of winter wheat seed due to a presowing treatment with an extremely high-frequency microwave field ensures a higher plant density throughout the growing season. The most effective way for increasing yield of winter wheat by 0.24 t/ha (or 4.5%) is a presowing seed treatment with EHF MF at the regime 1.8 kW/kg of seed and a 15 sec exposure with the additional treatment with the plant growth regulator Mars EL or with EHF MF at 0.9 kW/kg of seed and a 45 sec exposure.

References.

Gadzalo YaM. 2009. Mikrovolnovaya tehnologiya – shag v budushe agorarnoj otryasli. Zh Hranenie i pererabotka zerna **5**(119):26-28 (in Russian).

Kalinin LG, Tuchnij VP, Levchenko YeA, Kindruk MO, and Vishnevskij VV. 2000. Viznachennya vplivu mikrohvilovogo polya na posivni i urozhajni yakosti nasinnya zlakovih, olijnih i ovochevih kultur. Mikrovolnovye tehnologi v narodnom hozyajstve, 2- Odessa **3**:66-73 (in Ukrainian).

Kindruk MO, Vishnevskij VV, and Vishnevska AM. 2001. Mikrohvilova biostimulyaciya nasinnya, Zh. Hranenie i pererabotka zerna **4**:27-29 (in Ukrainian).

Kulbida M and Adamenko T. 2008. Usi sorti pshenici naroshuyut vmist bilka v zerni u miru zmenshennya geografichnoyi shiroti. Agronom **1**(9):12-15 (in Ukrainian).

Levchenko YeA. 2000. Prohresyvni napriamy borotby z shkidnykamy khlibnykh zapasiv (stan pytannia). Mykrovolnovie tekhnolohy v narodnom khoziaistve, sb. vipusk 2-3, Kyev-Odessa, 24-30 (in Ukrainian).

Medinec V. 2009. Moguchij tvorec kachestva zerna pshenicy. Zerno **6**(38)80-83 (in Ukrainian).

Nesterec VG. 2010. Agroklimatichni j tehnogenni faktori formuvannya vrozhajnosti zernovih kultur v umovah minlivosti klimatu v pivdenno- shidnij chastini Stepu. Zerno **6**:41-44 (in Ukrainian).

Petr I, Cherny V, and Grushna L. 1984. Formirovaniya urozhaya osnovnih selskohozyajstvennyh kultur. Per. s cheshskogo Z.K. Blagoveshenskoj. Moskva 111-112 (in Russian).

Polevik ND, Popov VM, and Bidyanov VA. 2011. Vliyanie predposevnoj SVCh obrabotki semyan golozernyh sortov yachmenya na ih produktivnost. Zh. Hranenie i pererabotka zerna **9**(147):22-24 (in Russian).

Ponomarenko SP, Nikolaenko TK, and Troyan VM. 1992. RRR na osnove oksidov proizvodnyh piridina. Fiziko – himicheskie svojstva i mehanizm dejstviya. RRR. Kiev 28-55 (in Russian).

Shevchenko AM, Volkogon VV, Goncharov AN, Retman SV, Vozhegova RA, and Sitnik VP. 2007. Znachenie mikrovolnovoj tehnologi v razvitii agropromyshlennogo kompleksa. Mikrovolnovye tehnologi v narodnom hozyajstve. Odessa **6**:8-9 (in Russian).

Vrkach F. 1984. Morfologicheskaya struktura otdelnogo rasteniya i vysokoproduktivnogo poseva. Formirovanie urozhaya osnovnyh selskohozyajstvennyh kultur, per. s cheshsk. Z.K. Blagoveshenskoj. Moskva 58-62 (in Russian).

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Aegilops tauschii: an ideal tool to characterize genes in wheat–Hessian fly interactions.

Subhashree Subramanyam.

The gall midge, Hessian fly (*Mayetiola destructor*), is a devastating pest of common bread wheat causing significant yield losses. Deployment of resistant wheat cultivars is the most effective and economical strategy to manage this insect pest. However, extensive planting of resistant cultivars with high level of antibiosis to the larvae exerts strong selection pressure on Hessian fly population, favoring the selection of virulent biotypes that can overcome deployed resistance, posing a threat to long-term production of wheat.

An alternate strategy to enhance and complement native H gene resistance is by employing forward genetics to develop wheat lines overexpressing candidate defense-response genes or negatively regulating genes involved in wheat

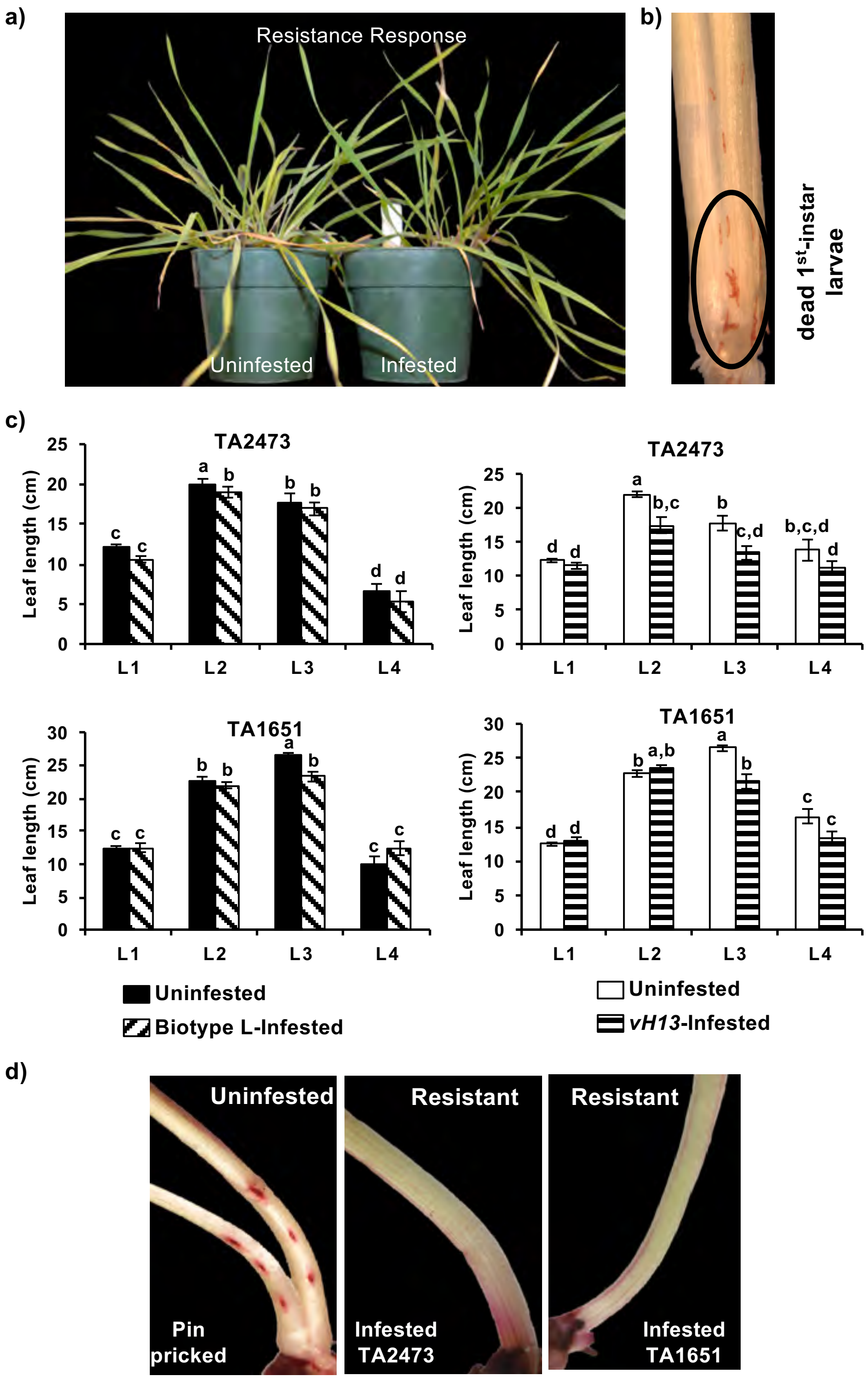

Fig. 1 Phenotypic response of *Ae. tauschii* to Hessian fly larval feeding: Diploid wheat accessions showing homozygous resistance response to feeding by Biotype L and *vH13* Hessian fly larvae. **a)** Plant growth; **b)** Representative plant showing dead 1st-instar avirulent larvae at the base of the crown tissue (the larval feeding site); **c)** Leaf (L) growth in leaves 1 to 4. Data are represented as mean ± standard error. The letters on top of the bars indicate significant differences based on Tukey's HSD test (p<0.05). Same letters indicate no difference between the two treatments. Different letters indicate significant differences between the two treatments; **d)** change in plant cell wall permeability determined by staining plants with Neutral Red.

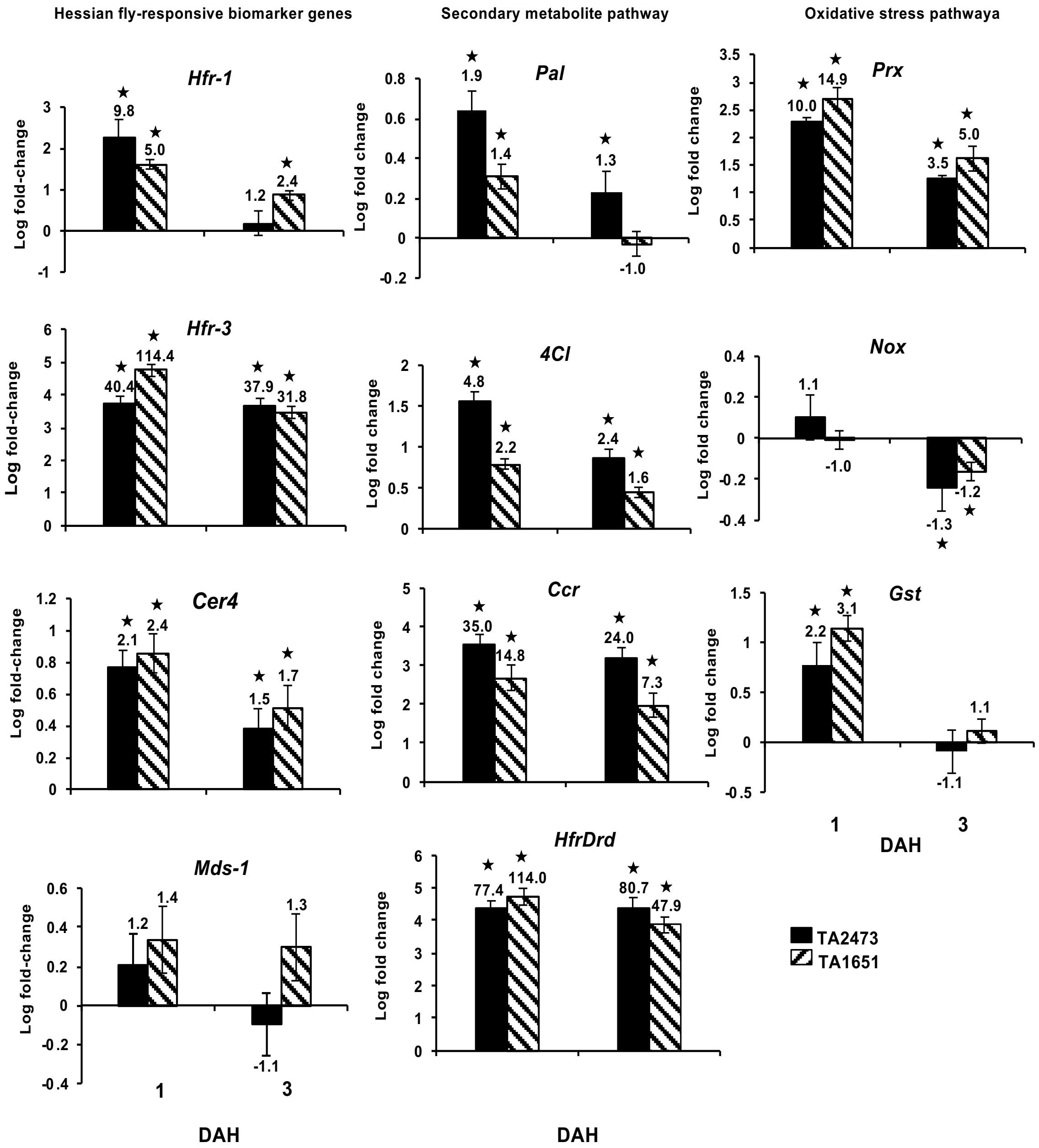

Fig. 2 Molecular response of *Ae. tauschii* to Hessian fly larval feeding: Expression of genes encoding Hessian fly-responsive biomarker proteins, secondary metabolites and oxidative stress in resistant diploid wheat lines at 1 and 3 Days After Egg Hatch (DAH) quantified by quantitative real-time PCR. Values are plotted as the log fold-change of infested compared to uninfested control plants with standard error bars for 3 biological replicates. Statistically significant (p<0.05) differences are indicated by '*' with linear fold-change values above each bar. *Hfr-1* (Hessian fly response gene 1); *Hfr-3* (Hessian fly response gene 3); *Cer4* (Fatty acyl CoA reductase); *Mds*-1 (*Mayetiola destructor* susceptibility gene 1); *Pal* (Phenylalanine-ammonia lyase); *4Cl* (4-coumarate-CoA ligase); *Ccr* (Cinnamoyl-CoA reductase); *HfrDrd* (Hessian fly-responsive disease resistance dirigent-like); *Prx* (Class III peroxidase); *Nox* (NADPH-dependent oxidase); *Gst* (Glutathione S-transferase) .

susceptibility to Hessian fly. Despite identification of hundreds of Hessian fly-responsive genes and associated biological pathways in common bread wheat, the functional validation of these genes via supplementation and/or mutational approaches have been challenging. This is largely attributed to large genome size, polyploidy, repetitive DNA, and limited availability of genetic resources for hexaploid wheat, thus necessitating a need to explore other less complex genomes as a models for functional characterization of candidate genes.

The diploid progenitor *Ae. tauschii*, D-genome donor of modern-day hexaploid wheat, offers an ideal surrogate eliminating the need to target all three homeologous chromosomes (A, B, and D) individually and, thereby, making the functional validation of candidate Hessian fly-responsive genes plausible. Furthermore, the well-annotated sequence of *Ae. tauschii* genome and availability of genetic resources amenable to manipulations makes the functional assays less tedious and time-consuming. However, the utilization of this diploid genome for downstream studies requires characterization of its physical and molecular responses to Hessian fly.

Phenotypic screening identified two *Ae. tauschii* accessions (TA2473 and TA1651) that exhibited a homozygous resistance response to feeding by virulent Hessian fly larval biotypes, vH13 and L. The resistant diploid wheat accessions resembled hexaploid wheat in their phenotypic responses, including larval developmental stages, leaf and plant growth, and cell wall permeability, to Hessian fly larval attack (Fig. 1, p. 81). Furthermore, resembling the resistant hexaploid wheat, the resistant diploid wheat lines mount an early defense strategy involving defense proteins including lectins, secondary metabolites and reactive oxygen species (ROS) radicals (Fig. 2, p. 82). These results reveal the suitability of the diploid progenitor for use as an ideal tool for functional genomics research in deciphering the wheat-Hessian fly molecular interactions. A similar approach can be employed by researchers and breeders working with other important insect pests of wheat and other economically important cereal crops.

Publication.

Nemacheck JA, Schemerhorn BJ, Scofield SR, and Subramanyam S. 2019. Phenotypic and molecular characterization of Hessian fly resistance in diploid wheat, *Aegilops tauschii*. BMC Plant Biol **19**:439 [https://bmcplantbiol.biomedcentral.com/articles/10.1186/s12870-019-2058-6].

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Water relations and cadmium uptake of wheat grown in soil with particulate plastics.

M.B. Kirkham.

Particulate plastics contaminate the terrestrial environment, yet no information exists concerning the water-relations of plants grown in soil with particulate plastics. Therefore, our first objective was to determine the growth, evapotranspiration rate, and stomatal resistance of wheat when grown in soil with particulate plastics. Because particulate plastics can be a vector for toxic trace-element uptake, our second objective was to determine the uptake of cadmium (Cd) to see if they enhanced its uptake. Wheat cultivar Everest was grown for 28 days under greenhouse conditions in pots with a commercial potting soil. The particulate plastic was polyethylene glycol with a molecular weight of 8000 (called PEG 8000). At the beginning of the experiment, pots were divided into three sets: pots with soil that received no PEG 8000 (called the no-PEG treatment); pots with soil into which dry PEG 8000 was mixed at a rate of 2% on a dry-weight basis (called the dry-PEG treatment); and pots with soil that received PEG 8000 via irrigation of a 2% solution of PEG 8000 (called the wet-PEG treatment). The three sets of pots were divided in half and, during the experiment, half of the pots were irrigated with a 100 µg/mL Cd solution. The pots in the no-PEG treatment and the dry-PEG treatment were irrigated with tap water or the 100 µg/mL Cd solution. The pots in the wet-PEG treatment were irrigated with a solution containing 2% PEG and no Cd or 2% PEG and 100 μg/mL Cd. During the experiment, height was measured with a ruler, evapotranspiration rate was determined by weighing the pots, and stomatal resistance was measured using a porometer.

Both with and without Cd, 18 days after planting, plants in the wet-PEG treatment were shorter than plants in the no-PEG treatment. Both with and without Cd, the evapotranspiration rate of plants in the wet-PEG treatment was reduced by 0.3 mm/day compared to plants in the no-PEG treatment. Without Cd, the stomatal resistances of plants grown in the wet-PEG treatment and in the no-PEG treatment were 295 s/m and 178 s/m, respectively; for plants grown with Cd, these values were 322 s/m and 231 s/m, respectively. Shoots of plants grown in the no-PEG treatment with Cd and in the dry-PEG treatment with Cd had an average Cd concentration of 130.0 mg/kg. Plants grown in the wet-PEG treatment with Cd had a Cd concentration of 204.8 mg/kg. The presence of wet PEG in the soil increased the Cd in the plants by 1.5 times (204.8 vs. 130.0 mg/kg). The results showed that PEG 8000 was a potent vector for the transport of Cd to wheat leaves.

News.

Reshma M. Antony, whose work on cold tolerance was reported in the 2019 *Annual Wheat Newsletter*, now is working as a Research Technologist, Ruminant Nutrition Laboratory, 110 Call Hall, Department of Animal Sciences and Industry, Kansas State University, Manhattan, KS 66506.

Publications.

Alghamdi A, Presley DR, Kirkham MB, and Hettiarachchi G. 2020. Efficacy of amendments on soil physical properties of mine waste materials at an abandoned lead and zinc mine. Agrosyst Geoscie Environ (in press)

Bradney L, Wijesekara H, Palansuriya KN, Obadamudalige N, Bolan NS, Ok YS, Rinklebe J, Kim K-H, and Kirkham MB. 2019. Particulate plastics as a vector for toxic trace-element uptake by aquatic and terrestrial organisms and human health risk. Env Internat **131**:104937 [https://doi.org/10.1016/j.envint.2019.104937].

Carver RE, Nelson NO, Roozeboom KL, and Kirkham MB. 2020. Species and termination method effects on phosphorus loss from plant tissue. J Environ Qual **49**:97-105 [https://doi.org./10.1002/jeq2.20019].

Chowdhury S, Bolan NS, Farrell M, Sarkar B, Sarker JR, Kirkham MB, and Kim GH. 2020. Role of cultural and nutrient management practices in carbon sequestration in agricultural soil. Adv Agron (in press).

Huo D, Bolan NS, Tsang DCW, Kirkham MB, and O'Connor D. 2020. Sustainable soil use and management: an interdisciplinary and systematic approach. Sci Total Environ 729:138961 [https://doi.org/10.1016/j.scitotenv.2020.138961].

Liu J, Shrestha P, Skabelund LR, Todd T, Decker A, and Kirkham MB. 2019. Growth of prairie plants and sedums in different substrates on an experimental green roof in Mid-Continental USA. Sci Total Environ **697**:134089 [https://doi.org/10.1016/j.scitotenv.2019.134089].

Opole RA, Prasad PVV, Djanaguiraman M, Vimala K, Kirkham MB, and Upadhyaya HD. 2018. Thresholds, sensitive stages and genetic variability of finger millet to high temperature stress. J Agron Crop Sci **204**(5):477-492 [https://doi.org/10.1111/jac.12279].

Xiong X, Yu IKM, Tsang DCW, Bolan NS, Ok YS, Igalavithana AD, Kirkham MB, Kim K-H, and Vikrant K. 2019. Value-added chemicals from food supply chain wastes: state-of-the-art review and future prospects. Chem Eng J 375:121983 [https://doi.org/10.1016/j.cej.2019.121983].

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Mining wheat's wild side for global food security.

The Wheat Genetics lab is receiving nearly $1 million from the U.S. Department of Agriculture's National Institute of Food and Agriculture, through its Agriculture and Food Research Initiative, for two projects to improve the genetic diversity of wheat. Centuries of focused breeding to increase yields and performance stability has reduced genetic diversity in most modern wheat cultivars. As the human population increases and climates become more variable, the lack of genetic diversity in modern wheat has the potential to compromise global food security. The grants to mine wheat wild relatives for genes that increase disease resistance, stress tolerance, and yield potential. Two reservoirs of untapped genetic diversityare *Aegilops speltoides* and the wild emmer *T. turgidum* subsp. *dicoccoides*. These new projects, supported through the National Institute of Food and Agriculture, will build on decades of work and genetic resources assembled in the Wheat Genetics Resource Center. Current industry partnerships in the NSF Industry-University Cooperative Research Center, have further strengthened the value of the germplasm collection. K-State can directly connect the work on wild wheat with companies and breeders delivering the new germplasm to farmers.

The first project is a collaboration between K-State, 2Blades Foundation, the University of Minnesota, and the John Innes Center. The extensive Wheat Genetics Resource Center collection of wild emmer will be leveraged to resequence the emmer genome and identify genes providing resistance to stripe, leaf, and stem rust, three diseases that cause nearly $\$3 \times 10^6$ in damage to global wheat crops annually. The second collaboration brings K-State Plant Pathology researchers together with the University of Haifa, Israel, to unlock genetic diversity in *Ae. speltoides*, a distant wild relative of wheat with huge diversity. This work will better characterize the collection of *Ae. speltoides* and use this information to identify genetic segments transferred into wheat with the aim of making better genetic markers for wheat breeders to use. These projects really complement the ongoing work of the WGRC to provide robust genetic resources to breeders and see this novel genetic diversity transferred to breeding companies and delivered to farmers.

Registration of Hessian fly-resistant germplasm KS18WGRC65 carrying H26 *in hard red winter wheat Overley background.*

Narinder Singh, Ryan Steeves, and Jesse Poland; Ming-Shun Chen and Mohammed El Bouhssini (Department of Entomology); and Mike Pumphrey (Washington State University, Pullman).

Hessian fly causes severe damage to wheat worldwide. Several resistance genes have been identified in wheat and wild relatives; however, HF populations are under strong selection pressure and evolve rapidly to overcome resistance. To ensure the availability of resistance sources, HF-resistant germplasm KS18WGRC65 (TA5110, Reg. no. GP-1042, PI 688251) was developed by Wheat Genetics Resource Center at Kansas State University as a breeding stock that carries resistance gene *H26* from *Ae. tauschii*. KS18WGRC65 is a cytogenetically stable, homozygous, $BC_3F_{3:6}$ line derived from the cross between *Ae. tauschii* accession KU2147 and hard red winter wheat recurrent parent Overley. KS18WGRC65 exhibited no penalty for yield or other agronomic characters, making it a suitable source of HF resistance for wheat breeding.

Harnessing the wild side to search for novel wheat blast resistance genes.

Paula Silva, Giovana Cruppe, Narinder Singh, John Raupp, Barbara Valent, and Jesse Poland; and Lidia Calderon (Instituto Nacional de Investigación Agropecuaria (INIA), Programa Nacional de Cultivos de Secano, Estacion Experimental INIA La Estanzuela, Ruta 50 km 11, 70006, Colonia, Uruguay).

When genetic diversity is scarce, plant breeding programs can turn to crop wild relatives as donors of novel sources of diversity. *Aegilops tauschii* is the donor of the D genome of the cultivated bread wheat and has been used as a valuable source of novel disease resistance genes. Wheat blast, caused by *Magnaporthe oryzae Triticum* (MoT) pathotype, is an emerging disease in South Asia that has the potential to devastate wheat production. Our objective was to characterize a panel of *Ae. tauschii* accessions for resistance to wheat blast and identify genomic regions associated with resistance that can be used in marker-assisted selection. We tested 138 accessions of *Ae. tauschii* form *strangulata* under controlled conditions in Bolivia. *Ae. tauschii* spikes were inoculated with the MoT Bolivian isolate 008, and disease severity was assessed at 10, 12, 14, 16, and 18 days after inoculation. Genomic regions associated with wheat blast resistance were mapped in a genome-wide association study (GWAS) using the area under the disease progress curve (AUDPC) as the trait and 13,135 SNP markers. Phenotypic values for the AUDPC ranged from 10 to 790, and six accessions were observed to be more resistant than the highly resistant check. GWAS resulted in the identification of six significant SNPs on chromosomes 4, 2, and 1. This study identified novel genomic regions involved in resistance to wheat blast in a wheat wild relative that have the potential to improve wheat blast resistance in cultivated wheat. Further analysis of these regions will identify candidate genes for these associations.

Preparing for the potential emergence of wheat blast in Uruguay.

Paula Silva, Liangliang Gao, and Jesse Poland; Silvia Pereyra, Silvia Germán, and Martin Quincke (Programa Nacional de Cultivos de Secano, Instituto Nacional de investigación Agropecuaria (INIA), La Estanzuela, 70006, Colonia, Uruguay); and Bettina Lado (Departamento de Estadística, Facultad de Agronomía, Universidad de la República, 12900, Montevideo, Uruguay).

Wheat blast, caused by *Magnaporthe oryzae* pathotype *Triticum*, is currently one of the most destructive diseases threatening wheat production worldwide. The disease is endemic in South America, first reported in 1985 in Brazil and subsequently has spread to Bolivia (1996), Paraguay (2002), northern Argentina (2007), and Bangladesh (2016). Despite this, wheat blast has not been detected in wheat in Uruguay, probably due to unfavorable environmental conditions for the infection and development of the pathogen during the crop cycle. However, *M. oryzae* has been reported in Uruguay in rice, ryegrass, and barley. To date, the alien chromosome fragment $2N^VS$ transferred from the wheat relative *Ae. ventricosa* holds the only useful source of wheat blast resistance. The presence of the $2N^VS$ fragment in Uruguayan wheat cultivars and breeding germplasm might be one of the reasons why wheat blast has not been detected in Uruguay. We evaluated the presence of the $2N^VS$ fragment in 3,977 wheat germplasm lines from the INIA (National Agricultural Research Institute) breeding program. The plant material included advanced wheat breeding lines and prebreeding germplasm, CIMMYT germplasm, and material from other global breeding programs introgressed into INIA-adapted material and cultivars bred abroad and released in Uruguay. In order to predict the presence of the $2N^VS$ fragment, we used skim-sequencing and a bioinformatic customized pipeline developed in house. Only 495 lines (14.2% of the total) resulted positive for the presence of $2N^VS$, suggesting that the alien fragment is present in a low proportion. Additionally, we checked for the presence of $2N^VS$ in some widely grown cultivars in Uruguay in 2018, which accounted for ~56,000 ha (one-fourth of the total wheat area). Interestingly, ~30% of the area was grown with resistant cultivars (positive for $2N^VS$), suggesting that resistance might have helped to prevent wheat blast establishment. Our results also suggest that the INIA wheat breeding program should start an introgression plan for the $2N^VS$ in order to prevent a future blast outbreak.

Harnessing the wild side to search for novel wheat curl mite resistance genes.

Paula Silva, Narinder Singh, Liangliang Gao, John Raupp, Michael Smith, and Jesse Poland.

Genetic diversity is the foundation for crop breeding. When genetic diversity is scarce, we can turn to crop wild relatives as donors of novel sources of diversity. *Aegilops tauschii,* the donor of the D genome of the cultivated bread wheat, has been used as a valuable source of novel genes for many economically important traits, such as pest and disease resistance. Wheat curl mite (WCM) is a threating pest for wheat, mainly because of vectoring wheat streak mosaic virus. Our objective was to characterize a diverse panel of *Ae. tauschii* accessions against WCM and identify genomic regions associated with resistance that can be used with marker-assisted selection to breed wheat against WCM. We tested 234 accessions of *Ae. tauschii* (109 from Lineage 1 and 125 from Lineage 2). Curl mite infestation was performed under controlled conditions and the plants were tested 14 days after infestation. Phenotypic response to WCM was recorded using a 0 to 4 scale, where 0 was resistant (R) and 1–4 different levels of susceptibility (S). Genotyping-by-sequencing data was used to map genomic regions associated with WCM resistance using genome-wide association study. The diverse panel resulted in 190 S and 44 R accessions. Strong population structure was identified within the accessions, consistent with the lineages. Mapping analysis resulted in a strong association to resistance on chromosome 6S. This study identified genomic regions involved in resistance to WCM in wild wheat. Further analysis of these regions will reveal if they are novel or already present in cultivated wheat cultivars.

Breeding strategies to fight a cereal killer.

Paula Silva, Giovana Cruppe, Byron Evers, Barbara Valent, and Jesse Poland; and Lidia Calderon (Unidad de Mejoramiento de Trigo, Asociación de Productores de Oleaginosas y Trigo (ANAPO), Santa Cruz de la Sierra, Bolivia, 2305).

Wheat blast, caused by the *Magnaporthe oryzae Triticum* pathotype, is an emerging disease in South Asia, with the potential to devastate wheat production. Wheat blast was first reported in Brazil in 1985, however, not until its emergence in Bangladesh in 2016 that international attention focused on this disease. To date, only four major resistance genes have been identified, *Rmg2*, *Rmg3*, *Rmg7*, and *Rmg8*. Currently, only *Rmg8* still holds potential for effectiveness under field conditions. Recently, the chromosome fragment $2N^VS$ from the wild relative *Aegilops ventricosa* is reported to contain the only useful source of wheat head blast resistance. However, there is unclear information regarding the level of resistance conferred by $2N^VS$ in different genetic backgrounds. Moreover, no information regarding which genes(s) on $2N^VS$ are responsible for effectively fighting blast. This project aims to characterize the wheat blast resistance conferred by the alien fragment $2N^VS$ and search for new resistance genes in the wild relative *Ae. tauschii*. To characterize $2N^VS$, we developed an EMS populations derived from five $2N^VS$ bread wheat cultivars showing different levels of blast resistance. These will be tested under field conditions in Bolivia in order to select for susceptible plants and segregating lines. To explore for new resistance genes, we are evaluating 156 *Ae. tauschii* form *strangulata* lines under controlled conditions. Resistant lines will be selected and, using whole-genome sequencing data, we expect to characterize new resistance genes. Overall, these breeding strategies will help researchers and breeders to better understand the disease and breed germplasm resistant to wheat blast.

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

Bikram S. Gill, M. 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. Although 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. They defy the controls of mitosis and meiosis and lead to acquired herbicide resistance in *Amaranthus palmeri*.

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

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

Glume color in the A-genome progenitors 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 yet illustrated. 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 SNP to understand the genetic architecture of the trait in these different species. Nine 96-plexed GBS libraries with *Pst*I-*Msp*I were constructed for 848 A-genome accessions, including 559 subsp. *aegilopoides*, 172 *T. urartu*, and 117 subsp. *monococcum*. The raw sequence data (pair-end 150 bp) were processed using the TASSEL5 GBSv2 pipeline, where reads were aligned to a *T. urart*u reference (tu2.0). The filtered SNPs and binary coded (0 = white, 1=color) phenotypes were tested for genome-wide association (GWAS) within each species using GAPIT, and the result was verified using rrBLUP mixed model. The top GWAS hit for all three species was observed on the short arm of chromosome 1 at about 5 Mb. Furthermore, 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 on chromosome 1. These results indicate that the wheat MYB ortholog on chromosome 1 could be a potential candidate gene for glume color in the A-genome species.

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

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

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 of large populations and is time and labor consuming. With next generation sequence resources available for wheat and related species, 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 rear, 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 sub-genomes, 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.

Paula Silva receives Early Career Award.

PhD candidate Paula Silva was named a prestigious Borlaug Global Rust Initiative (BGRI) 2020 Jeanie Borlaug Laube Women in *Triticum* (WIT) Early Career Award winner. The award provides training opportunities for innovative women scientists who have demonstrated traction in increasing gender parity in agriculture.

Paula is an excellent young scientist who shows vast potential that will be realized through her hard work and dedication. Along with her demonstrated experience and success, Paula embodies the type of young scientist that we want to cultivate and encourage in their research and career. Silva joined Jesse Poland's lab in 2016 as a Fulbright Fellow, where her research has focused on breeding for economically important and complex diseases, such as barley yellow dwarf, rusts, and wheat blast. In addition to her graduate work, in 2019 she was appointed to remotely lead the disease resistance breeding program and coordinate the Precision Wheat Phenotypic Platform for wheat diseases for INIA Uruguay—where she plans to return once completing her PhD this year.

Publications.

Adihikari L, Wu S, Raupp J, Poland J, Kratlinger SG. And Abrouk M. 2020. Genome-wide association mapping of glume color in the A-genome species of wheat. Plant and Animal Genome XVIII. Abstract PE0920.

Crain J, Bajgain G, Anderson J, Zhang X, DeHaan L, and Poland J. 2020. Enhancing crop domestication through genomic selection, a case study of intermediate wheatgrass. Front Plant Sci [https://doi.org/10.3389/fpls.2020.00319].

Jared Crain1, Prabin Bajgain2, James Anderson2, Xiaofei Zhang3, Lee DeHaan4* and Jesse Poland

Danilova TV, Development and application of genome-specific SNP markers for tracing alien introgressions in polyploid wheat genome. Plant and Animal Genome XVIII. Abstract PO0907.

Gill BS, Jungalem M, Friebe B, and Koo D-H. 2020. Fishing eccDNA elements that defy chromosome control of mitosis and meiosis and drive rapid adaptive evolution. Plant and Animal Genome XVIII. Abstract W796.

Koo D-H, Friebe B, and Gill BS. 2020. Homoeologous recombination: A novel and efficient system for broadening the genetic variability in wheat. MDPI Agronomy **10**(8);1059 [https://doi.org/10.3390/agronomy10081059].

Silva P, Gao L, Pereyra S, Lado B, Germán S, Quincke M, and Poland J. 2019. Preparing for the potential emergence of wheat blast in Uruguay. 1st Internat Wheat Cong, 21–26 July, Saskatoon, Saskatchewan, Canada. Abstract.

Silva P, Cruppe G, Calderon L, Singh N, Raupp J, Valent B, and Poland J. Harnessing the wild side to search for novel wheat blast resistance genes. 2020. National Association of Plant Breeders (NAPB) Annual Meeting (virtual, 16–20 August 2020). Abstract.

Silva P, Singh N, Gao L, Raupp J, Smith M, and Poland J. Harnessing the wild side to improve wheat curl mite resistance. 2020. Research and the State Graduate Students Summit, Capitol Building, Topeka, KS. 26 February 2020. Abstract.

Silva P, Cruppe G, Calderon L, Evers B, Valent B, and Poland J. 2020. Breeding strategies to fight a cereal killer. Plant and Animal Genome XVIII. Abstract.

Singh N, Raupp J, Koo D-H, Friebe B, Gill B, and Poland J. 2020. *In-silico* detection of aneuploidy and chromosomal deletions in wheat using genotyping-by-sequencing. Plant Methods **16**:45 [https://doi.org/10.1186/s13007-020-00588-3].

Singh N, Steeves, R, Chen M-S, El Bouhssini M, Pumphrey, M, and Poland J. 2020. Registration of Hessian fly-resistant germplasm KS18WGRC65 carrying *H26* in hard red winter wheat 'Overley' background. J Plant Reg **14**(2):206-209 [https://doi.org/10.1002/plr2.20003].

Wang X, Xuan H, Evers B, Shrestha S, Pless R, and Poland J. 2019. High-throughput phenotyping with deep learning gives insight into the genetic architecture of flowering time in wheat. bioR$_{x}$iv [doi: https://doi.org/10.1101/5279].

MINNESOTA

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Wheat leaf rust in the USA in 2019.

Occurrence and crop conditions. In 2019 wheat leaf rust, caused by *Puccinia triticina*, was widespread throughout the soft red winter wheat area of the Southeastern states, the Ohio Valley, and also was commonly found in the hard red winter area of the Great Plains and the hard red spring wheat area of the northern Great Plains. In the south Atlantic, Gulf coast region, southern Great Plains, and Ohio Valley region, the average temperatures in April were slightly higher than normal in April. Warm temperatures allowed infections of *P. triticina* to increase and spread across the winter wheat regions. In May and June, temperatures were very close to average throughout the soft red and hard red wheat regions. The above average temperatures early in the growing season and close to average temperatures later allowed leaf rust to spread and compete with stripe rust (*P. striiformis* f. sp. *graminis*), which favors lower temperatures compared to leaf rust. Temperatures in the spring wheat region of the northern Great Plains were also close to average in May and June. In Oklahoma losses due to leaf rust were estimated to be 8%, with 3% losses in Texas and Kansas. Losses in other states were at 1% or less. Overall estimated losses in the US due to leaf rust in 2019 were 24 x 10^6 bushels.

Races and virulence of *P. triticina*. In 2019, 32 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 252 isolates were processed for race identification. Race MNPSD was the most common race at 45.2% of all isolates. MNPSD was found in the soft red winter regions of the southeastern states, and Ohio Valley, in addition to the winter and spring wheat region of the Great Plains. MNPSD and the closely related race MPPSD at 11.9% 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*, *Lr39*, and *Lr37* that are in many of the hard red winter cultivars. Race MBTNB was the most common race in the southeastern states and Ohio Valley. MBTNB is virulent to *Lr11*, which is present in the soft red winter wheat cultivars grown in these regions. Races TBBGS was at the highest frequency in the hard red spring region of the northern Great Plains. TBBGS is virulent to *Lr21*, which is in many of the spring wheat cultivars in this region, in addition to *Lr39*. Virulence to *Lr24* and *Lr39* are highest in the southern to mid Great Plains region. Virulence to *Lr11* and *Lr26* is highest in the southeastern states, and virulence to *Lr18* was detected at low frequencies in all regions, but was most common in the Ohio Valley region. Virulence to *Lr2a* and *Lr21* was highest in Minnesota and South Dakota and North Dakota.

The complete race frequency and virulence frequency to individual *Lr* genes and information on the individual collections, location, date, cultivar collected from, and race designations of the derived isolates are given (Tables 1 and 2, p. 91).

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2019.

Race	Virulence combination (ineffective *Lr* genes)	Southeast		Ohio Valley		OK–TX		KS–NE		MN–ND–SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%
LBDSG	*1,17,B,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	22.2	2	0.8
LCDSG	*1,26,17,B,10,14a,28*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	33.3	3	1.2
MBDSB	*1,3,17,B,10,14a*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	22.2	2	0.8
MBDSD	*1,3,17,B,10,14a,39*	1	4.3	0	0.0	3	3.7	1	1.9	4	6.5	0	0.0	9	3.6
MBTNB	*1,3,3ka,11,17,30,B,14a*	8	34.8	10	40.0	3	3.7	0	0.0	1	1.6	0	0.0	22	8.7
MBTSB	*1,3,3ka,11,17,30,B,10,14a*	0	0.0	1	4.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
MCDSB	*1,3,26,17,B,10,14a*	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	22.2	2	0.8
MCDSD	*1,3,26,17,B,10,14a,39*	0	0.0	0	0.0	1	1.2	0	0.0	1	1.6	0	0.0	2	0.8
MDPSD	*1,3,24,3ka,17,30,B,10,14a,39*	1	4.3	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
MFJSB	*1,3,24,26,11,17,B,10,14a*	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.4
MJBGJ	*1,3,16,24,10,28,39*	0	0.0	0	0.0	1	1.2	0	0.0	0	0.0	0	0.0	1	0.4
MJBJG	*1,3,16,24,10,14a,28*	0	0.0	0	0.0	0	0.0	1	1.9	0	0.0	0	0.0	1	0.4
MLPSD	*1,3,9,3ka,17,30,B,10,14a,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.4
MNDSD	*1,3,9,24,17,B,10,14a,39*	0	0.0	0	0.0	0	0.0	1	1.9	0	0.0	0	0.0	1	0.4
MNPSD	*1,3,9,24,3ka,17,30,B,10,14a,39*	4	17.4	3	12.0	48	59.3	36	69.2	23	37.1	0	0.0	114	45.2
MNPTS	*1,3,9,24,3ka,17,30,B,10,14a,18,21,28,39*	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.4
MPDSD	*1,3,9,24,26,17,B,10,14a,39*	0	0.0	0	0.0	0	0.0	2	3.8	0	0.0	0	0.0	2	0.8
MPPSD	*1,3,9,24,26,3ka,17,30,B,10,14a,39*	0	0.0	1	4.0	11	13.6	8	15.4	10	16.1	0	0.0	30	11.9
MPTSD	*1,3,9,24,26,3ka,11,17,30,B,10,14a,39*	0	0.0	0	0.0	1	1.2	0	0.0	0	0.0	0	0.0	1	0.4
PCDGJ	*1,2c,3,26,17,10,28,39*	0	0.0	0	0.0	1	1.2	0	0.0	1	1.6	0	0.0	2	0.8
TBBGQ	*1,2a,2c,3,10,21,28*	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.4
TBBGS	*1,2a,2c,3,10,21,28,39*	0	0.0	0	0.0	5	6.2	0	0.0	14	22.6	0	0.0	19	7.5
TBRKG	*1,2a,2c,3,3ka,11,30,10,14a,18,28*	1	4.3	1	4.0	1	1.2	0	0.0	0	0.0	0	0.0	3	1.2
TBTNB	*1,2a,2c,3,3ka,11,17,30,B,14a*	2	8.7	3	12.0	0	0.0	0	0.0	0	0.0	0	0.0	5	2.0
TCTNB	*1,2a,2c,3,26,3ka,11,17,30,B,14a*	2	8.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	0.8
TFKGB	*1,2a,2c,3,24,26,11,17,30,10*	0	0.0	1	4.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.4
TFPSB	*1,2a,2c,3,24,26,3ka,17,30,B,10,14a*	0	0.0	1	4.0	0	0.0	0	0.0	0	0.0	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	3	5.8	2	3.2	0	0.0	5	2.0
TNBGS	*1,2a,2c,3,9,24,10,21,28,39*	0	0.0	0	0.0	1	1.2	0	0.0	0	0.0	0	0.0	1	0.4
TNBJJ	*1,2a,2c,3,9,24,10,14a,28,39*	0	0.0	0	0.0	4	4.9	0	0.0	0	0.0	0	0.0	4	1.6
TPBGJ	*1,2a,2c,3,9,24,26,10,28,39*	0	0.0	0	0.0	1	1.2	0	0.0	1	1.6	0	0.0	2	0.8
Total		23		25		81		52		62		9		252	

Table 2. Frequency (%) of isolates of *Puccinia triticina* collected in 2019 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	23	100.0	25	100.0	81	100.0	52	100.0	62	100.0	9	100.0	252	100.0
Lr2a	5	21.7	6	24.0	12	14.8	3	5.8	18	29.0	0	0.0	44	17.5
Lr2c	5	21.7	6	24.0	13	16.0	3	5.8	19	30.6	0	0.0	46	18.3
Lr3	23	100.0	25	100.0	81	100.0	52	100.0	62	100.0	4	44.4	247	98.0
Lr9	4	17.4	4	16.0	66	81.5	50	96.2	38	61.3	0	0.0	162	64.3
Lr16	0	0.0	0	0.0	1	1.2	1	1.9	0	0.0	0	0.0	2	0.8
Lr24	5	21.7	6	24.0	67	82.7	51	98.1	38	61.3	0	0.0	167	66.3
Lr26	6	26.1	7	28.0	15	18.5	10	19.2	15	24.2	5	55.6	58	23.0
Lr3ka	22	95.7	24	96.0	64	79.0	44	84.6	37	59.7	0	0.0	191	75.8
Lr11	17	73.9	20	80.0	5	6.2	0	0.0	3	4.8	0	0.0	45	17.9
Lr17	22	95.7	24	96.0	68	84.0	48	92.3	44	71.0	9	100.0	215	85.3
Lr30	22	95.7	25	100.0	64	79.0	44	84.6	37	59.7	0	0.0	192	76.2
LrB	22	95.7	23	92.0	67	82.7	48	92.3	43	69.4	9	100.0	212	84.1
Lr10	7	30.4	8	32.0	78	96.3	52	100.0	60	96.8	9	100.0	214	84.9
Lr14a	23	100.0	24	96.0	72	88.9	49	94.2	43	69.4	9	100.0	220	87.3
Lr18	1	4.3	1	4.0	1	1.2	0	0.0	1	1.6	0	0.0	4	1.6
Lr21	0	0.0	0	0.0	6	7.4	0	0.0	16	25.8	0	0.0	22	8.7
Lr28	1	4.3	1	4.0	14	17.3	4	7.7	20	32.3	5	55.6	45	17.9
Lr39	6	26.1	4	16.0	77	95.1	51	98.1	58	93.5	0	0.0	196	77.8
Lr42	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Total	**23**		**25**		**81**		**52**		**62**		**9**		**252**	

The postulated *Lr* genes in the ten most common hard red winter wheat cultivars in Texas, Oklahoma, and Kansas in 2019 are listed (Table 3) as are the postulated *Lr* genes in the ten most common hard red spring wheat cultivars in Minnesota and North Dakota in 2019 (Table 4).

Table 3. Hard red winter wheat cultivars grown in 2019 (when possible, an *Lr* gene was postulated; *?* indicates a gene postulation could not be made; + indicates that the cultivar was resistant to all isolates tested).

Texas	Oklahoma	Kansas	Nebraska
TAM 111–*Lr37*, *Lr39*	Gallagher–*Lr26*	SY Monument–*?*	SY Monument–*?*
Gallagher–*Lr26*	Doublestop CL–none	WB Grainfield–*Lr39*	SY Wolf–*Lr26, Lr34, Lr37*
TAM 112–*Lr39*	Bentley–*Lr21, Lr39*	WinterHawk–*Lr39*	Ruth *?*
TAM 114–*Lr18*	Iba–*Lr34*, *Lr37*	Everest–*Lr1 Lr14a*	WB Grainfield–*Lr39*
TAM 204 +	Duster–*Lr11 Lr34 Lr46 Lr77*	T158–*Lr37, Lr39*	Settler CL–*Lr11*
TAM 105	Endurance–*Lr1 Lr26*	LCS Mint	Robidoux–none
SY Razor	Jagger–*Lr37*	Gallagher–*Lr26*	Brawl CL Plus–*Lr3*, *Lr14a*
Greer–*Lr39*	SY Monument *?*	Joe–*Lr21*	Freeman–none

Table 4. Hard red spring wheat cultivars grown in 2019 (when possible, an *Lr* gene was postulated; *?* indicates a gene postulation could not be made; + indicates that the cultivar was resistant to all isolates tested).

Minnesota		North Dakota	
Linkert +	LCS Breakaway *?*	SY Ingmar +	Faller–*Lr21*
Shelly–*Lr21* +	MN–Washburn +	SY Valda +	Barlow–*Lr21*
Bolles +	SY Valda +	Bolles +	Glenn–*Lr21*
Lang-MN +	WB9590 +	SY Soren +	SY Rockford
Rollag +	WB 9590 *?*	Elgin-ND–*Lr21* +	Prosper–*Lr21*

MONTANA

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A transcriptomic-guided strategy to identify wheat rust targets and modification of the target enhanced host resistance against the pathogen.

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Transcriptional reprogramming is an essential feature of plant immunity and is governed by transcription factors (TFs) and co-regulatory proteins associated with discrete transcriptional complexes. On the other hand, effector proteins from pathogens have been shown to hijack these vast repertoires of plant TFs. Studies have begun targeting and editing some host genes that benefit pathogens to enhance plants' immunity to pathogens. However, our current knowledge on the role of host genes (including TFs) involved in host colonization is just based on research employing a few model plants such as Arabidopsis and rice with minimal efforts in wheat rust interactions. In this study, we identified the wheat MYC4 TF located on the chromosome 1B (TaMYC4-1B) was upregulated at 24 hours post-rust inoculation in a susceptible wheat line. Down-regulation of TaMYC4-1B using barley stripe mosaic virus-induced gene silencing (BSMV-VIGS) in the susceptible cultivar Chinese Spring enhanced its resistance to stem rust pathogen. Knockout of the TaMYC4 -1BL homeolog in Cadenza rendered new resistance to races of stem, leaf, and stripe rust pathogens. From this discovery, we have created new germplasm in wheat via modifications of the wheat TaMYC4 -1BL transcription factor.

A new mode of NPR1 action via an NB-ARC–NPR1 fusion protein negatively regulates the defence response in wheat to stem rust pathogen.

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Plants constantly battle with a variety of pathogens in the environment via their complex and effective innate immune systems. One strategy is the hypersensitive response, used to defend against biotrophic pathogens by which rapid programmed cell death occurs immediately surrounding the infection sites to restrict pathogens from further spreading and replications. NPR1 has been found to be a key transcriptional regulator in some plant defence responses. There are nine NPR1 homologues (TaNPR1) in wheat, but little research has been done to understand the function of those NPR1-like genes in the wheat defence response against stem rust pathogens. We used bioinformatics and reverse genetics approaches to study the expression and function of each TaNPR1. In wheat, six members of TaNPR1 were found to be located on homoeologous group-3 chromosomes (designated as TaG3NPR1) and three on homoeologous group-7 chromosomes (designated as TaG7NPR1). The group-3 NPR1 proteins regulate transcription of SA-responsive PR genes. Downregulation of all the TaNPR1 homologues via virus-induced gene co-silencing resulted in enhanced resistance to stem rust. More specifically, downregulating TaG7NPR1 homeologues or Ta7ANPR1 expression resulted in stem rust resistance phenotype. By contrast, knocking down TaG3NPR1 alone did not show visible phenotypic changes in response to the rust pathogen. Knocking out Ta7ANPR1 enhanced resistance to stem rust. The Ta7ANPR1 locus is alternatively spliced under pathogen inoculated conditions. We discovered a new mode of NPR1 action in wheat at the Ta7ANPR1 locus through an NB-ARC–NPR1 fusion protein negatively regulating the defence to stem rust infection.

Publication.

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Non-immunogenic wheat needed to feed 10% of the US population suffering from wheat-related disorders.

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Wheat is the primary food staple for 20% of the world's population as it is affordable and a good source of nutrients. Unfortunately, none of the natural wheat genotypes are gluten-free (Rustgi et al. 2019, 2020a), and many cannot digest gluten proteins due to the repetitive proline and glutamine tracts in their primary sequences (Osorio et al. 2012). The human immune system recognizes gluten peptides, and a native gluten-modifying enzyme as invaders and attacks them, leading to various reactions, such as celiac disease (CD), dermatitis herpetiformis, wheat allergy, wheat sensitivity, and gluten ataxia (Brouns et al. 2019). These disorders affect about 10% of the US population (Sapone et al. 2012). The current treatment for these disorders is avoiding wheat, which is impractical and negatively affects health by depriving consumers of other nutrients in the grain (Rustgi et al. 2019).

To mitigate this problem, we have developed reduced-gluten (Wen et al. 2012; Rustgi et al. 2014) and 'glutenase'-expressing transgenic wheat lines (Osorio et al. 2019). These genotypes, albeit useful, are unavailable to consumers due to the lack of general acceptance for genetically modified wheat. With an intent to identify a more widely acceptable solution, we set out to isolate reduced-gluten wheat mutants from landraces, and screen wheat genotypes exhibiting ABA insensitive/hypersensitive response or carry mutations in the wheat *DEMETER* or *Dre2* (Derepressed for Ribosomal protein S14) genes for their gluten profiles. The selection of genotypes for screening was based on the knowledge of the existence of variable gluten genotypes in wheat landraces (Rustgi et al. 2019), the transcriptional control of gluten proteins by the wheat *DEMETER*, and *DRE2* genes (Wen et al. 2012; Rustgi et al. 2020b) and that ABA biosynthesis/signaling genes influences protein and starch composition of the grains. The standard gel electrophoresis, densitometry, and chromatography were used to study the gluten content and composition of wheat genotypes. The reduced-gluten genotypes identified through the analysis constitute the required genetic resources to breed for non-immunogenicity in wheat. A few genetic crosses among the selected mutant lines were made (Kashyap 2020), and a few more will be performed in the future.

Wheat landraces and ABA-hypersensitive/insensitive mutants. Thirty-four wheat landraces and 27 ABA-biosynthesis or hypersensitive mutants (ABH) and ABA-signaling or insensitive mutants (ABI) were tested for their protein profiles using SDS-PAGE-based densitometric analysis and high-performance liquid chromatography. Gluten-banding patterns from the genotypes of a landrace or across landraces were compared, and the mutant types were identified. Mutants with different missing gluten proteins were selected for the genetic crossing to stack their effects on gluten content in a single genotype. The differences in the banding pattern observed in these genotypes were divided into two categories: qualitative differences and quantitative differences. The deficiency of a protein subunit (qualitative differences) was determined by comparing the protein profile of different genotypes of a landrace (analyzed three to four half-seeds per landrace). On the other hand, the quantitative differences were determined via densitometric analysis of corresponding bands (determined based on molecular weights, inferred from the migration patterns on the gel) among genotypes belonging to a landrace. Similar criteria were used to study quantitative and qualitative differences in protein profiles of the wheat ABA insensitive and hypersensitive mutants, except, in this case, comparisons were made with the respective wild type controls.

1. Quantitative/qualitative differences in protein profiles of wheat landraces. Different seeds analyzed from a landrace exhibited differences in the quantities of corresponding protein bands (Fig. 1a). Not to our surprise, some genotypes showed reduced accumulation of one gluten protein subfamily and over-accumulation of another subfamily upon loading equal amounts of gliadins/glutenins from different genotypes onto a gel. Altogether, eight (23.5%) out of 34 landraces showed differential accumulation of proteins when 3–4 seeds of each landrace were tested. It suggested the presence of different gluten genotypes in such landraces. In some instances, up to three different genotypes (based on protein profiles) were observed out of the four seeds tested for a landrace. Among these eight landraces, three landraces have genotypes that specifically showed a reduction in the content of gliadins, two in glutenins, and three in both gliadins and glutenins.

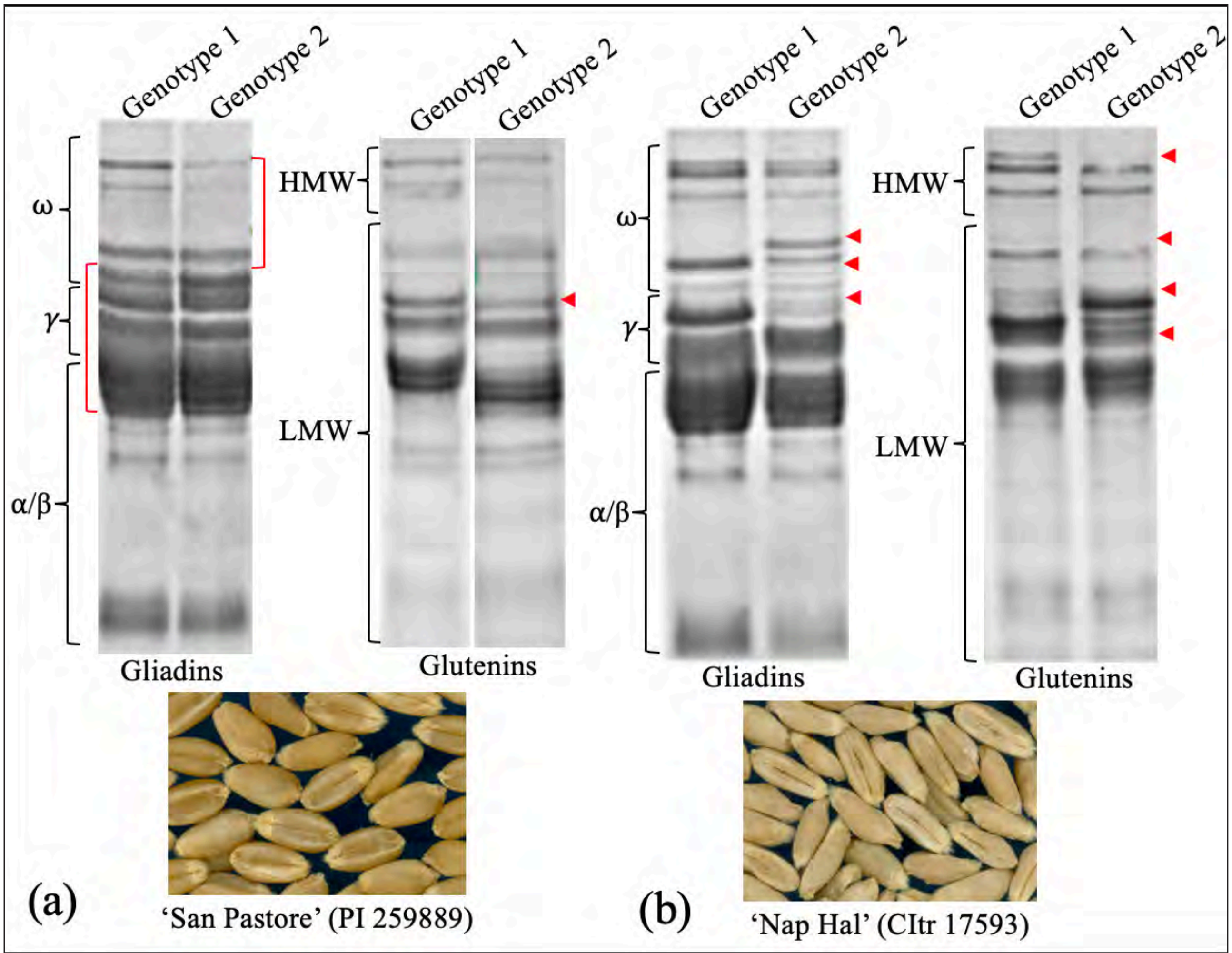

Fig. 1. SDS–PAGE gel analysis of gluten proteins derived from wheat landraces. Comparison of gliadin and glutenin profiles obtained from two individual seeds (endosperm half) of wheat landraces with each other to identify quantitative differences in the content of corresponding proteins exhibiting quantitative differences (a), or qualitative differences or missing proteins (b); arrowheads and brackets mark the regions of interest in each gel lane.

Similar to quantitative differences, the qualitative differences (presence/absence of specific protein bands) were monitored by loading an equal amount of gliadin/gluten proteins on to the gel (Fig. 1b). When comparisons were made across landraces using an arbitrary meta-reference (a gliadin/glutenin profile with all bands observed in studied landraces), 16 (47%) out of 34 landraces showed a deficiency of one or more protein bands. Among the 16 landraces, seven landraces have genotypes that specifically show missing glutenin bands, four showed missing gliadins bands, and the remaining five landraces showed missing glutenin and gliadin bands. Precisely, out of these 16 landraces, 10 showed deficiency in one or more of the ω-gliadins (including D-type ω-gliadins), four in LMW-glutenin subunits, three each in α/β- and γ-gliadins, and two in HMW-glutenin subunits.

2) ***Quantitative/qualitative differences in protein profiles of the wheat ABA biosynthesis/signaling mutants.*** Gliadins and glutenins were extracted from the ABA hypersensitive and ABA insensitive mutants to understand the effects of impaired ABA biosynthesis/signaling on the accumulation of wheat gluten proteins. The ABH wheat mutants used in the present study were derived wheat cultivar Chinese Spring (CS) and soft white winter wheat cultivar Brevor and soft white spring wheat cultivar Zak. Whereas, the ABI mutants were generated in the background of hard red spring wheat cultivar Scarlet. Seeds of ABH and ABI mutants were received from Dr. C.M. Steber, USDA–ARS. When gliadin and glutenin profiles from mutants were compared with the respective wild type genotypes three mutants, ScABI1b, ScABI1c (Fig. 2), and ScABI5 in the cultivar Scarlet background, one mutant, 144-29A in 'Brevor' background, and two mutants WARM1 and WARM6 in CS background showed quantitative/qualitative differences in gliadins and/or glutenins. In sum, out of 27 mutant genotypes tested, three were found to show quantitative differences in their gliadin and/or glutenin contents, and three showed qualitative differences (i.e., missing protein bands).

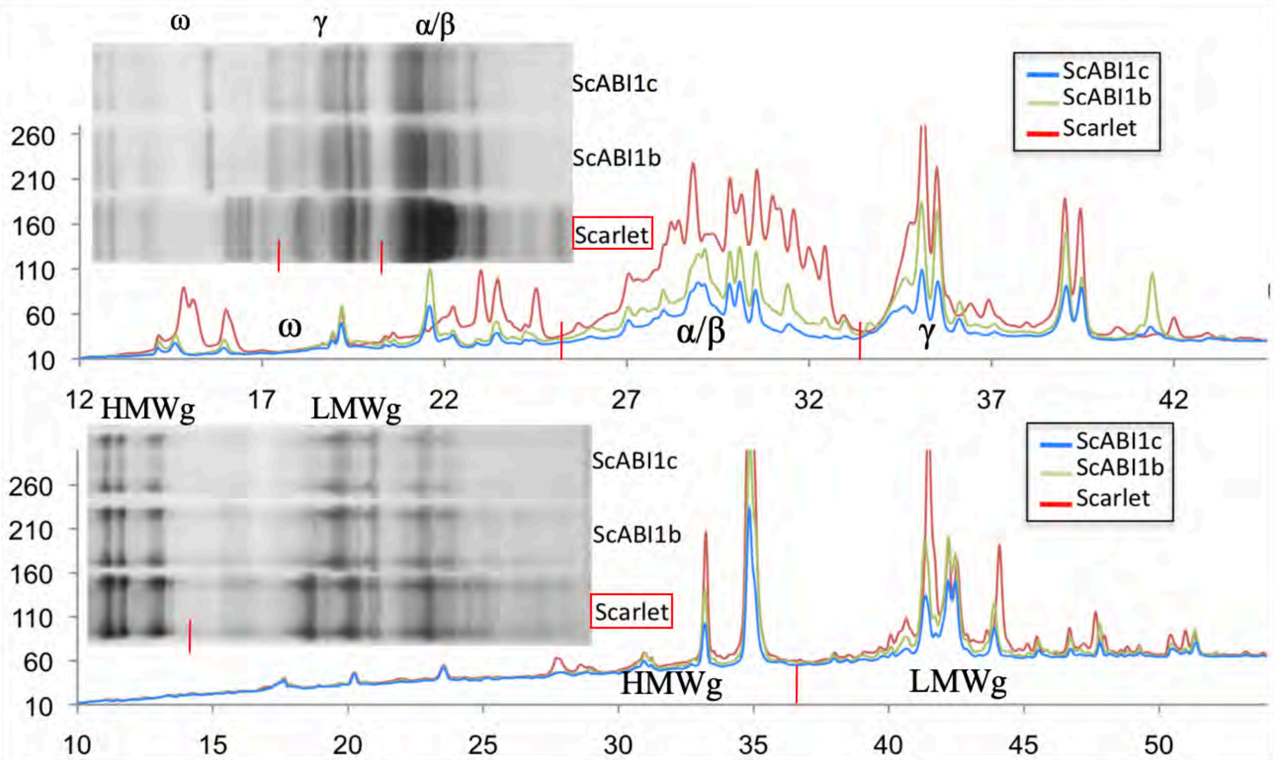

Fig. 2. Comparison of gliadin (first two lanes) and glutenin (next two lanes) profiles of ABI mutant, ScABI1b, and ScABI1c with wild type control cultivar Scarlet, obtained using SDS–PAGE gel analysis and reversed-phase high-performance liquid chromatography (RP–HPLC). Notice the differences in different components of gliadins and glutenins.

Wheat *DEMETER* mutants. Based on the knowledge that the enzyme coded by the wheat *DEMETER* gene is responsible for the transcriptional activation of the gluten genes in developing wheat grains (Wen et al. 2012), we screened two TILLING populations one each in cultivar Kronos and Express backgrounds, for mutations in the *DEMETER* genes. To reduce the workload, we confined our search for the mutants to one kb region in the active site of the *DEMETER* genes. Screen for mutations in Kronos and Express populations yielded 77 and 149 mutations, respectively. Seeds of the selected *DEMETER* mutants were obtained from Dr. C.P. Moehs of Arcadia Biosciences and analyzed for their gluten profiles. The single mutations in *DEMETER* homoeologues showed reductions in specific prolamins (Fig. 3a, p. 96). Crosses were made between the mutants carrying substitutions, premature stop codons, and splice site variations in A and B sub-genome *DEMETER* homoeologues to pyramid the effect of the individual mutations in a single genotype. Unfortunately, the crosses between the mutants carrying premature stop codons or splice site variations never yielded a double mutation. To determine the cause of the observed segregation distortion, we closely monitored the anther morphology, the number of viable pollens, and pollen germination. We observed, the nonsense mutations in wheat *DEMETER* genes have significantly reduced the anther locules size, the number of viable pollen, and negatively affected the pollen germinate. Thus, this analysis also suggested a vital role of *DEMETER* in pollen development and germination.

Wheat *Dre2* mutants. The Dre2 or Derepressed for Ribosomal protein S14 Expression facilitates the deposition of the iron–sulfur (Fe–S) cluster to the DEMETER apoenzyme, which is vital for its interaction with genomic DNA and its subsequent demethylation (Buzas et al. 2014). Given Dre2's role in DEMETER activation, we decided to test its effect on prolamin accumulation. As a first step, the TILLING population in Kronos background was screened for mutations in the wheat *Dre2* homoeologues. Thirteen mutants in the 2AL copy and three mutants in the 2BL copy of the *Dre2* gene were identified. Seed of the selected *Dre2* mutants were obtained from Dr. J. Dubcovsky, University of California, Davis and analyzed for their gluten profiles. The single mutations in the *Dre2* homoeologues showed reductions in specific prolamins (Fig. 3b). These single mutations are currently being crossed in the greenhouse to pyramid their effects. During these attempts, it was continuously noticed that the anther size for the Dre2-2AL mutants was significantly small than the wild type control.

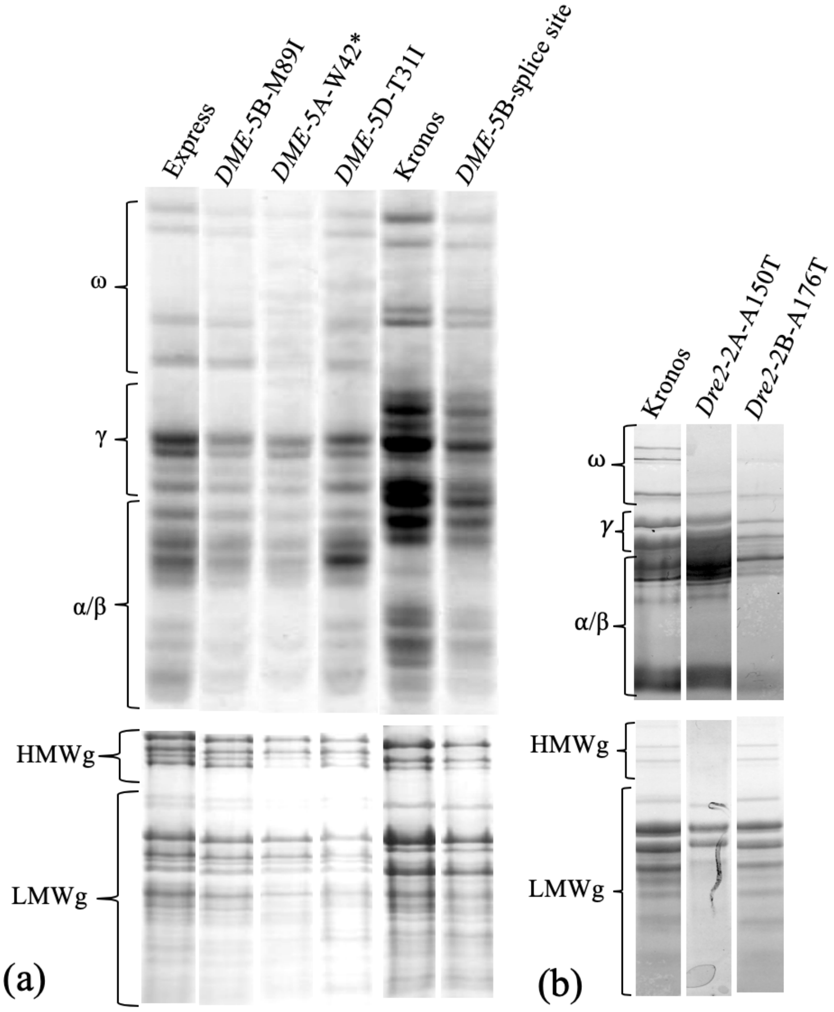

Fig. 3. Acid/SDS–PAGE gel analysis of gluten proteins derived from TILLING mutants of wheat *DEMETER* (a) and *Dre2* (b) genes in the background of common wheat cultivar Express and durum wheat cultivar Kronos. The type of mutation and the homeologous copy of the gene it exists is mentioned over each lane.

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References.

Brouns F, Van Rooy G, Shewry P, Rustgi S, and Jonkers D. 2019. Adverse reactions to wheat or wheat components. Comp Rev Food Sci Food Saf **18**:1437-1452.

Buzas DM, Nakamura M, and Kinoshita T. 2014. Epigenetic role for the conserved Fe-S cluster biogenesis protein AtDRE2 in *Arabidopsis thaliana*. Proc Natl Acad Sci USA **111**:13565-13570.

Kashyap S. 2020. Development of reduced immunogenicity wheat lines using molecular plant breeding approaches. Clemson University Master's Thesis.

Osorio C, Wen N, Gemini R, Zemetra R, von Wettstein D, and Rustgi S. 2012. Targeted modification of wheat grain protein to reduce the content of celiac causing epitopes. Funct Integr Genomics **12**:417-438.

Osorio CE, Wen N, Mejias JH, Liu B, Reinbothe S, von Wettstein D, and Rustgi S. 2019. Development of wheat genotypes expressing a glutamine-specific endoprotease from barley and a prolyl endopeptidase from *Flavobacterium meningosepticum* or *Pyrococcus furiosus* as a potential remedy to celiac disease. Funct Integr Genomics **19**:123-136.

Rustgi S, Kashyap S, Ankrah N, and von Wettstein D. 2020b. Use of microspore-derived calli as explants for biolistic transformation of common wheat. *In:* Biolistic DNA Delivery in Plants (Rustgi S and Luo H, Eds), Springer Nature, New York, NY. Pp 263-279.

Rustgi S, Shewry P, and Brouns F. 2020a. Health hazards associated with gluten consumption in susceptible individuals and current status of research on the dietary therapies. *In:* Wheat Quality for Improving Processing and Human Health (Igrejas G, Ikeda TM, and Guzmán C, Eds). Springer, Cham. Pp. 471-515.

Rustgi S, Shewry P, Brouns F, Deleu L, and Delcour JA. 2019. Wheat seed proteins - factors influencing their content, composition, and technological properties, and strategies to reduce adverse reactions. Comp Rev Food Sci Food Saf **18**:1751-1769.

Rustgi S, Wen N, Osorio C, Brew-Appiah RAT, Wen S, Gemini R, Mejias JH, Ankrah N, Moehs CP, and von Wettstein D. 2014. Natural dietary therapies for the 'gluten syndrome', 1st edition, The Royal Danish Academy of Sciences and Letters, Copenhagen, Denmark.

Sapone A, Bai JC, Ciacci C, Dolinsek J, Green PH, Hadjivassiliou M, Kaukinen K, Rostami K, Sanders DS, Schumann M, Ullrich R, Villalta D, Volta U, Catassi C, and Fasano A. 2012. Spectrum of gluten-related disorders: consensus on new nomenclature and classification. BMC Med **10**:13.

Wen S, Wen N, Pang J, Langen G, Brew-Appiah RAT, Mejias JH, Osorio C, Yang MM, Gemini R, Moehs CP, Zemetra RS, Kogel KH, Liu B, Wang X, von Wettstein D, and Rustgi S. 2012. Structural genes of wheat and barley 5-methylcytosine DNA glycosylases and their potential applications for human health. Proc Natl Acad Sci USA **109**:20543-20548.

Publications.

Alam T, Anco DJ, and Rustgi S. 2020. Management of aflatoxins in peanuts. Clemson University Land-Grant Press LGP 1073 [https://lgpress.clemson.edu/publication/management-of-aflatoxins-in-peanut/].

Brouns F, Van Rooy G, Shewry P, Rustgi S, and Jonkers D. 2019. Adverse reactions to wheat or wheat components. Comp Rev Food Sci Food Saf **18**:1437-1452.

Cong X, Miao Y, Xu L, Zhang Y, Yuan C, Wang J, Zhuang T, Lin X, Jiang L, Wang N, Ma J, Sanguinet KA, Liu B, Rustgi S, and Ou X. 2019. Transgenerational memory of gene expression changes induced by heavy metal stress in rice (*Oryza sativa* L.). BMC Plant Biol **19**:282.

Gandhi N, Kashyap S, Rawlins S, Kerr R, Hoover G, Campbell BT, Jones M, and Rustgi S. 2019. Breeding cotton for annual growth habit: Increasing cotton fiber yield by remobilization of reserves. *In:* 116th Annual Meeting of The Southern Association of Agricultural Scientists Biochemistry and Biotechnology Division, Birmingham, Al (4 February, 2019).

Kashyap S. 2020. Development of reduced immunogenicity wheat lines using molecular plant breeding approaches. Clemson University Master's Thesis.

Kashyap S, Gandhi N, Elkins A, Yang M, and Rustgi S. 2019. Novel Reduced-immunogenicity wheat for celiac patients. *In:* 1st International Wheat Congress, Saskatoon, Canada (21-26 July, 2019).

Narayanan S, Rustgi S, Zoong-Lwe ZS, and Welti R. 2019. Lipid metabolic changes contribute to heat tolerance in soybean. *In:* Annual meeting of the Crop Science Society of America, San Antonio, Texas (10-13 November, 2019).

Narayanan S, Zoong-Lwe ZS, Gandhi N, Welti R, Fallen B, Smith JR, and Rustgi S. 2020. Comparative lipidomic analysis reveals heat stress responses of two soybean genotypes differing in temperature sensitivity. Plants **9**:457.

Osorio CE, Mejias JH, and Rustgi S. 2019. Gluten detection methods and their critical role in assuring safe diets for celiac patients. Nutrients **11**:2920.

Osorio CE, Wen N, Mejias JH, Liu B, Reinbothe S, von Wettstein D, and Rustgi S. 2019. Development of wheat genotypes expressing a glutamine-specific endoprotease from barley and a prolyl endopeptidase from *Flavobacterium meningosepticum* or *Pyrococcus furiosus* as a potential remedy to celiac disease. Funct Integr Genomics **19**:123-136.

Osorio CE, Wen N, Mejias JH, Mitchell S, von Wettstein D, and Rustgi S. 2020. Directed-mutagenesis of Flavobacterium meningosepticum prolyl-oligopeptidase and a glutamine-specific endopeptidase from barley. Front Nutr **7**:11.

Pollmann S, Springer A, Rustgi S, von Wettstein D, Kang C, Reinbothe C, and Reinbothe S. 2019. Substrate channeling in oxylipin biosynthesis through a protein complex in the plastid envelope of *Arabidopsis thaliana*. J Exp Bot **70**:1483-1495.

Rustgi S, and Luo H. 2020. Biolistic DNA delivery in plants. Springer Nature, New York, NY. Pp. 334.

Rustgi S, and Skadhauge B. 2020. Diter von Wettstein, Professor of genetics and master of translating science into applications. *In:* Biolistic DNA Delivery in Plants (Rustgi S and Luo H, Eds.). Springer Nature, New York, NY. Pp. 3-18.

Rustgi S, Brouwer B, von Wettstein D, Reisenauer PE, Lyon S, Ankrah N, Jones S, Guy SO, and Chen X. 2020. Registration of 'Fritz', a two-row spring barley. J Plant Register DOI: 10.1002/plr2.20046.

Rustgi S, Gasic K, and Schnabel G. 2019. Eco-friendly treatment for pre and postharvest issues in peach production. *In:* Annual Peach research report for 2018 (Schnabel G, Ed). **XVIII**:66-81.

Rustgi S, Gasic K, and Schnabel G. 2020. Eco-friendly treatment for pre and postharvest issues in peach production. *In:* Annual Peach Research Report for 2019 (Schnabel G, Ed.). **XIX**:61-63.

Rustgi S, Kashyap S, and von Wettstein D. 2019. Tailoring non-immunogenic wheat genotypes for gluten-sensitive individuals. *In:* 1st International Wheat Congress, Saskatoon, Canada (21-26 July, 2019).

Rustgi S, Kashyap S, Ankrah N, and von Wettstein D. 2020. Use of microspore-derived calli as explants for biolistic transformation of common wheat. *In:* Biolistic DNA Delivery in Plants (Rustgi S and Luo H, Eds). Springer Nature, New York, NY. Pp 263-279.

Rustgi S, Kashyap S, Deleu LJ, and Delcour J. 2020. Reduced-immunogenicity wheat now coming to age. *In:* Physiological, Molecular, and Genetic perspectives of Wheat Improvement (Wani SH, Mohan A, and Singh GP, Eds). Springer Nature (in press).

Rustgi S, Kashyap S, Gandhi N, Naveed S, Windham J, Yang M, Gemini R, and Reisenauer P. 2019. A creative solution to gluten-induced disorders using a unique combination of multigene editing and nanoparticle-based gene-delivery. Ann Wheat Newslet **65**:79-84.

Rustgi S, Saski C, and Gasic K. 2020. Genome editing in peach. *In:* Annual Peach research report for 2019 (Schnabel G Ed). **XIX**: 64-77.

Rustgi S, Shewry P, and Brouns F. 2020. Health hazards associated with gluten consumption in susceptible individuals and current status of research on the dietary therapies. *In:* Wheat Quality for Improving Processing and Human Health (Igrejas G, Ikeda TM, and Guzmán C, Eds). Springer, Cham. Pp. 471-515.

Rustgi S, Shewry P, Brouns F, Deleu L, and Delcour JA. 2019. Wheat seed proteins - factors influencing their content, composition, and technological properties, and strategies to reduce adverse reactions. Comp Rev Food Sci Food Saf **18**:1751-1769.

Rustgi S, Springer A, Kang C, von Wettstein D, Reinbothe C, Reinbothe S, and Pollmann S. 2019. Two non-canonical cytochrome P450s in *Arabidopsis thaliana* and their different roles in plant defense. Internat J Mol Sci **20**:3064.

Rustgi S. 2019. Talking CRISPR & NBTs with Dr. Sachin Rustgi. https://crispr-agbio.com/about/media-hub/

Windham J, Sharma S, Kashyap MK, and Rustgi S. 2020. CRISPR/Cas12a (Cpf1) and its role in plant genome editing. *In:* RNA-based Technologies for Functional Genomics in Plants (Tang G, Teotia S, Tang X, and Singh D, Eds). Springer Nature (in press).

Windham J. 2020. Site-directed mutagenesis in peach (*Prunus persica*) via CRISPR-Cas12a. Clemson University Master's Thesis.

Yang M, Liu Y, Dong J, Zhao W, Kashyap S, Gao X, Rustgi S, and Wen S. 2020. Probing early wheat grain development via transcriptomic and proteomic approaches. Funct Integr Genomics **20**:63-74.

SOUTH DAKOTA

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Sunish Sehgal.

The South Dakota Wheat Commission (SDWC) has a long-standing partnership with South Dakota State University, providing a large portion of wheat checkoff funds to the SDSU winter and spring wheat breeding and cultivar development programs. This cooperation is truly a great example of achieving common goals of developing wheat cultivars that meet the needs of South Dakota producers, the food industry, and the consumer demands. The SDSU wheat breeding programs have been continuously working to provide producers in the northern Great Plains an opportunity, to select from a group of superior winter wheat cultivars that have great agronomics, a good disease package, and marketability.

Breeding and cultivar development is a slow and long-term effort that takes 10–12 years from crossing date to release of a new cultivar. This involves years of selection for agronomic traits and disease and pest resistance, followed by intensive yield trials by the breeder at 8–9 locations. The SDSU Crop Performance Testing (CPT) further evaluates the yield potential and quality characteristics of the new experimental breeding lines along with 20–25 commercially released wheat cultivars at about 15 locations throughout South Dakota. Data collected includes grain yield, protein content, disease resistance, response to fungicides, heading, plant height, straw strength, and milling and baking characteristics. Finally, if the experimental line is superior to the check commercial varieties and if better adapted to the state or region, it is released as a new variety after intensive testing for about three years under CPT trials and a seed production increase during that last year prior to release.

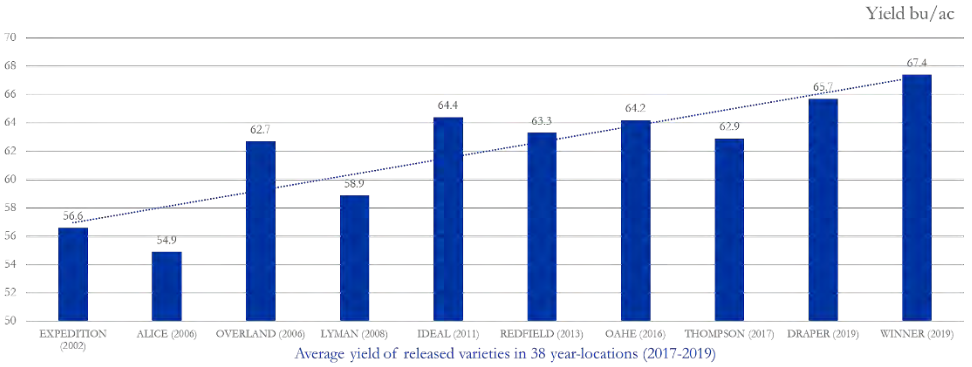

Fig. 1. Winter wheat cultivars released from the South Dakota public wheat breeding program with support from the South Dakota wheat check off.

In the last 17 years, the SDWC investment had led to the release of 10 winter wheat cultivars, including two new hard red winter wheat cultivars **Winner** and **Draper**, released in autumn 2019 for certified seed growers (Fig. 1). Release of new cultivars such as Winner (released 2019) offers producers approximate 11-bushel advantage when compared to Expedition (released in 2002). This increase in yield potential can result in an increased revenue of $40/acre for the producers when compared to Expedition, demonstrating the economic impact of variety development.

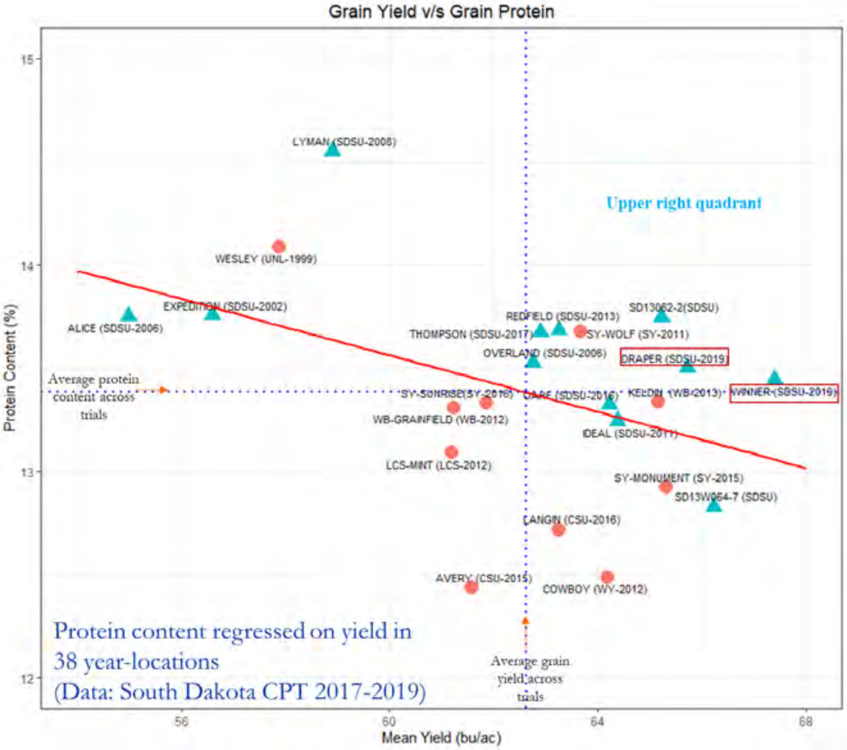

Fig. 2. The grain yield and grain protein content in commercial wheat cultivars evaluated in the South Dakota Crop Performance Test (CPT) for three years (2017–19). The green triangles show SDSU winter wheat cultivars and red dots indicate other commercial cultivars.

In addition to yield, the SDSU winter wheat cultivars offer good end-use quality and marketability (Fig. 2). Of course, the credit goes to the South Dakota wheat producer for excellent management of the wheat crop as the variability in protein among environments is generally much larger than variability among cultivars. However, the inherent protein content of the cultivar also plays a crucial role in determining the bread-baking quality and marketability of wheat. In order to maximize economic return, a producer would like to select a cultivar that maximizes grain yield and grain protein. However, grain yield and grain protein have a widely known inverse relationship, the higher-yielding cultivars produce more kernels and, thus, each kernel proportionally has less protein. The producer should pick higher-yielding cultivars that have comparatively higher protein (the cultivars above the trend line in Fig. 2, p. 99). The newly released hard red winter wheat cultivars Winner and Draper are very competitive and shows a good yield potential while maintaining a good grain protein content. The two new cultivars also showed above average to good baking quality in wheat quality council test.

The cultivars in the upper right quadrant show both above average grain yield and protein content. Cultivars above the trend line show a positive deviation for protein content at that yield and must be preferred (Table 1).

Other characteristics of Winner and Draper include medium height, medium-early heading, good straw strength, and a moderate disease resistance package.

Table1. Grain protein deviation (GPD) scores (1 = good to 9 = poor) of cultivars tested in the 2017–19 SDSU Crop Performance and Testing cultivar trials across 38 year-locations (2017–19).

High positive grain protein deviation (1–3)		Medium grain protein deviation (4–6)		High negative grain protein deviation (7–9)	
Winner	1	Keldin	4	Langin	7
Draper	1	Overland	4	SD13W064-7	7
Lyman	1	Oahe	4	Cowboy	7
Wesley	1	Ideal	4	Avery	8
SD13062-2	1	SY Sunrise	5		
SY Wolf	2	Expedition	5		
Thompson	2	WB Grainfield	5		
Redfield	2	Alice	5		
		LCS Mint	6		
		SY Monument	6		

New cultivars.

Winner (HRW-2019). Winner hard red winter wheat has excellent yield potential with good baking quality, disease resistance and straw strength package and is better suited for good-moisture environments. Winner was developed from the cross 'T154/SD07165' and has a medium height and medium maturity, similar to that of Lyman, and good winter hardiness and straw strength. Winner has demonstrated an excellent yield potential in the 2017 (2nd), 2018 (4th), and 2019 (4th) USDA Northern Regional Performance Nurseries, demonstrating broad adaptation. Winner also topped South Dakota Crop Performance Trials in central South Dakota and did well in both the eastern and western South Dakota trial locations over last three years. Winner has avreage test weight and protein concentration but good milling and baking chracteristics. Winner is moderately resistant to stem rust and intermediate reaction to stripe, leaf rust, and Fusarium head blight.

Draper (HRW-2019). Draper was developed from the cross 'T154/SD06069' and has medium height and medium maturity, similar to that of Wesley, and has very good winter hardiness and straw strength. Draper has demonstrated an excellent yield potential (ranked 2nd) in the 2018 and 2019 USDA Northern Regional Performance Nurseries. In the South Dakota Crop Performance Trials across 41 environments over three years, Draper ranked 3rd in central SD and 1st in western SD locations. This cultivar has moderate test weight and protein concentration. Draper is moderately resistant to resistant to soil-borne mosaic virus and shows an intermediate response to Fusarium head blight, and stripe and leaf rust. Marker data indicated it possibly has *Lr46*, however, gene postulation has suggested *Lr14a*. Draper as acceptable milling and baking characteristics. Draper is better suited in dry conditions having strong drought tolerance. Therefore, it is well-adapted for western South Dakota.

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New Small Grains Breeder at Virginia Tech.

After more than 31 years of service at Virginia Tech, Dr. Carl A. Griffey will retire at the end of 2020. We are very excited to announce that Dr. Nicholas Santantonio (nsant@vt.edu), Ph.D. at Cornell University, will join Virginia Tech as the new Small Grains Breeder August 2020.

2019 Wheat production in the Commonwealth of Virginia.

Growing season. A wet autumn in 2018 resulted in some small grain acres not planted, but those acres that were seeded were mostly planted on time, with 44% of wheat acres seeded by 21 October and and 66% by 11 November. These proportions mirrored the 5-year average for planting progress. December and January were drier with variable but seasonal temperatures. Due to later planting of some wheat acres and wet soils, only 61% of the small grain crop was rated as good or excellent in January. Significant statewide precipitation in February resulted in a decline in small grain ratings with only 43% of the crop rated good or excellent (Figs. 1 and 2). Over 80% of acres were reported to have excess topsoil moisture. By 31 March, only 15% of acres were reported to have excess topsoil moisture, and 55% of the wheat crop was rated as good or excellent. Favorable weather continued through most of April and resulted in 9% of the wheat crop headed by 21 April, compared with a 5-year average of 12%. By 6 May, half the wheat crop was headed, which was very near the 5-year average but well below the 78% headed mark reported by this date in 2018. Rain in early June hampered some harvesting efforts, but farmers were still able to harvest 11% of the crop by 10 June. Farmers pushed to harvest fields

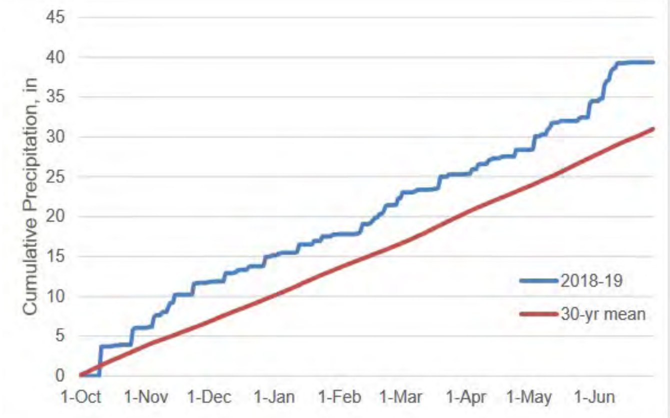

Fig. 1. 2018–19 and 30-yr mean cumulative growing season.

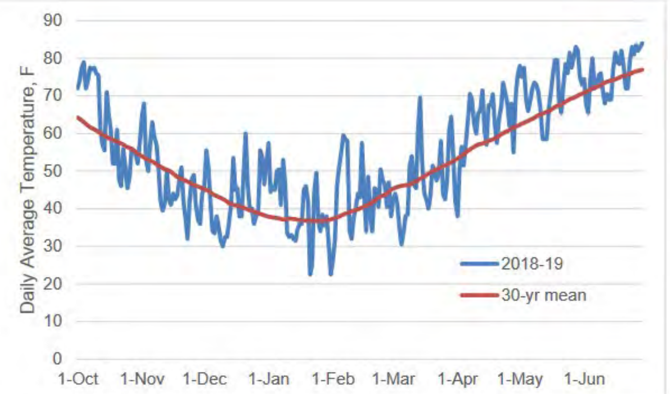

Fig. 2. Growing season daily average temperature, 2018–19 and 30-yr mean.

as quickly as possible but continued periods of heavy rain in mid and late June resulted in delays and declining grain quality.

Production. Because of unplanted acres and wet, unfavorable conditions through much of the winter, the Virginia wheat crop was expected to produce only 7.6 x 10^6 bu, an 18% reduction from 2018 production. Yields were estimated at 66 bu/acre, up 6 bu/acre from 2018 and up 4 bu from May. Virginia farmers planted a total of 180,000 acres in autumn of 2018 with 115,000 acres intended to be harvested for grain. The remaining 65,000 acres were planted as cover crop or to be cut as silage or hay.

Disease incidence and severity. Several wheat diseases were prevalent across the Commonwealth of Virginia in 2019; however, stripe rust was not found at any of the six state wheat testing sites. Low to moderate levels of leaf rust, rated on a 0 (no disease) to 9 (severe disease) scale, were noted in the state wheat trial on the Eastern Shore (0–5, mean of 0.4) in Accomack County, while significant levels (1–9, mean of 3.4) of leaf rust were noted in the trial conducted at Blacksburg (Montgomery County) in southwestern Virginia. Leaf rust samples from wheat trials conducted in these two counties were sent to Dr. James Kolmer at the USDA–ARS Cereal Disease Lab for race identification. Races MBTNB (virulence for genes *Lr1, 3, 3ka, 11, 17, 30, B,* and *14a*) and MCTNB (virulence for genes *Lr1, 3, 26, 3ka, 11, 17, 30, B,* and *14a*) were identified in both Accomack and Montgomery counties, whereas race TBTNB (virulence for genes *Lr1, 2a, 2c, 3, 3ka, 11, 17, 30, B,* and *14a*) was identified only in Accomack County. Powdery mildew was low to moderate (0–4, mean of 0.5), and only rated in the Eastern Shore trial. *Barley yellow dwarf virus* infection was low to moderate (1–4, mean of 2.0) in the Southern Piedmont trial near Blackstone, VA.

State cultivar tests. The Virginia 2018–19 soft red winter wheat Official Variety Trial included 148 entries that were planted no-till at the Tidewater test site at 48 seeds per square foot. Tests in the southwestern and northeastern regions, Eastern Shore, and southern and northern Piedmont regions were planted conventional-till at 44 seed/ft^2. A period of unseasonably hotter than normal temperatures during later grain-fill stages followed by frequent rain showers following physiological maturity at some locations resulted in swelling and exposure of grain in the spikes and subsequent pre-harvest sprouting in some lines. Delayed harvest due to rain at some locations resulted in significant reductions in grain volume weight and quality. Mean grain yields at six test sites varied from 43.5 bu/acre (2,923 kg/ha) in the southeastern Tidewater region to 105.9 bu/ac (7,116 kg/ha) in the northern Piedmont. Over the six test sites, 30 entries produced mean grain yields that were significantly ($P < 0.05$) higher than the overall trial average of 83.4 bu/acre (5,604 kg/ha). The highest yielding entry (SY Viper) had an overall mean yield of 92.6 bu/acre (6,223 kg/ha). Twelve other entries, including Pioneer Brand 26R59, USG 3316, SY 100, SY Richie, USG 3790, Warrior, and six experimental lines had overall mean grain yields that did not differ significantly from the top yielding line. Mean test weights of the 148 entries varied from 56.2 lb/bu (74.0 kg/hl) at the southern Piedmont test site to 59.3 lb/bu (78.0 kg/hl) at the northern Piedmont site with an over location mean test weight of 57.7 lb/bu (76.0 kg/hl). The entry having the highest overall test weight (61.3 lb/bu, 80.6 kg/hl) was DH13SRW023-201, which was approved for release in 2020.

Newly released cultivars. Three soft red winter wheat cultivars, including **Liberty 5658** (DH12SRW056-058), **Laverne** (VA09MAS2-131-6-2), and **Featherstone 125** (VA09MAS1-12-5-1-1), and one hard red winter wheat **Hardy 2519** (VA14HRW-25) were released by the Virginia Agricultural Experiment Station in May 2019.

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

Table 1. Results of the Virginia Wheat Yield Contest for soft (SRW) and hard (HRW) red winter wheat.

Rank	Wheat class	Grower	Farm	County	Yield (bu/acre)	Yield (kg/ha)
1	SRW	Justin Welch	Welch Farms Inc.	Northumberland	109.8	7,379
2	SRW	Alan Welch	Welch Farms Inc.	Northumberland	108.6	7,298
1	HRW	Josh Long	Brann and Long Farms	Montgomery	80.6	5,416
2	HRW	Dan Brann	Brann Farms	Montgomery	79.4	5,336
3	HRW	Robert Pollok	Hill View Farm	Pittsylvania	72.7	4,885
4	HRW	Katie Myer	Laurel Springs Grains	Richmond	72.1	4,845

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

Joseph Oakes (Eastern Virginia Agricultural Research and Extension Center), and Maria Balota, Wade Thomason, Alexandre-Brice Cazenave, and Sayantan Sarkar (Virginia Tech).

Optimum wheat yields require high tiller density and adequate nitrogen (N) throughout the growing season. Often the decision of whether to apply N at GS 25 is based on the number of tillers present at a particular growth stage. However, applying N based on tiller density is often not utilized by growers due to the time involved and field variability. UAVs give us the ability to fly a field with a sensor and determine the crop's nutrition status. Our objectives to 1) identify aerial indices that are best correlated with tiller density and 2) determine a threshold for whether or not to apply N at GS 25 with aerial indices examined. Plots were grown at Warsaw, VA, in 2020 to examine these two objectives. In previous years, we exclusively examined the relationship between tiller density and aerial indices throughout the growing season. We used this season's data to fine-tune the tiller density/aerial index relationship; we also focused on using the aerial indices as a basis of when to apply N. We found a positive, significant relationship between aerial indices and tiller density in 2019 (Figs. 3 and 4). Two aerial indices were examined: normalized difference vegetative index (NDVI) and normalized difference red edge (NDRE). Nitrogen was applied to plots at GS 25 based on tiller density and aerial indices. Plots that had 50 or more tillers/ft^2 did not receive any nitrogen at GS 25, whereas those with less than 50 tillers did. Based on relationship generated from this study the past two years, an NDVI of 0.60 and an NDRE of 0.31 corresponded to 50 tillers/ft^2. Plots with an NDVI greater than 0.60 and an NDRE greater than 0.31 did not receive any nitrogen at GS 25, whereas those with lower values did. At GS 30, N applications were made to bring to 120 total lbs N after planting. The goal is to compare the yields between the tiller and aerial to determine the efficacy of applying N based on aerial indices. Yields will be analyzed and compared after harvest.

Acknowledgements. We would like to thank the Delmarva Cooperative Seed Grant and the Virginia Small Grains Board for their funding of this research.

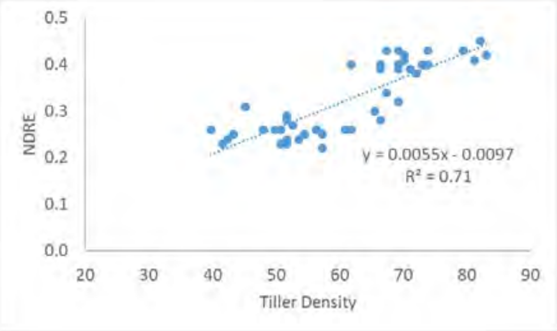

Fig. 3. Relationship between winter wheat tiller density and NDRE (normalized difference red edge)measurements collected with a MicaSense RedEdge multispectral sensor at GS 25 in Warsaw, VA.

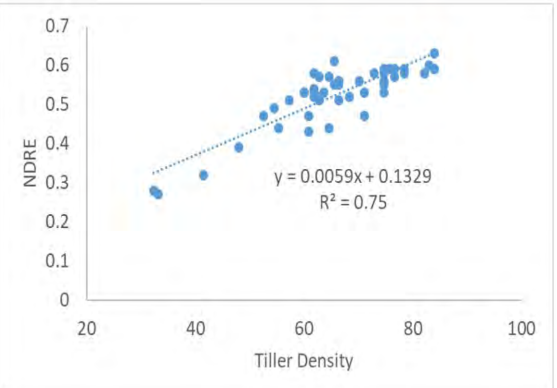

Fig. 4. Relationship between winter wheat tiller density and normalized difference red edge (NDRE) measurements collected with a MicaSense RedEdge multispectral sensor at GS 30 in Warsaw, VA.

Integrated disease management for soft red winter wheat in Virginia.

Navjot Kaur (PhD student) and Hillary Mehl.

Wheat disease management research conducted in Virginia in 2019 included 1) assessment of flag leaf and flowering applications of commercial standards for control of foliar and head diseases, 2) evaluation of different fungicide application timings for control of Fusarium head blight (FHB), and 3) quantification of the integrated effects of fungicide treatment and genetic resistance on FHB severity and deoxynivalenol (DON) contamination, with emphasis on a new fungicide, Miravis Ace. Experiments were conducted at the Tidewater Agricultural Research and Extension Center in Suffok, VA, and the diseases observed were Stagonospora nodorum leaf blotch, powdery mildew, FHB, and trace amounts of leaf rust. For leaf blotch, fungicide applications at flowering generally reduced disease severity more than flag leaf applications. Trivapro, Priaxor +Tilt, and Tilt applied at the flag leaf stage provided the greatest control of powdery mildew. Prosaro, Caramba, and Miravis Ace applied at flowering provided similar levels of FHB and DON control, and flowering applications were more effective than heading applications for all fungicides tested. Integrated disease management experiments demonstrated that high-yielding wheat cultivars with moderate FHB resistance have greater yields, less disease, and lower concentrations of DON in harvested grain compared to susceptible varieties regardless of fungicide program.

Publications.

Brasier K, Oakes J, Balota M, Reiter M, Jones N, Pitman R, Sneller C, Thomason W, and Griffey C. 2019. Genotypic variation and stability for nitrogen use efficiency in winter wheat. Crop Sci **60**:32-49 [doi.org/10.1002/csc2.20006].

Brasier K, Ward B, Smith J, Seago J, Oakes J, Balota M, Davis P, Fountain M, Brown-Guedira G, Sneller C, Thomason W, and Griffey C. 2020. Identification of quantitative trait loci associated with nitrogen use efficiency in winter wheat. PloS One **15**(2):p.e0228775.

Kaur N, Byrd-Masters L, and Mehl HL. 2020. Evaluation of the integrated effects of fungicide treatment and genetic resistance on FHB and DON, with emphasis on a new fungicide, Miravis Ace in wheat in Virginia, 2019. Plant Dis Manag Rep.

Kaur N, Byrd-Masters L and Mehl HL. 2020. Comparison of the efficacy of Miravis Ace when applied at heading or at anthesis to that of standard anthesis application of Prosaro or Caramba to control scab in wheat in Virginia, 2019. Plant Dis Manag Rep.

Kaur N, Byrd-Masters L and Mehl HL. 2020. Comparison of flag leaf and flowering applications of commercial standards for foliar diseases of wheat in Virginia, 2019. Plant Dis Manag Rep.

Kaur N, Byrd-Masters L, and Mehl HL. 2020. Comparison of flag leaf and flowering fungicide applications for control of scab and foliar diseases of wheat in Virginia, 2019. Plant Dis Manag Rep.

Liu L, Barnett MD, Griffey CA, Malla S, Brooks WS, Seago JE, Fitzgerald J, Thomason WE, Rucker EG, Behl HD, et al. 2019. Registration of 'Vision 50' Wheat. J Plant Reg **13**(2):193-198.

Pittman KB, Barney JN, Cahoon CW, and Flessner ML. 2019. Influence of hairy vetch seed germination and maturation on weediness in subsequent crops. Weed Res **59**:427-436 [doi: 10.1111/wre.12380].

Santantonio N, Jannink J-L, and Sorrells M. 2019. Homeologous epistasis in wheat: the search for an immortal hybrid. Genetics **211**(3):1105-1122 [doi.org/10.1534/genetics.118.301851].

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Craig F. Morris, Douglas A. Engle, Mary Baldridge, Gail Peden, William Kelley, Shelle Lenssen, Eric Wegner, Alecia Kiszonas, Shawna Vogl, Janet Luna, Stacey Sykes, Robin Saam, Eden Stout, Deidrea Power, Galina Mikhaylenko, Kelly Leonard, Susan Conrad, Yvonne Thompson, Carlos Munoz, Melissa Rauch, Ujwala Ganjyal, and Nate Ovetz.

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

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

Publications.

Delwiche SR, Morris CF, and Kiszonas AM. 2020. Compressive strength of Super Soft wheat endosperm. J Cereal Sci **91**:102894.

Geng HW, Shi J, Fuerst EP, Wei J, and Morris CF. 2019. Physical mapping of peroxidase genes and development of functional markers for *TaPod-D1* on bread wheat chromosome 7D. Front Plant Sci **10**:523.

Ibba MI, Kiszonas AM, See DR, Skinner DZ, and Morris CF. 2019. Mapping kernel texture in a soft durum (*Triticum turgidum* subsp. *durum*) wheat population. J Cereal Sci **85**:20-26.

Ibba MI, Zhang M, Cai X, and Morris CF. 2019. Identification of a conserved *ph1b*-mediated 5DS-5BS crossing over site in soft-kernel durum wheat (*Triticum turgidum* subsp. *durum*) lines. Euphytica **215**:200.

Kiszonas AM, Higginbotham R, Chen XM, Garland-Campbell K, Bosque-Perez NA, Pumphrey M, Rouse MN, Hole D, Wen N, and Morris CF. 2019. Agronomic traits in durum wheat germplasm possessing puroindoline genes. Agron J **111**:1254-1265.

Kumar N, Kiszonas AM, Ibba MI, and Morris CF. 2019. Identification of loci and molecular markers associated with Super Soft kernel texture in wheat. J Cereal Sci **87**:286-291.

Kumar N, Orenday-Ortiz JM, Kiszonas AM, Boehm Jr, JD, and Morris CF. 2019. Genetic analysis of a unique 'super soft' kernel texture phenotype in soft white spring wheat. J Cereal Sci **85**:162-167.

Morris CF. 2019. The antimicrobial properties of the puroindolines, a review. World J Microbio Biotech **35**:86.

Morris CF. 2019. Development of soft kernel durum wheat. Front Agric Sci Eng **6**:273-278.

Morris CF and Kiszonas AM. 2019. NOTE: A device for the efficient detection of wheat seeds with waxy endosperm. Cereal Chem **96**:797-801.

Morris CF, Kiszonas AM, and Peden GL. 2020. Registration of extra-hard kernel near-isogenic hexaploid wheat genetic stocks lacking puroindoline genes. J Plant Reg **14**:92-95.

Zhan S, Ren Y, Liu J, Fuerst EP, Xia X, Lv W, Morris CF, and Geng HW. 2019. Genome-wide association study of feruloyl arabinoxylan content in common wheat grain. J Cereal Sci **89**:102787.

IV. CULTIVARS AND GERMPLASM

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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
690713	*Aegilops tauschii*	AUS22980	Australia	New South Wales
690717 PVP	*Triticum aestivum* subsp. *aestivum*	KWS060	Germany	
690718 PVP	*Triticum aestivum* subsp. *aestivum*	112383W	Germany	
690719 PVP	*Triticum aestivum* subsp. *aestivum*	112382W	Germany	
690720 PVP	*Triticum aestivum* subsp. *aestivum*	KWS147	Germany	
690766 PVP	*Triticum aestivum* subsp. *aestivum*	TCG-Glennville	United States	North Dakota
691501	*Triticum aestivum* subsp. *aestivum*	UI Bronze Jade	United States	Idaho
691531 PVP	*X Triticosecale spp*.	343CMS	United States	Texas
691547 PVP	*Triticum aestivum* subsp. *aestivum*	SY Wolverine	United States	Iowa
691548 PVP	*Triticum aestivum* subsp. *aestivum*	SY 576	United States	Iowa
691549 PVP	*Triticum aestivum* subsp. *aestivum*	SY Richie	United States	Iowa
691550 PVP	*Triticum aestivum* subsp. *aestivum*	AP Venom	United States	Iowa
691551 PVP	*Triticum aestivum* subsp. *aestivum*	AP Octane	United States	Iowa
691552 PVP	*Triticum aestivum* subsp. *aestivum*	AP Redeye	United States	Iowa
691553 PVP	*Triticum aestivum* subsp. *aestivum*	Rock Star	United States	Iowa
691554 PVP	*Triticum aestivum* subsp. *aestivum*	AP Coachman	United States	Iowa
691555 PVP	*Triticum aestivum* subsp. *aestivum*	AP Kimber CL2	United States	Iowa
691556 PVP	*Triticum aestivum* subsp. *aestivum*	AP Mondaci CL2	United States	Iowa
691557 PVP	*Triticum aestivum* subsp. *aestivum*	Stingray CL+	United States	Washington
691558 PVP	*Triticum aestivum* subsp. *aestivum*	Purl	United States	Washington
691600 PVP	*Triticum aestivum* subsp. *aestivum*	Crescent AX	United States	Colorado
691601 PVP	*Triticum aestivum* subsp. *aestivum*	Battle AX	United States	Colorado
691602 PVP	*Triticum aestivum* subsp. *aestivum*	Canvas	United States	Colorado
691603 PVP	*Triticum aestivum* subsp. *aestivum*	Whistler	United States	Colorado
691604 PVP	*Triticum aestivum* subsp. *aestivum*	Byrd CL Plus	United States	Colorado
691605 PVP	*Triticum aestivum* subsp. *aestivum*	Snowmass 2.0	United States	Colorado
691606 PVP	*Triticum aestivum* subsp. *aestivum*	Monarch	United States	Colorado
691609 JPR	*Triticum aestivum* subsp. *aestivum*	WQL 18RE5	United States	Washington
691610 JPR	*Triticum aestivum* subsp. *aestivum*	WQL 18CS5	United States	Washington
691656 JPR	*Triticum aestivum* subsp. *aestivum*	VA11DH-P46xTrib-28	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
691657 JPR	*Triticum aestivum* subsp. *aestivum*	VA11DH-P46xTrib-99	United States	Virginia
691658 JPR	*Triticum aestivum* subsp. *aestivum*	VA11DH-P46xTrib-103	United States	Virginia
691746	*Triticum aestivum* subsp. *aestivum*	Skagit 1103-8	United States	Washington
691747	*Triticum aestivum* subsp. *aestivum*	Skagit 1113-3	United States	Washington
691748	*Triticum aestivum* subsp. *aestivum*	Skagit 1112-17	United States	Washington
691749	*Triticum aestivum* subsp. *aestivum*	WA007976	United States	Washington
691750	*Triticum aestivum* subsp. *aestivum*	WA007977	United States	Washington
691751	*Triticum aestivum* subsp. *aestivum*	WA008068	United States	Washington
691832 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Photon AX	United States	Colorado
691833 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Shine	United States	Colorado
691834 PVP	*Triticum aestivum* subsp. *aestivum*	LCS Ghost	United States	Colorado
691847 JPR	*Triticum aestivum*	WQL19WX7A	United States	Washington
691848 JPR	*Triticum aestivum*	WQL19WX4A	United States	Washington
691849 JPR	*Triticum aestivum*	WQL19WX7D	United States	Washington
691850 JPR	*Triticum aestivum*	WQL19WX7A.A4	United States	Washington
691851 JPR	*Triticum aestivum*	WQL19WX7A.7D	United States	Washington
691852 JPR	*Triticum aestivum*	WQL19WX4A.7D	United States	Washington
691978 PVP	*Triticum aestivum* subsp. *aestivum*	AAC Wildfire	Canada	Ontario
691979 PVP	*Triticum aestivum* subsp. *aestivum*	UC-Amarillo	United States	California
691981 PVP	*Triticum spp*.	WB4394	United States	Minnesota
691982 PVP	*Triticum spp*.	WB4595	United States	Minnesota
691983 PVP	*Triticum spp*.	WB4699	United States	Minnesota
691984 PVP	*Triticum spp*.	WB4792	United States	Minnesota
691985 PVP	*Triticum spp*.	WB7696	United States	Minnesota
691986 PVP	*Triticum spp*.	WB9490	United States	Minnesota
691987 PVP	*Triticum spp*.	WB9699	United States	Minnesota
691988 PVP	*Triticum spp*.	WB9990	United States	Minnesota
692074 PVP	*X Triticosecale spp*.	Nitrous	Canada	Ontario
692126 PVP	*Triticum aestivum*	Whitetail	United States	Michigan
692132 JPR	*Triticum aestivum* subsp. *aestivum*	USDA Lori	United States	Washington
692251	*Triticum turgidum* subsp. *durum*	Kronos EMS mutant T4-0865	United States	California
692252	*Triticum turgidum* subsp. *durum*	Kronos EMS mutant T4-1280	United States	California
692253	*Triticum turgidum* subsp. *durum*	Kronos EMS mutant T4-2197	United States	California
692613 PVP	*Triticum aestivum* subsp. *aestivum*	Hardy 2519	United States	Virginia
692614 PVP	*Triticum aestivum* subsp. *aestivum*	Liberty 5658	United States	Virginia
692615 PVP	*Triticum aestivum* subsp. *aestivum*	Laverne	United States	Virginia
692616 PVP	*Triticum aestivum* subsp. *aestivum*	Featherstone 125	United States	Virginia
692618 PVP	*X Triticosecale spp*.	APB 249	United States	Arizona
692619 PVP	*Triticum aestivum* subsp. *aestivum*	122014W	United States	Iowa
692620 PVP	*Triticum aestivum* subsp. *aestivum*	122013W	United States	Iowa
692944	*Triticum aestivum* subsp. *aestivum*	UI Cookie	United States	Idaho
692956 PVP	*Triticum aestivum*	310R2	United States	Iowa
692957 PVP	*Triticum aestivum*	321R2	United States	Iowa
692958 PVP	*Triticum aestivum*	401W1	United States	Iowa
692959 PVP	*Triticum aestivum*	14006	United States	Iowa
692960 PVP	*Triticum aestivum*	112385W	United States	Iowa
692961 PVP	*Triticum aestivum*	112386W	United States	Iowa

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
692962 PVP	*Triticum aestivum*	16162698	United States	Iowa
692963 PVP	*Triticum aestivum*	16162700	United States	Iowa
692964 PVP	*Triticum aestivum*	16162701	United States	Iowa
692965 PVP	*Triticum aestivum*	16162705	United States	Iowa
692966 PVP	*Triticum aestivum*	16162707	United States	Iowa
692973 JPR	*Triticum aestivum* subsp. *aestivum*	UX1334-4-3	United States	Virginia
692974 JPR	*Triticum aestivum* subsp. *aestivum*	UX1362-6-2	United States	Virginia
692977 JPR	*Triticum aestivum* subsp. *aestivum*	Fahari	United States	Minnesota
692978 JPR	*Triticum aestivum* subsp. *aestivum*	Kulungu	United States	Minnesota
692979 JPR	*Triticum aestivum* subsp. *aestivum*	Ngiri	United States	Minnesota
692980 JPR	*Triticum aestivum* subsp. *aestivum*	Paka	United States	Minnesota
692981 JPR	*Triticum aestivum* subsp. *aestivum*	Pasa	United States	Minnesota
692982 JPR	*Triticum aestivum* subsp. *aestivum*	Popo	United States	Minnesota
692983 JPR	*Triticum aestivum* subsp. *aestivum*	LMPG-6	United States	Minnesota
693154 PVP	*Triticum aestivum*	LCS Ghost	United States	Colorado
693155 PVP	*Triticum aestivum*	LCS Shine	United States	Colorado
693156 PVP	*Triticum aestivum*	LCS Photon AX	United States	Colorado
693157 PVP	*Secale cereal*	ND Gardner	United States	North Dakota
693222 PVP	*Triticum aestivum* subsp. *aestivum*	Siege	United States	Nebraska
693223 PVP	*Triticum aestivum* subsp. *aestivum*	Valiant	United States	Nebraska
693224 PVP	*X Triticosecale spp*.	NT13443	United States	Nebraska
693235 PVP	*Triticum aestivum*	Bobcat	United States	Montana
693236 PVP	*Triticum aestivum*	StandClear CLP	United States	Montana
693237 PVP	*Triticum aestivum*	Flathead	United States	Montana
693269 PVP	*Triticum aestivum* subsp. *aestivum*	GA 08535-15LE29	United States	Georgia

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2020 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, and 2019 also are available at those sites as well as this *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.

Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1. Sphaerococcum

S-D1. 3DS: Add '11415' to the references.

S-D1b. Add syn: *Tasg-D1* {11415}.
v: Add: Nongda 4332 {11415}.
ma: Located between markers *Xgwm341-3DS* and *Xgdm72-3DS* {11415}.
c: The sphaerococcum phenotype is caused by a gain of function mutation in serine/threonine kinase glycogen synthase kinase 3 (STKc_GSK3) that in rice affects the brassinosteroid signaling pathway and grain shape {11415}. There is a Lys286Glu substitution in the ninth exon of *TraesCSD01G137200* {11415}.

11. Boron tolerance

Bo1. Add syn: *Bot-B5b* {11432}.
c: Boron transporter-like gene {M2239}. GenBank KF148625.
Bo1 functions as a boron transporter {11432}.

Bo4 {11432}. *BOT(TP4A-B5C)* {11432}. 4AL {11431}.
v: G61450 {11431}.
Bo4 is a dispersed duplication of *Bo1* {11432}.
Add note following the *Bo4* entry: A homoeologous nomenclature based on annotated boron transporters inferred from the IWGS CS sequence is provided in Extended Data Table 1 in {11432}.

18. Dormancy (seed)

18.3. Pre-harvest sprouting

Annong 0711 (res) / Henong 825 (sus): RIL population. Differences in germination index were attributed to a 33-bp insertion in the promoter (possibly the AP2 binding site) of *TaMFT-3A* in Annong 0711 relative to Henong 825. *TaMFt-3A* encodes a phosphatidyl ethanolamine-binding protein {11410}.

Totoumai (res) / Siyong (sus): RIL population: A QTL on chromosome 4AL was delimited to a 2.9-cM interval flanked by GBS109947 and GBS212432; nine and two SNP were associated with minor QTL on chromosomes 5A and 5B, respectively {11408}.

Add at end of section: A GWAS identified 12 QTL for PBS resistance among which those on chromosomes 3AS and 4AL were most commonly detected {11409}.

29. Glaucousness (Waxiness/Glossiness)

29.1. Genes for glaucousness

Add at the beginning: The *W* loci are complexes of closely linked genes involved in beta-diketone synthesis.

W1. **v:** Bethlehem {11458}. **tv:** Kofa+*Lr19* {11458}.
w1. **su:** Bethlehem CASL*/*T. turgidum* subsp. *dicoccoides* TTD140 2BS(2B) {11458}.
tv: AUS2499 {11458}.
c: *W1* is a highly duplicated, variable gene cluster containing type-III polyploid synthase, hydrolase and cytochrome P450 genes and is homologous to the *Cer-cqu* cluster in barley {11458}.
W3 {11456}. 2BS {M22063}. **v:** Bobwhite {11456}
w3. **v:** Bobwhite Mutant #056 {11456}.
ma: *Xwmc764-2B* – 0.6 cM – *Xwmc770*/*Xgwm148-2B* – 5.5 cM – *W3* {11456}.
W4 {11457}. 3DL {11457}. **dv:** *Aegilops tauschii* KU-2126 {11457}.
w4. **dv:** *Aegilops tauschii* KU-2104 {11457}; KU-2105 {11457}.
ma: *Xgwm645-3DL* – 8.0 cM – *W4* – 8.9 cM – *Xbarc42-3DL* {11457}.

Add at the end of section: Glaucous synthetics LDN/KU-2104 and LDN/KU-2105 are presumed to have genotype *W1W1W4W4*.

29.2. Epistatic inhibitors of glaucousness

Iw1. **c:** *IW1* encodes a long non-coding RNA (LncRNA) that putatively arose from an inverted repeat of a carboxylesterase gene (80% homology) in the W1 cluster that consists of WI-COE (non-annotated carboxylesterase), WI-PKS (*Traes_2BS_9E10D26DB*, polykedide synthase), and WI-CYP (*Traes_2BS_163390FC4*, cytochrome P450-type hydroxylase) {11459}. GenBank C-DNA sequence, KX823910. The IR region has >94% identity to an IR region in *Ae. tauschii* chromosome 2 that also produces MiRNA and a marker-based location similar to that of *Iw2* {11459}.
Iw3. **sutv:** Add: Langdon*/*T. turgidum* subsp. *dicoccoides* 1B {11455}.
ma: *XWL1967*/*Xfcp168-1B* – 0.15 cM – *XWL3096* – 0.015 cM – *Iw3* – 0.12 cM – *Xpsp3000-1B* {11455}.

29.4. Leaf glaucousness

RAC875 (non-glaucous leaf) / Kukri (glaucous leaf): *QW.aww-3A*, nearest marker *Xwmc264-3A*, accounted for 36–40% of the phenotypic variation; other QTL were located on chromosomes 1D, 2B (2 QTL), 4D, 5B, and 2D {11460}.

GWAS of flag leaf glaucousness in a large panel of genotypes identified major QTL on chromosomes 2B (W1/IW1) and 3A {11482}.

49.2. Early leaf senescence

Els2 {11472}. 2BL {11472}. **v:** LF2099 {11472}.
ma: *Xgpw4043-2B* – 8.87 cM – *Els2* – 22.27 cM *Xwmc149-2B* {11472}.

The incompletely dominant *Els2* mutant was found in an EMS-treated M_2 population of H261 {11472}.

44. Height

44.2. Reduced height: GA-sensitive

ht12. **i:** N98-2105, Yangmai 5*5 / Karcagi 522M7K {11428}.
ma: The *Rht12* phenotype is due to deletion of a 10.73-Mb terminal deletion of chromosome 5AL {11428). Reduced plant height might be due to activation of *TaGA2ox-A14* {11428}.

44.3 Reduced height QTL

QHt.nau-2D {11463}. Recessive. Gibberellin-sensitive. 2DS {11463}.

bin: 2DS-0.47-1.00. **v:** EMS-Induced Dwarf Wangshuibai {11463}.

ma: *Xbarc-2D* – 2.6 cM-*2D* – *QHt.nau-2D* – 0.3 cM-*2D* – *Xgpw361-2D* {11463}.

49. Leaf Characteristics

49.1. Leaf erectness Currently: 49. Leaf Erectness

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

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

49.4. Early leaf senescence

Insert after '…. *Ne2*.'in the comments section: A similar situation was described in {11423} where a claimed a putatively novel gene was designated as *yglw-1*'.

48. Lack of Ligules

Add note at end of section:

An erect leaf mutant involving *TaSPL8* (SQUAMOSA promoter-binding protein-like transcription factor), a homolog of *LG1* in maize and rice and was located in chromosome 2D. Knockout mutants of *TaSPL8* orthologs led to a fully liguleless phenotype. The gene in 2D was identified as *TraesCS2D01G502900*. *TaSPL8* transcript was highly expressed in the laminar joint region and young spike. *TaSPL8*-2D transcript was produced at much higher levels than *TaAPL-2B,* whereas *TaSPL-2A* was produced at a minimal level {11401}.

53. Male Sterility

53.1. Chromosomal

Ms1. **c:** *Ms1* is a phospholipid-binding protein {11421}. Sequence: SRP113340. Encodes a 219 amino acid polypeptide with similarity to a large family of GPI-anchored lipid transfer proteins affecting exine development {11422}. *Ms-A1 = TraesCS4A02G295900*; *Ms-B1 = TraesCS 4B02G017900).*

ms1a. **c:** Terminal deletion {11422}.

ms1b. **c:** Interstitial deletion {11422}.

ms1c. **c:** Terminal deletion {11422}.

ms1d. **v:** Add: Ningchen mutants *msd.1* and *msd.2* {11421}.
c: G329A {11421, 11422}.

ms1e. **c:** G1431A del1432 {11421}; C1435T del {11422}.

ms1f. **c:** G155A {11422}.

ms1g {11421}. **c:** Deletion of entire sequence {11421}.

ms1h {11421}. **v:** Ningchun 4 mutant {11421}.
c: C1762T {11421}.

ms1i {11421}. **v:** Ningchun 4 mutant {11421}.
c: G1603A {11421}.

ms1j {11421}. **v:** Ningchun 4 mutant {11421}.
c: C1775A {11421}.

ms1k {11421}. **v:** Ningchun 4 mutant {11421}.
c: G1397A {11421}.

ms1l {11421}. **v:** Ningchun 4 mutant {11421}.
c: C226T {11421}.

ms1m {11421}. **v:** Ningchun 4 mutant {11421}.
c: C1472T {11421}.

ms1n {11421}. **v:** Ningchun 4 mutant {11421}.
c: T164A {11421}.

ms1o {11421}. **v:** Ningchun 4 mutant {11421}.
c: G281A {11421}.

ms1p {11421}. **v:** Ningchun 4 mutant {11421}.
c: G155A {11421}.

ms1q {11421}. **v:** Ningchun 4 mutant {11421}.
c: C148T {11421}.

Ms1r [{11422}]. *Ml1h* {11422}.
v: Tilling mutant in Qual2000 {11422}.
c: G178A {11422}.
Add at end of section: *Ms1* orthologs in the A and D genomes were epigenetically silenced {11421}.

Ms5. 3AL {11427}.
c: Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is required for pollen exine development {11427}. *TraesCS3A02G217000* {11427}. GenBank MK577897.

ms5. *ms5a* {11427}.
v: H45 {11427}.
c: A G101A {11427}.

Complete sterility conferred by *ms5* is dependent on the homoeologous *ms-D* genotype – Ecalibur, Gladius, and RAC 875 have an *ms-D* allele that restores fertility to *ms5* genotypes {11427}.
Two non-functional *ms-B* alleles (Chinese Spring and Synthetic W7984 types) were identified {11427}.

57. Meiotic Characters

57.5. Unreduced gametes and polyploidization

QTug.sau-3B {11471}. **bin:** 5BS5-0.07-0.03.
ma: *Xgwm285-3B* – 1.0 cM – *Xcfp11012-3B* {11471}.
Identified in *T. turgidum*/*Ae. tauschii* hybrids involving Langdon durum (high unreduced gamete formation) crossed with AS313 and AS2225 (low unreduced gamete formation) topcrossed with *Ae. tauschii* AS60. The QTL was located near *Ttam*, a homologue of the *TAM* (tardy asynchronous meiosis/CYCA1;2) cyclin gene from Arabidopsis {11471}.

XX. Red Seed Colour

Add at end of section: A fourth QTL for red seed colour was detected on chromosome 1B in a GWAS of U.S winter wheat {11409}.

67. Response to Photoperiod

67.1. PPD1

QTL:
Insert at the beginning of section:
QPpd.zafu-4AL {11443}. 4AL {11443}.
s: CASL 4AL {11443}.
tv: *T. turgidum* subsp. *dicoccoides* TTD140 {11443}.
ma: Flanked by *M576* and *Xwmc468-4AL* in a 1.2-cM region {11443}.
Other publications reporting *Ppd* genes/QTL in the same region are reviewed in {11443}.

67.2. CONSTANS

Wheat genes *CONSTANS1* and *CONSTANS2* interact with *PPD1* to regulate photoperiodic response {11495}.

CONSTANS1
Triticum aestivum: *CO-A1* = *TraesCS7A02G211300*; *CO-B1* = *TraesCS7B02G118300*; *CO-D1* = *TraesCS7D02G212900*.
Triticum turgidum subsp. *durum* cv. Kronos: GenBank accession numbers: MT043302 (*CO-A1*); MT043303 (*CO-B1*) {11495}.

CONSTANS2
Triticum aestivum: *CO-A2* = *TraesCS6A02G289400*; *CO*-B2 = *TraesCS6B02G319500*; *CO-D2* = *TraesCS6D02G269500*.
Triticum turgidum subsp *durum* cv. Kronos: GenBank accession numbers MT043304 (*CO-A2*) and MT043305 (*CO-B2*) (11495}.

71. Restorers for Cytoplamic Male Sterilty

71.1 Restorers for *T. timpheevii* cytoplasm

Rf3. **v:** Add: Primepi {11476}.
ma: Add: *Xbarc128-1Bs* – 5.3 cm – *IWB14060* – 2.0 cM – *Rf3*/*IWB72107*/*IWB73447* – 14.5 cM – *Xwmc406-1B* {11476}.

Rf7 [{11473}]. *Rf6* {11473}. 5DS {11473}.
v2: Primepi *Rf3* {11474}.

Rf8 {11474}. 2DS {11474}. **v:** PWR4099 {11474}.
ma: *Xwmc503-2D* – 3.3 cM – *Rf8* – 5.8 cM – *Xgwm296-2D* – 0.9 cM – *Xwmc112-2D* {11474}.

Rf9 {11475}. 6AS {11475}. **v:** Gerek 79 {11475}.
ma: *IWB72413-6A* – 4.3 cM – *Rf9* – 4.7 cM – *IWB1550*-6A {11475}.

71.5. Restorers for multi-species cytoplasm

Restorer of *Ae. kotschyi*, *Ae. uniaristata,* and *Ae. mutica* cytoplasmic male sterility.

Rf^{multi} {11477}. 1BS {11477}.
v: All common wheat genotypes except *T. aestivum* subsp. *spelta* var. *duhamelianum* {11477}.
ma: Localized to a 2.9 cM region in a 1BS map {11477}.

rf^{multi}. **v:** *T. aestivum* subsp. *spelta* var. *duhamelianum* {11477}.

Sterility in the same plasmons is also found in lines with the T1BL·1RS translocation. Hohn & Lukaszewski {11478} produced a chromosome $1B_{1:6}$ translocation with a short rye insert replacing the Rf^{multi} region (rf^{multi} equivalent) causing partial sterility that can be restored by most common wheat genotypes.

81. Tiller Inhibition

Following the *tin1* add note:

A near recessive gene, *ftin*, was located proximal to the *Tin1* locus in putative *Agropyron cristatum* derivative Pubing3558{11462}: *Xgwm136-1A* – 4.3 cM – *Xpsp2999-1A* – 0.7 cM – *Xcfa2153-1A* – 1.0 cM – *Ftin* {11462}.

Three QTL were located on chromosomes 2DL (*Qltn.siau-2D*), 2BL, and 5AL in a RIL population from 'H461 (low tillering) / CN16 (high tillering)', but only the 2DL QTL was confirmed in RIL populations from 'H461 / cM107' and 'H461 / MM37' {11465}.

84. Yield and Yield Components

84.3.2 1,000-grain weight

TaCKX6-D1 {11407}. 3D {11407}. Encodes a cytokinin oxidase/dehydrogenase.
v: Hap a associated with high TKW has an 18-bp deletion relative to hap b: Wenmai 6, Yanzhan 1, Lumai 14 {11407}; Hap b: Bainong 321, Chinese Spring, Hanxuan 10, Neixiang 188 {11407}.
ma: *Xcfd70-3D* – 3.7 cM – *TaCKX6-D1* – 2.0 cm – *Xwmc533-3D* {11407}.

TaGW2-6A. Insert at end of section: Encodes an E3 RING ligase {11122}.

84.7. Spikelet number/ear

QSns.sau-2DS {11424}. 2DS {11424}.
v: RIL populations from 'Line 20828 / Chuanong 16', 'Line 20828 / Shumai 51', and 'Line 20828 / Sy95-71'; LOD score 3.47–38.24, PV 10–46% in eight environments. Located in a 2-cM interval flanked by *Ax-109836946* (32.8 Mb) and *AX-111956072* (34.43 Mb) {11424}.

QSns.ucw-7AL {11496}. 7AL {11496}. Underlying gene: *WHEAT ORTHOLOG OF APO1* (*WAPO1*), which is an orthologue of rice gene *ABER RANT PANICLE ORGANIZATION 1* (*APO1*).

WAPO-A1. *TraesCS7A02G481600* {11496}.

WAPO-A1a. Associated with low SNS; has a 115-bp promoter deletion and a D384N amino acid change {11496}.
v: RAC875, Clark, Lancer, CDC Lanmark, Julius, Arina, Jagger, Cadenza, Robigus, and SY_Mattis {11496}.
tv: Kronos, Ben {11496}. Most frequent allele in durum {11496}.

WAPO-A1b. Associated with high SNS; has a C47F amino acid change and no promoter deletion {11496}.
v: Berkut, Ning7840, PI 41025, MPV57, Platte {11496}. Most frequent allele in *T. aestivum*.
tv: Rare in durum {11496}.

WAPO-A1c. Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion {11496}.

v: AGS2000, LA95135, 26R61 {11496}.

tv: *T. turgidum* subsp. *dicoccoides* PI 471033 and PI 355455; *T. turgidum* subsp. *dicoccum* CItr 14135, PI 94638, and PI 298586; *T. turgidum* subsp. *durum* PI 286539 {11496}.

WAPO-A1d. Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion but differs from *WAPO-A1c* by a C667 and G764A DNA changes {11496}.

tv: *T. durum* Rusty and Lang; *T.dicoccum* CItr14919, PI 193877, PI 193882, PI 217640, PI 221400, PI 225332, PI 273980, and PI 94657 {11496}.

86. Proteins

86.3. Endosperm storage proteins

86.3.1. Glutenins

86.3.1.1. *Glu-1*

Glu-B1

Glu-B1d.	6+8.	**tv:**	Kronos {11497}.

Simultaneous and individual truncation mutations were found *Glu-B1x* and *Glu-B1y* subunits in Kronos mutant lines {11497}. Germplasm was accessioned as PI 692251 (T4-0865, *Bx6* single mutant), PI 692253 (T4-2197, *By8* single mutant), and PI 692252 (T4-1280, *Bx6* + *By8* combined mutant).

Add:

Glu-B1cf {11490}.	20*+33* {11490}.	**tv:**	*T. turgidum* subsp. *durum* Mexican landrace accession 22 (CWI52215) {11490}.
Glu-B1cg {11490}.	13+16* {11490}.	**tv:**	*T. turgidum* subsp. *durum* Mexican landrace accession 19 (CWI52200) {11490}.
Glu-B1ch {11490}.	7+22 {11490}.	**v:**	*T. aestivum* subsp. *aestivum* cv. Wilbur (CW13735) {11490}.
Glu-B1ci {11490}.	7+22* {11490}.	**tv:**	*T. turgidum* subsp. *durum* Iranian landrace accession 51 (CWI57280) {11490}.
Glu-B1cj {11490}.	13*+15* {11490}.	**tv:**	*T. turgidum* subsp. *durum* Iranian landrace accession 46 (CWI56913) {11490}.
Glu-B1ck {11491}.	15 {11491}.	**v:**	*T. aestivum* subsp. *compactum* PI 157920 {11491}.
Glu-B1cl {11491}.	14+8 {11491}.	**v:**	*T. aestivum* subsp. *macha* PI 272554, PI 278660, PI 290507 {11491}.
Glu-B1cm {11491}.	6+8* {11491}.	**v:**	*T. aestivum* subsp. *macha* PI 428177 {11491}.
Glu-B1cn {11491}.	17 {11491}.	**v:**	*T. aestivum* subsp. *sphaerococcum* CItr 4531, PI 272581, PI 282452 {11491}.
Glu-B1co {11493}.	20+22* {11493}.	**tv:**	*T. turgidum* subsp. *durum* Moroccan landraces MGB-2963, MGB-3152 {11493}.
Glu-B1cp {11493}.	20* {11493}.	**tv:**	*T. turgidum* subsp. *durum* North American cv. MGB-66023 {11493}.

Glu-B1-1

Add:

Glu-B1-1ao {11490}.	20* {11490}.	**tv:**	*T. turgidum* ss subsp p. *durum* Mexican landrace accession 22 (CWI52215) {11490}.

Glu-B1-2

Add:

Glu-B1-2al {11490}.	33* {11490}.	**tv:**	*T. turgidum* s subsp sp. *durum* Mexican landrace accession 22 (CWI52215) {11490}.
Glu-B1-2am {11490}.	22* {11490}.	**tv:**	*T. turgidum* s subsp sp. *durum* Iranian landrace accession 51 (CWI57280) {11490}.

86.3.1.2 *Glu-2*

Glu-B2

Add:

Glu-B2d {11493}.	12.1 {11493}.	**tv:**	*T. turgidum* subsp. *durum* Moroccan landrace MGB-3125 {11493}.

86.3.1.3. *Glu-3*

Glu-A3

Add:

Glu-A3ay {11490}.	6+20 {11492}.	**tv:** *T. turgidum* subsp. *durum* landraces BGE047515 and BGE047516 {11492}; Mexican durum landrace accession 10 (CWI52016) {11490}.
Glu-A3az {11490}.	6+10+11* {11490}.	**tv:** *T. turgidum* subsp. *durum* Mexican landrace accession 3 (CWI51941) {11490}.
Glu-A3ba {11490}.	5+11 {11492}.	**tv:** *T. turgidum* subsp. *turgidum* landrace BGE047535 {11492}; Iranian landrace accession 77 (CWI73342) {11490}.
Glu-A3bb {11493}.	20 {11492}.	**tv:** *T. turgidum* subsp. *dicoccon* landrace BGE047498 {11492}; *T. turgidum* subsp. *turgidum* landrace BGE047531 {11492}; *T. turgidum* subsp. *durum* Moroccan landrace MGB-16563 {11493}.
Glu-A3bc {11493}.	5** {11493}.	**tv:** *T. turgidum* subsp. *durum* Moroccan cv. MGB-20 {11493}.

Glu-B3

Add:

Glu-B3ae {11490}.	1+3+16 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 56 (CWI57386) {11490}.
Glu-B3af {11490}.	1+3+17 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 74 (CWI71827) {11490}.
Glu-B3ag {11490}.	2+4+16 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 46 (CWI56913) {11490}.
Glu-B3ah {11490}.	8+9+16 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 65 (CWI57719) {11490}.
Glu-B3ai {11490}.	2+4+14+18 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 62 (CWI57615) {11490}.
Glu-B3aj {11490}.	19 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 77 (CWI73342) {11490}.
Glu-B3ak {11490}.	2+4+6*+15+19 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 69 (CWI71627) {11490}.
Glu-B3al {11490}.	2+4+7*+15+16 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 61 (CWI57614) {11490}.
Glu-B3am {11490}.	1+3+6*+13'+17 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 72 (CWI71759) {11490}.
Glu-B3an {11490}.	8+9+13'+17 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 58 (CWI57522) {11490}.
Glu-B3ao {11490}.	1+3+8'+17 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 50 (CWI57256) {11490}.
Glu-B3ap {11490}.	2+4+6*+9'+14+19 {11490}.	**tv:** *T. turgidum* subsp. *durum* accession 78 (CWI73350) {11490}.
Glu-B3aq {11493}.	2+4+8+15+19 {11492}.	**tv:** *T. turgidum* subsp. *durum* landraces BGE045634 {11492}; MGB-2963 {11493}.
Glu-B3ar {11493}.	1+3+7+15+18 {11493}.	**tv:** *T. turgidum* subsp. *durum* landrace MGB-16563 {11493}.
Glu-B3as {11493}.	1+3+8+13+16+19 {11493}.	**tv:** *T. turgidum* subsp. *durum* landrace MGB-3152 {11493}.
Glu-B3at {11493}.	2+4+17 {11493}.	**tv:** *T. turgidum* subsp. *durum* landrace MGB-3125 {11493}.
Glu-B3au {11493}.	2+4+7+15+19 {11493}.	**tv:** *T. turgidum* subsp. *durum* landrace MGB-5963 {11493}.
Glu-B3av {11493}.	9+13+16 {11493}.	**tv:** *T. turgidum* subsp. *durum* landrace MGB-3101 {11493}.

86.3.2. Gliadins

Following the introductory paragraph insert:

A catalogue of common wheat gliadin genes and alleles is provided in {11437}.

86.5.6. Puroindolines and grain softness protein

Toward the end of the section expand on the sentence regarding the transfer to durum:

The soft kernel trait was transferred to durum; firstly, to Langdon durum Selection 1-674 and then by backcrossing to cultivar Svevo {10899}, which was in turn used to develop backcross derivatives in cultiars Alzada, Havasu, Kyle, and Strongfield {11444}. Genetic evidence indicated that ~24.4 Mbp from CS chromosome 5DS replaced ~20 Mbp of 5BS {11444}. Further cytogenetic analysis identified the translocation breakpoint in a 39-bp region within a putative glcosyl-transferase gene {11489}.

89. Reaction to *Bipolaris sorokiniana*

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

Pm3. Add note: *Pm3* has 92.9% identity with *Pm8* at the protein level {11398}.

Pm6. Add to comments: *Pm6* was localized to a 0.9 Mb physical region in chr 2BL {11451}.

Pm8. Add notes: *Pm8* has 92.9% identity with *Pm3* at the protein level {11398}. *Pm8* is an allele of *Pm17* in rye and orthologue of *Pm3* {11398}.

Pm17.
v: Embrapa 16 {11398}; Hugenoot {11398}.
al: Insave rye Nr 10458 {11398}.
c: GenBank MH077963 {11398}.

Pm17 is an allele of *Pm8* in rye and orthologue of *Pm3* {11398}.

Pm24. Replace *Pm24a* and *Pm24b* with a new section as follows.

Pm24 {571, 11414}. *Pm24a* {571}; *Pm24b* {10994}, *MlHLB* {2020}.
bin: 1DS-0.54-1.00.
v: Baihulu {10994, 11414}; Chicacao {571, 11414}; Hongmangmai {11414}; Hulutou {11413, 11414}.
ma: *Xgwm789/Xgwm603-1D* – 2.4 cM – *Pm24* 3.6 cM – *Xbarc229-1D* {10109, 10957, 10994}. Located in a 9.3-cM region flanked by *Xgwm337-1D* and *Xcfd83/Xcfd72-1D* {11413}.
c: *Pm24* encodes a tandem kinase protein with putative pseudokinase domains. The gene was designated *Wheat Tandem Kinase 3* (WLK30) – this gain of function mutation was conferred by a 6-bp deletion of lysine/glycine codons (K400G401) in the KIN1 domain {11414}. GenBank MK950855.

Pm41.
c: Encodes a unique CC-NBS-LRR gene {11454}. GenBank MN395289. Orthologs: in tv: Zavitan (*TRIDC3BG077810*) and Svevo (*TRITD3Bv1G261150.1*), but not in Chinese Spring {11454}.

Pm60. Add note at end of section: Gene *PmU*, flanked by *Xwmc273-7A* and *Xpsp3003-3A*, was transferred to common wheat from *T. urartu* accession UR206 (JIC 10100015) {11402}. *Xwmc273-7A* was 7.8 cM proximal to *Pm60* {11250}.

Pm67 {11426}. *Pm1V#5* {11426}. 1D (T1DL·1VS#5) {11426}.
v: NAU18105 {11426}.
s: NAU18103 (1V(1D)) {11426}.
al: *Dasypyrum villosum* 011140 {11426}.

Lines with *Pm67* showed complete immunity as seedlings but adult plants produced some conidial development on leaves whereas the culms were mildew-free {11426}.

Pm68 {11466}. 2BS {11466}.
bin: 2BS-0.84-1.00.
dv: *T. turgidum* subsp. *durum* TRI 1796 {11466}.
ma: *Xdw04* (TRITD2Bv1G010030, chr2B:21587671-21591163) – 0.22 cM – *Pm68* – 0.22 cM – *Xdw12* (TRITD2Bv1G010880, chr2B:23374401-23375310) – 3.0 Mb – *Pm26/Xcau516-2B* (TRITD2Bv1G012960, chr2B:26398438-26414596) – 36.8 cM – *Pm42* {11466}.

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

pmDHT {11447}. Recessive. 7BL {11447}.
v: Dahongtou S761 {11447}.
ma: *XBE443877/Xwmc526-7B* – 0.8 cM – *pmDHT* – 0.8 cM – *Xgwm611/Xwmc581-7B* – 0.9 cM – *XBF473539/Xgwm577-7B* – 0.9 cM – *Xgwm577-7B* {11447}.

PmG3M {11479}. 6BL {11479}. **bin:** 6BL1-0-70-1.00.
tv: *T. turgidum* subsp. *dicoccoides* G-305-3M {11479}.
ma: *Xgpw7262-6B* – 6.9 cM – *PmG3M* – 4.5 cM – *Xedm149-6B* {11479}; *Xgpw7262 – 6B* – 13.6 cM – *PmG3M* – 3.5 cM – *Xuhw213-6B* – 5.7 cM – *Xedm149-6B* {11479}.

PmJM23 {11445}. 5DS {11445}.

v: Jimai 23 {11445}.

ma: *Xytu3004* – 0.7 cM – *PmJM23/Xytu201/Xbwm21/Xcfd81-5D* – 1.8 cM – *Xswgi068/Xbwm20* {11445}.

PmQ {11461}. Recessive.

v: Hongxinmai {11461}.

ma: *Xstars419-2B* – 0.6 cM – *Xicsq405 2B* – 0.8 cM – *PmQ* – 0.2 cM – *XWGGBH913-2B* {11461}.

PmQ is very close to *Pm51, Pm63,* and *Pm64*.

PmSGD {11453}. Recessive. 7BL {11453}.

v: Shangeda {11453}.

ma: *SNP2-58* – 0.4 cM – *PmSGD* – 0.8 cM – *SNP2-46* {11453}.

***PmTm4*.** **ma:** Add: *XWGGC6892* – 0.6 cM – *PmTm4/XWGGC5746* – 0.03 cM – *XWGGC891* {11452}.

Ml92145E8-9 {11436}. 2AL {11436}. **bin:** 2AL1-0-0.85.

v: Line 92145E8-9 {11436}.

ma: *Xwmc181-2A* – 9.3 cM – *Xsdauk682-2A* – 2.8 cM – *Ml92145E8-9* – 0.8 cM – *Xsdauk-2A* – 18.7 cM – *Xgwm356-2* {11436}.

96. Reaction to *Fusarium* spp.

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

***Fbb5*.** Add note following the gene listing: According to {11487} *Fhb5* might be the same as *Qfhs.ifa-5Ac* but the issue remained ambivalent.

***Fhb7*.** **ma:** Add: Located to a 245-kb region flanked by *Xsdau86* and *Xsdau88* {11483}.

c: Gene Tel7E01T1020600.1 encodes a glutathione S-transferase that detoxifies trichothecene toxin {11483}. Sequence data can be found at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA540081.

Fhb7 was considered to be a horizontal gene transfer from an *Epichloe* spp. endophyte {11483}.

***Qfhs.ifa-5A*.** Add: Fine mapping divided this QTL into two components, *Qfhs.ifa-5Ac* located in the centromere region at 245.9 Mbp and a less effective *Qfhs.ifa 5AS* located at 290 Mbp. Both QTL were significantly associated with higher anther extrusion and plant height {11487}.

97. Reaction to *Heterodera* spp.

***Cre5*.** Add syn: *QCre-ma2A* {11394}.

v2: Move Madsen to this group and insert as 'Madsen *Cre9*' with same reference.

Add note: *Cre5* conferred resistance to *H. avenae* but not to *H. filipjevi* {11394}.

Cre9 {11394}. *QCre-ma7D* {11394. 7DL {11394}.

v1: VPM-1/Moisson 951{11394}.

v2: Madsen *Cre5* {11394}; VPM-1 *Cre5* {11394}.

ma: Flanked by *Xics7D-27-7D* and *BS00129645* {11394}. KASP markers *BS00021745*, *BS00150072*, and *BS00154302* were developed {11394}.

Cre9 conferred resistance to Chinese isolates of *H. filipjevi* but not to *H. avenae*.

99.2. Reaction to *Magnaporthe oryzae*.

***Rmg1*.** **v:** Change to **v1:** Delete Norin 4.

v2: Norin 4 *Rmg6* {302, 11470}.

Rmg1 was present in 87% of surveyed genotypes {11470}.

***Rmg6*.** *Rwt3* {11470}.

v1: Delete Norin 4. Add: IAC-5 {11470}; Transfed {11470}.

v2: Norin 4 *Rmg1* {11470}.

Rmg6 was present in 77% of surveyed genotypes 11470}.

Add at end of section: The wheat blast pathogen became established on wheat cultivar Anahuac (*rmg1 rmg6*) in Brazil in the mid-1980s. It was initially avirulent on cultivars such as IAC-5 with *Rmg6* but later acquired virulence allowing it to attack most wheat genotypes {11470}.

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

Stb5. **v:** Add: Baldus {11446}; Chaucer {11446}; Israel 493 {11446}; Longbow {11446}; Olaf {11446}; Senat {11446}; Veranopolis {11446}.

v2: Gene *Stb10* {11446}; Frontana *Stb10* {11446}; Mentana *Stb10* {11446}.

Stb6. *TaWAKL4* {11434}. **v:** Add: Cadenza {11434}; Flame {11434}.

ma: *Xgwm369-3A* – 4.3 cM – *Stb6* – 3.8 cM – *Xgwm132-3A* {11434}.

c: Encodes a wall-associated receptor kinase (WAK)-like protein {11434}.

Stb6 is common in *T. turgidum* subsp. *dicoccum* {11434}.

Stb10. **v2:** Gene *Stb5* {11446}; Frontana *Stb5* {11446}; Mentana *Stb5* {11446}.

Temporary designation

TmStb1 {11446}. Resistance to IPO323.

dv: *T. monococcum* subsp. *monococcum* MDR043 {11446}.

QTL

Spelt HRTI1410 (R) / 3 wheat parents: 135 DH lines: mapped using SNP polymorphisms common to all three S parents: four QTL identified on chromosomes 5AL (74.2–82.4 cM; $r^2 = 0.18$); 4B (52.9–56.9 cm, $r^2 = 0.09$) contributed by the susceptible parents; and 7B.1 (41.2–57.0 cM, $r^2 = 0.09$) and 7B.2 (58.2–67.4 cM, $r^2 = 0.15$) contributed by the susceptible parents {11430}.

At the end of section add: For a review of qualitative and quantitative resistance {11439}.

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

102.2. Sensitivity to SNB toxins (necrotrophic effectors)

Snn1. **ma:** *Xfcp618-1B* – 1.9. cM – *Snn1* – 0.16 cM – *Xfcp624-1B* {11433}.

c: *Snn1* is a wall-associated kinase (*TaWAK*) {11433}. GenBank (cDNA) KP091701.

Add note: Lebsock durum carried an intact *Snn1* but it was not expressed {11433}.

snn1. **s:** CS*/Hope 1B {11433}.

105. Reaction to *Puccinia graminis* Pers.

Sr2. **ma:** Add: *Bs0006276* – 0.3 cM – *Yr57* – 1.3 cm – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B* {11480}.

Sr7a. **v2:** Jagger *Sr38* {11420}.

ma: *Xwmc313-4A* – *SNP1067* – 0.8 cM – *Sr7a* – 2.7 cM – *Xbarc78-4A* – 2.7 cM – *SNP7126* {11420}.

Sr7b. **v2:** PI 177906 *Sr28 SrTmp* {11419}.

ma: Located at 147–164 in the Wang et al. (2014) consensus map {11419}.

Sr8a. **v:** Harvest {11418}.

v2: SD4297 *Sr28* {11418}; PI 177906 *Sr7b SrTmp* {11419}.

ma: Terminally located; SNP markers within 2 cM {11416}. *Sr8a* – 2.2 cM – *Xgwm459-6*A {11418}.

Sr9h. *SrWLR* {11485}. **v:** Matlabas {correct:10058, add: 11486}.

ma: *Xgwm47-2B* – 1.8 cM – *Sr9h* (*SrWLR*) – 7.0 cM – *Xwmc332-2B* {11485}; *AWA543-HRM* – *Sr9H* – *Xgwm47-2B*.

SR13.

Sr13a. **c:** GenBank KY924305 for Langdon and ST464 (Haplotype R1); KY825225 for Kronos and Khapstein (Haplotype R3) {11217}.

Sr13b. **c:** GenBank KY225226 (Haplotype R3) {11217}.

Sr22. **c:** *Sr22* encodes a CC-NBS-LRR protein with 941 aa {11404}. EBI LN883743, GenBank CUM44200.1.

Sr28. **v2:** SD4297 *Sr8a* {11419}.

The *Sr28* allele in SD4297 was originally reported as *Sr9h* {11418}.

Sr38. **v2:** Jagger *Sr7a* {11420}.

Sr45. **c:** *Sr22* encodes a 1,230 aa CC-NBS-LRR protein {11404}. EBI LN883757.

Add to existing note: Cloning of *Sr45* showed that *Sr45* and *Sr21* were different genes.

Sr46. **madv:** Flanked by *Xgwm1099-2D* and *Xbarc297-2D* {11405}.
c: Cloned by AgRenSeq and map-based methods *Sr46* has a CC-NBS-LRR structure {11405}. GenBank MG851023.

Sr50. **c:** *Sr50* was shown to encode a CC-NBS-LRR protein homologous to the barley *Mla* gene {11403}. GenBank KT725812.

Sr60. Reproduced here and updated in full.

Sr60 {11208}. 5A^{m}S {11208}.
dv1: PI 277130 {11385}; PI 277131-2 {11385}; PI 277135 {11385}; PI 306540 {11385}; PI 306545 {11385}; PI 306547 {11385}; PI 428158 {11385}; PI 435001 {11385}.
dv2: PI 306540 *Sr21 SrTm4 SrTm5* {11208}.
v: PI 689563, PI 306540/Kronos/2/UC1361/4UC12014-36 {11385}.
ma: *Pinb-5A*^{m}*S……GH724575/DK22976/CA5012332* – 0.25 cM – *Sr60/LRRK123.1* – 0.19 cM – *CJ942731/CJ884584* {11208}; *GH724575* – 1.56 cM – *Sr60/ LRRK123.1* – 0.52 cM – *FD475316* {11208}. *Sr60F2R2* {11385}.
c: *Sr60* from *T. monococcum* subsp. *monococcum* PI 306540 encodes a protein with two putative kinase domains designated *Wheat Tandem Kinase 2* (*WTK2*) {11208,11385}. GenBank MK629715 {11385}. The gene is orthologous to *T. aestivum* gene *TraesCS5A02G005400* {11385}.

Sr60 in UC12014-36+Sr60 (PI 689563) is linked with puroindoline genes for grain softness that were also introgressed from the diploid parent {11385}.

Sr61 {11397}. *SrB* {11337}. 6AL (T6AS·6AL-6Ae#1-6Ae#3) {11338, 11397}.
v2: AGG91586WHEA *Sr26* {11397}.
su: W3757 = SA8123 {11337}.

The recombinant AGG91586WHEA was produced after crossing the shortened 6Ae#1 recombinant WA-5 (AUS91436) carrying *Sr26* with SA8123. A separate line carrying *Sr61* alone is currently being selected for *Ph1* homozygosity.

SrTA1662. **v:** KS05HW14 {11405}.
c: An SrTA1662 candidate identified by AgRenSeq encoded a CC-NBS-LRR candidate gene (GenBank MG763911) with 83% homology with *Sr33* {11405}.

SrTA10276-2V {11395}. 2V {11395}. **d:** TA7753 {11395}.
al: *D. villosum* TA10276 {11395}.

SrTmp. **v2:** PI 177906 *Sr7b Sr28* {11419}.
ma: *SrTmp* – 3.1 cM – *IWB49086* {11419}.

Suppressor of Stem Rust Resistance 1

A suppressor of stem rust resistance in cultivar Canthatch was known from the 1980s based on the response of an extracted tetraploid and aneuploid derivatives of Canthach as well as mutation analysis ({11410, 11411}) and references therein.

SuSr-D1 {11411}. 7DL {11412, 11417}.
v: Canthatch CTH-K RL5451 {11411}; Columbus {11417}; Katepwa {11417}. Other Canadian Thatcher derivatives {11417}.
ma: Localised to a 1.3 cM genetic interval flanked by *Xkwh239* and *Xkwh281* {11412}.
c: *TraesCS7D01G526100*. Encodes a mutant form of *TaMed15b.D*, a subunit of the Medicator complex {11412}.

suSr-D1 [{11411}].**v:** Thatcher {11411}; NS1 RL5863 {11412}; NS2 RL5864 {11412}.
c: *TraesCS7D01G526100* {11412}.

106. Reaction to *Puccinia striiformis* Westend.

106.1. Designated genes for resistance to stripe rust

Yr15. Add synonyms: *YrH52* {0003}, *YrG303* {11429}, *Wtk1* {11392}.
Chromosome location add reference: {0003}.
tv: Add: *T. turgidum* subsp. *dicoccoides* H52 {0003, 11429}; *T. turgidum* subsp. *dicoccodes* G303 {11429}.
ma: *T. turgidum* subsp. *dicocoides* H52 {0003}.
ma: distal ...*Yr15* – 9.6 cM – *YrH52* – 1.4 cM – *Nor-B1* – 0.8 cM – *Xgwm264a* – 0.6 cM – *Xgwm18*{3}; *Xgmw273a* – 2.7 cM – *YrH52* – 1.3 cM – *Xgwm413/Nor1*...centromere {108}.
c: Add: GenBank MG649384 and MG674157 {11392}, MK188918 (*YrH52*) {11429}, and MG18819 (*YrG303*).

Yr28. *YrAS2388* {10822, 11438}. **c:** See *YrAs2388*.
Yr57. **ma:** Add: *Bs0006276* – 0.3 cM – *Yr57* – 1.3 cm – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B* {11480}.
Yr58. Add: Adult plant resistance. *QYr.sun-3BS* {10964}.
Change current listing to: **v2:** Sonora W195 AUS 19292 *Yr46* {10964}.
Yr81. **ma:** Replace with: *KASP_3077* – 2.7 cM – *Yr81* – 6.4 cM – *Xgwm459-6A* – 1.0 cM *KASP_11315* {11262}.
Yr83 {M11396}. 6A (T6AL·6RL {11396}.
tr: T6AL·6RL C19.3 {11396}.
ad: Wheat + 6R {11396}; Wheat + 6RL {11396}.
su: CS + 6R(6D) {11396}.
al: Triticale accession T-701 {11396}.
ma: Deletion mapping indicated that *Yr83* was located in 6RL bin FL 0.73-1.00 containing PCR markers KU.86, TNAC1823, TNAC1826, TNAC1844) {11396}.

The only previously designated *Yr* gene derived from *Secale cereale* is *Yr9* from chromosome 1RS.

106.2. Temporarily designated genes for resistance to stripe rust

YrAs2388. Add: *Yr28* {11438}, *NLR*$_{4D\text{-}1}$ {11438}.
v: Shumai 1675 {11438}.
dv: Add: *Ae. tauschii* Clae9 {11438}; PI5111383 {11438}; PI511384 {11438}.
c: *Yr28* has a CC-NBS-LRR structure, alternative splicing in the NBS region and duplicated 3' UTR {11438}. GenBank MK73661 – MK73666 {11438}.

Yr28 was present in all tested accessions of *Ae. tauschii* ssp. *strangulata* and some accessions of ssp. *tauschii* {11438}. Often suppressed in synthetic and derived wheat backgrounds.

YrH52. Delete. Synonymous with *Yr15*; moved to *Yr15* section.
YrH9020 {11450}. Derived from *Psathyrostachys huashanica*.
2DS {11450}. **v:** H9020-1-6-8-3 {11450}.
ma: *Xgwm455-2DS* – 5.8 cM – *YrH9020* – 4.4 cM – *Xgwm261-2DS* {11450}.
al: *Psathyrostachys huashanica* 0503383 {11450}.
Yru1 {11494}. 5AL {11494}. **bin:** 5AL10-0.57-0.78.
dv: *T. urartu* PI 428309 {11494}.
ma: *Xgwm186-5A* – 30.5 cM – *Yru1* – 10.8 cM – *Xgpw7007-5A*, then fine mapped with 82 additional polymorphic markers {11494}.
c: *TuG1812G0500003718*. *Yru1* has as NBS-LRR structure with N-terminal ankyrin and C-terminal WRKY repeats {11494}. GenBank MT018453.

The *Yru* resistance allele was present in a number of *T. urartu* accessions, but not in G1812 {11494}.

106.3. Stripe rust QTL

Correction: The reference for the listing 'Luke (MR) / 2174' in the 2019 supplement should be renumbered to {11393}.

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chromosomes 2AL, 2BL, 2BS, and 3BS were from Capo and one on 5BL was from Arina; the QTL on 2AL, 2BL, and 3BS were co-located with QTL for resistance to stripe rust {11449}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

Lr13. *LrZH22* {11467, 11468}; *LrLC10* {11468}.
bin: 2BS1-0.35-0.75.
v: Liaochen 10 {11468}; Zhoumai 22 {11467, 11468}.
ma: *Xbarc55-2B* – 2.4 cM – *LrZH22* – 4.8 cM – *Xgwm374-2B* {11467}; *Xbarc55-2B* – 2.2 cM – *XCAUT163* – 1.10 cM – *LrLC10* – 0.55 cM – *Lseq22* – 6.05 cM – *Xbarc18-2B* {11468}.
Lr39. **i:** TC*4 / Overley, GSTR 447 {11498}.
Lr42. **i:** TC*4 / Century, GSTR 448 {11498}.
Lr49. **ma:** Add: *Xgwm251-4B* – 8.6 cM – *XsunKASP_21* – 0.4 cM – *Lr49* – 0.6 cM – *XsunKASP_24* – 8.1 cM – *Xwmc349-4B* {11484}.

Lr64. Revise to: **v:** TC/RL6149-RIL13, GSTR 451{11399, 11498}.
v2: RL6149 *LrX* {10550, 11399}.
ma: Add: *K-IWB38521* – 1.0 cM – *Lr64*/*K-IWB59855* – 2.9 cM – *K-IWB72197* – 10 cM – *K-IWB73609* {11399}.
A second recessive gene (*LrX*) in in the previous near-isogenic line RL6149 was located in chromosome 1DS: *K-IWB577* – 11.2 cM – *LrX*/*IWB38437* {11399}.

Lr67. **v:** Chapingo 48 {11070}; Chapingo 53 {11070}; Yaqui 53 {11070}.
v2: NP876 *Lr46* {11441}; Sujata *Lr46* {11440, 11442}.

Add note: *Lr67* was predicted in 51 accessions mainly collected in the Indian subcontinent {11448} on the basis of the gene-specific marker SNP1-TM4 {11070}.

Lr68. **v2:** Sujata *Lr46 Lr67* {11442}.
Lr77. **v:** TC*2 / Toropi, GSTR 449 {11498}.
Lr78. **v:** TC*2 / Santa Fe, GSTR 450 {11498}.
Lr80 {11464}. *LrH2* {11464}. 2DS {11464}.
v: FLW6-Selection AGG95499WHEA {11464}.
ma: *Xgdm35-2D* – 7.5 cM – *Xcau96-2D* – 0.4 cM – *Lr80* – 0.2 cM – *Xbarc124-2D* – 13.2 cM – *Xgwm296-2D* {11464}.

107.3. QTL for reaction to *P. triticina*

Immediately above the heading 'Tetraploid wheat' insert:
Review of QTL in hexaploid wheat {11442}.

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chromosomes 2AL, 2BL, 2BS, and 3BS were from Capo and one on 5BL was from Arina; the QTL on 2AL, 2BL, and 3BS were co-located with QTL for resistance to stripe rust {11449}.

109. Reaction to *Pyrenophora tritici-repentis*

109.1. Resistance to tan spot

QTL

Add at the end of section: A QTL analysis of 4 durum crosses identified 12 QTL on chromosomes 1B, 2B (2), 3A (3), 5A (5), and 7A {11481}.

XXX. Reaction to *Sitobiplosis mosellana* (Gehin)

Henong 215 (R) / Yanyou (S) and 6218 (S) / Jimai 24 (R): selected RIL populations: Several QTL identified: *QSm.hbau-4A.2* with LOD scores 5.58–29.22 and PVE 24.4–44.8% were mapped to a 4.9-Mb interval; nearest markers *AX-109543456, AX-108942696* and *AX-110928325* {11425}.

112. Reaction to *Schizaphis graminum*

116. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa* J.G. Kuhn

Bt12. Add syn.: *QBt.ifa-7DS* {11469}. 7DS {11469}.
ma: Associated with 13 markers in a distally located physical region of ~4.3 Mbp {11469}. Validated KASP markers were derived from *IWB61302* and *IWB50978* {11469}. Although appearing to be proximal to *QDB.ui*-7DS {11182} the genes were not clearly distinguished.

QTL

Add: IDO835 (R)/Moreland (S): DH population: *Q.DB.ui-6DL* (PVE 0.53, *Bt9* region) and *Q.DB.ui-7AL* (PVE 0.38) {11400}.

XXX. Reaction to Soil-Borne Cereal Mosaic Virus

Insert immediately following the *SBWMV1* entry:

Sbwm1 {11435}. **v:** Heyne {11435}. 5D {11435}.
ma: *Xgwm272-5D* – 20.2 cM – *Sbwm1* – 2.2 cM – *wsnp_CAP11_c209_198467* – 0.7 cM – *wsnp_JD_c4438_5568170* – 8.7 cM – *Xgwm469* {11435}.

Change the note to: *Sbm1* and *Sbwm1* are likely the same gene.

118. Reaction to *Ustilago tritici*

Ut11 {11406}. 7BS {11406}.
v: DH line TD14XDIA*B0075, CN 120264 {11406}; Sonop, TD-14 {11406}.
ma: Co-segregation with *BS00022562_51, Excabibur_C3489_182* and *Kukri_rep_c71778_644* at 0.43, 1.20 and 1.25 Mbp {11406}.

Ut11 conferred resistance to race T2 but not T9 and T39; resistance to those races (and race T2) was conferred by *QUt.mrc-5B* {11406}.

119. Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)

Wss1. Add note: A number of secondary translocations were induced, the smallest of which was NAU421 (FL 0.78-1.00) {11488}.

References.

Updates

10786. Delete the names Simkova H and Dolezel from this reference.
10801. Replace with: Williamson VM, Thomas V, Ferris H and Dubcovsky J 2013 An *Aegilops ventricosa* translocation confers resistance against root-knot nematodes to common wheat. Crop Science 53: 14120-14128.
11060. Change title to: High-density mapping of the major FHB resistance gene *Fhb7* derived from *Thinopyrum ponticum* and its pyramiding with *Fhb1* by marker-assisted selection. Theoretical and Applied Genetics 128: 2301-2316. DOI: 10.1007/s00122-015-2586-x.
11155. Hao M, Liu M, Luo JT, Fan CL, Yi YJ, Zhang LQ, Yuan ZW, Ning SZ, Zheng YL and Liu DC 2018 Introgression of powdery mildew resistance gene *Pm56* on rye chromosome arm 6RS to wheat. Frontiers in Plant Science 9, 1040. DOI: 10.3389/fpls.2018.01040.
11356. Replace the 2019 reference with: Li GQ, Cowger C, Wang XW, Carver BF and Xu XY 2019 Characterization of *Pm65*, a new powdery mildew resistance gene on chromosome 2AL of a facultative wheat cultivar. Theoretical and Applied Genetics 132: 2625-2632. DOI: 10.1007/s00122-019-03377.
11364. Update: 2020 Theoretical and Applied Genetics 133: 1149-1159. DOI: 10.1007/s00122-020-03538-8.
11378 Xu XY, Li GQ, Carver BF and Scott Armstrong JS 2020 *Gb8*, a new gene conferring resistance to economically important greenbug biotypes in wheat. Theoretical and Applied Genetics 133: 615-622. DOI: 10.1007/s00122-019-03491-1.
11262. Replace with: Gessese M, Bariana H, Wong D, Hayden M and Bansal W 2019 Molecular mapping of stripe rust resistance gene *Yr81* in common wheat landrace AUS27430. Plant Disease 103: 1166-1171. DOI: 10.1094/PDIS-06-18-1055-RE.
11328 In the 2019 Supplement: *Yr17*: Change reference '19008' to '11328'.
11385. Chen S, Rouse MN, Zhang W, Zhang X, Guo Y, Briggs J and Dubcovsky J 2019 Wheat gene *Sr60* encodes a protein with two putative kinase domains that confers resistance to stem rust. New Phytologist 225: 948–959. DOI: 10.1111.nph.16169.

New

11393. Liu MY, Lei L, Powers C, Liu ZY, Campbell KG, Chen XM, Bowden RL, Carver BF and Yan LL 2016 *TaXa21-A1* on chromosome 5AL is associated with resistance to multiple pests in wheat. Theoretical and Applied Genetics 129: 345-355. DOI: 10.1007/s00122-015-2631-9.
11394. Cui L, Qiu D, Sun L, Sun Y, Ren YK, Zhang HJ, Li JT, Zou JW, Wu PP, Hu JH, Xie JZ, Liu HW, Yang L, Zhou Y, Wang Y, Lv Y, Liu ZY , Murray TD and Li HJ 2019 Resistance to *Heterodera filipjevi* and *H. avenae* in winter wheat is conferred by different QTL. Phytopathology, in review.
11395. Ando K, Krishnan V, Rynearsa S, Rouse MN, Danilova T, Friebe B, See D and Pumphrey M 2019 Introgression of a novel Ug-99-effective stem rust resistance gene into wheat and development of *Dasypyrum villosum* chromosome-specific markers vis genotyping-by-sequencing (GBS). Plant Disease 103: 1068-1074. DOI: 10.1094/PDIS-05-18-0831-RE.
11396. Li JB, Dundas I, Dong CM, Li GR, Trethowan R, Yang ZJ, Hoxha S and Zhang P 2020 Identification and characterization of a new stripe rust resistance gene *Yr83* on rye chromosome 6R in wheat. Theoretical and Applied Genetics 133: 1095-1107. DOI: 10.1007/s00122-020-03534-y.

11397. Zhang JP, Hewitt TC, Boshoff WHP, Upadhyaya N, Chandramohan S, JLi JB, Patpour M, Dundas I, Pretorius ZA, Hovmøller M, Park RF, Mago R, Periyannan S, Schnippenkoetter W, Richardson T, Bhatt D, Hoxha S, Steuernagel B, Ayliffe M, Wulff BH, McIntosh RA, Zhang P and Lagudah ES 2020 Resolution of the broad-spectrum wheat stem rust resistance genes *Sr26* and *Sr61* from tall wheat grass. Draft manuscript.

11398. Singh SP, Hurni S, Ruinelli M, Brunner S, Sanchez-Martin J, Krukowski P, Peditto D, Buchmann G, Zbinden H and Keller B 2018 Evoluionary divergence of the rye *Pm17* and *Pm8* genes reveals ancient diversity. Plant Molecular Biology 98: 249-260. DOI: 10.1007/s11103-018-0780-3.

11399. Kolmer JA, Bernardo A, Bai G, Hayden MJ and Anderson JA 2019 Thatcher wheat line RL6149 carries *Lr64* and a second leaf rust resistance gene on chromosome 1DS. Theoretical and Applied Genetics 132: 2809-2814. DOI: 10.1007/s00122-019-03389-y.

11400. Wang R, Gordon T, Hole D, Zhao WD, Isham K, Bonman JM, Goates B and Chen JL 2019 Identification and assessment of two major QTLs for dwarf bunt resistance in winter wheat line 'ID085'. Theoretical and Applied Genetics 132: 2755-2766. DOI: 10.1007/s00122-019-03385-2.

11401. Liu KY, Cao J, Yu KH, Liu XY, Gao YJ, Chen Q, Zhang WJ, Peng HR, Du JK, Xin MM, Hu ZR, Guo WL, Rossi V, Ni ZF, Sun QX and Yao YY 2019 Wheat *TaSPL8* modulates leaf angle through auxin and brassinosteroid signalling. Plant Physiology 181: 179-194. DOI: 10.1104/pp.19.00248.

11402. Qiu YC, Zhou RH, Kong XY, Zhang SS and Jia JZ 2005 Microsatellite mapping of a *Triticum urartu* Tum. derived powdery mildew resistance gene transferred to common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 111: 1424-1531. DOI: 10.1007/s00122-005-0081-5.

11403. Mago R, Zhang P, Vautrin S, Simkova H, Bansal U, Luo M-C, Rouse M, Karaoglu H, Periyannan S, Kolmer J, Jin Y, Ayliffe MA, Bariana H, Park R, McIntosh R, Dolezel J, Berges H, Spielmeyer W, Lagudah ES, Ellis JG and Dodds P 2015 The wheat *Sr50* gene reveals rich diversity at a cereal disease resistance locus. Nature Plants 1, 15186. DOI: 10.1038/nplants.2015.186.

11404. Steuernagel B, Periyannan SK, Hernandez-Pinzon I, Witek K, Rouse MN, Yu GT, Hatta A, Ayliffe M, Bariana H, Jones JDG, Lagudah ES and Wulff BH 2016 Rapid cloning of disease resistance genes in plants using mutagenesis and sequence capture. Nature Biotechnology 34. DOI: 10.1038/nbt.3543.

11405. Arora S, Steuernagel B, Gaurav K, Chandramohan S, Long YM, Matny O, Johnson R, Enk J, Periyannana S, Singh N, Hatta MAM, Athiyannan N, Cheema J, Yu GT, Kangara N, Gosh S, Szabo LJ, Poland J, Bariana H, Jones JDG, Bentley AR, Ayliffe M, Olsen E, Xu SS, Steffenson BJ, Lagudah E and Wulff BBH 2019 Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nature Biotechnology 37: 139-143. DOI: 10.1038/s41587-018-0007-9.

11406. Thambugala D, Menzies JM, Knox RE, Campbell H and McCartney C 2020 Genetic analysis of loose smut (*Ustilago tritici*) resistance in Sonop spring wheat. BMC Plant Biology 20, 314. DOI: 10.1186/s12870-020-02525-x.

11407. Zhang L, Zhao YL, Gao LF, Zhao GY, Zhou RH and Zhang BS 2012 *TaCKX6-D1*, the ortholog of rice *OsCKX2*, is associated with grain weight in hexaploid wheat. New Phytologist 195: 574-584.

11408. Lin M, Cai SB, Wang S, Liu SH and Zhang GR 2018 Genotyping-by-sequencing (GBS) identified SNP tightly linked to QTL for pre-harvest sprouting resistance. Theoretical and Applied Genetics 128: 1385-1395. DOI:10.1007/s00122-015-2513-1.

11409. Lin M, Zhang DD, Liu SB, Zhang GR, Yu JM, Fritz AK and Bai GH 2016 Genome-wide association analysis on pre-harvest sprouting resistance and grain color in U.S. winter wheat. BMC Genetics: 17, 794. DOI:10.1186/s12864-016-3148-6.

11410. Jiang H, Zhao LX, Chen XJ, Cao JJ, Wu ZY, Liu K, Zhang C, Wei WX, Xie HY, Li L, Gan YG, Lu J, Chang C, Zhang HP, Xia XC, Xiao SH and Ma CX 2018 A novel 33-bp insertion in the promoter of *TaMFT-3A* is associated with pre-harvest sprouting resistance in common wheat. Molecular Breeding 38, 69. DOI: 10.1007/s11032-018-0830-1.

11411. Kerber ER and Green GJ 1980 Suppression of stem rust resistance in the hexaploid wheat cv. Canthatch by chromosome 7DL. Canadian Journal of Botany 58: 1347-1350. DOI: 10.1139/g91-144.

11412. Hiebert CW, Moscou MJ, Hewitt T, Steuernagel B, Hernández-Pinzón I, Green P, Pujol V, Zhang P, Rouse MN, Jin Y, McIntosh RA, Upadhyaya N, Bhavani S, Vrána J, Karafiátová M, Huang L, Fetch T, Doležel J, Wulff BH, Lagudah E and Spielmeyer W 2020 Stem rust resistance in wheat is suppressed by a subunit of the Mediator complex. Nature Communications 11, 1123. DOI: 10.1038/s41467-02014937-2.

11413. Wang ZZ, Li HW, Zhang DY, Guo L, Chen JJ, Chen YX, Wu QH, Xie JZ, Xie JZ, Zhang Y, Sun QX, Dvorak J, Luo M-C and Liu ZY 2015 Genetic and physical mapping of powdery mildew resistance gene *MlHLT* in Chinese landrace Hulutou. Theoretical and Applied Genetics 128: 365-373, DOI: 10.1007/s00122-014-2436-2.

11414. Lu P, Guo L, Wang ZZ, Li BB, Li J, Li YH, Qiu D, Shi WQ, Yang LJ, Wang N, Guo GH, Xie JZ, Wu QH, Chen YX, Li MM, Zhang HZ, Dong LL, Zhang PP, Zhu KY, Yu DZ, Zhang Y, Deal KR, Huo NX, Liu CM, Luo M-C, Dvorak J, Gu YQ, Li HJ and Liu ZY 2020 A rare gain of function mutation in a wheat tandem kinase confers resistance to powdery mildew. Nature Communications 11, 680. DOI: 10.1038/s41467-020-14294-0.

11415. Cheng XJ, Xin MM, Xu RB, Chen ZY, Cai WL, Chai LL, Xu HW, Jia L, Feng ZY, Wang ZH, Peng HR, Yao YY, Hu ZR, Ni ZF and Sun QX 2020 A single amino acid substitution in STKc_GSK3 kinase conferring semisphaerical grains and its implications for the origin of *Triticum sphaerococcum* Perc. The Plant Cell 32: 923-034. DOI: 10.1105/tpc.19.00580.

11416. Guerrero-Chavez R, Glover KD, Rouse MN and Gonzalez-Hernandez JL 2015 Mapping of two loci conferring resistance to wheat stem rust pathogen races TTKSK (Ug99) and TRTTF in the elite hard red spring wheat line SD4279. Molecular Breeding 35, 8. DOI: 10.1007/s11032-015-0198-4.

11417. Kerber ER 1991 Stem-rust resistance in 'Canthatch' hexaploid wheat induced by a nonsuppressor mutation on chromosome 7DL. Genome 34: 935-939. doi.org/10.1139/g91-144.

11418. Hiebert CW, Rouse MN, Nirmala J and Fetch T 2017 Genetic mapping of stem rust resistance to *Puccinia graminis* f. sp. *tritici* race TRTTF in the Canadian wheat cultivar Harvest. Phytopathology 107: 192-197. DOI: 10.1095/PHYTO-05-16-0186-R.

11419. Babiker EM, Gordon TC, Chao S, Rouse MN, Wanyera R, Brown-Guedira and Bonman JM 2017 Molecular mapping of stem rust resistance loci effective against the Ug99 race group of the stem rust pathogen and validation of a single nucleotide polymorphism marker linked to rust resistance gene *Sr28*. Phytopathology 107: 208-215. DOI: 10.1094/PHYTO-08-160294-R.

11420. Turner MK, Jin Y, Rouse MN and Anderson JA 2016 Stem rust resistance in 'Jagger' winter wheat. Crop Science 56: 1719-1725. DOI: 10.2135/cropsci2015.11.0683.

11421. Wang Z, Li JI, Chen SX, Heng YF, Chen Z, Yang J, Zhou KJ, Pei JW, He H, Deng XW and Ma LG 2017 Poaceae-specific *Ms1* encodes a phospholipid-binding protein for male fertility in bread wheat. Proceedings of the National Academy of Sciences of the United States of America 114: 12614-12609. DOI:10.1073/pnas.1715570114.

11422. Tucker EJ, Baumann U, Kouidri A, Suchecki R, Baes M, Garcia M, Okada T, Dong CM, Wu YZ, Sandhu A, Singh M, Langridge P, Wolters P, Albertsen MC, Cigan AM and Whitford R 2017 Molecular identification of the wheat male fertility gene *Ms1* and its prospects for hybrid breeding. Nature Communications 8, 869. DOI: 10.1038/s41467-017-00945-2.

11423. Li XJ, Ding WH, Chen XD, Li G, Jiang XL, Dong N, Xiao YJ, Ren CC, Gao XH and Ru ZG 2018 Genetics and mapping of the novel leaf-colour mutant gene *yglw-1* on wheat chromosome arm 2BS. Crop & Pasture Science 69: 955-965. DOI: 10.1071/CPI18321.

11424. Ma JA, Ding PY, Liu JJ, Li T, Zou YY, Habib A, Mu Y, Tang HP, Jiang QT, Liu YX, Chen GY, Wang JR, Deng M, Qi PF, Li W, Pu ZE, Zheng YL, Wei, YM and Lan XJ 2019 Identification and validation of a major and stably expressed QTL for spikelet number per spike in bread wheat. Theoretical and Applied Genetics 132: 3155-3167. DOI: 10.1007/ss00122-019-03415-z.

11425. Zhang LJ, Geng MM, Zhang Z, Zhang Y, Yan GJ, Wen SM, Liu GR and Wang RH 2020 Molecular mapping of major QTL conferring resistance to orange wheat blossom midge (*Sitodiplosis mosellana*) in Chinese wheat varieties with selective populations. Theoretical and Applied Genetics 133: 491-502. DOI: 10.1007/s00122-019-03480-4.

11426. Zhang RQ, Xiong CX, Yao RN, Mu HQ, Meng XR, Fan YL, Kong LN, Xing LP, Wu JH, Feng YG and Cao AZ 2020 Characterization of powdery mildew resistance gene *Pm1V* on *Dasypyrum villosum* chromosome arm 1VS in wheat. Draft Manuscript.

11427. Pallotta MA, Warner P, Kouidri A, Tucker EJ, Baes M, Suchecki R, Watson-Haigh N, Okada T, Garcia M, Sandhu A, Singh M, Wolters P, Albertsen MC, Cigan AM, Baumann U and Whitford R 2019 Wheat *ms5* male-sterility is induced by recessive homoeologous A and D genome non-specific lipid transfer proteins. The Plant Journal 99: 673-68. DOI: 10.1111/tpj.14350.

11428. Sun LH, Yang WL, Li YF, Shan QQ, Ye XB, Wang DZ, Yu K, Lu WW, Xin PY, Pei Z, Guo XL, Liu DC, Sun JZ, Zhan KH, Chu JF and Zhang AM 2019 A wheat dominant dwarfing line with *Rht12*, which reduces stem cell length and affects gibberellic acid synthesis, is a terminal deletion line. The Plant Journal 97: 887–900. DOI: 10.1111/tpj.14168.

11429. Klymiuk V, Fatiukha A, Raats D, Bocharova V, Huang L, Feng LH, Jaiwar S, Pozniak C, Coaker G, Dubcovsky J and Fahima T 2020 Three previously characterized resistances to yellow rust are encoded by a single locus *Wtk1*. Journal of Experimental Botany 71: 2561-2572. DOI: 10.1093/jxb/eraa020.

11430. Karlstedt F, Kopahnke D, Perovic D, Jacobi A, Pillen K and Ordan F 2019 Mapping of quantitative trait loci (QTL) for resistance against *Zymoseptora tritici* in the winter spelt accession HTR11410 (*Triticum aestivum* subsp. *spelta*). Euphytica 215, 108. DOI: 10.1007/s10681-019-2432-3.

11431. Paull JG, Nable RO and Rathjen AJ 1992 Physiological and genetic control of the tolerance of wheat to high concentrations of boron and implications for plant breeding. Plant and Soil 146: 251-260.

11432. Pallota M, Schnurbusch T, Hayes J, Hay A, Baumann U, Langridge P and Sutton T 2014 Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. Nature 514: 88-9. DOI: 10.1038/nature13538.

11433. Shi GJ, Zheng ZC, Friesen TL, Raats D, Fahima T, Brueggeman RS, Lu SW, Trick HN, Liu ZH, Chao W, Frenkel Z, Xu SS, Rasmussen JB and Faris JD 2016 The hijacking of a receptor-driven pathway by a wheat fungal pathogen leads to disease. Science Advances 2:e1600822. DOI: 10.1126/sciadv.1600822.

11434. Saintenac C, Lee W-S, Cambon F, Rudd JJ, King RC, Marande W, Powers SJ, Berges H, Phillips AL, Uauy C, Hammond-Kosack KE, Langin T and Kanyaka K 2018 Wheat receptor-kinase-like resistance to fungal pathogen *Zymoseptoria tritici*. Nature Genetics 50: 368-374. DOI: 10.1038/s41588-018-0051-x.

11435. Liu SB, Yang XP, Zhang DD, Bai GH, Chao SM and Bockus W 2014 Genome-wide association analysis identified SNPs closely linked to a gene resistant to soil-borne wheat mosaic virus. Theoretical and Applied Genetics 127: 1039-1047. DOI: 10.1007/s00122-014-2277-z.

11436. Yu YC, Ren SZ, Zhao LF, Guo J, Bao YG, Ma YX, Wan HW, Ohm HW, Yu DZ, Li HJ and LR Kong 2018 Molecular mapping of a novel wheat powdery mildew resistance gene *Ml9214E8-9* and its application in wheat breeding by marker-assisted selection. The Crop Journal 6: 621-627. DOI: 10.1016/j.cj.2018.04.cn.

11437. Metakovsky E, Melnik V, Rodriquez-Quijana M, Upelniek V, and Carillo JL 2018 A catalog of gliadin alleles: Polymorphism of 20th century common wheat germplasm. The Crop Journal 6: 628-641. DOI: 10.1016/j.cj.2018.02.003.

11438. Zhang CZ, Huang L, Zhang HF, Hao QQ, Lyo B, Wang MN, Epstein L, Liu MA, Kou CL, Qi JA, Li MK, Gao G, Ni F, Zhang LQ, Gao M, Wang JR, Chen XM, Luo M-C, Zheng YL, Wu JJ, Liu DC and Fu DL 2019 An ancestral NB-LRR with duplicated 3'UTRs confers stripe rust resistance in wheat and barley. Nature Communications 19, 4023. DOI: 10.1038/s41467-019-11872-9.

11439. Brown JKM, Chartrain L, Lasserre-Zuber P and Saintenac C 2015 Genetics of resistance to *Zymoseptoria tritici* and applications to wheat breeding. Fungal Genetics and Biology 79: 33-41. DOI: 10.1016/j.fgb.2015.04.017.

11440. Lan CX, Zhang SA, Herrera-Foesse SA, Basney BR, Huerta-Espina J, Lagudah ES and Singh RP 2015 Identification and characterization of pleiotropic and co-located resistance loci to leaf rust and stripe rust in bread wheat cultivar Sujata. Theoretical and Applied Genetics 128: 549-561.DOI: 10.1007/s00122-015-2454-8.

11441. Ponce-Molina LJ, Huerta-Espina J, Singh RP, Basnet BR, Lagudah ES, Aguilar-Rincon VH, Alvarado G, Lobato-Ortiz R, Garcia-Zavala J and Lan CX 2018 Characterization of adult plant resistance to leaf rust and stripe rust in Indian wheat cultivar 'New Pusa 876'. Crop Science 58: 630-638. DOI: 10.2135/cropsci2017.06.0396.

11442. Pinto da Silva GB, Zanella CM, Martinelli JÁ, Chaves MS, Hiebert CW, McCallum BD and Boyd LA 2018 Quantitative trait loci conferring leaf rust resistance in hexaploid wheat. Phytopathology 108: 1344-1354. DOI: 10.1094/PHYTO-016-18-0208-RVW.

11443. Yu JS, Miao YZ, Shi ZB, Miao NN, Ding MQ, Zhang H, Jiang YR, and Rong JK 2019 Identification and mapping of a photoperiod response gene (*QPpd.zafu-4A*) on wild emmer wheat (*Triticum turgidum* L.) chromosome 4AL. Euphytica 125, 146. DOI: 10.1007/s10681-019-2469-3.

11444. Boehm JD, Zhang MY, Cai XW and Morris CF 2017 Molecular and cytogenetic characterization of the 5DS-5BS chromosome translocation conditioning soft kernel texture in durum wheat. The Plant Genome 10, 3. DOI: 10.3835/plant genome2017.04.0031.

11445. Jia MS, Xu HX, Liu C, Mao RX, Li HS, Liu JJ, Du WX, Wang WR, Zhang X, Han R, Wang XL, Wu LR, Liang X, Song JC, He HG and Ma PT 2020 Characterization of the powdery mildew resistance gene in the elite wheat cultivar Jimai 23 and its application in marker-assisted selection. Frontiers in Genetics 11, 241. DOI: 10.3389/fgene.2020.00241.

11446. Jing H-C, Lovell D, Gutteridge R, Jenk D, Kornyukhin D, Mitrofanova OP, Kema GHJ and Hammond-Kosack KE 2008 Phenotypic and genetic analysis of the *Triticum monococcum – Mycosphaella graminicola* interaction. New Phytologist 179: 1121-1132. DOI: 10.1111/j.1469-8137.2008.02526.x.

11447. Qie YM, Sheng YA, Xu HX, Jin YL, Ma FF, Li LH, Li XQ and An DG 2019 Identification of a new powdery mildew resistance gene *pmDHT* at or closely linked to the *pm5* locus in the Chinese wheat landrace Dahongtou. Plant Disease 103: 2645-2651. Doi: 10.1094/PDIS-02-0401-RE.

11448. Riaz A, Athiyannan N, Periannan S, Afanasenko O, Mitrafanova O, Aitken EAB, Lagudah E and Hickey LT 2017 Mining Vavilov's treasure chest of wheat diversity for adult plant resistance to *Puccinia triticina*. Plant Disease 101: 317-323. DOI: 10.1094/PDIS-05-16-0614-RE.

11449. Buerstmayer M, Matiasch L, Mascher F, Vida G, Ittu M, Robert O, Holdgate S, Flath K, Neumayer A and Buerstmayer H 2014 Mapping of quantitative adult plant field resistance to leaf rust and stripe rust in two European winter wheat populations reveals co-location of three QTL conferring resistance to both rusts. Theoretical and Applied Genetics 127: 2011-2028. DOI: 10.1007/s00122-014-2357-0.

11450. Li Q, Huang J, Hou H, Liu P, Jing JX, Wang BT and Kang ZS 2012 Genetic and molecular mapping of stripe rust resistance gene in wheat-*Psathyrostachys huashanica* translocation line H9020-1-6-8-3. Plant Disease 96: 1482-1487. DOI: 10.1094/PDIS-03-11-0204-RE.

11451. Wan WT, Xiao J, Li ML, Tang Xo, Wen MX, Cheruiyot AK, Li YB, and Wang HY 2020 Fine mapping of wheat powdery mildew resistance gene *Pm6* using 2B/2G homoeologous recombinants induced by the *ph1b* locus. Theoretical and Applied Genetics 133: 1265-1275. DOI: 10.1007/s00122-020-03546-8.

11452. Xie JZ, Wang LL, Wang Y, Zhang HZ, Zhou SH, Wu QH, Chen YX, Wang ZZ, Wang GX, Zhang DY, Zhang Y, Hu TZ and Liu ZY 2017 Fine mapping of powdery mildew resistance gene *PmtM4* in wheat using comparative genomics. Journal of Integrative Agriculture 16: 540-550. DOI: 10.1016/S2095-3119(16)61377-1.

11453. Xu XD, Li QA, Ma Zh, Fan JR and Zhou YL 2018 Molecular mapping of powdery mildew resistance gene *PmSGD* in Chinese wheat landrace Shangeda using RNA-seq with bulk segregant analysis. Molecular Breeding 38, 23. DOI: 10.1007/s11032-018-0783-4.

11454. Li MM, Dong LL, Li BB, Wang ZZ, Xie JZ, Qiu D, Li YH, Shi WQ, Yang LJ, Wu QH, Chen YX, Lu P, Guo GH, Zhang HZ, Zhang PP, Zhu DZ, Li UYW, Zhang Y, Wang TG, Yuan CG, Liu W, Yu DZ, Luo M-C, Fahima T, Nevo E, Li HJ and Liu ZY 2020 A CNL protein in wild emmer wheat confers powdery mildew resistance. New Phytologist June 2020. DOI: 10.1111/nph.16761.

11455. Wang J, Li WL and Wang W 2014 Fine mapping and metabolic and physiological characterization of the glume glaucousness inhibitor locus *Iw3* derived from wild wheat. Theoretical and Applied Genetics 127: 831-841. DOI: 10.1007/s00122-014-2260-8.

11456. Zhang ZZ, Wei WJ, Zhu HL, Challa GS, Bi CL, Trick HN and Li WL 2015 *W3* is a new wax locus that is essential for biosynthesis of beta-diketone, development of glaucousness, and reduction of cuticle permeability in common wheat. PLoS One 10(10)e0140524. DOI: 10.1371/journal.pone.0140524.

11457. Nishijima R, Tanaka C, Yoshida K and Takumi S 2018 Genetic mapping of a novel recessive allele for non-glaucousness in wild diploid wheat *Aegilops tauschii*: implications for the evolution of common wheat. Genetica 146: 249-254.

11458. Hen-Avivi S, Savin O, Racovita RC, Lee W-S, Adamski NM, Malitsky S, Almekias E, Levy M, Vautrin S, Berges H, Friedlander G, Kartvelishily E, Ben-Zvi G, Alkan N, Uauy C, Kanyuka K, Jetter R and Distelfeld A 2016 A metabolic gene cluster in the wheat *W1* and barley *Cer-cqu* loci determines beta-diketone biosynthesis and glaucousness. The Plant Cell 28: 1440-1460.

11459. Huang DQ, Feurtado JA, Smith MA, Flatman LK, Koh C and Cutler AY 2017 Long noncoding miRNA gene represses wheat beta-diketone waxes. Proceedings of the National Academy of Sciences of the United States of America 114: E3149-E3158. DOI: 10.10-73/pnas.1617483114.

11460. Bennett D, Izanloo, Edwards J, Kuchel H, Chambers K, Tester M, Reynolds M, Schnurbusch T and Langridge P 2012 Identification of novel quantitative trait loci for days to ear emergence and flag leaf glaucousness in a bread wheat (*Triticum aestivum*) population adapted to southern Australian conditions. Theoretical and Applied Genetics 124: 697-611. DOI: 10.1007/s00122-011-1740-3.

11461. Li YH, Shi XH, Hu JH, WU PP, Qiu D, Qu YF, Xie JH, Wu QH, Zhang HJ, Yang L, Liu HW, Zhou Y, Liu ZY and Li HJ 2020 Identification of a recessive gene *PmQ* conferring resistance to powdery mildew in wheat landrace Qingxinmai using BSR-Seq analysis. Plant Disease 104: 743-751. DOI: 10.1094/PDIS-08-19-1745-RE.

11462. Zhang JP, Wu J, Liu WH, Lu XA, Yang XM, Gao AN, Li XQ, Lu YQ and Li LH 2013 Genetic mapping of a fertile tiller inhibition gene, *ftin*, in wheat. Molecular Breeding 31: 441-449. DOI: 10.1007/s11032-012-9801-0.

11463. Xu T, Bian NF, Wen MX, Xiao J, Yuan CX, Cao Az, Zhang SZ, Wang XE and Wang HY 2017 Characterization of a common wheat (*Triticum aestivum*) high-tillering dwarf mutant. Theoretical and Applied Genetics 130: 483-404. DOI: 10.1007/s00122-016-2826-6.

11464. Kumar S, Bhardwaj SC, Gangwar OP, Kumaran VV, Khan H, Prasad P, Singh GP, Sharma K, Verma H, Bariana HS and Bansal U 2020 *LrH2* - a new gene for leaf rust resistance in wheat. Manuscript.

11465. Wang ZQ, Liu YX, Shi HR, Mo Hj, Wu FK, Lin Y, Gao S, Wang JR, Wei YM, Liu CJ and Zheng YL 2016 Identification and validation of low-tiller number QTL in common wheat. Theoretical and Applied Genetics 129: 603-612. DOI: 10.1007/s00122-015-2653-4.

11466. He HG, Liu RK, Zhang HH, Du HN, Ma PT 3 and Zhu SY 2020 Characterization of *Pmxx*, a new broad-spectrum powdery mildew resistance gene on chromosome 2BS, in Greek durum wheat accession TRI 1796. Manuscript.

11467. Wang CF, Yin GH, Xia XC, He ZH, Zhang PP, Yao ZJ, Qin JY, Li ZF and Liu DQ 2016 Molecular mapping of a new temperature-sensitive gene *LrZH22* for leaf rust resistance in Chinese wheat cultivar Zhoumai 22. Molecular Breeding 36, 18. DOI: 101007/s11032-016-043703.

11468. Qiu LN, Wang HF, Li YH, Wang WD, Liu YJ, Mu JY, Geng MM, Guo WL, Hu ZR, Ma J, Sun QX and Xie CJ 2020 Fine mapping of the wheat leaf rust resistance gene *LrLC10* (*Lr13*) and validation of its co-segregation markers. Frontiers in Plant Science 11, 470. DOI: 10.3389/fpls.2020.00470.

11469. Muellner AE, Eshonkulnov B, Hagenguth J, Pachler B, Michel S, Buerstmayr M, Hole D and Buerstmayr H 2020 Genetic mapping of the common and dwarf bunt resistance gene *Bt12* descending from the wheat landrace PI119333. Euphytica 216, 83. DOI: 10.1007/s10681-020-02614-w.

11470. Inoue Y, Vy TTP, Yoshida K, Asano H, Mitsuoka C, Asuke S, Anh VL, Cumagun CJR, Chuma I, Terauchi R, Kato K, Mitchell, Valent B, Farman M and Tosa Y 2017 Evolution of the wheat blast fungus through functional losses in a host specificity determinant. Science 357: 80-83. DOI: 10.1126/science.aam9654.

11471. Hao M, Luo JT, Zeng DY, Zhang L, Ning SZ, Yuan ZW, Yan ZH, Zhang HG, Zheng YL, Feuillet C, Choulet F, Yen Y, Zhang LQ and Liu DC 2014 *QTug.sau-3B* is a major quantitative trait locus for wheat hexaploidization. G3. 4. DOI:10.1534/g3.114.013078.

11472. Wang N, Xie YZ, Li YZ, Wu SN, Wei HS and Wang CS 2020 Molecular mapping of a novel early leaf-senescence gene *els2* in common wheat by SMP genotyping arrays. Crop & Pasture Science 71: 356-367. DOI: 10.1071/CP19435.

11473. Mukai Y and Tsunewak K 1979 Basic studies on hybrid wheat breeding. Theoretical and Applied Genetics 54: 153-160.

11474. Sinha P, Tomar SMS, Vinod, Singh VK and Balyan HS 201 Genetic analysis and molecular mapping of a new fertility restorer gene *Rf8* for *Triticum timopheevi* cytoplasm in wheat (*Triticum aestivum* L.) using SSR markers. Genetica 141:431-441. DOI: 10.1007/s10709-013-9742-5.

11475. Shahinnia F, Geyer M, Block A, Mohler M and Hartl L 2020 Identification of a new gene *Rf9* and unravelling the genetic complexity for controlling fertility restoration in hybrid wheat. bioRxiv. DOI: 10.1101/2020.06.20.162644.

11476. Geyer M, Bund A, Albrecht T, Hartl L and Mohler V 2016 Distribution of the fertility-restoring gene *Rf3* in common and spelt wheat determined by an informative SNP marker. Molecular Breeding 36, 167. DOI: 10.1007/s11032-016-0592-6.

11477. Tsunewaki K 2015 Fine mapping of the first multi-fertility-restoring gene, Rf$^{\mathrm{multi}}$, of wheat for three *Aegilops* plasmons, using 1BS-1RS recombinant lines. Theoretical and Applied Genetics 128:723-732. DOI: 10.1007/s00122-015-2467-3.

11478. Hohn CE and Lukaszewsk AJ 2016 Engineering the 1BS chromosome arm in wheat to remove the Rf^{multi} locus restoring male fertility in cytoplasms of *Aegilops kotschyi*, *Ae. uniaristata* and *Ae. mutica*. Theoretical and Applied Genetics 129: 1769-1774. DOI: 10.1007/s00122-016-2738-7.

11479. Xie WL, Ben-David R, Zeng B, Distelfeld A, Roder MS, Dinoor A and Fahima T 2012 Identification and characterization of a novel powdery mildew resistance gene *PmG3M* derived from wild emmer wheat, *Triticum dicoccoides*. Theoretical and Applied Genetics 124: 911-922. DOI: 10.1007/s00122-011-1756-8.

11480. Lodhi S, Bariana H, Randhawa M, Gul A, John P and Bansal U 2019 Identification of recombinants carrying stripe rust resistance gene *Yr57* and adult plant stem rust resistance gene *Sr2* through marker-assisted selection. Plant Breeding 138: 148-153. DOI: 10.1111/pbr.12674.

11481. Liu YA, Zhang QJ, Salsman E, Fiedler JD, Hegstad JB, Liu ZH, Faris JD, Xu SS and Li XH 2020 QTL mapping of resistance to tan spot induced by race 2 of *Pyrenophora tritici-repentis* in tetraploid wheat. Theoretical and Applied Genetics 133: 433-442. DOI: 10.10087/s00122-019-03474-2.

11482. Würschum T, Langer SM, Longin CFH, Tucker MR and·Leiser WL 2020 Refining the genetic architecture of flag leaf glaucousness in wheat. Theoretical and Applied Genetics 133: 981-991. DOI: 10.1007/s00122-019-03522-x.

11483. Wang HW, Sun SL, Ge WY, Zhao LF, Hou BQ, Wang K, Lyu ZF, Chen LY, Xu SS, Guo J, Li M, Su PS, Li XF, Wang GP, Bo CY, Fang XJ, Zhuang WW, Cheng XX, Wu JW, Dong LH, Chen WY, Li W, Xiao GL, ZhaoJX, Hao YC, Xu Y, Gao Y, Liu WJ, Liu YH, Yin HY, Li JZ, Li X, Zhao Y, Wang XQ, Ni F, Ma X, Li AF, Xu SS, Bai GH, Nevo E, Gao CX, Ohm H and Kong LR 2020 Horizontal gene transfer of *Fhb7* from fungus underlies Fusarium head blight resistance in wheat. Science 368, eaba5435. DOI: 10.1126/science.368.6487.122.

11484. Nsabiyera V, Baranwal D, Qureshi N, Kay P, Forrest K, Valarik M, Dolezel J, Hayden MJ, Bariana HS and Bansal UK 2020 Fine mapping of *Lr49* using 90K NNP chip array and flow-sorted chromosome sequencing in wheat. Frontiers in Plant Science 19, 1787. DOI: 10.3389/fpls.2019.01787.

11485. Zurn JD, Newcomb M, Rouse MN, Jin Y, Chao SM, Sthapit J, See DR, Wanyera R, Njau P, Bonman JM, Brueggeman and Acevedo M 2014 High-density mapping of a resistance gene to Ug99 from the Iranian landrace PI 626573. Molecular Breeding 34: 871-0881. DOI: 10.1007/s11032-014-0081-8.

11486. Wessels E, Prins R, Boshoff WHP, Zurn JD, Acevedo M and Pretorius ZA 2019 Mapping a resistance gene to *Puccinia graminis* f. sp. *tritici* in the bread wheat cultivar 'Matlabas'. Plant Disease 102: 2327-2344.

11487. Steiner B, Buerstmayr M, Wagner C, Danler A, Eshonkulov B, Ehn M and Buerstmayr H 2019 Fine-mapping of the Fusarium head blight resistance QTL *Qfhs.ifa-5A* identifies two QTL associated with anther extrusion. Theoretical and Applied Genetics 132: 2039-2053. DOI: 10.1007/s00122-019-03336-x.

11488. Zhao RH, Wang HY, Xiao J, Bie TD, Cheng SH, Jia Q, Yuan CX, Zhang RQ, Cao AH, Chen PD and Wang XE 2013 Induction of 4VS chromosome translocations and mapping of the wheat yellow mosaic virus resistance gene from *Haynaldia villosa*. Theoretical and Applied Genetics 126: 2921-2930. DOI: 10.1007/s00122-013-2181-y.

11489. Ibba MI, Zhang MY, Cai XW and Morris CF 2019 Identification of a conserved *ph1b*-mediated 5DS-5BS crossing over site in soft-kernel durum wheat (*Triticum turgidum* subsp. *durum*) lines. Euphytica 215, 200. DOI: 10.1007/s10681-019-2518-y.

11490. Hernández-Espinosa N, Payne T, Huerta-Espino J, Cervantes F, Gonzalez-Santoyo H, Ammar K and Guzmán C 2019 Preliminary characterization for grain quality traits and high and low molecular weight glutenins subunits composition of durum wheat landraces from Iran and Mexico. Journal of Cereal Science 88: 47-56. DOI:10.1016/j.jcs.2019.05.007.

11491. Alvarez JB and Guzmán C 2019 Recovery of wheat heritage for traditional food: genetic variation for high molecular weight glutenin subunits in neglected/underutilized wheat. Agronomy 9: 755. DOI:10.3390/agronomy9110755.

11492. Ruiz M, Bernal G and Giraldo P 2018 An update of low molecular weight glutenin subunits in durum wheat relevant to breeding for quality. Journal of Cereal Science 83: 236–244. DOI:10.1016/j.jcs.2018.09.005.

11493. Chegdali Y, Ouabbou H, Essamadi A, Cervantes F, Ibba MI and Guzmán C 2020 Assessment of the glutenin subunits diversity in a durum wheat (*T. turgidum* ssp. *durum*) collection from Morocco. Agronomy 10: 957. DOI:10.3390/agronomy10070957.

11494. Wang Hu, Zou SH, Li YW, Lin FY and Dingzhong Tang 2020 An ankyrin-repeat and WRKY-domain-containing immune receptor confers stripe rust resistance in wheat. Nature Communications 11:1353. DOI: 10.1038/s41467-020-15139-6.

11495. Shaw LM, Li C, Woods DP, Alvarez MA, Lin H, Lau MY, Chen A and Dubcovsky J 2020 Epistatic interactions between *PHOTOPERIOD-1*, *CONSTANS 1* and *CONSTANS 2* modulate the photoperiodic response in wheat. PLoS Genetics. In press. bioRxiv preprint DOI: 10.1101/2020.04.29.067959.

11496. Kuzay S, Xu Y, Zhang J, Katz A, Pearce S, Su Z, Fraser M, Anderson JA, Brown-Guedira G, DeWitt N, Peters Haugrud A, Faris JA, Akhunov E, Bai GH and Jorge Dubcovsky J 2019 Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping. Theoretical and Applied Genetics 132: 2689-2705. DOI: 10.1007/s00122-019-03382-5.

11497. Zhang Y, Schonhofen A, Zhang W, Hegarty J, Carter C, Vang T, Laudencia-Chingcuanco D and Dubcovsky J 2020 Contributions of individual and combined *Glu-B1x* and *Glu-B1y* high-molecular-weight glutenin subunits to semolina functionality and pasta quality. Journal of Cereal Science 93, 102943. DOI: 10.1016/j.jcs.2020.102943.

11498. Kolmer JA 2020 Personal communication.

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 67 MANUSCRIPT GUIDELINES.

The required format for Volume 67 of the *Annual Wheat Newsletter* will be similar to previous editions edited from Kansas State University.

CONTRIBUTIONS MAY INCLUDE:

—Current activities on your projects.
—New cultivars and germ plasm released.
—Special reports of particular interest, new ideas, etc., normally not acceptable for scientific journals.
—A list of recent publications.
—News: new positions, advancements, retirements, necrology.
—Wheat stocks; lines for distribution, special equipment, computer software, breeding procedures, techniques, etc.

FORMATTING & SUBMITTING MANUSCRIPTS:

Follow the format in volume 44–66 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@k-state.edu.

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The *Annual Wheat Newsletter* also will continue to be available (Vol. 37–66) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.