

# ANNUAL WHEAT NEWSLETTER

Volume 68



Contribution no. 23-035-B from the Kansas Agricultural Experiment Station,  
Kansas State University, Manhattan.

# **ANNUAL WHEAT NEWSLETTER**

Volume 68

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## IN DEDICATION TO

**CRAIG F. MORRIS**

Dr. Craig Franklin Morris of Pullman, WA, passed away at home on 25 October, 2021, at the age of 64 after a courageous battle with cancer, surrounded by his loved ones.

Craig was born on 18 September, 1957, in Winterset, Iowa, to George and Maxine (Shorb) Morris where he spent his early life on the family farm. After graduating from Winterset High School, he attended Iowa State University receiving his B.S., and later his M.S. and Ph.D. degrees from Kansas State University. He moved to Pullman in 1987 for a postdoc at Washington State University where he later would become Director of the USDA–ARS Western Wheat & Pulse Quality Laboratory (WW&PQL), a position he held for 32 years.



Craig led with humility, and often expressed his joy in collaborating and mentoring his employees and fellow scientists. He served as an Adjunct Professor at Washington State University, the University of Idaho, and Colorado State University. He was an Honorary Research Professor at the National Wheat Improvement Center, the Crop Science Research Institute, and the Chinese Academy of Agricultural Sciences. Additionally, Craig was a Fellow and president of the Cereals & Grains Association and editor-in-chief Emeritus of the journal *Cereal Chemistry*. He was awarded five patents, the Thomas Burr Osborne Medal for recognition of his scientific achievements in the field of cereal chemistry, and was widely published. His success was the result of his ardent curiosity and constant desire to expand his mind and the field of cereal chemistry.

Craig viewed life as a privilege and an adventure, often remarking how grateful he was for his work, friends, and family. A devoted father and excellent craftsman, he built his daughters treehouses, sandboxes, swings, and many other projects that brought his family joy. Never was there a problem or broken item that he could not fix through application of the scientific method and his inventive mind. He loved nothing more than spending a day on the water with his loving partner Patricia and her children Lily and Max in their little wooden boat. He was always ready for the next adventure, whether it be travel, a new project, or spending time with his exceptional friends. Patient and kind, he always acted intentionally, in thoughtful consideration of others.

In addition to his wonderful friends and employees, Craig is survived by his daughters Effy and Ana and their mother, Kay, his partner Patricia, her children Lily and Max, and his sister-in-law Sally. He was preceded in death by his brother, Sterling Morris and his parents George and Maxine Morris.

Craig was honored with a celebration of life on 6 November, 2021, at the Simpson Methodist Church in Pullman, a nondenominational service followed by a reception.

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**I. SPECIAL REPORTS****INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM**

<http://www.wheatgenome.org/>

In the last year, the IWGSC focused its efforts on several activities: releasing new versions of the IWGSC Chinese Spring reference sequence (IWGSC RefSeq) assembly and annotation, developing genomics tools for the wheat community, working to secure funding for the wheat diversity project, conducting its webinar series, and securing new sponsorships.

As of 30 June 2022, the IWGSC has 3,400 members, representing 918 research institutions and companies in 72 countries. The organization is supported by ten financial sponsors: CIMMYT, Curio Genomics, Daicel Arbor Biosciences, BASF, Florimond Desprez, Illumina, INRAE, the Kansas Wheat Commission, RAGT, and Syngenta.

***Reference Sequence and Annotation v2.1.***

An updated version of the Chinese Spring reference sequence (**IWGSC RefSeq v2.1**) was made available to the community in April 2021. This new version was completed under the leadership of Mingcheng Luo and Jan Dvorak (University of California, Davis, CA, USA) and with funding from the US National Science Foundation and the USDA Agricultural Research Service CRIS.

IWGSC RefSeq v2.1 integrates new datasets, resolves ambiguities, closes gaps, and increases the contiguity of the reference genome. IWGSC RefSeq v1.0 was revised using whole-genome optical maps and contigs assembled from whole-genome-shotgun (WGS) PacBio SMRT reads. The revisions involved approximately 10% sequence length of the IWGSC RefSeq v1.0.

To complement the new assembly, a new version of the annotation (**IWGSC RefSeq Annotation v2.1**) was also released in April 2021, integrating functional and manual annotation, as well as manually curated genes submitted by the wheat community. This new annotation was generated by Frédéric Choulet and H el ene Rimbert (INRAE, GDEC, France) with funding from the French Government managed by the Research National Agency (ANR) under the Investment for the Future program (BreedWheat). IWGSC RefSeq Annotation v2.1 contains 266,753 genes, comprising 106,913 HC genes and 159,840 LC genes.

The annotation of the IWGSC Chinese Spring RefSeq is in continuous improvement and the IWGSC will continue to integrate manually curated genes received from the community into upcoming releases. See the website (link below) for details on how to submit manually and functionally annotated genes for inclusion in future annotation releases.

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

**Reference.**

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

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***Genomics Tools.***

The IWGSC is committed to helping develop genomic resources useful for the wheat community and is continuously discussing opportunities with service providers.

As part of the IWGSC ongoing collaboration with Daicel Arbor Biosciences, a promoter capture array was developed under the leadership of Jorge Dubcovsky (University of California, Davis, CA USA) and Jacob Enk (Daicel Arbor Biosciences), in collaboration with researchers from INRAE (France). The panel is designed to capture ~168 Mbp of genomic space as measured on RefSeq v1.0. The kit was released in January 2022.

***Wheat Diversity Project.***

In this project, the IWGSC plans to develop platinum quality sequences of a core set of eight to twelve landraces and to add to these data elite and founder lines sequenced to varying levels of quality, as well as publicly available sequences.

Several of the landraces will be sequenced as part of a 3D-wheat project led by Moussa Benhamed which was funded recently through a European Research Council Grant. The IWGSC is now in the process of finalizing a proposal to sequence the remaining landraces.

***Webinar Series.***

The IWGSC webinar series continues to be very popular in the wheat community. The monthly webinars are free to attend and are posted subsequently on the IWGSC YouTube channel [<https://www.youtube.com/c/internationalwheat-genomesequencingconsortium>].

***Data access.***

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

***Links.***

- IWGSC website <http://www.wheatgenome.org/>
- How to submit manually curated genes: <https://www.wheatgenome.org/Resources/Annotations/How-to-submit-manually-curated-genes>
- IWGSC YouTube Channel <https://www.youtube.com/c/internationalwheatgenomesequencingconsortium>



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**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<sub>1</sub> 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 BRAZIL****BRAZILIAN AGRICULTURAL RESEARCH CORPORATION — EMBRAPA TRIGO  
C.P. 3081, 99.050–970 Passo Fundo, Rio Grande do Sul, Brazil.*****Performance of wheat cultivars in Rio Grande do Sul state, Brazil, 2020.***

Ricardo Lima de Castro, Eduardo Caierão, João Leonardo Fernandes Pires, and Pedro Luiz Scheeren (Embrapa Trigo), 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 Rio Grande do Sul state (STWC-RS), with the aim of supporting the indications of cultivars. This work evaluates the wheat cultivar grain yield performance of the STWC-RS in 2020.

The yield grain performance of 30 wheat cultivars (BRS 327, BRS Belajoia, BRS Marcante, BRS Reponde, CD 1303, Celebra, Esporão, FPS Amplitude, FPS Certero, FPS Regente, Inova, LG Fortaleza, LG Oro, LG Supra, ORS 1401, ORS 1403, ORS Agile, ORS Citrino, ORS Madrepérola, ORS Vintecinco, TBIO Astro, TBIO Aton, TBIO Audaz, TBIO Duque, TBIO Ponteiro, TBIO Sinuelo, TBIO Sonic, TBIO Sossego, and TBIO Toruk) was studied in nine environments (Coxilha – season 1, Coxilha – season 2, Cruz Alta – season 1, Cruz Alta – season 2, Sertão, Vacaria – season 1, Vacaria – season 2, Vacaria – season 2 with no fungicide application on the aerial part of the plants, and São Borja), in the state of Rio Grande do Sul in 2020. The experiments were in a randomized block design with three or four repetitions. Each plot consisted of five 5-m rows with a 0.2 m spacing between rows. The plant density was about 330 plants/m<sup>2</sup>. Grain yield data (kg/ha) were subjected to individual analysis of variance (for each environment) and to grouped analysis of variance (for all environments). The grouped analysis of variance was performed employing the mixed model (fixed cultivar effect and randomized environment effect). The grain yield performance of wheat cultivars was evaluated by analysis of adaptability and stability, employing the method of distance from the ideal cultivar, weighed by the coefficient of residual variation, proposed by Carneiro (1988).

In this analysis, the ideal cultivar was considered as the cultivar with high grain yield, high stability, low sensitivity to adverse conditions of unfavorable environments and the ability to respond positively to improvement of favorable environments. The general average of the STWC-RS in 2020 was 5,498 kg/ha. The experiment conducted in Vacaria – season 1 had the highest average wheat grain yield at 6,347 kg/ha. The maximum wheat grain yield was 7,440 kg/ha, in Vacaria – season 1 (cultivar CD 1303). Cultivars TBIO Aton, BRS Reponde, BRS Belajoia, CD1303, and TBIO Ponteiro had adaptability and stability in favorable environments (environments with average of wheat grain yield higher than the general average). BRS Reponde, LG Supra, CD 1303, TBIO Aton, and BRS Belajoia had adaptability and stability in unfavorable environments (environments with average of wheat grain yield lower than the general average). In general, the average of all environments, TBIO Aton (6,104 kg/ha), BRS Reponde (6,051 kg/ha), CD 1303 (5,899 kg/ha), BRS Belajoia (5,927 kg/ha), and TBIO Ponteiro (5,855 kg/ha) were the cultivars that came closest to the ideal cultivar.

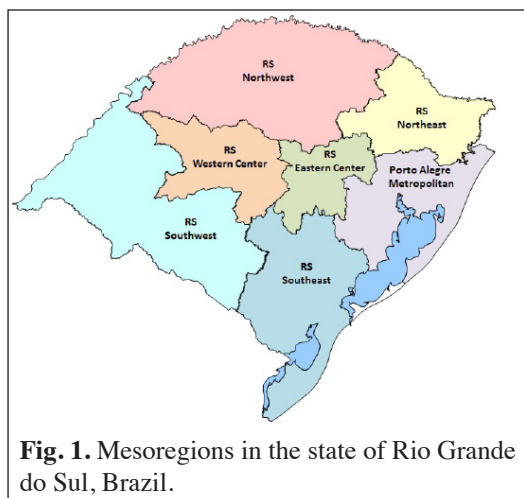
**Reference.**

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

**The wheat crop in the state of Rio Grande do Sul, Brazil, 2020.**

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

The state of Rio Grande do Sul (RS) is one of the main wheat producing states in Brazil. The objective of this study was to analyze the wheat crop in Rio Grande do Sul in 2020. In 2020, Rio Grande do Sul harvested 953,382 ha of wheat (39.2% of the total area harvested in Brazil), producing 2,104,160 tons of wheat (33.1% of the Brazilian production), with an average of grain yield of 2,207 kg/ha (400 kg/ha below the Brazilian average of 2,607 kg/ha). Among the geographical mesoregions of Rio Grande do Sul state (Fig. 1), the RS Northwest mesoregion harvested the largest wheat area at 742,854 ha (77.9% of the cropped area in the state) and had the largest production, 1,535,955 tons of wheat grain (73.0% of state’s production) (Table 1). However, the average wheat grain yield obtained in this mesoregion was the lowest of the state at 2,068 kg/ha (139 kg/ha below the state average) (Table 1), which was due mainly to late frosts during flowering.



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

The RS Northeast mesoregion harvested 43,829 ha of wheat (4.6% of the cropped area in the state), produced 159,272 tons of wheat grain (7.6% of state production), and had the highest average wheat grain yield of the state at 3,634 kg/ha (1,427 kg/ha above the state’s average) (Table 1).

The wheat crop in Rio Grande do Sul in 2020 had some unfavorable environmental conditions, notably (i) the occurrence of yellow rust (until then with rare occurrence in Brazil), (ii) the breakdown of leaf rust resistance (race B62) in some resistant cultivars, and (iii) the occurrence of late frosts that coincided with flowering and the beginning of grain filling, especially in the RS Northwest mesoregion. Comparing the wheat crop data with the results of the State Test of Wheat Cultivars in Rio Grande do Sul (STWC-RS) in 2020, we observed that the average of wheat grain yield of commercial crops was 3,291 kg/ha below the average of (5,498 kg/ha).

**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 2020 (Source: IBGE, 2022).

Mesoregion	Area harvested		Production		Grain yield (kg/ha)
	ha	%	tons	%	
RS Northwest	742,854	77.9	1,535,955	73.0	2,068
RS Northeast	43,829	4.6	159,272	7.6	3,634
RS Western Center	53,945	5.7	135,05	6.4	2,504
RS Eastern Center	15,807	1.7	39,971	1.9	2,529
Porto Alegre Metropolitan	2,044	0.2	4,879	0.2	2,387
RS Southwest	86,098	9.0	206,333	9.8	2,396
RS Southeast	8,805	0.9	22,645	1.1	2,572
<b>Rio Grande do Sul State</b>	<b>953,382</b>	<b>100.0</b>	<b>2,104,160</b>	<b>100.0</b>	<b>2,207</b>

Reference.

IBGE. 2022. Produção Agrícola Municipal. Disponível in <<https://www.ibge.gov.br/estatisticas/economicas/agricultura-e-pecuaria/9117-producao-agricola-municipal-culturas-temporarias-e-permanentes.html?=&t=resultados>>. Accessed on 30 April, 2022. Note: Aggregate database of studies and surveys carried out by IBGE.

## ITEMS FROM GERMANY

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

A. Börner, V. Aleksandrov, A.M. Alqudah, M.V. Chebataveva, E. Esquisabel, S.I. Golik, T. Kartseva, A.G. Klykov, S.B. Lepekhov, U. Lohwasser, S. Misheva, M. Pardi, V.A. Petin, T.A. Pshenichnikova, M.S. Röder, M. Schierenbeck, V.P. Shamanin, L.V. Shchukina, M.R. Simón, V.I. Yakubovskiy, and K. Zaynali Nezhad.

***The impact of Rht alleles on cross-pollination efficiency traits with relevance for hybrid breeding in wheat.***

Hybrid breeding and the ability to exploit heterosis is one of a few high-priority wheat breeding strategies that have the potential to rapidly improve yield and stability. Yield improvements associated with hybrid vigor were demonstrated to be in the order of a 10–25% increase in grain yield as well as improved resistance against biotic/abiotic stresses and grain quality. Faced with these scenarios, the identification of factors affecting the development of hybrid wheats is of fundamental importance in order to accelerate the rate of genetic gain of the crop. Due to the prevalence and usefulness of *Rht* ‘Green revolution’ dwarfing alleles, it is important to gain a better understanding of how these alleles affect those traits related to the development of hybrid wheat seed production. Up to now, the expected influence of these alleles/genes on wheat flowering-related traits was evaluated based on mapping populations or genome-wide association studies, without taking into account the actual effect of each *Rht* allele in particular. In this project, we propose to explore the effect of different *Rht* alleles using many near-isogenic lines. The experiments were performed at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK Gatersleben, Germany) and the Faculty of Agricultural Sciences and Forestry (National University of La Plata, Argentina) during three growing seasons. Four sets of NILs carrying the alleles of *Rht* genes: *Rht1* (*Rht-B1b/Rht-D1a*), *Rht2* (*Rht-B1a/Rht-D1b*), *Rht3* (*Rht-B1c/Rht-D1a*), *Rht 1+2* (*Rht-B1b/Rht-D1b*), *Rht 2+3* (*Rht-B1c/Rht-D1b*), and *rht* (*tall; Rht-B1a/Rht-D1a*) in the genetic backgrounds of the wheat cultivars April Bearded, Bersee, Maris Huntsman, and Maris Widgeon were evaluated. Traits associated with cross-pollination efficiency (flowering date, plant height, spike length, anther extrusion, anther and filament length, and spikelets/spike) were studied. Preliminary results showed that the extreme dwarf alleles *Rht3*, *Rht1+2*, and *Rht2+3* presented the greatest effects in all the variables analyzed. Plant height showed reductions from 22–25% (*Rht1* and *Rht2*), 50–57% (*Rht3* and *Rht1+2*), and 66% (*Rht2+3*) compared to *rht* (*tall*). Spike length was increased up to 14% (*Rht1+2* vs. *rht*) and 3–9% for the rest of *Rht* alleles compared to *rht*, whereas spikelets/spike were increased up to 6% (*Rht2+3* vs. *rht*). In comparison to *rht* (*tall*), the floral organs were negatively influenced by *Rht* alleles; decreases from 8–13% (*Rht 1*, *Rht2*, and *Rht3*) to 17–25% (*Rht1+2* and *Rht2+3*) in anther length, and reductions from 16–44% in filament length were observed. For their part, anthers extrusion decreased between 15–27% (*Rht1*, *Rht2*, and *Rht3*) to 32–35% for *Rht1+2* and *Rht2+3* compared with that of *rht*. No significant differences were detected for flowering time among the alleles evaluated. These preliminary results indicate that *Rht* alleles combination are involved in multiple traits of interest for hybrid wheat production in breeding programs. Moreover, the magnitude of the negative impact of *Rht* alleles on floral organs depends on the combination of the alleles involved.

***Impact of fungal 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 the grain weight, being variations more associated to the grain number. Grain number per spike 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. 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. The present work aims to assess the effect of fungal foliar diseases on FE identifying genotypes able to keep FE stable under high disease severity conditions. The experiments were carried out 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 recombinant inbred lines previously mapped originated from the cross between 'Synthetic W 7984 × Opatá', 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), first node detectable (GS31), anthesis (GS60), and early dough grain (GS82), and the area under disease progress curve (AUDPC) was estimated. The number of grains/spike, spike dry weight, and heading date were assessed, and FE calculated as the ratio between the number of grains/spike and the spike dry weight at maturity (SDW). Data were analyzed using ANOVA for split-plot designs. Preliminary results showed no associations between FE and heading date. Fungicide applications reduced the AUDPC by 35%, being the genotypes mostly affected by leaf rust (*Puccinia triticina* Eriks) and tan spot (*Pyrenophora tritici-repentis* (Died.) Drechs). For the grain number, values ranged from 9.1 to 76.5 grains/spike, being the mean value 27.2 grains/spike. The SDW showed a variation between 0.21 and 2.2 g/spike, with a mean value of 0.77 g/spike. For FE, the lowest value was 15.1 grains/gSDW, and the highest 87.6 grains/gSDW. The FE remained stable under diseased treatments in the parental cultivar Synthetic W7984, whereas showed reductions of 20% in Opatá. Several genotypes showed the same behavior as Synthetic W7984 where FE remained stable in the diseased treatment or it was even higher than in the fungicide treatment. The SDW was on average more reduced by the diseased treatment than the number of grains/spike, resulting in those genotypes with similar or higher FE values in the diseased treatment compared to the treatment with fungicides. Our results suggest that FE is not reduced by fungal foliar diseases in some genotypes and could be used as a promising trait associated with disease tolerance. Molecular markers will be associated with the studied traits.

### ***SNP-based assessment of genetic diversity and population structure of Bulgarian bread wheat germplasm.***

Knowledge about genetic diversity in a crop germplasm could facilitate its utilization in breeding programs. In this study, we explored aspects of DNA genetic diversity, population structure, and linkage disequilibrium (LD) in a bread wheat collection comprising 51 old accessions (tall historic cultivars and landraces) and 128 contemporary semidwarf cultivars from Bulgaria. The panel was SNP-genotyped using an optimized wheat 25K Infinium iSelect array. For analyses, 19,019 polymorphic SNPs were used. The A, B, and D genomes contained 41, 42, and 11% of the total number of markers, respectively, and 6% were not assigned to any chromosome. The Nei's gene diversity (GD) was within the range of 0.1 to 0.5, and the polymorphism information content (PIC) ranged from 0.1 to 0.4. The old and modern sets differed slightly regarding GD and PIC, whereas significant differences were revealed between the two groups with respect to LD. Two approaches, STRUCTURE and the k-mean clustering algorithm, allocated the wheat accessions to three subgroups. The vast majority of the old germplasm formed a distinct subgroup. The inferred structure for the modern cultivars reflected the different strategies adopted by the breeding centers. A high level of gene migration between the two subgroups of contemporary cultivars was suggested. However, the estimated low rate of gene flow from the old accessions towards the modern subgroups evidenced the underutilized potential of the old germplasm by the breeders.

### ***Evaluation of a bread wheat collection for biotic and abiotic stresses.***

This project is being conducted at Gorgan University of Agricultural Sciences and Natural Resources, Iran, in 2022. The plant materials include 700 landraces and modern bread wheat cultivars from many countries from all over the world. These genotypes were all spring types and have been received kindly from the genebanks at IPK-Gatersleben, Germany, ICARDA in Syria, the Czech Republic, and the Seed and Plant Improvement Institute (SPII) in Iran. These genotypes were cultivated at field in two separate experiments. The first experiment is for abiotic stress and it is being performed for post-anthesis drought stress applying potassium iodide (0.5 percent w/v) over the whole canopy including spikes. Anthesis days were recorded for each genotype and 14 days later the treatment was performed using hand operated spray machine. This treatment simulate the response of wheat plant against drought stress via stem reserve mobilization. In the second experiment the same plant material was evaluated for Fusarium Head Blight as well as brown and yellow rust diseases tolerance. In order to spread rust pathogens a susceptible genotype was cultivated surrounding and among the



plant materials. The plants were rated in the field for rust, using a scale which ranged from 1 (resistant) to 9 (susceptible). Infection type and disease severity were recorded. For Fusarium head blight, the plant pathogen interaction characters, disease index, disease incidence and fusarium damaged kernels were evaluated three times after inoculation. Disease intensity and area under the disease progress curve also will be calculated. The data will be used for GWAS and also parents selection to develop segregation populations for wheat breeding purposes.

**Table 1.** Technological and physical properties of grain and flour in three rivet wheat accessions grown in the field (Gatersleben, Germany) and greenhouse (Novosibirsk, Russia) (TKW = 1,000-kernel weight; W = dough strength in units of alveograph; P = tenacity; L = extensibility).

ACCESSION NUMBER	ACCESSION NAME	TECHNOLOGICAL PROPERTIES					PHYSICAL PROPERTIES OF DOUGH (ALVEOGRAPH)				
		TKW (G)	VITREOUSNESS (%)	FLOUR PARTICLE DIAMETER (MK)	PROTEIN CONTENT (%)	GLUTEN CONTENT (%)	GLUTEN QUALITY (HAND WASHING)	W (UA)	P (MM)	L (MM)	P/L RATIO
TRI 1256	Rivets Grannen	42.2	67.2	25.5	16.9	30.8	Light, elastic	303	151	37.0	4.10
TRI 24752	Rivets Grannen ( <i>Triticum</i> sp.)	36.3	54.3	23.4	23.9	32.9	Not washable, disintegrates	51	66.0	24.7	2.69
TRI 28386	England Rivet Wheat	50.7	76.8	24.8	22.2	38.0	Sticky, gray	65	66.0	34.5	3.17

### ***Isolation of a genetic factor associated with increase in protein and gluten content in the grain of bread wheat originated from chromosome 2A of *Triticum timopheevii*.***

A chromosome 2A introgression from *T. timopheevii* was transferred from the experimental line 821 to bread wheat cultivar Saratovskaya 29 (S29). The obtained single-chromosome substitution line S29 (821 2A) showed an increased protein and gluten content in grain in a greenhouse when growing under normal and restricted water supply. Therefore, the line was grown in five different geographical locations situated 1,000 kilometers apart in different climatic regions. The regions differed in temperature, humidity, soil conditions, and agronomic practices. We found that under all conditions, protein and gluten contents in grain of line S29 (821 2A) was significantly higher by 1–2% and 3–4%, respectively, compared to that of the parental cultivar. In most cases, this introgression did not reduce grain yield and retained 1,000-kernel weight. The line had high rheological properties of dough comparable to the high-quality cultivar S29. It has been suggested that the new genetic factor may belong to the homoeoallelic series of gene *Gpc-2* for high grain protein content.

### ***Technological properties of grain, flour and other agronomic properties of rivet wheat accessions from the collection of IPK.***

Rivet wheat (*Triticum turgidum* subsp. *turgidum*) is an underutilized cereal that was often cultivated in the Mediterranean region, United Kingdom, Germany, and Switzerland until 20th century. Now, rivet wheats are kept in different gene banks and need more detailed phenotyping to return them into breeding process. Three accessions from the IPK gene bank were investigated for technological properties of grain, flour, and several other morphological and agronomical traits. The diversity for these traits is presented (Tables 1 and 2 (p. 10)). No variability was found for flour particle size, which was rather high; this is characteristic of tetraploid wheats that lack the D-genome gene *Ha* for endosperm softness. For the same reason, the physical properties of the dough were similar to that of durum wheat, which are characterized by low extensibility and high P/L ratio. The accession TRI 1256 was in contrast with two others by a good gluten quality, which was demonstrated both by hand washing and with the use of alveograph. This accession had a high dough strength, comparable with that of high-quality bread wheats (Table 2, p. 10). This grain can be used for food purposes, in those products where the flour with a high strength is required. The accessions TRI 24752 and TRI 28386 had a higher protein and gluten content in grain. They may serve as a feed wheat. Additionally, the accessions were evaluated for morphological and quantitative traits. Their spikes were of different shape and all were pubescent (Fig. 1, p. 10). Two of them had black awns and colored glumes. TRI 24752 had the shortest stem and TRI 28386 – the longest (Table 2, p. 10). All had large grains with the highest TKW in

**Table 2.** Yield components demonstrated by the three rivet wheat accessions grown in the field (Gatersleben, Germany) and greenhouse (Novosibirsk, Russia) (TKW = 1,000-kernel weight).

ACCESSION NUMBER	ACCESSION NAME	MORPHOMETRIC PARAMETERS											
		STEM LENGTH (CM)	NUMBER OF TILLERS	SPIKE LENGTH (CM)	SPIKELET NUMBER	NUMBER OF GRAINS (MAIN SPIKE)	NUMBER OF GRAINS (SECONDARY SPIKES)	GRAIN WEIGHT (MAIN SPIKE G)	GRAIN WEIGHT (SECONDARY SPIKES G)	FERTILITY (MAIN SPIKE)	TKW (G)	NUMBER OF GRAINS (TOTAL)	GRAIN WEIGHT (TOTAL G)
TRI 1256	Rivets Grannen	76.7	7	7.3	24	39	237	1.67	11.02	1.6	46.0	276	12.6
TRI 24752	Rivets Grannen ( <i>Triticum</i> sp.)	68.7	5	7.3	26	33	98	1.37	4.03	1.3	41.2	131	5.4
TRI 28386	England Rivet Wheat	91.9	6	9.2	24	15	162	0.87	9.91	0.6	60.9	177	10.7



**Fig. 1.** Spikes of the three rivet wheat accessions. From left to right: TRI 24752, TRI 1256, and TRI 28386. Inset in upper left shows spike glume pubescence.

TRI 28386. Rivet wheat accessions remain understudied and underutilized, where polymorphism could be useful for enlarging the genetic background of modern durum wheats.

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## ITEMS FROM INDIA

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

The Department of Genetics and Plant Breeding at Ch. Charan Singh University Meerut (India) now has been working on the genetics of wheat for over five decades. Initially, we worked on cytogenetics, mutation research, biometrical analysis, and classical breeding for the first 25 years. Thereafter, for more than the past two decades, our research is focused on genetics, genomics, and molecular breeding in wheat (primarily spring bread wheat). We primarily worked in the area of biotic and abiotic stress tolerance (disease resistance, tolerance to drought and heat), resource use efficiency (nitrogen use efficiency), agronomic traits, grain quality, and biofortification (grain Zn and Fe concentrations). These studies mainly involved interval mapping, genome-wide association studies (GWAS), and epigenomics. We focus mainly on the role of DNA methylation, histone modifications (both methylation and acetylation), and non-coding RNA (miRNA and lncRNA), in regulating expression of the genes involved in downstream pathways involved in resistance against leaf rust due to two major leaf rust resistance genes (all-stage resistance gene *Lr28* and adult-plant stage resistance gene *Lr48*). We also have been involved in introgression and pyramiding of a variety of genes/QTL for abiotic and biotic stress tolerance, grain quality and rust resistance. These studies were funded by national and international funding agencies. Here, we present a brief summary of our work during last year (2021–22).

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

**Meta-QTL, ortho-MQTL, and candidate genes for thermotolerance.** Meta-QTL analysis for thermotolerance in wheat was conducted to identify robust meta-QTL (MQTL). In this study, 441 QTL related to 31 heat-responsive traits were projected on the consensus map with 50,310 markers. This exercise resulted in the identification of 85 MQTL with confidence intervals (CI) ranging from 0.11 to 34.9 cM with an average of 5.6 cM. This amounted to a 2.96-fold reduction relative to the mean CI (16.5 cM) of the QTL used. Seventy-seven of these MQTL also were compared and verified with the results of recent GWAS. The above 85 MQTL included seven MQTL that are particularly useful for breeding purposes (we call them ‘breeders’ MQTL’).

Seven ortho-MQTL involving wheat and rice genomes also were identified using synteny and collinearity. The MQTL were used to identify 1,704 candidate genes (CGs). In silico expression analysis of these CGs permitted identification of 182 differentially expressed genes (DEGs), which included 36 high confidence CGs with known functions previously reported to be important for thermotolerance. These high-confidence CGs encoded proteins belonging to the following families: protein kinase, WD40 repeat, glycosyltransferase, ribosomal protein, SNARE associated Golgi

protein, GDSL lipase/esterase, SANT/Myb domain, and K homology domain. Thus, the study resulted in the identification of MQTL (including breeders' MQTL), ortho-MQTL, and underlying CGs, which could prove useful not only for molecular breeding for the development of thermotolerant wheat cultivars, but also for future studies focused on understanding the molecular basis of thermotolerance.

**QTL for terminal heat stress tolerance.** In order to discover genomic regions associated with morphological, physiological, and yield and yield-contributing traits under heat stress, a bi-parental mapping population consisting of 177 doubled-haploid (DH) lines derived from a cross between two diverse cultivars PBW343 (heat sensitive) and Giza168 (heat tolerant parent) was used. The parents and the DH lines were grown in alpha-lattice designs with three replications under three sowing dates, timely sown (non-stress), late sown (moderate heat stress), and very late sown (severe terminal heat stress) over three years (2018, 2019, and 2020) in Meerut and two years (2018 and 2019) in Lucknow. The experimental lines were phenotyped for following 18 traits: (i) days-to-heading, (ii) days-to-anthesis, (iii) days-to-maturity, (iv) grain-filling duration, (v) plant height, (vi) number of tillers, (vii) spike length, (viii) number of seeds/spike, (ix) spikelet density, (x) number of florets/spike, (xi) number of grains/spike, (xii) floret fertility, (xiii) grain weight/main spike, (xiv) grain weight/side spikes, (xv) 1,000-kernel weight, (xvi) biological yield, (xvii) grain yield, and (xviii) harvest index. Genotyping of the DH population and parents was conducted using the genotyping-by-sequencing (GBS) approach, which identified 26,213 polymorphic SNP markers. High-quality SNPs were physically mapped on 21 wheat chromosomes. Using the above phenotypic and genotypic data, QTL analysis has begun using single marker analysis (SMA) composite interval mapping (CIM). Preliminary results of pooled data from the timely sown dates (Lucknow location) revealed 70 significant QTL for the 18 traits. These QTL were distributed on 20 of the 21 wheat chromosomes (excluding 4B). Maximum QTL were associated with days-to-heading and harvest index, whereas only a solitary QTL was detected for grain yield. Average LOD scores of these QTL ranged from 2.50 to 9.43 and explained up to 40% of the phenotypic variation. QTL analysis for other trials from the two locations is underway.

**Meta-QTL and ortho-metaQTL for drought-responsive traits.** Meta-QTL (MQTL), ortho-MQTL, and CGs were identified for eight drought-responsive yield and yield-related traits: days-to-heading, plant height, days-to-maturity, 1,000-kernel weight, grain weight/spike, grain number/spike, spikes/plant and grain yield. For this purpose, 318 QTL reported using 16 different wheat mapping populations were utilized. A total of 56 MQTL were identified. The confidence interval (CI) for individual MQTLs was narrow (compared to the original QTL), and ranged from 0.7 to 21 cM (mean = 5.95 cM), equivalent to 0.18 to 673.93 Mb (mean = 168.35 Mb). Forty-five of these MQTL also were verified using MTAs reported in GWAS.

Ortho-MQTL also were identified using synteny/collinearity among the wheat, rice, and maize genomes. This exercise allowed us to identify 12 ortho-MQTL. We also identified 1,497 CGs within the above 56 MQTL regions. *In silico* expression analysis of the genes identified 64 differentially expressed genes (with  $\pm 2$  fold change) under water deficit conditions. Nine MQTL with small CI (<1 cM) were declared as breeders' MQTL, because these have the potential for use in marker-assisted breeding for drought tolerance. The results can be utilized by breeders for developing cultivars with improved yield under water stress and by geneticists/biotechnologists for basic strategic research involving fine-mapping leading to cloning of QTL/genes across the three cereals involved.

**GWAS for yield-related traits under drought.** GWAS for grain yield under drought was conducted using nine multi-locus and six single-locus models. For this purpose, phenotypic and genotypic data (9,627 SNPs) on a wheat association mapping (WAM) panel comprising 320 genotypes was available from our previous study. For recording phenotypic data in the earlier study, the WAM panel was raised under irrigated (IR) and rainfed (RF) conditions each at two different locations, Meerut (Northern India (28°0.97'N 77°0.74'E)) located in mega environment-1 and Powarkheda (Central India (22°0.07'N 73°0.98'E)) located in mega environment-5. These two locations provided the following four environments: Meerut IR (E1), Meerut RF (E2), Powarkheda IR (E3), and Powarkheda RF (E4). Nine multi-locus models (FASTmrEMMA, FASTmrMLM, ISISEM-BLASSO, and pKwMEB, and pLARmEB, mrMLM, FarmCPU, and Blink, MLMM) gave 404 MTAs, and the six single-locus models (MLM, CMLM, SUPER, P3D/EMMAX, GLM, and ECMLM) gave 231 MTAs. The distribution of 404 MTAs from the multilocus models was as follows: 61 (FarmCPU), 49 (Blink), 27 (MLMM), 15 (FASTmrEMMA), and 38 (FASTmrMLM), and 59 (ISISEM-BLASSO), 45 (mrMLM), 40 (pKwMEB), and 70 (pLARmEB). Similarly, the distribution of 231 MTAs among six SLMs was as follows: 18 (MLM), 83 (GLM), 16 (CMLM), 18 (ECMLM), 18 (P3D/EMMAX), and 78 (SUPER). Only one solitary QTN was common in all the nine multi-locus models and all six single locus models; two QTNs were identified using each of the nine multi-locus models and five QTNs were common in all the six SLMs. Forty-five QTNs were available in at least two multilocus models,

21 MTAs were common in one or more multi-locus models, and one or more single-locus models. Candidate genes for QTNs that were common in more than one model are being identified for further detailed analysis.

**GWAS for grain-weight related traits under drought.** A multi-locus genome-wide association study (ML-GWAS) was conducted for four grain weight-related traits (days-to-anthesis, grain-filling duration, grain number/spike, and grain weight/spike) using data recorded under irrigated (IR) and rain-fed (RF) conditions. Seven stress-related indices were estimated for these four traits, (i) drought resistance index, (ii) geometric mean productivity, (iii) mean productivity index, (iv) relative drought index, (v) stress tolerance index, (vi) yield index, and (vii) yield stability index. The association panel consisted of a set of 320 spring wheats representing 28 countries. The panel was genotyped using 9,627 SNPs. The GWA analysis provided 30 significant MTAs, distributed as follows: (i) IR (15 MTAs), (ii) RF (14 MTAs), and (iii) IR+RF (1 MTA). In addition, 153 MTAs were available for the seven stress-related indices. Five MTAs co-localized with previously reported QTL/MTAs. Candidate genes associated with different MTAs also were identified. Gene ontology analysis and expression analysis together allowed the selection of the two CGs, which may be involved in the drought stress response. These two CGs included TraesCS1A02G331000, encoding an RNA helicase, and TraesCS-4B02G051200, encoding the microtubule-associated protein 65. The results not only supplement current knowledge on genetics for drought tolerance in wheat but may also be used for future wheat breeding programs to develop drought-tolerant wheat cultivars.

**QTL and CGs for preharvest-sprouting tolerance in wheat.** A mapping population of 386 DH lines produced from a cross of two Canadian white-seeded spring wheat genotypes, SC8021-V2 (PHS tolerant) and AC Karma (moderately susceptible to PHS), was used for QTL analysis. Sprouting scores (SS) (scale 1–9) and falling number (FN) were measured on spikes collected from two different environments (Meerut and Pantnagar locations) in 2018–19 and 2019–20. Continuous frequency distributions for SS and FN suggested segregation of multiple genomic regions for the two traits, which are negatively correlated.

The DH population and the parental genotypes were genotyped with an Infinium iSelect 90K SNP chip and a high-density genetic map with 6,114 SNPs covering 3,526.0 cM was constructed. QTL analysis was conducted using composite interval mapping and Bayesian interval mapping (BIM). A total of 43 QTL, including 30 for SS and 13 for FN, were identified. The phenotypic variation explained by these QTL ranged from 1.16–8.63% for SS and 2.11–10.93% for FN. Composite interval mapping allowed detection of 16 QTL (14 for SS and 2 for FN), whereas 17 QTL (12 for SS and 5 for FN) were identified through BIM. As many as 10 QTL (4 for SS and 5 for FN, and 1 for SS/FN) were detected by both methods. The 43 QTL, significant for the two traits, were mapped on 13 different wheat chromosomes. A majority of these QTL were mapped in regions known to contain factors affecting different components of PHS tolerance like seed dormancy, seed coat color, ABA responsiveness, and alpha-amylase activity. We also identified the CGs underlying the QTL regions. A total of 302 putative CGs were identified in 35 of 43 QTL associated with SS and FN. These putative CGs encoded as many as 42 proteins/domains types, of which 22 proteins were related to the ABA-signalling pathway. The functional annotations of identified CGs were verified from published reports to understand their possible roles in controlling the targeted preharvest-sprouting traits. We found 41 promising CGs belonging to 16 domains on chromosome 5A around SNP marker *Kukri\_c108256\_381* associated with FN across environments and methods. The above QTL/genes could be useful for marker-assisted breeding for tolerance to preharvest sprouting in wheat.

### ***Genetics of tolerance to biotic stresses: rusts, powdery mildew, spot blotch, MDR (multiple disease resistance) and cereal cyst nematodes.***

**Meta-QTL and candidate genes for stem rust resistance.** Stem rust is generally treated as a qualitative trait and ~70 *Sr* genes are known. More recently, the trait has been treated as a quantitative trait, and many QTL identified in a number of studies. Individual QTL have a large confidence interval (CI) and are less reliable than the meta-QTL (MQTL). Therefore, an MQTL analysis using a consensus genetic map was begun, containing 71,778 markers and 177 QTL reported in 32 studies involving 42 mapping populations derived from 62 different parental lines of durum and common wheat. The study resulted in 37 MQTL located on 18 wheat chromosomes (excluding 1D, 2D, and 4D). The average CI of the MQTL was mostly lower than the CI of the original QTL. Individual MQTL contained two to seven original QTL. The PVE (%) due to an individual MQTL ranged from 4.58 to 82.58. The MQTL identified during the present study should help in marker-assisted selection for pyramiding minor and partial-effect resistance genes to develop cultivars with durable resistance to stem rust. The knowledge of MQTL and the associated candidate genes should facilitate further work on cloning of QTL.



**Meta-QTL and candidate genes for stripe rust.** In bread wheat, a meta-QTL analysis for stripe rust was conducted using 353 known QTL. When projected onto a dense consensus map comprised of 76,753 markers, only 184 QTL with the required information could be utilized, leading to the identification of 61 MQTL spread over 18 of the 21 chromosomes (excluding 5D, 6D, and 7D). The range of the mean  $R^2$  (PVE %) was 1.9% to 48.1%, and that of the CI was 0.02 to 11.47 cM. These CIs also carried 37 Yr genes. Using these MQTL, 385 CGs were identified. Of these, 241 CGs encoded known R proteins and 120 showed differential expression due to stripe rust infection at the seedling stage. The remaining 24 CGs were common, in the sense that they encoded R proteins as well as showed differential expression. The proteins encoded by CGs carried the following widely known domains: NBS-LRR domain, WRKY domains, ankyrin repeat domains, and sugar transport domains. Thirteen breeders' MQTL (PVE > 20%), including four pairs of closely linked MQTL, are recommended for use in molecular breeding for future studies to understand the molecular mechanism of stripe rust resistance and for gene cloning.

**Meta-QTL for multiple disease resistance (MDR) to three rusts.** Developing cultivars with MDR to leaf (LR), stem (SR), and yellow (YR) rusts is a major goal in wheat breeding programs worldwide. Therefore, this study used meta-QTL and CGs using 152 individual QTL mapping studies to identify resistance to all three rust diseases. From these 152 studies, a total of 1,146 QTL for resistance to the three rusts were retrieved, including 368 for LR, 291 for SR, and 487 for YR. Of these 1,146 QTL, only 718 could be projected onto a consensus map saturated with 2,34,619 markers. Meta-analysis of the projected QTL resulted in 86 MQTL, which included 28 MDR-MQTL. Ten of these MDR-MQTL were breeders' MQTL. Seventy-eight of the 86 MQTL also could be anchored to the physical map of wheat genome and 54 MQTL were validated by MTAs identified during earlier GWAS. Twenty MQTL (including 17 MDR-MQTL) were co-localized with 42 known R genes. *In silico* expression analysis identified several differentially expressed candidate genes encoding proteins carrying each one of the following domains: NBS-LRR, WRKY domains, F-box domains, sugar transporters, and transferases. The introgression of these MDR loci in high-yielding cultivars should prove useful for developing high-yielding cultivars with resistance to all three rusts.

**Meta-QTL for MDR for five diseases (*Septoria tritici* blotch, *Septoria nodorum* blotch, *Fusarium* head blight, Karnal bunt, and loose smut).** We identified MQTL and candidate genes for MDR against five diseases, *Septoria tritici* blotch (STB), *Septoria nodorum* blotch (SNB), *Fusarium* head blight (FHB), Karnal bunt (KB), and loose smut (LS). For this purpose, information on a total of 493 QTL for STB (126), SNB (103), FHB (184), KB (33), and LS (14) were collected from 58 independent studies. Of these QTL, 291 QTL were projected onto a consensus genetic map. This exercise resulted into 63 MQTL. The CI of individual MQTL ranged from 0.04 to 15.31 cM, with a mean of 3.09 cM; a significant reduction (~4.39 fold) from the CI of the original QTL used. Thirty-eight of these 63 MQTL were validated using MTAs derived from GWAS. Three promising MQTL (MQTL2B.2, MQTL3B.2, and MQTL4A.1) were recommended for marker-assisted breeding for MDR in wheat. Furthermore, a number of R and defense genes also were detected within these MQTL regions. *In silico* expression analysis revealed 194 differentially expressed candidate genes; 85 of these genes have been previously reported to be associated to disease resistance. These findings could be useful in focusing on hot spots on different chromosomes for fine mapping of genes for MDR and marker-assisted breeding.

**GWAS and interval mapping for resistance to cereal cyst nematodes (CCN).** Cereal cyst nematode (*Heterodera avenae*) is among the most important plant parasitic nematode species reported worldwide, causing significant yield losses in wheat. Genome-wide association studies and QTL interval mapping were used to study the genetics of resistance against *H. avenae*.

**Genome-wide association studies.** Two association mapping panels were used for GWAS analysis. The first panel consisted of 180 exotic wheat genotypes (genotyped with a 15K SNP array; genotyping data obtained from IPK, Gatersleben, Germany). The second panel consisting of 141 indigenous wheat genotypes (genotyped with a 35K SNP array) obtained from NBPGR, New Delhi. Both panels were screened for resistance to *H. avenae* under controlled environmental conditions for 2 years with a minimum of five replicates of each genotype. For both studies, ANOVA showed significant phenotypic variation for number of cysts in the roots and in the soil. Single-locus (GLM, MLM, CMLM, and ECMLM) and multi-locus (FarmCPU, Blink, and MLM) models were used to identify the MTAs. This study further suggested that few MTAs co-localized with the previously reported MTAs/QTL for CCN. A more detailed analysis of the results is being carried out.

**Interval mapping.** For interval mapping, the novel doubled-haploid ITMI mapping population (114 individual lines) derived from the cross 'synthetic wheat M6/Opata' and a RIL mapping population consisting of 149 lines derived from the cross 'HUW468/C306' were phenotyped for QTL related to CCN resistance. Genotyping data for both the

populations was available. The phenotypic and genotypic data are being used to study the genetic architecture of the plant–nematode interaction and identify QTL for CCN resistance. These QTL could serve as target regions for MAS in breeding programs aimed at development of wheat genotypes that are resistant to CCN.

**GWAS for powdery mildew resistance.** A spring wheat panel was phenotyped for resistance to powdery mildew. Using the Dunnett test, 29 genotypes were identified as resistant to powdery mildew in comparison to the check cultivar WL711. This panel was mapped with 17,937 polymorphic SNPs of a 90K SNP array. The panel was structured and was divided into four subpopulations, G1, G2, G3, and G4. The four subpopulations included 40 (G1), 21 (G2), 35 (G3), and 129 (G4; admixture) genotypes. Based on a principle component analysis, the percentage of variance for first, second, and third component was 8.6, 4.2, and 3.0, respectively. GWAS conducted using data collected over 2 years gave 23 MTAs ( $P < 0.0001$ ). Three of these MTAs were detected over both the years, suggesting their stable nature. Using a 200-kb window (100-kb upstream and 100-kb downstream) for each the 23 MTA, 124 CGs were identified. Gene ontology analysis showed the involvement of CGs in different pathways. These genes contained the following domains: tubulin, leucine rich repeat 4, histone H2A, histone H2B, F-box domain, zinc finger, RING-type, protein kinase domain, cytochrome P450, and leucine-rich repeat. Digital expression analysis showed differential expression of 24 genes in different tissues and organs following infection with powdery mildew. Our results may be utilized in developing powdery mildew-resistant cultivars.

**GWAS for spot blotch resistance.** We used a spring wheat reference set (SWRS) comprised of 303 accessions that were genotyped for 12,160 SNP markers (generated using DArT-seq at Diversity Array Technology Pvt. Ltd., Australia, under the ‘Seed for Discovery’ project at CIMMYT). This panel was phenotyped at BHU, Varanasi (Uttar Pradesh), and the BISA Farm, Samastipur (Bihar) for the following three spot blotch disease related traits: (i) area under disease progress curve (AUDPC), (ii) incubation period, and (iii) lesion number. GWAS was conducted using four single-locus models (SLMs) (GLM, MLM, CMLM, and SUPER (available in GAPIT)) and nine multi-locus models (MLMs) (mrMLM, FASTmrMLM, FASTmrEMMA, ISISEM-BLASSO, pKwMEB, pLARmEB (computed in R with the package mrMLM), MLMM, FarmCPU, and BLINK (available in GAPIT)). A threshold  $p$ -value ( $p < 0.001$ ) was adopted to declaring a MTA/QTN. A total of 148 MTAs/QTNs were detected by four SLM models, whereas 381 MTAs/QTNs were detected by nine MLM models. The maximum number of MTAs was found for lesion number (62) in SLM using all the four models, whereas all the nine MLM models together detected the maximum number of MTAs (173) for the AUDPC. The MTAs from both model types (SLM and MLM) are being subjected to identification of CGs. Identified CGs and QTNs/MTAs may prove useful for molecular breeding for the development of spot blotch-resistant wheat cultivar and also may be the potential target for future molecular studies.

### ***Genetics of some other traits: nitrogen use efficiency (NUE), yield, grain morphology, grain mineral content, and grain quality.***

**Genetic variability for NUE and its components.** Nitrogen (N) is one of the essential macro-nutrients for plant growth and development. Excessive use of N fertilizers in commercial wheat cultivation causes severe environmental degradation. Breeding of genotypes with improved NUE may give high yield at a low or optimum level of N. Thus, examining the genetic variability for NUE and its two component traits, namely N uptake efficiency (NUpE) and N utilization efficiency (NUE), as well as other agronomic traits in wheat is necessary. In this study, a set of 21 Indian wheat cultivars was evaluated under four different N levels (0, 60, 120, and 180 kg/ha) in a split-plot design over 3 years at the IIFSR, Modipuram, Meerut. An ANOVA showed significant variation among cultivars for all traits except days-to-anthesis under all the four N levels. The ‘genotype  $\times$  N level’ interaction also was significant for all the traits with a few exceptions. NUE was negatively correlated with grain yield at increasing N levels. Three wheat cultivars (HUW468, PBW343, and HD2967) had a relatively high NUE and a high grain yield over different N levels. Cultivar HUW468 (high NUE) was crossed with a tall cultivar, C306 (low NUE), and an RIL mapping population was developed. This mapping population is being used for QTL analysis for NUE and related traits.

**QTL analysis for NUE and its component traits.** Genetics of NUE and related traits was examined using 149 RILs, derived from a cross between the cultivars HUW468 (with high NUE) and C306 (low NUE parent). The mapping population was grown in an augmented block design under four different N levels (0, 60, 120, and 180 kg/ha) over 3 years. Phenotypic data on NUE, NUpE, and NUtE was collected on the parents and RILs. Genotyping used the GBS (genotyping-by-sequencing) approach, where 5,717 polymorphic markers were available for linkage analysis. Eventually only 518 marker loci could be mapped, which were distributed on 26 linkage groups with a total coverage of 2,837.24 cM.

This genetic map and phenotypic data were used for QTL interval mapping. A varying number of significant main effect QTL (range of LOD=2.5 to 9.26) were detected on 11 different chromosomes (1B, 1D, 2B, 3A, 4B, 5A, 5B, 5D, 6A, 6D, and 7A) for NUE (25), NUpE (18), and NuTE (08). Twenty-eight QTL were detected across N levels of 60, 120, and 180 kg/ha. Overall, nine QTL also were detected for two or all the three traits under different N levels. The QTL explained up to 7.09 % to 22.89 % of the phenotypic variation. Thirty-eight (38) epistatic QTL (E-QTLs) distributed on nine different chromosomes (1B, 1D, 2A, 4B, 4D, 5A, 5D, 6B, and 6D) also were detected, including nine QTL for NUE, 11 for NUpE, and 18 for NuTE. Twelve of the E-QTL were major QTL with PVE ranging from 15.48–20.52%. A set of 19 E-QTL were identified under more than one N level. These QTL could prove useful for marker-assisted breeding for improvement of NUE in wheat.

**Meta-QTL for NUE and related traits.** MQTL, ortho-MQTL, and CGs for NUE and associated traits were identified. For this study, information on 1,788 QTL was collected from 24 publications (2006–2020). Of these, 1,098 QTL were projected onto a consensus map, giving 118 MQTL. The average confidence interval (CI) of the MQTL was reduced by up to 8.56 times compared to the CI of the original QTL. Out of 118 MQTL, 112 could be physically anchored to the wheat reference genome. MQTL were located within the physical intervals ranging from 0.02 to 666.18 Mb (average = 94.36 Mb). Eighty-eight of the 112 MQTL were verified using MTAs reported in earlier GWAS. The verified MQTL also included nine of the most robust MQTL, or breeders' QTL. MQTL also identified nine ortho-MQTL for wheat and maize. Among 1,991 CGs available from the MQTL, 97 were selected to be significant for the traits under study. In the MQTL regions, 49 orthologs of 35 rice genes were detected based on homology analysis and expression patterns. These findings could prove useful when developing a better selection approach for yield potential, stability, and performance under N-limited conditions.

**Meta-QTL for grain yield and its components.** A large number of QTL are identified in wheat for grain yield and its component traits. However, in practical wheat breeding, these QTL have been seldom used. In order to make use of these QTL in wheat breeding and basic research, a meta-QTL analysis was undertaken. For this purpose, 8,998 known QTL, including 2,852 significant QTL for grain yield and 10 related traits were used: (i) grain weight, (ii) grain morphology related traits, (iii) grain number, (iv) spike-related traits, (v) plant height, (vi) tiller number, (vii) harvest index, (viii) biomass yield, (ix) days-to-heading/flowering and maturity and (x) grain-filling duration. The QTL included in this work were collected from 230 reports based on 190 mapping populations (1999–2020). The analysis revealed 141 MQTL with an average confidence interval (CI) of 1.37 cM (an 8.87-fold reduction), compared to an average CI of >12.15 cM of the original QTL. These included 63 robust MQTL, each based on at least 10 original QTL, with 13 MQTL classified as breeders' QTL. Following a functional analysis of these MQTL, 1,202 CGs were discovered, including 18 known genes. The MQTL also contained 50 wheat genes that were homologous to 35 known rice, barley, and maize genes for yield-related traits. Additionally, using synteny and collinearity, we identified 24 ortho-MQTL among wheat, barley, rice, and maize. The findings of this study should be useful for wheat breeding and basic research across these four cereal crops. Breeders QTL, in particular, can be exploited for marker-assisted selection for grain yield and fine mapping leading to cloning of QTL/genes for yield and associated traits.

**Meta-QTL, ortho-MetaQTL, and candidate genes for grain Fe (GFe) and Zn (GZn) content.** For the purpose of MQTL analysis for GFe and GZn contents, information on QTL was collected from 12 studies that utilized 14 mapping populations. Information about 141 QTL for both the traits were collected and 32 of these QTL could be projected utilizing a high-resolution genetic map of wheat consisting of 76,743 markers. This exercise identified 11 MQTL for GFe and GZn content, which included nine novel MQTL. Eight MQTL were located on three A-genome chromosomes (5A, 6A, and 7A) and three MQTL were located on a chromosome 5B. Eight of these 11 MQTL controlled both GFe and GZn; the remaining three MQTL controlled only GZn. The MQTL3.5A also was verified using reported GWAS-MTAs. The confidence intervals of the MQTL were narrower (0.51–15.75 cM) relative to those of the corresponding QTL. Two ortho-MQTL conserved over three cereals (wheat, rice, and maize) and 101 CGs underlying the MQTL also were identified. The proteins encoded by the 12 prioritized CGs contained important domains (zinc finger, RING/FYVE/PHD type, and FAD linked oxidase), which are involved in metal ion binding, heme binding, and iron binding. A qRT-PCR analysis conducted for four of the 12 CGs showed a significant differential expression in the genotypes differing for GFe and GZn content at 14 and 28 days-after-anthesis. The identified MQTL/CGs may be utilized in marker-assisted selection for improvement of GFe/GZn content and also for the understanding of the molecular basis of GFe/GZn homeostasis in wheat.

**GWAS and meta-GWAS for GFe, GZn, and phytate contents.** A set of 310 wheat genotypes (Indian wheat cultivars, landraces from Watkin's collection and genetic stocks with improved grain quality) is being used as an association mapping panel for grain GFe, grain GZn, and phytate concentrations. The panel previously was genotyped using a wheat Illu-

mina iSelect 90 K Infinium SNP array and was planted in alpha lattice design at three locations (Meerut, Pantnagar, and Ludhiana) during the current crop season for collecting phenotypic data. This panel also was phenotyped during 2020–21 at the three locations, but only at Meerut during 2019–20. The GFe and GZn concentrations were estimated using ED-XRF. Mean concentration ranged from 24.9 to 45.88 ppm for GZn and from 20.25 to 44.22 ppm for GFe. GWAS will be conducted using phenotypic data collected from all the locations and years. Meta-GWAS also is planned to detect stable MTAs with significant effects across multiple association mapping panels and environments. The linked markers and associated candidate genes will be identified and validated in new biparental mapping populations for marker-assisted breeding.

**GWAS for grain morphology traits.** The genetic architecture for six grain morphology traits, (i) grain cross-sectional area (GCSA), (ii) grain perimeter (GP), (iii) grain length (GL), (iv) grain width (Gwid), (v) grain length-width ratio (GLWR), and (vi) grain form-density (GFD), was examined using an association mapping panel consisting of 225 diverse spring wheat genotypes. The panel was genotyped for 10,904 SNPs markers and phenotyped for two consecutive years (2017–19). GWAS was conducted using five different models including two single-locus models (CMLM and SUPER), one multi-locus model (FarmCPU), one multi-trait model (mvLMM), and a model for ‘Q x Q’ epistatic interactions. False discovery rate (FDR) ( $p\text{-value} -\log_{10}(p) \geq 5$ ) and Bonferroni correction ( $p\text{-value} -\log_{10}(p) \geq 6$ ) (corrected  $p\text{-value} < 0.05$ ) were applied to eliminate false positives due to multiple testing. This exercise gave 88 main effect and 29 epistatic MTAs after FDR and 13 main effect and six epistatic MTAs after Bonferroni corrections. MTAs obtained after Bonferroni corrections were further utilized for identification of 55 CGs. *In silico* expression analysis of CGs in different tissues and different parts of the seed at different developmental stages was made. MTAs and CGs identified during the present study are a useful addition to available resources for MAS to supplement wheat-breeding programs after due validation and also for future strategic basic research.

**GWAS for grain mineral contents.** For conducting GWAS for a variety of mineral contents (comprising macro- and micro-elements) in wheat grains, a set of 310 genotypes (Indian wheat cultivars, landraces from Watkin’s collection, and genetic stocks with improved grain quality) were sown in November 2021 at three locations, (i) Agriculture Research Farm, Ch. Charan Singh University, Meerut (U.P.), (ii) Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pant Nagar (Uttarakhand), and (iii) Punjab Agriculture University, Ludhiana (Punjab), in two replications in the alpha lattice experimental design. Variation was noted for heading date and anthesis among the genotypes at the three locations. Grain mineral contents will be analyzed using harvested seed. The grain mineral data and genotypic data will be used to find significant MTAs using a variety of single-locus and multi-locus models, which should prove useful for identification of candidate genes and development of molecular markers for future wheat breeding.

### ***Wheat QTL database.***

**WheatQTLdb (v2.0).** We curated and released a largest database for hexaploid wheat QTL (WheatQTLdb: [www.wheatqtl.net](http://www.wheatqtl.net)) in 2021 that included 11,552 QTL. More recently we released version 2.0 of the database, which includes information on QTL, meta-QTL, and epistatic QTL for a variety of traits reported in hexaploid wheat (*Triticum aestivum*) and seven related species *T. turgidum* subsps. *durum*, *turgidum*, *dicoccoides*, and *dicoccum*; *T. monococcum* subsps. *monococcum* and *aegilopoides*; and *Aegilops tauschii*. WheatQTLdb v2.0 includes 27,518 main-effect QTL, 202 epistatic QTL, and 1,321 meta-QTL, along with links to their genetic maps and references. This newly released WheatQTLdb v2.0 will provide plant breeders and geneticists much more valuable options to search and choose the category, trait and chromosome-wise data for QTLs for their research or breeding programs.

### ***Breeding using molecular marker-assisted selection (abiotic/biotic stress tolerance and grain quality).***

**MAS for drought tolerance.** A marker-assisted, back-cross breeding scheme was followed in two crosses involving SQ1 as a donor parent and the two recipient Indian wheat cultivars HD2967 and DBW88. In each generation, foreground MAS used SSR marker *Xwmc273.3* (linked to QTL *Qyld.csdh.7AL*) until BC<sub>2</sub>F<sub>3</sub> for the selection of plants homozygous for the QTL followed by phenotypic selection of the positive plants that resembled the recipient parents. These selected homozygous plants were advanced to the BC<sub>2</sub>F<sub>5</sub> following selfing. The BC<sub>2</sub>F<sub>5</sub> progenies were screened for rust resistance and a total of 94 BC<sub>2</sub>F<sub>6</sub> resistant (stripe rust) progenies of the above two crosses were selected. These selected progenies, along with nine high-yielding checks, were evaluated in a preliminary yield trial under irrigated and rainfed conditions (only one irrigation, 40 DAS) during the 2020–21 crop season at the research farm of CCS University,



Meerut (U.P.). Phenotypic data were scored on 10 traits: (i) days-to-heading, (ii) days-to-anthesis, (iii) days-to-maturity, (iv) plant height, (v) chlorophyll content, (vi) grains/spike, (vii) 1,000-kernel weight, (viii) grain yield, (ix) biomass, and (x) harvest index. The selfed BC<sub>2</sub>F<sub>7</sub> progenies of both crosses are being evaluated again in the 2021–22 crop season at CCS University, Meerut, and the Agharkar Research Institute (ARI), Pune (Maharashtra) under similar conditions. Data on the above 10 traits is being recorded at both the locations. After the analysis of data, high-yielding progenies with improved drought tolerance will be submitted for testing under IPSPN and national varietal development trials conducted by ICAR-Indian Wheat and Barley Research (IIWBR), Karnal.

#### **Pyramiding of genes for grain protein content, grain quality, and rust resistance (a multi-institutional effort).**

Improvement of grain protein content (GPC), loaf volume, and resistance to three rusts was achieved in 11 Indian wheat cultivars that are widely grown in four different agro-climatic zones of India. We used marker-assisted, back-cross breeding for introgression and pyramiding of the following genes: (i) the high GPC gene *Gpc-B1*; (ii) HMW-glutenin subunits 5+10 at the *Glu-D1* loci, and (iii) rust resistance genes, *Yr36*, *Yr15*, *Lr24*, and *Sr24*. GPC increased by 0.8% to 3.3%, although high GPC was generally associated with a yield penalty. Further selection among the high GPC lines identified progenies with higher GPC associated with improvement in 1,000-kernel weight and grain yield in the backgrounds of four cultivars, NI5439, UP2338, UP2382, and HUW468. The high GPC progenies (derived from NI5439) also were improved for grain quality using HMW-glutenin subunits 5+10 at the *Glu-D1* loci. Similarly, progenies combining high GPC and rust resistance were obtained in the backgrounds of five cultivars, Lok1, HD2967, PBW550, PBW621, and DBW1. These improved, prebreeding lines developed with a multi-institutional effort should prove a valuable source for developing cultivars with improved nutritional quality and rust resistance in ongoing wheat-breeding programs.

**Pyramiding of rust resistance genes into high grain quality wheat lines.** Marker-assisted selection was used to pyramid QTL/genes for improved grain quality (GPC and preharvest sprouting tolerance) and resistance to all the three rusts using the improved cultivars HD2967 and Lok1: (i) HD2967 (*Gpc-B1/Yr36 + Lr24*), (ii) HD2967 (*Lr19/Sr25 + Yr10 + Lr34*), and (iii) Lok1 (*Gpc-B1/Yr36 + Lr24 + Qphs.dpivic.4A.2*). Using these three genotypes, we attempted the following two crosses: (1) 'HD2967 (*Gpc-B1/Yr36 + Lr24*) × HD2967 (*Lr19/Sr25 + Yr10 + Lr34*)' and (2) 'Lok1 (*Gpc-B1/Yr36 + Lr24 + Qphs.dpivic.4A.2*) × HD2967 (*Lr19/Sr25 + Yr10 + Lr34*)'. Foreground MAS for all the genes/QTL was conducted from the F<sub>2</sub> to F<sub>4</sub> generations. Selected F<sub>5</sub> plants, homozygous for the above QTL/genes, were raised simultaneously at the Research Farm of CCS University, Meerut, for seed multiplication and screening for rust resistance under high-disease pressure in field conditions at IIWBR, Karnal. Selected F<sub>6</sub> progenies pyramided with QTL/genes were raised at Wellington, Tamil Nadu, to evaluate for disease resistance and seed multiplication. A preliminary yield trial was conducted for the selected resistant F<sub>7</sub> progenies at the Research Farm of CCS University, Meerut, during 2020–21 crop season and the data recorded. Promising progenies are being evaluated this year (2021–22) in trials at CCS University, Meerut, and GBPUA&T Pantnagar. High-yielding progenies with improved grain quality and rust resistance will be identified and submitted for testing under national varietal development trials conducted by IIWBR, Karnal.

Pyramiding of rust resistance genes in genotypes with improved grain quality is being undertaken in parallel for two new crosses involving the widely adapted cultivar PBW723 (*Lr37/Yr17/Sr38 + Lr76/Yr70*) as donor and HD2967 (*Gpc-B1/Yr36 + Lr24*) and Lok1 (*Gpc-B1/Yr36 + Lr24 + Qphs.dpivic.4A.2*) as recipients. Thirty F<sub>2</sub> plants were selected from the cross 'HD2967 (*Gpc-B1/Yr36 + Lr24*) × PBW723 (*Lr37/Yr17/Sr38 + Lr76/Yr70*)' and 22 F<sub>2</sub> plants were selected from the cross 'Lok-1 (*Gpc-B1/Yr36 + Lr24 + Qphs.dpivic.4A.2*) × PBW723 (*Lr37/Yr17/Sr38 + Lr76/Yr70*)' on the basis of foreground selection in the 2020–21 crop season. Derived F<sub>3</sub> populations are being raised in 2021–22 and foreground MAS for pyramiding of a number of genes is being carried out.

**MAS for heat stress tolerance.** Marker-assisted selection was initiated to transfer desirable alleles of 10 QTL reported earlier for six different heat-responsive traits from the high-yielding, heat-tolerant, Egyptian cultivar Giza168 into the background of the popular Indian wheat PBW343 following a marker-assisted, back-cross breeding scheme. BC<sub>2</sub>F<sub>1</sub> plants carrying 3–8 QTL and resembling the recipient parent were selected in 2018–19 and backcrossed to the recipient parent. Foreground MAS and phenotypic selection in the BC<sub>3</sub>F<sub>1</sub> during the 2019–20 crop-season led to selection of 780 plants containing a combination of 2–5 different QTL and having a high degree of resemblance to the recipient parent PBW343. Selected BC<sub>3</sub>F<sub>1</sub> plants were selfed and the BC<sub>3</sub>F<sub>2</sub> seed obtained. In the current crop season, 2021–22, the BC<sub>3</sub>F<sub>2</sub> progenies of 780 plants (along with check cultivars) are being evaluated in an augmented block design at the Research Farm, CCS University, Meerut (UP), under late-sown conditions. These progenies are being phenotyped for 10 traits: (i) days-to-heading, (ii) days-to-anthesis, (iii) canopy temperature, (iv) chlorophyll content, (v) maximum rate of senescence, (vi) grain-filling duration, (vii) plant height, (viii) days-to-maturity, (ix) kernel weight of main spike, and (x)

grain yield/plot. Selected, high-yielding progenies will be evaluated in preliminary yield trials under heat stress conditions during 2022–23 to identify desirable lines.

**MAS for high grain Fe and grain Zn content.** Fe and Zn deficiency is a serious problem worldwide, especially in developing countries. *Aegilops kotschy* has a genetic system for micronutrient uptake, translocation, and sequestration that is distinct from that in wheat cultivars. Segments of *Ae. kotschy* with metal homeostasis genes were transferred into wheat by Professor H.S. Dhaliwal at Eternal University, Baru Sahib (H. P.). These segments were found to be compensating. The introgressed lines showed higher GFe and GZn content, which was associated with improved yield relative to elite wheat cultivar PBW343 LrP. The intron targeted amplified polymorphic (ITAP) markers developed for the *YSL15*, *IREG*, *FRO7*, *NAS2*, and *ZIP2* genes controlling high GFe and GZn in wheat for use in MAS. Three crosses involving the introgression lines and carrying different genes were attempted to pyramid genes, (i) 'EU13124-25-2-2-4 (*YSL15*) x EU13124-25-2-2-2 (*YSL15*, *FRO1-7BS-2*)', (ii) '77-33-2-5-2 (*IREG*) x EU13124-25-2-3-4 (*YSL15*)', and (iii) 'PRH3-15-5 (*YSL15*) x 49-1-73-8-5 (*IREG*, *FRO7*, *NAS2*, *ZIP2*)'. Foreground MAS for all the genes was conducted in the F<sub>2</sub> and F<sub>3</sub> generations at Eternal University, Baru Sahib. Selected F<sub>4</sub> plants are being raised at the Research Farm of CCS University, Meerut, during 2021–22 for further foreground selection for pyramiding of genes for high GFe and GZn content available in the introgressed parental lines.

### ***Other marker-assisted selection trials.***

We also are conducting four trials of our material that was developed earlier using MAS during the current season (2021–22) to collect data on 10 agronomic traits. The collected data will be utilized for registration of the tested lines with ICAR-National Bureau of Plant Genetic Resources, New Delhi.

**Lines with high grain protein content (GPC) and leaf rust resistance.** We have introgressed the high-GPC gene *Gpc-B1* and *Lr24* into the wheat cultivars Lok1 and HD2967 using MAS. Five improved lines in the Lok1 background and one improved line in a HD2967 background were selected on the basis of foreground MAS followed by phenotyping for three consecutive years at multiple locations. The GPC level in the Lok1 background ranged from 12.9% to 13.3%, compared to 12% in recipient Lok1 parent, and the line in the HD2967 background contained 14% GPC, compared to 12.9% in recipient HD2967 with no yield penalty. A station yield trial in randomized block design with three replications is being carried out for the above lines along with the six national checks (HD3086, WH1124, DBW187, WH1105, DBW173, and DBW71) during the current 2021–22 season.

**Preharvest sprouting tolerance (PHST), high GPC, and leaf rust resistant lines.** A major QTL for PHST (*QPhs.dpi.vic.4A.2*) was introgressed by us earlier into Lok1 wheat (PHS susceptible) from two PHS-tolerant, white-grained cultivars AUS1408 and CN19055. The PHST lines were used for pyramiding the PHST QTL with one gene each for high grain protein content (*Gpc-B1*) and leaf rust resistance (*Lr24*). This resulted into four lines containing the PHST QTL with *Gpc-B1* and *Lr24* genes. These lines exhibited a high level of PHST (PHS score 2–3) associated with significant improvement in GPC (1–2%) with no yield penalty, but carrying resistance against leaf rust under artificial epidemic conditions. A station yield trial of the above lines along with six national checks (HD3086, WH1124, DBW187, WH1105, DBW173, and DBW71) is being carried out during the 2021–22 crop season in a randomized block design with three replications.

**Lines with genes/QTL for disease resistance, GPC, gluten content, grain weight, and PHST.** We have pyramided genes/QTL for GPC (*Gpc-B1*), gluten content (*Glu-A1-1/GluA1-2*), PHST (*QPhs.ccsu-3A.1*), grain weight (*QGw.ccsu-1A.3*), leaf rust (*Lr76*, *Lr37*, *Lr24*), stem rust (*Sr38* and *Sr24*), and stripe rust (*Yr17*, *Yr36*, and *Yr70*) in the background of wheat cultivar PBW343. Following foreground MAS and phenotyping at multiple locations, six lines were selected that showed improved GPC with high yield and also resistance to five pathotypes of *Puccinia triticina*, seven pathotypes of *P. graminis* f. sp. *tritici*, and two pathotypes of *P. striiformis* f. sp. *tritici* that occur in major wheat-growing areas of India. In 2021–22, we are conducting a station yield trial of these lines along with six national checks (HD3086, WH1124, DBW187, WH1105, DBW173, and DBW71) in randomized block design with three replications for collection of data on 10 agronomic traits.

**Lines with improved drought tolerance.** In an earlier study, we introgressed a major QTL (*Qyld.csdh.7AL*) contributing to >20% higher yield/spike yield under stress environments (including drought stress) from wheat genotype SQ1 into four popular Indian wheat cultivars (HUW234, HUW468, K307, and DBW17) using MABB. After phenotypic evaluations for 2 years at two locations and under rainfed conditions, five lines in the background of cultivar HUW234 were

selected on the basis of higher yield under drought stress. The high-yielding progenies also were significantly superior for two or more of the following seven traits: (i) grain number/spike, (ii) grain weight/spike, (iii) tiller number/m<sup>2</sup>, (iv) harvest index, (v) biomass, (vi) canopy temperature, and (vii) chlorophyll content. A station yield trial is being carried out of the above selected five lines with three national checks (GW322, WH1105, and WH1142) under rainfed and irrigated conditions during the 2021–22 season in a randomized block design with three replications for collection of data on 10 agronomic traits.

### *In silico identification and characterization of genes/gene families.*

**RuvBL helicase genes for abiotic stress (heat/drought) tolerance.** *RuvB* family of helicase genes is a conserved family of genes, which occur widely ranging from single-celled organisms (bacteria, yeast) to multicellular organisms (*Drosophila*, human, *Arabidopsis thaliana*, *Oryza sativa*). In this study, nine wheat *RuvBL* genes (*TaRuvBL2a-2A*, *TaRuvBL2a-2B*, *TaRuvbl2a-2D*, *TaRuvBL1b-3A*, *TaRuvBL1b-3B*, *TaRuvbl1b-3D*, *TaRuvBL1a-4A*, *TaRuvBL1a-4B*, and *TaRuvBL1a-4D*) ranging in length from 1,647 to 2,197 bp were identified. For these genes, we also examined (i) promoter analysis, (ii) miRNAs and their targets in *TaRuvBL* genes, (iii) proteins encoded by these genes and their detailed structure (including secondary and tertiary structures and motifs), and (iv) phylogeny. *In silico* expression analysis of these genes suggested that they are differentially regulated under heat and drought. We hope that the results of this study may prove useful in developing wheat cultivars with heat/drought tolerance.

**SIZ1 gene for abiotic stress tolerance.** In plants, ubiquitin and small ubiquitin-like modifier (SUMO) are related small proteins that are members of the large ubiquitin superfamily of post-translational modifiers. The ubiquitinated proteins are destined to 26S proteasome for degradation, whereas SUMO-conjugated (SUMOylation) proteins influence numerous cellular processes such as a plant's response to abiotic stress, such as heat, drought, or salinity. In rice, the SUMO E3 ligase gene *OsSIZ1* has been shown to play an important role in plant response to abiotic stresses. Loss of function of *OsSIZ1* leads to increased sensitivity to drought, heat, and salt stress. Using full-length cDNA and protein sequences of *OsSIZ1* gene as reference, putative orthologs of *SIZ1* were identified in eight monocot and two dicot species. The sequence similarity at the cDNA level ranged from 78.81 to 82.6% in monocots and 58.25 to 59.5 % in dicots. The coding DNA sequence (CDS) similarity ranged from 78.25 to 85.57% in monocots and 60.48 to 63.25% in dicots. Protein sequence similarity ranged from 44.78 to 81.27% in monocots and 47.9 to 52.99% in dicots. Among all the species, 10 distinct motifs belonging to *SIZ1* were identified; eight were novel and two were reported in previous studies. The *SIZ1* proteins were characterized by a single, conserved domain belonging to the PHD\_Bye1p\_SIZ1\_like domain present in all the monocots and dicots. Quantitative real-time polymerase chain reaction analyses revealed that *SIZ1* transcripts were significantly upregulated in wheat seedlings under 6 h heat stress. Two heat tolerant wheat genotypes (Giza168 and IC2538749) showed significant up regulation (>2-fold change) as compared to the two heat sensitive wheat genotypes (PBW343 and HD2967), which showed non-significant up-regulation. Findings from this study provide evidence for conservation of the *SIZ1* gene in different monocot and dicot species and the expression pattern of *TaSIZ1* lays the foundation for further research related to heat tolerance breeding in wheat.

**VMT gene for accumulation of GZn and GFe.** Essential metals, such as Fe and Zn, in grains are important sources for seed germination and to meet the nutritional requirements. However, the molecular mechanism underlying loading of Fe and Zn into grains is poorly understood. The transporter gene *OsVMT* (VACUOLAR MUGINEIC ACID TRANSPORTER) in rice (*Oryza sativa*) has been reported to play an important role in the preferential distribution of mineral elements to the grains. This gene belongs to a major facilitator superfamily. The putative orthologs of VMT in seven monocot and three dicot species were identified using cDNA and protein sequence of *OsVMT* gene as a reference. The sequence similarity at cDNA level ranged from 63.59 to 83.23% in monocots and 51.09 to 60.04 % in dicots. CDS similarity ranged from 71.21 to 84.56% in monocots and 60.07 to 64.44% in dicots. Protein similarity ranged from 44.78 to 81.27% in monocots and 47.9 to 52.99% in dicots. Compared to cDNA, CDS and protein sequences, the genomic sequence similarity was lowest both in the monocots (36.04–61.24%) and dicots (46.95–52.33). In the VMT proteins of the different species, 10 distinct motifs were identified, eight of which were novel and two were already reported for Major Facilitator Superfamily. The VMT proteins were characterized by a single, conserved domain belonging to Major Facilitator Superfamily domain and was present in all the monocots and dicots. In wheat, qRT-PCR differential expression of six *TaVMT* genes at two grain filling stages (14 DAA and 28 DAA) was examined in four pairs of genotypes, which included two genotypes, each containing high GZn and GFe content (FAR4 and WB02), and another two genotypes with low GZn and GFe content (K8027 and HD3226). In each pair, the expression in the high GZn and GFe containing genotype (first genotypes) was compared with the low GZn and GFe containing genotype (second genotype).

All six genes most often showed significant differential expression (>2-fold and >-2-fold) between pairs of genotypes in both grain-filling stages suggesting their possible role in accumulation of Zn and Fe in the grains.

### ***Epigenetic regulation of leaf rust.***

**DNA methylation due to *Lr28* using BS-seq.** Continuing our earlier studies aimed at understanding the role of epigenetic regulation of defense genes during leaf rust resistance mediated by *Lr28* gene in wheat, a pair of wheat NILs for the *Lr28* gene (R) in the background of an Indian cultivar HD2329 (S) was used to study DNA methylation-mediated regulation of gene expression. Leaf samples were collected at 0 h before (S0 and R0) and 96 h after inoculation (S96 and R96). The DNA samples, subjected to BS-Seq and BS-Seq libraries, were used to identify differentially methylated/demethylated regions and genes (DMRs and DMGs) from the following four pairs of comparisons: S0 vs S96, S0 vs R0, R0 vs R96, and S96 vs R96. A major role of CHH methylation relative to that of CG and CHG methylation was observed. Some important observations include the following: (i) an abundance of CHH-methylation among DMRs; (ii) a predominance of DMRs in intergenic region, relative to other genomic regions (promoters, exons, introns, TSS, and TTS); (iii) an abundance of transposable elements in DMRs with CHH context; (iv) a demethylation-mediated, high expression of genes during susceptible reaction (S0 vs S96) and a methylation-mediated low expression of genes during resistant reaction (R0 vs R96 and S96 vs R96); (v) major genes under regulation encode proteins, which differ from those encoded by genes regulated during susceptible reaction; and (vi) ~500 DMGs carried differential binding sites for H3K4/K27me3 marks, suggesting joint involvement of DNA and H3 methylation. Thus, CHH methylation, either alone or in combination with histone methylation, plays a major role in regulating the expression of genes involved in wheat-leaf rust interaction.

### ***Reviews written during 2021–22.***

***SWEET* genes for disease susceptibility.** *SWEET* genes in several crops are exploited by pathogens for the supply of sugar and, thus, cause infection. The subject was reviewed in Gupta (2021) and Gupta et al. (2021).

**SVs and k-mers for GWAS.** New molecular markers for GWAS are regularly developed to be used for QTL interval mapping and GWAS. SVs and k-mers are two such new marker systems that have been developed in recent years and utilized in a number of studies. The subject has been summarized in a Forum article in *Trends in Genetics* and a full length review was published in *BioEssays* (Gupta 2021a, 2021b).

**Earth Biogenome Project.** Earth Biogenome Project, which involves sequencing of the genomes of all  $1.8 \times 10^6$  species of eukaryotes (including single celled protozoan eukaryotes) that was launched in 2018 has already made significant progress. The subject was covered in a Special Feature in the 25 November, 2021, issue of the *Proceedings of the National Academy of Sciences*. This subject was briefly covered in an Forum article that is due to appear as an invited article in *Trends in Genetics* (Gupta 2022).

### ***Wheat stocks and lines for distribution (developed using MAS).***

The following material developed by us is available for distribution for use in genetic and breeding studies after signing a MOA.

- (i) high protein and leaf rust resistant lines containing *Gpc-B1+Lr24* in the backgrounds of the cultivars Lok1 and HD2967 and
- (ii) a line containing a major QTL (*Qyld.csdh.7AL*) for drought stress in the background of the cultivar HUW234. This line had similar yields under irrigated and rainfed environments.

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***Evaluation of wheat germplasm under the All-India Coordinated Research Program on Wheat (AICRP Wheat), crop season 2021–22.***

As one of the voluntary funded centers in Northern Hill Zone for evaluation of advanced wheat breeding lines before their release as cultivars, a set of 16 advanced breeding lines received under Initial Varietal Trails (IVTs) and a set of eight advanced breeding lines received under Advanced Varietal Traits (AVTs) were evaluated for a variety of traits in a randomized complete-block design with four and six replications, respectively. These lines are being evaluated for different morphological, phenological, biotic/abiotic stress, and yield and yield related traits. Promising lines for different traits will be selected and used in different wheat-breeding programs. In addition, segregating stock nursery is being evaluated during the current cropping season for a variety of traits, to select promising transgressive segregants for future breeding programs.

***A multi-tier evaluation of diverse germplasm for understanding the mechanism of cold tolerance.***

A large core set of wheat germplasm containing 4,575 genotypes including checks is being evaluated for cold tolerance in the Kashmir division of J&K, India (Fig. 1, p. 27). Different screening tiers are being used to screen this huge germplasm set. Data was recorded for cold/freezing in the field under natural conditions and under controlled conditions in the greenhouse. The evaluation for cold/freezing tolerance revealed a substantial phenotypic variation available in our germ-

plasm set. The evaluation for cold stress tolerance, based on electrolyte leakage, also depicted substantial variation in the germplasm. Based on this first-tier screening, the germplasm was narrowed down to 10%, constituting a mini-core set. This mini-core currently is being screened in a second-tier for cold tolerance by performing biochemical assays that will help us understand the balance between the generation of reactive oxygen species and activation of antioxidant enzymes in diverse genotypes in response to cold stress. Based on the results of second-tier screening, we will select candidate genotypes that will be evaluated for cold tolerance using more sophisticated approaches, such as metabolomics, lipidomics, and gene expression studies.

### ***Germplasm characterization and introgression of the *Gpc-B1* allele into early maturing wheat.***

In addition to quality, improving the early maturity trait is one of the important objectives in wheat-breeding programs in the western Himalayas of Kashmir Valley. In this region, a successful rice–wheat crop rotation is considered very crucial in achieving self-sufficiency in food production. In the Kashmir Valley, the wheat crop takes ~8 months from sowing to harvest (15 October–15 June) and does not vacate land in time for the cultivation of next crop, i.e., rice. With this back drop, we evaluated a set of 450 germplasm lines for early maturity and quality traits at three different locations in the valley. Substantial genetic variation was found for almost all the traits in the germplasm set evaluated and some promising early maturing, high-yielding, disease-resistant, and highly nutritional lines were identified. Crossing was done to introgress grain protein content (*Gpc-B1*) allele from the cultivar Lok1 into the early maturing wheat WW-101 during the main wheat cropping season of 2020–21. The *Gpc-B1* gene is known to enhance grain Zn, grain Fe, and grain protein concentrations simultaneously, and it regulates senescence. The  $F_1$  seed was sown in pots in the greenhouse as an off-season crop on 15 June, 2021. The  $F_2$  seed was harvested in October 2021 and sown in the main field in November 2021. The  $F_2$  population was evaluated for early maturity through visual observation and genotyped for the *Gpc-B1* allele using the linked markers. Some important segregants, containing both early maturity and the *Gpc-B1* allele, were identified and single plants were harvested. The  $F_{2,3}$  seed was sown in the research field in November 2021 in separate rows with space planting to study the genetics of early maturity and nutrition traits. Segregants containing both early maturity and *Gpc-B1* will be selected and advanced through further generations to obtain the lines with the desired target traits.



**Fig. 1.** Evaluation of a diverse core set of wheat for cold stress tolerance in the fields of the Faculty of Agriculture at the Sher-E-Kashmir University of Agriculture Sciences and Technology.

### ***Characterizing and evaluating wheat germplasm for resistance to biotic stress.***

Under the DBT-funded network project ‘Germplasm Characterization and Trait Discovery in Wheat Using Genomics Approaches and its Integration for Improving Climate Resilience, Productivity, and Nutritional Quality,’ a large, diverse set of wheat germplasm consisting of 4,575 genotypes including checks is being evaluated in the temperate conditions of Kashmir at SKUAST-K, Wadura, under the supervision of Drs. Reyazul Rouf Mir (PI) and Mohd Anwar Khan (Co-PI) (Fig. 2, p. 28). The diverse germplasm with five (05) checks was sown in an augmented block design (ABD) at research farms of the Faculty of Agriculture in October, 2021. This diverse germplasm set is being screened for various biotic stresses including, diseases, such as stripe rust (*P. striiformis*), leaf blight (*Alternaria triticina*), Septoria leaf blotch (*Zymoseptoria tritici*), and spot blotch (*Bipolaris sorokiana*), and insect damage by cereal leaf beetle (*Oulema melanopus*). Substantial variability in the diverse germplasm for these diseases and insect damage has been observed. In addition, the germplasm also is under evaluation for various agro-morphological, phonological, and yield and yield-related traits, using the guidelines released by IIW&BR, Karnal. A large amount of variability for the traits has been observed and high-yielding and early maturing genotypes, which can fit in the rice–wheat double cropping system in the valley, are expected. Furthermore, attempts are being made to transfer genes conferring disease resistance in to the early maturing genotypes through hybridization.



### ***A genome-wide association study for mapping genes for culm strength and related traits.***

Lodging in cereal crops in general, and wheat in particular, poses a serious threat to agricultural production as it reduces wheat yield by 61% and also results in a loss of bread-making consistency. Therefore, breeding for lodging resistant wheat cultivars is one of the most important subject areas of wheat research. During this study, we made an effort to study the natural variation for culm cellulose content/related traits and identify/validate related genes/QTL in Indian Wheats. Experiments were conducted at two locations, at the Faculty of Agriculture, Wadura, SKUAST-K, Sopore, and the Mountain Research Centre for Field Crops, Khudwani, following an augmented block design with 16 blocks in 2019–20 and 2020–21. Each block contained 20 genotypes (16 test and four check entries). Trait data was recorded for 13 important quantitative traits. Some promising genotypes with respect to high cellulose were identified during the study. In addition, a marker-trait association (MTA) study was made using the phenotypic data recorded and genotypic data already available. The study identified some significant MTAs for all the traits in both environments. Validation was done using five SSR markers for culm cellulose content and related traits, among which two markers were found to be associated with three traits lodging traits.



**Fig. 2.** A view of the wheat field and some team members of the wheat research group of Faculty of Agriculture at the Sher-E-Kashmir University of Agriculture Sciences and Technology.

### ***A genetic study of ‘spring × winter’ wheat crosses for yield and yield-related traits.***

Introgression of winter wheat genes into spring wheat is considered one of the best approaches to improve disease resistance, early maturity, and yield and yield-contributing traits in wheat. With this starting point, crosses between ‘spring × winter’ genotypes were made during the 2019–20 crop season (Fig. 3). The  $F_1$  seed was harvested in June 2020 and sown in pots to obtain the  $F_2$  seed. The resulting  $F_2$  population of 1,000 plants was sown in the field in November 2020 and evaluated for different agro-morphological, phenological, disease resistance, and yield and yield-related traits. Many promising transgressive segregants for different traits were obtained. Single plants were harvested from the  $F_2$  population in June 2021, and the  $F_{2,3}$  families were sown in the field during the present cropping season (2021–22). These families are now being evaluated to study the inheritance of different agro-morphological, phenological, disease resistance, and yield and yield-related traits.



**Fig. 3.** Parental genotypes, winter wheat (left) and spring wheat (right) used to develop a ‘spring × winter’ population. These two genotypes differ for plant height, flowering, maturity, awns, leaf size, and disease resistance.

### ***Screening wheat for stripe rust resistance in multiple environments.***

Wheat production in the western Himalayan region is affected by various biotic and abiotic stresses, of which yellow (or stripe) rust, caused by *P. striiformis* f. sp. *tritici*, is the most serious threat. This study screened wheat germplasm for stripe rust resistance at multiple locations of the western Himalayan region of the Kashmir Valley (Fig. 4, p. 29). We investigated spontaneous variation in 262 Indian wheat cultivars released in India over the past 100 years (1906–2006). Adult-plant stripe rust resistance was evaluated during the rabi crop season of 2020–21 at three locations of the western Himalayan region. When graded at the adult-plant stage

following the modified Cobb scale (Peterson et al. 1948) under field conditions, some promising wheat lines with various levels of resistance to yellow rust were obtained. These resistant lines are being evaluated again this cropping season to validate their resistance potential. Resistant lines identified will be used as a potential source for developing stripe rust resistant cultivars in the future.

### ***Characterizing wheat germplasm for pre-harvest sprouting tolerance (PHST).***

Pre-harvest sprouting in wheat is a problem that occurs all over the world to varying degrees. The problem occurs when high humidity accompanies rainfall on standing mature wheat crops before harvest, and seeds in the spike germinate. As the consequence of this, wheat quality as well as quantity are affected, reducing nutritional value and yield. Keeping this in mind, we evaluated a set of 250 bread wheat lines for PHST during the current cropping season. The germplasm set was sown in field at research farm in November, 2021, in an augmented block design using four checks. Any PHS-tolerant lines will be validated with relevant SSR markers. Random SSR markers already available also will be utilized for genotyping of the contrasting lines to identify new marker trait associations for PHST. Crossing will transfer PHST genes/QTL from resistant lines into adapted, high-yielding, but PHST susceptible, lines.



**Fig. 4.** Stripe rust inoculation and identification of stripe rust susceptible genotype in the field of the Faculty of Agriculture at the Sher-E-Kashmir University of Agriculture Sciences and Technology.

### ***Evaluating Indian wheat cultivars for foliar leaf blight.***

Leaf blight of wheat is caused by the fungus *Alternaria triticina*. In the recent past, with changes in the cropping system, foliar blight has now become a major disease in India. We evaluated Indian wheat cultivars for foliar blight in order to find promising candidate genotypes resistant to this disease (Fig 5). A set of 262 Indian wheat cultivars were evaluated for their tolerance to foliar blight disease at four different locations in the Kashmir Valley in an augmented block design. Disease severity was recorded at six different growth stages, from tillering to maturity. Infected leaves showing typical symptoms of circular concentric rings were collected from all four locations. Fresh samples of infected leaves were collected and used to isolate the pathogen. These lines also were grown in the greenhouse for pathogenicity tests to ensure the actual pathogens. We concluded that *Alternaria* spp. were responsible for the disease development in all locations. Of the 262 genotypes screened for resistance to foliar blight, none were 100% resistant to leaf blight at any location. However, 22 genotypes showed a resistance level of 90–99%, another 50 genotypes showed 70–89% resistance; the remaining genotypes were susceptible to the leaf blight. Molecular characterization of the associated pathogen also was carried out using the ITS1 and ITS4 primers. Different isolates of the pathogen obtained by molecular characterization with ITS1/4 have been selected for sequencing.



**Fig. 5.** Leaf blight susceptible genotypes identified during screening of wheat germplasm in the field of the Faculty of Agriculture, Sher-E-Kashmir University of Sciences and Technology.

### ***Wheat field day.***

The Faculty of Agriculture, Wadura campus, SKUAST–Kashmir, is at forefront in developing early maturing wheat cultivars for the Kashmir Valley. Efforts will be made to organize a wheat field day either in the last week of May or first week of June (Fig. 6, p. 30). The main aim of this day will be to make the public, and farmers in particular, aware of the different research activities being carried out by the Faculty of Agriculture. They also will get an opportunity to visualize the status of two early maturing wheat cultivars, WW101 and WW102, developed by SKUAST–K. These cultivars mature by the end of May or the first week of June. We hope that they will play an important role in ensuring food security



in the valley by fitting in the rice–wheat double cropping system. This way, farmers will be encouraged to cultivate wheat after paddy to double their income. Besides these early maturing lines, awareness regarding huge wheat germplasm currently being bred by the Faculty of Agriculture for different traits, including nutritional traits to mitigate hidden-hunger and malnutrition, biotic stress (such as leaf blight, rust, and *Septoria* leaf blotch), abiotic stress (cold and high temperature stress), and physical stress (lodging and preharvest sprouting), with the aim to prevent yield losses caused by these factors. They will also be given an awareness regarding various government schemes of in place for their benefit.



**Fig. 6.** Officials visit the fields of the Faculty of Agriculture at the Sher-E-Kashmir University of Agriculture Sciences and Technology.

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## **CALIFORNIA**

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#### ***Updated annotation of Affymetrix Wheat Genome Array microarray probes.***

Rachel Waymack and Debbie Laudencia-Chingcuanco.

The Affymetrix Wheat Genome Array is a widely used set of microarray probes designed to target over 55,000 transcripts across the wheat genome. This set of probes continues to be used to understand wheat transcriptional activity across a wide range of conditions including drought (Kumar et al. 2018), seed development (Tuan et al, 2019), and viral infection (Kumar et al, 2021). Although a still very useful resource, the Wheat Genome Array probes were designed and annotated prior to the assembly and release of the completed reference wheat genome (Appels et al. 2018). With the completed reference wheat genome, and particularly the most recently updated version (Zhu et al. 2021), many original annotations have become outdated, whereas other probes initially lacking annotations may now be able to accurately be assigned to known genes (De Leeuw et al. 2008). An updated annotation of the Affymetrix Wheat Genome Array probes would improve the knowledge gained by studies utilizing these microarray probes by providing a more accurate picture of the genes and corresponding functions differentially regulated in any tested condition.

Probe IDs in which individual probes mapped to multiple gene IDs in the reference that are all known homeologs were retained and assigned all of the matching homeologous gene IDs. Probe IDs where the individual probes mapped to multiple gene IDs in the reference that are not all known homeologs were dropped and considered unannotated. The 32,971 probe sets were assigned to a gene ID (or multiple homeologous gene IDs) through this mapping to the HC v2.1 reference. The remaining probe IDs where none of the individual probes mapped to the HC reference were then attempted to be annotated using the Affymetrix probe ID on the Ensembl Plants database, allowing an additional 1,216 probe sets to be annotated. Lastly, the remaining probes that both did not map to any sequences in the HC reference and did not have an assigned annotation on Ensembl Plants based on Affymetrix probe ID were mapped to the low confidence (LC) v2.1 reference transcriptome. These mapping results were filtered in the same way as the HC mapping results to only include probe IDs where all individual probes mapped to a single gene ID or multiple gene IDs all known to be homeologs. Mapping to the LC reference resulted in 3,554 more probe sets being assigned a gene ID. In total, we were able to assign 37,741 of the 61,127 probe sets – roughly 62% – on the Wheat Genome Array to a gene ID (or set of homeologous gene IDs).

We hope this updated annotation to the Affymetrix Wheat Genome Array will be useful to wheat researchers both implementing new studies as well as analyzing existing data. The updated probe annotations will allow a more accurate understanding of gene expression regulation and therefore enhance our understanding of the wide array of processes assessed with these probes. We are happy to provide a file containing a list of the updated probe annotations with the newly assigned gene ID for each probe ID, as well as additional information including gene description and GO terms for genes which these features are known. Please contact Dr. Laudencia-Chingcuanco at [debbie.laudencia@usda.gov](mailto:debbie.laudencia@usda.gov) to request a copy of this annotation file

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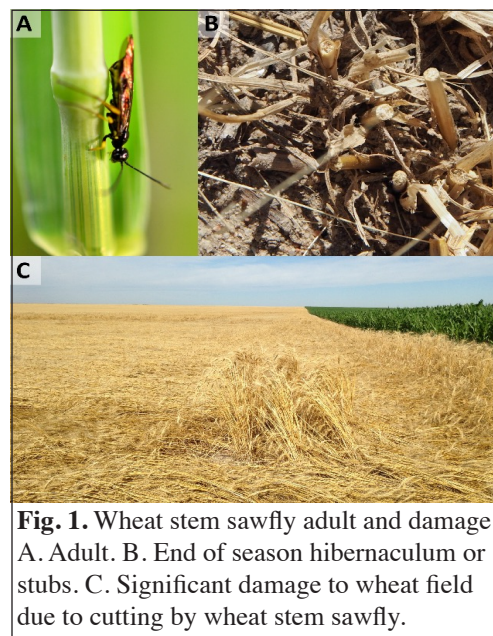
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### ***Wheat stem sawfly: A re-emerging pest in the central Great Plains.***

Punya Nachappa and Erika Peirce.

Among arthropod pests that impact wheat production, the wheat stem sawfly (*Cephus cinctus*) (WSS) is considered one of the most damaging, with grain-yield loss exceeding  $\$350 \times 10^6$  in the northern Great Plains. The WSS is difficult to study and control as most of its univoltine life cycle occurs inside the host stem. The adult WSS lay eggs within the stem of their host, and the larvae feed within the stems until the wheat is nearly mature (Fig. 1A–C). The larva then moves to soil level and cut a V-shaped notch around the interior of the stem (girdling). This girdled section is then filled with frass, which creates a protective solid plug in the pith cavity of the wheat plant, weakening the stem and predisposing it to lodge. Lodged stems result in fallen wheat heads, which are difficult to harvest and prone to being blown away (Fig. 1C). Equally damaging are the impacts in terms of crop residue losses, soil organic matter depletion, and yield losses experienced in crops following wheat in diversified crop rotations.

Major wheat-growing states including Colorado and Nebraska reported initial infestations from WSS in 2010 and 2011. Since then, WSS has been reported in every wheat-growing county in Colorado (Fig 2, p, 34). Initial surveys have detected WSS in Kansas, the top winter wheat-producing state, and damages are expected to increase as WSS host, and geographic range expands. To date, host plant resistance has proven to be most effective way to manage WSS. Solid stem varieties of wheat have been shown to be effective in impeding larval development and movement, thus reducing larval survival. The primary source of stem solidness in wheat is under genetic control of a QTL on chromosome 3B (*Qss.msub-3BL*) originally derived from the Portuguese landrace wheat S-615. However, there are reports from Montana that suggest sawflies may be adapting to this source of stem solidness. In addition, the solid-stemmed cultivars may not be preferred by grow-



**Fig. 1.** Wheat stem sawfly adult and damage. A. Adult. B. End of season hibernaculum or stubs. C. Significant damage to wheat field due to cutting by wheat stem sawfly.

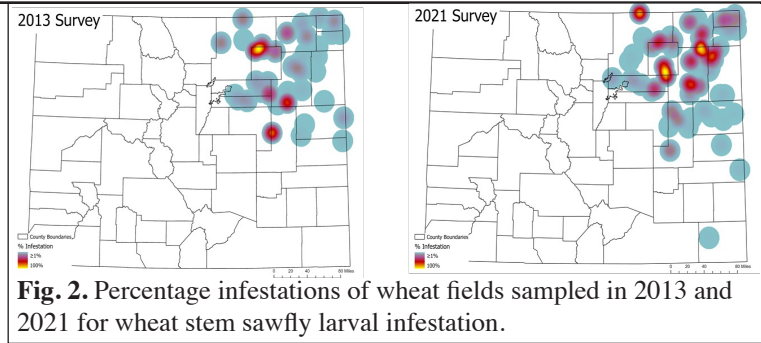
ers because of low yield (10–15% reduction) compared to hollow-stemmed cultivars and inconsistent solidness expression.

In 2020, researchers at Colorado State University teamed up with the Wheat Genetic Resource Center (WGRC) at Kansas State University to explore potential resistance traits to the wheat stem sawfly in wild wheat relatives. Wheat breeders can use wild wheat relatives as untapped sources of genet-

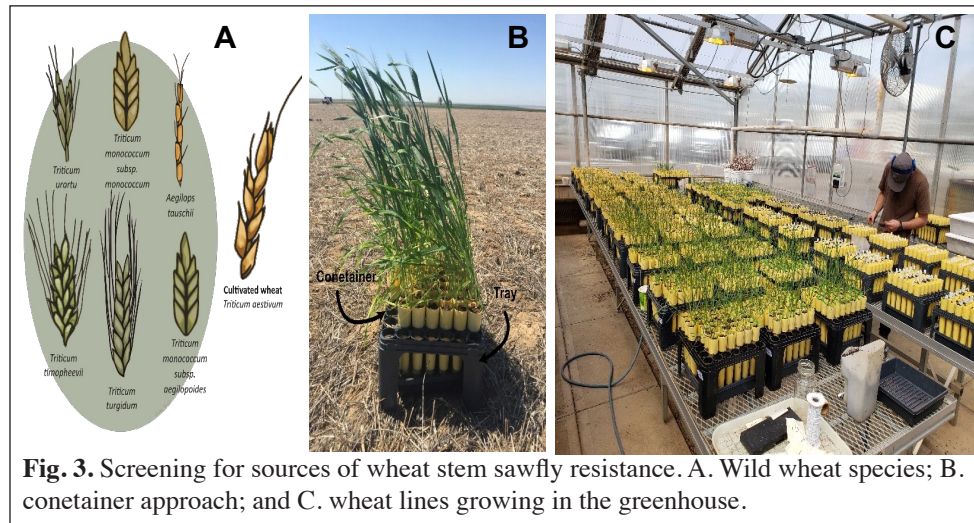
ics to enhance development of resistant cultivars. The WGRC provided six species of wild wheat (Fig. 3A). We screened each species to assess attractiveness, larval development, and infestation rates (whether larvae were present in the stem or not). Plants were grown in the greenhouse in cone-tainers as wild wheat is challenging to grow in the field (Figs. 3B and 3C). Then, we transported the plants to the field so adult sawfly could lay their eggs within the stems. We dissected the

stems at different stages of development. Using this experimental method, researchers can compare the host suitability of wild wheat species to cultivated wheat.

To complement the greenhouse experiment, the Colorado State University Wheat Breeding Program tested lines developed by the WGRC with wild wheat relatives as part of their pedigrees. Lines were planted in head rows in New Raymer, CO, and visually assessed for the number of stems cut per plot. Using this screening method, some lines that included *T. turgidum* and *A. tauschii* as part of their pedigree experienced less cutting than highly susceptible lines. These preliminary results look promising, and *T. turgidum* and *A. tauschii* might be good candidates for further evaluation and integration into wheat breeding programs. Currently, we are screening a series of synthetic hexaploids from crosses between the WGRC core collection accessions of *T. turgidum* subsp. *dicoccoides* and *Ae. tauschii* that that may have resistance to WSS.



**Fig. 2.** Percentage infestations of wheat fields sampled in 2013 and 2021 for wheat stem sawfly larval infestation.



**Fig. 3.** Screening for sources of wheat stem sawfly resistance. A. Wild wheat species; B. cone-tainer approach; and C. wheat lines growing in the greenhouse.

## INDIANA

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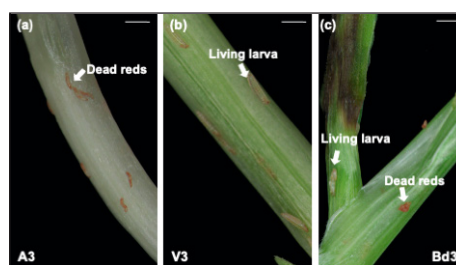
*Comparative Hessian fly larval transcriptomics provides novel insight into host and nonhost resistance.*

Subhashree Subramanyam, Jill A. Nemacheck, Shaojun Xie, Ketaki Bhide, Jyothi Thimmapuram, Steven R. Scofield, and Nagesh Sardesai.

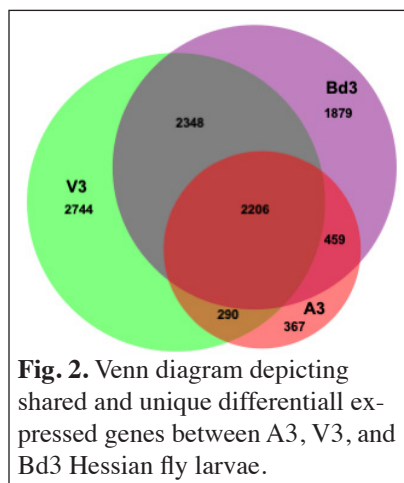
Hessian fly (*Mayetiola destructor*) is an economically important pest of wheat in the U.S. and around the globe. Although planting resistant wheat cultivars is the most environmentally friendly and economically sound strategy, there is prevailing fear of breakdown of resistance due to development of virulent biotypes. Alternate molecular strategies that can complement native durable resistance are imperative, requiring a thorough understanding of the plant-insect interaction at the molecular level. To expand our understanding of this interaction, we analyzed the transcriptomes of Hessian fly larvae feeding on host susceptible (V3) and resistant (A3) wheat as well as larvae feeding on *Brachypodium distachyon* plants (Bd3) at 3 days after egg-hatch (Fig. 1). *Brachypodium* exhibits nonhost resistance resembling the resistant host wheat phenotypically but displaying molecular responses that are intermediate between resistant and susceptible host wheat.

Comparative transcriptome analysis revealed similar molecular responses between V3 and Bd3 larvae that were very distinct from those observed in A3 larvae (Fig. 2). Differentially expressed genes involved in energy and amino acid metabolism, ROS (Reactive Oxygen Species) pathway, proteases, lipases, and detoxification (Fig. 3) were significantly up-regulated in both V3 and Bd3 larvae and are beneficial for the growth and development of the larvae. Genes from most of these pathways were either down-regulated or not differentially expressed in A3 larvae

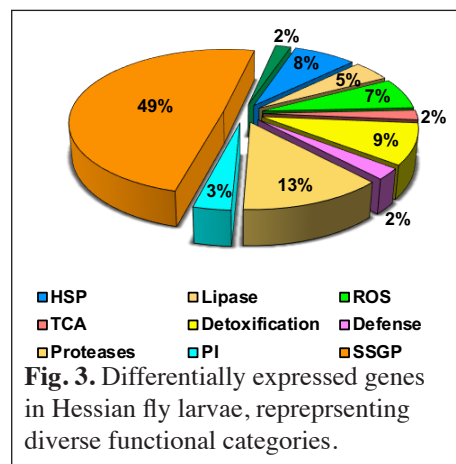
(Subramanyam et al. 2021). A large number of secreted salivary gland proteins were significantly up-regulated in all three larval samples (Fig. 3). Despite sharing common molecular responses, Bd3 larvae are unable to induce susceptibility in nonhost plants, unlike the V3 larvae. The primary factor responsible for this may be the relatively decreased transcriptional abundance of the differentially expressed genes in Bd3 as compared to the V3 larvae, which allows some of the Bd larvae to form developmentally delayed 2nd-instars with prolonged larval survival, ultimately yielding to the nonhost resistance defense mechanisms and dying (Subramanyam et al. 2019). In contrast, in susceptible host wheat, due to the lack of corresponding H-gene-mediated defense responses, the virulent larvae are able to successfully establish permanent feeding sites, alter the host plant physiology, and complete their development. In resistant wheat, the H-gene-



**Fig. 1.** Phenotypic responses of avirulent Hessian fly larvae (A3) on resistant wheat, virulent larvae (V3) on susceptible wheat, and larvae (Bd3) on nonhost *Brachypodium distachyon* plants.



**Fig. 2.** Venn diagram depicting shared and unique differentially expressed genes between A3, V3, and Bd3 Hessian fly larvae.



**Fig. 3.** Differentially expressed genes in Hessian fly larvae, representing diverse functional categories.



mediated early defense induces resistance, which is reflected in a lack of dynamic transcriptional change in the avirulent larvae during attempted feeding. Understanding the insect global molecular responses and adaptation strategies will be crucial in developing effective management strategies to control these insect pests.

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## KANSAS

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### *Problems from plastics used in agriculture.*

M.B. Kirkham.

Last year, I reported about microplastics that arise from the breakdown of plastics used in agriculture (Kirkham 2021), which was a summary of a chapter I wrote on the topic (Kirkham 2020). As a result of that work, people have contacted me about problems that they have had resulting from the use of plastics in agriculture. I here report those issues.

The main problem is the tillage of plastic mulch into soil. There is no way to get rid of plastic, once it has been tilled into the soil, unless it is picked out, piece by piece. And once the plastic has broken down into microplastics due to weathering, they remain in the soil.

Two lawyers representing different clients called me to find out how plastics tilled into the soil could be removed. In both cases, tenant farmers had tilled plastic sheets into the soil before they left the land in order to dispose of the plastic. One lawyer represented a client in Monterey County, California, who had bought a flower farm. The previous tenant used plastic and disposed of it by discing the plastic into the soil. The plastic buried in the soil violated solid waste disposal rules in the county. The county does not allow accumulation of any solid waste either on the surface of the ground or buried beneath the ground, except a person may accumulate food waste, yard waste, or green waste for the purpose of composting. Penalties for the improper disposal could amount to \$2,500.00/day. The State of California told the tenant farmer to desist doing this, but he continued. Now, the new owner of the land must get rid of the tiny bits of plastic in the soil. The County of Monterey Health Department issued a notice of violation both to the former tenant and the current owner. The land is on a slope and goes into a creek, which then goes into an estuary near Monterey. The area floods every few years, and, in the next flood, the plastic is going to be washed into the creek and estuary. The plastic particles are lighter than soil textural classes (sand, silt, and clay) and get easily washed off during flooding. They float on the surface and are subjected to washing and erosion. The only solution in this case is to grow buffer-strip plants on the bank of the creek, so that the plastics could get trapped. The trapped particles then might be collected and disposed of in a landfill.

Another case occurred on a farm in Indiana where soybeans were grown. A lawyer representing the owner of the farm called me to tell me about the situation. Approximately 86 acres were planted for three years by a tenant farmer, who left plastic debris in the soil, including black plastic sheets, plastic drip irrigation hoses, and green sheets of plastic wrap. Instead of removing the debris, the tenant farmer tilled it into the soil. The land then was taken over by its owner, who assumed the role of farm manager. She did not plant a crop in hopes that the plastic could be removed, with the unintended consequence of weeds. The lawyer tried to get damages from the tenant who polluted her soil with plastic. However, she had to settle the court case, because the defendants had more financial resources than she did.

Plastics are used in many different aspects of agriculture, including coatings of seeds and fertilizers. In 2022, the Minnesota House of Representatives introduced HF (House Files) 3751, which states 'Certain fertilizer coatings prohibited: A person may not sell, offer for sale, or apply a fertilizer coated with plastic or another material that is not readily biodegradable.' Such a ruling would impact wheat farmers, if they used polymer-coated urea.

Biodegradable mulch has drawbacks. It is not certified for use in organic agriculture in the United States due to utilizing fossil fuel resources and genetically modified bacteria in manufacturing, which is an ironic situation given that polyethylene (plastic) mulch is approved for organic use despite being made from 100% fossil fuel resources (Kirkham 2020, p. 32). The USDA National Organic Standards Board (NOSD) must decide if biodegradable plastic films should be allowed in organic farming (Asa Bradman, University of California at Merced, personal communication, 1 September, 2020). Even if biodegradable mulches are approved by NOSD, they do not fully breakdown (Kirkham 2020, p. 30-32) and contribute to microplastic pollution in the soil. The chair of the certification body for composting in the United Kingdom said that his group needs to consider microplastics in compost (Stephen Nortcliff, University of Reading, personal communication, 23 September, 2020).

Hemp production was banned throughout the USA in 1937. The 2018 Farm Bill authorized the production of hemp again. Fabrics used to be made out of hemp. Instead of using plastic, fertilizer bags and seed bags could be made of hemp. An herbalist in Madison, Wisconsin, called me to suggest that perhaps hemp could be used to remediate land contaminated with microplastics (Alan Robinson, personal communication, 5 May, 2021). He said they could be taken up by the hemp, and, because hemp was not eaten, they would not pose a threat to the food chain. Studies on the uptake of microplastics by plants are limited, due to the fact that instrumentation is not readily available to analyze for microplastics in crops or soils. The general rule of thumb is that particles less than 6 nm in one dimension may be able to permeate the cell wall, but larger particles cannot (Kirkham 2020, p. 27). Therefore, it is assumed that microplastics may not be taken up by plants. However, if the plants have broken roots, they can be taken up through the cracks in the roots. Broken roots are a common occurrence (Yan Jin, University of Delaware, personal communication, 14 April, 2022). It has been my experience using polyethylene glycol (PEG) (a microplastic) as an osmotic agent that the PEG is taken up by plants if the roots are damaged. The uptake is evidenced by a white efflorescence along the edges of the leaves where the PEG collects as water transpires from a leaf. We need more studies of the uptake of microplastics by plants.

These situations show that plastics used in agriculture, and the microplastics resulting from their breakdown, are going to become an important legal and environmental issue in the U.S.A.

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### *Personnel changes at the Wheat Genetics Resource Center.*

We are happy to welcome Eduard Akhunov as the new director of the Wheat Genetics Resource Center and the NSF-funded Industry–University Cooperative Research Center.

Buket Sahin defended her Master's Degree thesis in December 2021 on the 'Phenotypic evaluation of seedling and adult-plant stripe, leaf, and stem rust resistance in the A-genome diploid relatives of wheat.' A summary of this research appears in this contribution (pp. 40-42). Duane Wilson retired in June 2022, and we thank him for his many years of service with the WGRC managing all the greenhouse and field experiments.

## ***Phenotypic evaluation of seedling and adult-plant stripe, leaf, and stem rust resistance in the A-genome diploid relatives of wheat.***

Buket Sahin (Cereal Rust Research Center in Aegean Agricultural Research Institute, Turkey), and Duane Wilson and Bernd Friebe.

Global food security relies on increasing production of two main grain crops – rice and wheat. Among these, wheat has greater significance in terms of tonnage. The various rust diseases that attack this crop, leaf rust (*Puccinia triticina*), stripe rust (*P. striiformis* f. sp. *tritici*) and stem rust (*P. graminis* f. sp. *tritici*), are important limitations for increasing wheat production worldwide. In order to stay ahead of constantly evolving rust pathogens, increasing genetic diversity by identifying genetic resistance from sources besides common wheat is necessary. The wild relatives of wheat are valuable sources of wheat rust resistance genes. A minicore collection of diploid A-genome species covering about 90 percent of the genetic variation of these species, includes 59 accessions of *T. monococcum* subsp. *aegilopoides*, 24 accessions of *T. monococcum* subsp. *monococcum*, and 25 accessions of *T. urartu*, spanning their entire area of geographic distribution was established using genotype-by-sequencing. These accessions were evaluated for their seedling resistance to leaf and stem rust under greenhouse conditions and for adult-plant resistance under both greenhouse and field conditions (Table 1, pp. 39–42). Resistance to stripe rust was found in 41.6% of *T. monococcum* subsp. *monococcum* and 13.5% *T. monococcum* subsp. *aegilopoides*, and 91.6% *T. monococcum* subsp. *monococcum* and 5% *T. monococcum* subsp. *aegilopoides* were resistant to leaf rust at the seedling stage. A significant percentage the accessions were found to be resistant to stripe rust at the adult-plant stage under greenhouse conditions, 52.6% *T. monococcum* subsp. *monococcum*, 65% *T. monococcum* subsp. *aegilopoides*, and 23.8% *T. urartu*. About 63% and 10.6% of *T. monococcum* subsp. *monococcum* and 7.5% and 10.3% *T. monococcum* subsp. *aegilopoides*, respectively, exhibited resistance to leaf and stem rust at the adult-plant stage under greenhouse conditions. Resistance to stripe rust at the adult-plant stage under field conditions was 4.2% in *T. monococcum* subsp. *monococcum* and 3.4% in *T. monococcum* subsp. *aegilopoides*, however resistance to leaf and stem rust was only moderate. Among the evaluated accessions, *T. monococcum* subsp. *monococcum* showed a good number of resistant accessions, followed by *T. monococcum* subsp. *aegilopoides*, and *T. urartu*. Consequently, these A-genome species may have a high potential for breeding superior rust resistant wheat cultivars.

The major goals of wheat breeding projects often comprise developing new cultivars with higher yield, quality, and resistance to abiotic/biotic stresses. The rust diseases of wheat are the most important factor limiting wheat production and cause significant losses in wheat yield and quality. Regardless of the target product in breeding studies, the most critical step in achieving success is the accessibility of a diverse set of germplasm to screen for genes for the traits of interest. Wild wheat relatives are a potential genetic resource for improving abiotic and biotic stress in wheat. The diploid A-genome wheat species have been identified as an important and valuable genetic resource. However, no comprehensive research has uncovered the disease resistance potential of A-genome diploid wheat maintained in gene banks. Here, we evaluated a diverse set of A-genome accessions maintained at the Wheat Genetics Resource Center, Kansas State University, for their seedling and adult-plant rust resistance. Several accessions with single and multiple resistance to different rusts were identified, which can be the starting point of using these genes in wheat improvement.

**Stripe rust–seedling reaction.** Eighteen (16.6%) accessions were scored as resistant with six highly resistant. Nineteen (17.5%) accessions were scored as intermediate, and 71 (65.7%) were susceptible to stripe rust at the seedling stage. Ten (41.6%) accessions of *T. monococcum* subsp. *monococcum* and eight (13.5%) accessions of *T. monococcum* subsp. *aegilopoides* were resistant, however no *T. urartu* accessions were resistant. Six (25%) *T. monococcum* subsp. *monococcum* accessions, 11 (18.6%) *T. monococcum* subsp. *aegilopoides* accessions, and two (8%) *T. urartu* accessions had intermediate reactions. The majority of accessions were scored as susceptible to stripe rust at the seedling stage; eight (33.4%) *T. monococcum* subsp. *monococcum*, 40 (67.7%) *T. monococcum* subsp. *aegilopoides*. and 23 (92%) *T. urartu*.

**Stripe rust–adult-plant stage.** A composite culture pathogen isolates was used for stripe rust inoculation in the greenhouse. Out of 80 A-genome diploid wheat accessions tested, 13.8% showed a susceptible reaction (IT=7–9). About 52% of the accessions exhibited a resistance response (IT=0–3), and 28 (35%) showed intermediate reactions (IT=4–6). Out of 80 accessions tested in the greenhouse, *T. monococcum* subsp. *aegilopoides* exhibited the most resistance (65%), followed by *T. monococcum* subsp. *monococcum* (52.6%) and *T. urartu* (23.8%).

**Stripe rust–field reaction.** Different stripe rust reaction types were observed in the 108 accessions. Based on their final rust severity, the wheat genotypes were placed into three groups; high (0–20%), intermediate (20–40%), and low (40–100%) resistance. Four accessions were resistant, 42 were moderately resistant, 57 moderate, four moderately

**Table 1.** Rust reactions of A-genome lines tested for resistance to stem, leaf, and stripe rusts. For reaction scale, see footnotes at end of table (p. 42).

LINE	SPECIES OR SUBSPECIES	STEM RUST			LEAF RUST			STRIPE RUST	
		SEEDLING	ADULT	FIELD	SEEDLING	ADULT	FIELD	ADULT	FIELD
TA136	<i>monococcum</i>	2+	7	20M	;	10MR	15MR	60S	15S
TA177	<i>aegilopoides</i>	3+	3	25M	3	1R	15M	25S	30S
TA190	<i>aegilopoides</i>	2+	4	20M	2	20M	20MR	20M	15S
TA249	<i>aegilopoides</i>	3-	2	15MR	3	5M	15MR	20MS	15MS
TA250	<i>aegilopoides</i>	3-	—	5R	2+	—	10MR	—	10MR
TA252	<i>aegilopoides</i>	3+	6	25M	3	10M	10MR	30MS	20MS
TA261	<i>aegilopoides</i>	3	2	20M	3	5MR	20MR	10R	10M
TA278	<i>aegilopoides</i>	3+	—	30MS	3	—	15M	—	30S
TA284	<i>aegilopoides</i>	3	1	15M	3+	5MR	30M	20M	50S
TA285	<i>aegilopoides</i>	3-	2	20M	3-	1R	20MR	30M	20MS
TA299	<i>aegilopoides</i>	3+	7	30M	3	30MS	25MR	30M	30S
TA306	<i>aegilopoides</i>	3	1	15MR	3	30MS	10M	20M	25S
TA309	<i>aegilopoides</i>	3	—	10MR	3+	—	15M	—	10M
TA316	<i>aegilopoides</i>	2	3	20MR	3-	20MS	10MS	50S	40S
TA346	<i>aegilopoides</i>	3-	4	20M	3	25MS	15M	20MR	15M
TA362	<i>aegilopoides</i>	3-	3	20M	3	5R	15M	—	40S
TA366	<i>aegilopoides</i>	1+	—	15MR	3+	—	15M	—	10M
TA394	<i>aegilopoides</i>	3	1	20M	3+	10M	20M	40S	30S
TA396	<i>aegilopoides</i>	1	3	15M	2+	10MR	15M	20MS	50S
TA408	<i>aegilopoides</i>	1+	3	20M	3	10M	20M	15S	20MS
TA412	<i>aegilopoides</i>	3+	4	15MR	3	20MS	25M	30S	10MS
TA438	<i>aegilopoides</i>	3+	—	20MR	3	—	15M	—	10M
TA443	<i>aegilopoides</i>	3+	—	15MR	3	—	15M	—	10MS
TA447	<i>aegilopoides</i>	3+	6	25M	3	5M	20MR	10M	25S
TA466	<i>aegilopoides</i>	3-	3	15M	2	5MR	15M	20MS	20MS
TA473	<i>aegilopoides</i>	3	3	10MR	3	10MS	10M	50S	30MS
TA479	<i>aegilopoides</i>	3	—	15MS	3+	—	15M	—	10MS
TA488	<i>aegilopoides</i>	2	—	15M	3+	—	15M	—	30S
TA502	<i>aegilopoides</i>	3	3	20M	3	5M	20MR	15MR	15S
TA526	<i>aegilopoides</i>	3	—	15M	3+	—	20M	—	10M
TA534	<i>aegilopoides</i>	2+	3	20MR	2-	10MR	10MR	10MR	20MS
TA544	<i>aegilopoides</i>	3+	5	10M	3	5M	15M	30MS	10MS
TA580	<i>aegilopoides</i>	1	3	20MR	1-	30MR	10MR	10M	25MS
TA585	<i>aegilopoides</i>	2+	3	20MR	3-	10M	15M	30M	20MS
TA590	<i>aegilopoides</i>	1+	—	30M	3+	—	15M	—	5M
TA593	<i>aegilopoides</i>	3+	2	20M	3	10MR	15M	30M	20MS
TA632	<i>aegilopoides</i>	1-	—	25MR	3	15M	—	—	5M
TA647	<i>aegilopoides</i>	2-	—	25M	2	10M	—	—	10M
TA661	<i>aegilopoides</i>	3	6	30M	3	15MS	20M	40S	30S
TA686	<i>aegilopoides</i>	1-	2	15MR	3	5M	25M	20M	30S
TA709	<i>urartu</i>	3+	8	40MS	3+	25MS	20MS	60S	40S
TA721	<i>urartu</i>	3	3	15MR	3	10M	25M	20M	20MS
TA724	<i>urartu</i>	3+	7	20M	3	50S	20MS	50S	40S
TA748	<i>aegilopoides</i>	2-	—	20M	3	—	15M	—	10M
TA756	<i>aegilopoides</i>	3	—	15M	3	—	10M	—	5MS
TA790	<i>urartu</i>	2+	—	20M	3+	—	15M	—	30S
TA792	<i>urartu</i>	3	4	10MR	3	25MS	15M	50S	30S
TA800	<i>urartu</i>	3+	7	20M	3	10MS	15M	40S	20S
TA810	<i>urartu</i>	3+	6	30M	3	10MS	20MS	40S	30S
TA827	<i>urartu</i>	3-	2	5R	3+	25MS	20MS	40S	25S
TA832	<i>urartu</i>	3+	7	25M	3	40MS	20MS	30S	40S
TA834	<i>urartu</i>	3+	—	30MS	3+	—	20M	—	20S
TA 841	<i>urartu</i>	3	3	25MR	3	25MS	20M	40S	30S



**Table 1.** Rust reactions of A-genome lines tested for resistance to stem, leaf, and stripe rusts. For reaction scale, see footnotes at end of table (p. 42).

LINE	SPECIES OR SUBSPECIES	STEM RUST			LEAF RUST			STRIPE RUST	
		SEEDLING	ADULT	FIELD	SEEDLING	ADULT	FIELD	ADULT	FIELD
TA 850	<i>urartu</i>	3+	6	20S	3+	10S	30MS	30S	20MS
TA 1212	<i>aegilopoides</i>	3-	1	15M	3	20MS	10M	30M	15S
TA1254	<i>aegilopoides</i>	3-	—	15MR	3+	—	20M	—	15M
TA 1266	<i>aegilopoides</i>	3-	3	10M	3	10MS	15M	40S	20S
TA 1282	<i>urartu</i>	3	6	15MR	3	20MS	10M	25S	50S
TA1313	<i>urartu</i>	3+	7	20M	3-	15MS	20M	50S	50S
TA1314	<i>urartu</i>	3+	8	30M	3	10MS	15MS	40S	40S
TA1315	<i>urartu</i>	3-	4	20MR	3-	10M	15M	—	40S
TA2012	<i>aegilopoides</i>	2+	1	15MR	2	20MR	20MR	10R	10M
TA2021	<i>aegilopoides</i>	1-	—	25M	3+	—	15M	—	10MR
TA2022	<i>aegilopoides</i>	2	2	20M	3	20MS	15M	30MS	15M
TA2025	<i>monococcum</i>	1+	4	25M	;	5R	20MR	20M	10MS
TA2032	<i>monococcum</i>	1+	—	20MR	;	—	20MR	—	5M
TA2035	<i>monococcum</i>	2+	6	20M	;	1R	15M	50M	20S
TA2716	<i>monococcum</i>	3	5	15M	;	5R	15MR	40S	30S
TA2719	<i>monococcum</i>	3-	6	20MR	2-	5R	20MR	10R	15MR
TA2720	<i>monococcum</i>	2+	4	30M	2-	5R	30M	30S	20S
TA2723	<i>monococcum</i>	2+	2	30M	1-	20MR	20M	20MS	40S
TA2724	<i>monococcum</i>	3	7	30M	1-	20R	15MR	5M	40S
TA10418	<i>monococcum</i>	1	2	20MR	;	5R	20MR	20MS	10MS
TA10546	<i>aegilopoides</i>	3	—	15MR	;	—	20MR	—	10M
TA10569	<i>monococcum</i>	1+	2	15MR	1-	10MR	20M	30S	60S
TA10573	<i>aegilopoides</i>	3	7	25M	2	10M	15M	10R	15MS
TA10574	<i>monococcum</i>	1-	3	15MR	;	5R	15MR	20MS	10S
TA10581	<i>monococcum</i>	1-	—	15MR	;	—	20MR	—	15MR
TA10587	<i>monococcum</i>	3-	6	10MR	1	30M	10MR	20M	30S
TA10588	<i>monococcum</i>	1	3	20M	;	20MR	15M	40MS	10MS
TA10593	<i>aegilopoides</i>	3	6	15M	3+	60S	20M	20M	20MS
TA10595	<i>aegilopoides</i>	3+	6	15M	3	40MS	30MS	40S	30S
TA10603	<i>aegilopoides</i>	3	5	10MR	3+	50S	30MS	50S	20MS
TA10612	<i>monococcum</i>	3-	—	10R	1-	—	20MR	—	5M
TA10629	<i>monococcum</i>	3-	6	20M	1	25MR	15M	15R	15MR
TA10630	<i>monococcum</i>	1	2	15MR	1+	1R	15MR	20S	15S
TA10634	<i>monococcum</i>	3	3	20M	1-	5R	20MR	30MS	20S
TA10636	<i>monococcum</i>	1	—	15M	1	—	10M	—	20S
TA10642	<i>monococcum</i>	1-	3	10MR	;	5R	15MR	25MS	25S
TA10652	<i>monococcum</i>	3-	2	20M	1+	20MR	20M	20MS	10MR
TA10873	<i>urartu</i>	3-	—	10MR	3	—	15M	—	—
TA10876	<i>urartu</i>	3	3	10MR	3+	25MS	20M	50S	50S
TA10878	<i>urartu</i>	3+	5	25M	3+	30S	40MS	80S	25S
TA10879	<i>urartu</i>	3	—	5MR	3	—	15M	—	10MS
TA10884	<i>urartu</i>	3-	4	15M	3	10M	15M	50S	30S
TA10887	<i>urartu</i>	3+	6	20M	3	20S	15MR	40S	20S
TA10888	<i>urartu</i>	2+	2	30M	3	20M	20M	10M	10MR
TA10889	<i>urartu</i>	3	4	15MR	3	15M	10MR	40MS	25S
TA10891	<i>urartu</i>	3-	7	10MR	3	10MS	15M	50S	40S
TA10896	<i>monococcum</i>	2+	—	25M	1-	—	20MR	—	10M
TA10900	<i>aegilopoides</i>	2+	2	10MR	3	10MS	15M	10MS	20MS
TA10902	<i>aegilopoides</i>	2	4	30M	3	30MS	15M	15MR	15MS
TA10904	<i>aegilopoides</i>	3	2	20M	3	5MR	15M	20M	40S
TA10907	<i>aegilopoides</i>	3-	—	25MR	3+	—	20M	—	10MS
TA10909	<i>aegilopoides</i>	3	—	5R	3+	—	15MR	—	—
TA10916	<i>aegilopoides</i>	3	3	15MR	;	10MR	15M	10R	10MR

**Table 1.** Rust reactions of A-genome lines tested for resistance to stem, leaf, and stripe rusts. For reaction scale, see footnotes at end of table (p. 42).

LINE	SPECIES OR SUBSPECIES	STEM RUST			LEAF RUST			STRIPE RUST	
		SEEDLING	ADULT	FIELD	SEEDLING	ADULT	FIELD	ADULT	FIELD
TA11012	<i>aegilopoides</i>	3-	5	10MR	3	20MS	15MR	10MS	15MS
TA10622	<i>monococcum</i>	2	2	5MR	;	10 R	15MR	15MR	5MR
Morocco	S check	3+	8	60S	3+	40S	100S	50S	60S
Avery	S check	3+	—	70S	;	—	60S	—	60S
King Bird	R check	—	—	15MR	—	—	10MR	—	10MR
Joe	R check	3	6	30MS	2+	20MR	15MR	—	10MR
<b>Stakman Scale</b> Stem rust – seedling Stem rust – adult Leaf rust – seedling		For seedlings, disease response was scored 14–16 days after inoculation on a 0 to 9 with 0 = no visible signs or symptom; 1 = necrotic and/or chlorotic flecks, no sporulation; 2 = necrotic and/or chlorotic blotches or stripes, no sporulation; 3 = necrotic and/or chlorotic blotches or stripes, trace sporulation; 4 = necrotic and/or chlorotic blotches or stripes, light sporulation; 5 = necrotic and/or chlorotic blotches or stripes, intermediate sporulation; 6 = necrotic and/or chlorotic blotches or stripes, moderate sporulation; 7 = necrotic and/or chlorotic blotches or stripes, abundant sporulation; 8 = chlorosis behind sporulating area, abundant sporulation; and 9 = no necrosis or chlorosis, abundant sporulation. Plants with a score of 0-3 were rated resistant, those with a score of 4-6 were called intermediate, and those with a score of 7-9 were considered susceptible.							
<b>Modified Cobb Scale</b> Stem rust – field Leaf rust – adult plant Leaf rust – field Stripe rust – adult plant Stripe rust – field		The modified Cobb scale includes both percent leaf area and/or stem area affected (90–100%) and host response. For the host response, R (Resistant) = no uredinia present and necrotic areas without pustules; MR (Moderately Resistant) = small uredinia with slight sporulation, chlorosis and/or necrosis surrounding small uredinia as a result of an incomplete reaction; M (Moderate) = small to moderate sized uredinia with moderate to heavy sporulation, some chlorosis may be visible; MS (Moderately Susceptible) = medium size uredinia with moderate to heavy sporulation, some chlorosis may still be possible; and S (Susceptible) = large uredinia with abundant sporulation, uredinia often coalesced to form lesions without any visible chlorosis or necrosis.							

susceptible, and one was susceptible. Despite the heavy stripe rust disease pressure, one (4.2%), 10 (41.6%), 13 (54.2%) accessions *T. monococcum* subsp. *monococcum* showed R, MR, and M reactions, respectively; no moderately susceptible or susceptible response was observed. For *T. monococcum* subsp. *aegilopoides*, 2 (3.4%), 21 (35.6%), 34 (57.6%), 2 (3.4%) accessions exhibited R, MR, M, and MS reactions, respectively. After the final scoring, one (4%) accession of the 25 *T. urartu* accessions showed resistance, 10 (40%) were MR, 11 (44%) were M, two (8%) were MS, and one accession (4%) was susceptible.

**Leaf rust–seedling reaction.** Twenty-five (23.2%) accessions were scored resistant and 20 were highly resistant. Ten (9.3%) accessions were intermediate, and 73 (67.5%) accessions were susceptible to leaf rust at the seedling stage. Twenty-two (91.6%) accessions of *T. monococcum* subsp. *monococcum* and three (5%) of *T. monococcum* subsp. *aegilopoides* were resistant, however no *T. urartu* accessions was recorded as resistant. Two (8.3%) *T. monococcum* subsp. *monococcum* accessions, eight (13.5%) *T. monococcum* subsp. *aegilopoides* accessions, and no (0%) *T. urartu* accessions were intermediate. The majority of accessions were scored as susceptible to leaf rust seedling stage; no (0%) *T. monococcum* subsp. *monococcum*, 48 (81.3%) *T. monococcum* subsp. *aegilopoides*, and 25 (100%) *T. urartu* were scored as susceptible. All *T. monococcum* subsp. *monococcum* were considered either resistant or intermediate, whereas all *T. urartu* were susceptible.

**Leaf rust–adult-plant reaction.** Leaf rust severity varied greatly, ranging from 0 to 60% in the greenhouse. Final rust severity represents the cumulative results of all resistance factors. Based on the final rust severity, the accessions were placed into three groups; resistant, moderate, and susceptible, having 0–20%, 20–40%, and 40–60%, respectively. During the experiment, 31 accessions had resistant to moderately resistant (R–MR) reactions, whereas 32 accessions were moderately susceptible to susceptible (MS–S) responses, and 17 had a moderate (M) response. On the other hand, *T.*

*monococcum* subsp. *monococcum* accessions showed only R (63.2%), MR (31.5%), and M (5.3%) reactions. However, *T. urartu* was scored generally as moderately susceptible (57.2%), susceptible (19.1%), and moderately resistant (23.8%). No *T. urartu* accessions were resistant or moderately resistant to leaf rust in the greenhouse. In *T. monococcum* subsp. *aegilopoides*, 7.5% were R, 25% were MR, 27.5% were M, 35% were MS, and 5% had an S response. The check cultivars Morocco (susceptible) and Joe (resistant) wheats were 50S and 20 MR, respectively.

**Leaf rust–field reaction.** Resistance to susceptibility was observed at the Rocky Ford Experiment Station in 2020 and 2021 placing the accessions into three groups, resistant (0–20%), moderate (20–40%), and susceptible (40–100%). During the experiment, 32 accessions were resistant to moderately resistant, whereas 11 showed moderately susceptible to susceptible responses, and 65 accessions had a moderate response. Only MR (62.5%) and M (33.4%) reactions were observed in *T. monococcum* subsp. *monococcum* accessions. However, *T. urartu* and *T. monococcum* subsp. *aegilopoides* were scored generally as moderately resistant, moderate, and moderately susceptible. The susceptible checks Morocco (100 S, 2020) and Avery (2021, 60 S) and the resistant checks were King Bird (2020 10 MR) and Joe (2021, 15 MR).

**Stem rust–adult-plant reaction.** The 80 A-genome accessions tested for adult-plant stem rust under greenhouse conditions were classified into five groups. The first group contained six (7.5%) accessions resistant to stem rust. In the second group, five (60.3%) accessions showed an MR response with a severity between 10–20%. The third group consisted of 19 (23.8%) accessions that were moderately (M) resistant. In the fourth group, 16 (20%) accessions showed an MS reaction with a severity between 20–40%. In the fifth group, the remaining 32 (40%) accessions showed S reactions with severity between 20–80% in all three species. Two (10.6%) and one (5.3%) accessions of *T. monococcum* subsp. *monococcum* and four (10.3%) accessions of *T. monococcum* subsp. *aegilopoides* were resistant or moderately resistant, however no (0%) *T. urartu* accessions were resistant. Four (21.1%) and seven (36.8%) accessions of *T. monococcum* subsp. *monococcum*, 13 (33.4%) and eight (20.6%) of *T. monococcum* subsp. *aegilopoides*, and two (10%) and one (5%) *T. urartu* were moderate (M) and moderately susceptible (MS), respectively. The majority of accessions were scored as susceptible to stem rust at the adult-plant stage; five (26.3%) of *T. monococcum* subsp. *monococcum*, 10 (25.6%) of *T. monococcum* subsp. *aegilopoides*, and 17 (85%) of *T. urartu*.

**Stem rust–field observations.** Of the 108 A-genome diploid accessions of wheat tested, moderate resistance to stem rust was detected in nine (8.5%), a moderate response was detected in 17 (16.1%), 28 (26.4%) were moderately susceptible, and 52 (49.1%) were susceptible. Although no highly resistant (R) accession was found, the response of three different subspecies to stem rust was variable. Five (20.8%) accessions of *T. monococcum* subsp. *monococcum*, three (5.2%) of *T. monococcum* subsp. *aegilopoides*, and one (4.2%) of the *T. urartu* accessions were moderately resistant. Moderate resistance was observed in three (12.5%) *T. monococcum* subsp. *monococcum*, 14 (24.2%) *T. monococcum* subsp. *aegilopoides*, and no (0%) *T. urartu* accessions. Moderate susceptibility was in three (12.5%) *T. monococcum* subsp. *monococcum* accessions, 22 (37.9%) *T. monococcum* subsp. *aegilopoides* accessions, and three (12.5%) *T. urartu*. The majority of accessions were scored as susceptible to stem rust at the adult-plant stage; 13 (54.2%) *T. monococcum* subsp. *monococcum*, 19 (32.7%) *T. monococcum* subsp. *aegilopoides*, and 20 (83.3%) *T. urartu* in the field experiments in 2020 and 2021. The susceptible checks were Morocco (2020; 60 S) and Avery (2021, 60 S) and the resistant checks were King Bird (2020 10 MR) and Joe (2021, 10 MR).

### ***Genetic characterization and curation of diploid A-genome wheat species.***

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The A-genome diploid wheats represent the earliest domesticated and cultivated wheat species in the Fertile Crescent and include the donor of the wheat A sub-genome. The A-genome species encompass the cultivated einkorn (*T. monococcum* subsp. *monococcum*), wild einkorn (*T. monococcum* subsp. *aegilopoides*), and *T. urartu*. We evaluated the collection of 930 accessions in the Wheat Genetics Resource Center genebank using genotyping-by-sequencing and identified 13,860 curated single-nucleotide polymorphisms. Genomic analysis detected misclassified and genetically identical (>99%) accessions, with most of the identical accessions originating from the same or nearby locations. About 56% (n = 520) of the A-genome species accessions were genetically identical, supporting the need for genomic characterization for effective curation and maintenance of these collections. Population structure analysis confirmed the morphology-based classifications of the accessions and reflected the species geographic distributions. We also showed that *T. urartu* is the closest

A-genome diploid to the A-subgenome in common wheat through phylogenetic analysis. Population analysis within the wild einkorn group showed three genetically distinct clusters, which corresponded with wild einkorn races  $\alpha$ ,  $\beta$ , and  $\gamma$ , described previously. The *T. monococcum* genome-wide FST scan identified candidate genomic regions harboring a domestication selection signature at the *non-brittle rachis 1 (Btr1)* locus on the short arm of chromosome 3A<sup>m</sup> at ~70 Mb. We established an A-genome core set (79 accessions) based on allelic diversity, geographical distribution, and available phenotypic data. The individual species core set maintained at least 79% of allelic variants in the A-genome collection and constituted a valuable genetic resource to improve wheat and domesticated einkorn in breeding programs.

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

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

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

### **Publications.**

Adhikari L, Raupp J, Wu S, Wilson D, Evers B, Koo D-H, Singh N, Friebe B, and Poland J. 2022. Genetic characterization and curation of diploid A-genome wheat species. *Plant Physiol* **188**(4):2101-2114 [<https://doi.org/10.1093/plphys/kiac006>].

Gill BS, Koo DH, Jugulam M, Friebe B, and Koo D-H. 2022. Fishing eccDNA elements that defy chromosome control of mitosis and meiosis and drive rapid adaptive evolution. PAG Abstract W796.

## **MINNESOTA**

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### ***Wheat leaf rust in the United States in 2021.***

In 2021, wheat leaf rust caused by *Puccinia triticina*, was reported from 16 states. Incidence and severity levels were at low levels in 2021. Temperatures in the southern winter wheat regions were close to the long-term averages from March to June. In southern Texas, leaf rust was increasing at the end of March and was at high severity levels on susceptible

cultivars by mid April. Leaf rust was present in fields in Oklahoma by mid April and was present in at low levels across the state by mid May. In Kansas, leaf rust was present at low levels in some areas by mid June. High levels of leaf rust were observed in plots in eastern Nebraska in early June. Leaf rust was widespread, but at low severity levels, in late May in the Coastal Plain and Tidewater region of eastern North Carolina. In late May and June, extremely hot and dry weather in the northern plains greatly restricted the infection and spread of leaf rust across the spring wheat region of Minnesota, South Dakota, and North Dakota. The number of collections from this region was greatly reduced compared to that of previous years. Leaf rust was observed at very low levels in plots of susceptible cultivars throughout Minnesota in July. Leaf rust infections were not seen in any plots of the commonly grown spring wheat cultivars in northern and central Minnesota. Leaf rust was present at low levels in plots of winter and spring wheat in east central North Dakota in mid July.

In 2021, estimated losses due to leaf rust were highest in Pennsylvania at 5%, Oklahoma at 3%, 1% in Texas, and New York at 0.5%. Losses in all other states were at trace levels or no loss at all. The total estimated losses across the United States was 5,9315,260 bushels.

### ***Races and virulence of Puccinia triticina.***

In 2021, 24 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 207 isolates were processed for race identification. Travel restrictions related to COVID19, and the extremely hot and dry weather in the northern Great Plains region, reduced the number of collections received in 2021.

MNPSD was the most common race across the United States at 35.7% of all isolates. Isolates with this race designation were found at very high levels throughout the hard red wheat regions of the Great Plains and at low levels in the southeastern states and in Washington State. MNPSD is virulent to wheat lines with *Lr24*, *Lr37*, and *Lr39*. These genes are present in hard red winter wheat cultivars. MBDSO was the second most common race at 23.2% of all isolates. This race was found at high levels throughout the Great Plains region. MBDSO is virulent to wheat lines with *Lr37* and *Lr39*. MPPSD was the third most common race, at 19.3% of overall isolates. This race was found in the same regions as MNPSD, in addition to the Ohio Valley region. MPPSD is virulent to wheat lines with *Lr24*, *Lr26*, *Lr37*, and *Lr39*. Races MNPSD, MBDSO, and MPPSD, have been selected by the hard red winter wheat cultivar SY Monument that was widely grown in Oklahoma, Kansas, and Nebraska in 2021.

In the soft red winter wheat region of Area 1, MCTNB was the most common race. MCTNB and MBTNB have been the most common races in this region since 2013. The related races TBTNB and TCJTB, also were present in this region. All of these races have virulence to *Lr11*, which is present in many soft red winter wheat cultivars. Races MCTNB and TCJTB are also virulent to *Lr26*, which is also present in many soft red winter wheat cultivars.

Races MJBIG (found in Area 4 and Area 6) and MJMIG (found in Area 4) are virulent to *Lr16* and *Lr24*. Commonly grown hard red spring wheat cultivars such as Linkert have *Lr16*. Some hard red winter wheat cultivars also have *Lr16*.

A single isolate of race TNBJS and two isolates of TBBGS, which are virulent to *Lr21*, were present in Area 6. Many hard red spring wheat cultivars have *Lr21*. Races with virulence to *Lr21* were very frequent in previous years surveys. The lower frequency in 2021 was due to most collections in this region coming from susceptible wheat cultivars, not the prevalent hard red spring wheat cultivars.

The complete listing of races found in the United States in 2021 is given (Table 1, p. 46). The frequency of isolates with virulence to the individual Lr genes is given in Table 2 (p. 47). The complete listing of collections, host cultivars, date of collection, collectors, location of collections, and identified races are given in Table 3 (pp. 47-50). The most commonly grown cultivars grown in 2021 in the hard red winter wheat states of Oklahoma, Kansas, and Nebraska, and also the most prevalent hard red spring wheat cultivars in Minnesota and North Dakota are listed in Table 4 (p. 51). When possible, the Lr genes were postulated based on infection type data to different races of *P. triticina* and also on molecular marker data obtained from testing of the SRPN and NRPN and the UHRSWN by USDA–ARS genotyping laboratories in Manhattan, KS, and Fargo, ND.



**Table 1.** Number and frequency (%) of the predominant virulence phenotypes of *Puccinia triticina* in the United States in 2021 identified by virulence to 20 lines of Thatcher wheat with single genes for leaf rust resistance.

RACE	VIRULENCE COMBINATION (INEFFECTIVE <i>Lr</i> GENES)	MS, GA, LA, AL, NC, AND VA		NY		MO, IN, KY, OH, AND IL		TX AND OK		KS AND NE		MN, SD, AND ND		ID AND WA		TOTAL	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
LCDSG	1,26,17,B,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	14.3	1	0.5
MBDSD	1,3,17,B,10,14a,39	0	0.0	0	0.0	0	0.0	10	18.5	19	32.2	19	30.6	0	0	48	23.2
MBTNB	1,3,3ka,11,17,30,B,14a	1	6.3	0	0.0	0	0.0	0	0.0	1	1.7	3	4.8	0	0.0	5	2.4
MCDSG	1,3,26,17,B,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	28.6	2	1.0
MCQHB	1,3,26,3ka,11,10,18	0	0.0	1	16.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	0.5
MCTNB	1,3,26,3ka,11,17,30,B,14a	5	31.3	1	16.7	0	0.0	0	0.0	1	1.7	1	1.6	0	0.0	8	3.9
MJBIG	1,3,16,24,10,14a,28	0	0.0	0	0.0	0	0.0	2	3.7	0	0.0	2	3.2	0	0.0	4	1.9
MJMIG	1,3,16,24,3ka,30,10,14a,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	3.2	0	0.0	2	1.0
MLPSD	1,3,9,3ka,17,30,B,10,14a,39	0	0.0	0	0.0	0	0.0	0	0.0	2	3.4	0	0.0	0	0.0	2	1.0
MNPSD	1,3,9,24,3ka,17,30,B,10,14a,39	1	6.3	0	0.0	0	0.0	30	55.6	22	37.3	20	32.3	1	14.3	74	35.7
MPPSD	1,3,9,24,26,3ka,17,30,B,10,14a,39	4	25.0	2	33.3	0	0.0	11	20.4	13	22.0	8	12.9	2	28.6	40	19.3
PBDQJ	1,2c,3,17,B,10,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.5
TBBGS	1,2a,2c,3,10,21,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	3.2	0	0.0	2	1.0
TBTNB	1,2a,2c,3,3ka,11,17,30,B,14a	2	12.5	0	0.0	0	0.0	0	0.0	0	0.0	2	3.2	0	0.0	4	1.9
TBTSE	1,2a,2c,3,3ka,11,17,30,B,10,14a	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.5
TCJTB	1,2a,2c,3,26,11,17,B,10,14a,18	2	12.5	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	1.0
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	14.3	1	0.5
TCTLB	1,2a,2c,3,26,3ka,11,17,30,B	0	0.0	0	0.0	0	0.0	0	0.0	1	1.7	0	0.0	0	0.0	1	0.5
TCTNB	1,2a,2c,3,26,3ka,11,17,30,B,14a	0	0.0	0	0.0	1	33.3	0	0.0	0	0.0	0	0.0	0	0.0	1	0.5
TCTSE	1,2a,2c,3,26,3ka,11,17,30,B,10,14a	0	0.0	2	33.3	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	2	1.0
TDPSB	1,2a,2c,3,24,3ka,17,30,B,10,14a	0	0.0	0	0.0	1	33.3	0	0.0	0	0.0	0	0.0	0	0.0	1	0.5
TFTSE	1,2a,2c,3,24,26,3ka,11,17,30,B,10,14a	1	6.3	0	0.0	1	33.3	0	0.0	0	0.0	0	0.0	0	0.0	1	0.5
TNBGJ	1,2a,2c,3,9,24,10,28,39	0	0.0	0	0.0	0	0.0	1	1.9	0	0.0	0	0.0	0	0.0	1	0.5
TNBJS	1,2a,2c,3,9,24,10,14a,21,28,39	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	1.6	0	0.0	1	0.5
Total isolates		16		6		3		54		59		62		7			207

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

RESISTANCE GENE	MS, GA, LA, AL, NC, AND VA		NY		MO, IN, KY, OH, AND IL		TX AND OK		KS AND NE		MN, SD, AND ND		ID AND WA		TOTAL	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%		
Lr1	16	100.0	6	100.0	3	100.0	54	100.0	59	100.0	62	100.0	7	100.0	207	100.0
Lr2a	5	31.3	2	33.3	3	100.0	1	1.9	1	1.7	6	9.7	1	14.3	19	9.2
Lr2c	5	31.3	2	33.3	3	100.0	1	1.9	1	1.7	7	11.3	1	14.3	20	9.7
Lr3	16	100.0	6	100.0	3	100.0	54	100.0	59	100.0	62	100.0	6	85.7	206	99.5
Lr9	5	31.3	2	33.3	0	0.0	42	77.8	37	62.7	29	46.8	3	42.9	118	57.0
Lr16	0	0.0	0	0.0	0	0.0	2	3.7	0	0.0	4	6.5	0	0.0	6	2.9
Lr24	6	37.5	2	33.3	2	66.7	44	81.5	35	59.3	33	53.2	3	42.9	125	60.4
Lr26	12	75.0	6	100.0	2	66.7	11	20.4	15	25.4	9	14.5	6	85.7	61	29.5
Lr3ka	14	87.5	6	100.0	2	66.7	44	81.5	35	59.3	33	53.2	3	42.9	125	60.4
Lr11	11	68.8	4	66.7	2	66.7	0	0.0	3	5.1	7	11.3	1	14.3	28	13.5
Lr17	16	100.0	5	83.3	3	100.0	51	94.4	59	100.0	55	88.7	6	85.7	195	94.2
Lr30	14	87.5	5	83.3	3	100.0	41	75.9	40	67.8	37	59.7	4	57.1	144	69.6
LrB	16	100.0	5	83.3	3	100.0	51	94.4	59	100.0	55	88.7	6	85.7	195	94.2
Lr10	8	50.0	5	83.3	2	66.7	54	100.0	56	94.9	56	90.3	7	100.0	188	90.8
Lr14a	16	100.0	5	83.3	3	100.0	53	98.1	58	98.3	59	95.2	7	100.0	201	97.1
Lr18	2	12.5	1	16.7	0	0.0	0	0.0	0	0.0	0	0.0	1	14.3	4	1.9
Lr21	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	3	4.8	0	0.0	3	1.4
Lr28	0	0.0	0	0.0	0	0.0	3	5.6	0	0.0	8	12.9	4	57.1	15	7.2
Lr39	5	31.3	2	33.3	0	0.0	52	96.3	56	94.9	51	82.3	3	42.9	169	81.6
Lr42	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Total	16		6		3		54		59		62		7		207	

**Table 3.** Information on individual collections and race designations of derived leaf rust isolates.

COLLECTION / ISOLATE	RACE	CITY	COUNTY	STATE	COLLECTOR	COLLECTION DATE	VIRULENCE FORMULA	CULTIVAR	COMMENT
5001.1	MNPSD	Egypt	Wharton	TX	Simoneaux B	03/23/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Siouxland	
5001.2	MPPSD	Egypt	Wharton	TX	Simoneaux B	03/23/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Siouxland	
5001.3	MNPSD	Egypt	Wharton	TX	Simoneaux B	03/23/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Siouxland	
5002.1	MNPSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 204	
5002.2	MNPSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 204	
5003.1	MNPSD	College Station	Brazos	TX	Simoneaux B	03/22/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalean	
5003.2	MNPSD	College Station	Brazos	TX	Simoneaux B	03/22/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalean	
5003.3	MNPSD	College Station	Brazos	TX	Simoneaux B	03/22/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalean	
5004.1	MNPSD	College Station	Brazos	TX	Simoneaux B	03/22/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 110	
5006.1	MPPSD	Egypt	Wharton	TX	Simoneaux B	03/23/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	TAM 110	
5006.2	MPPSD	Egypt	Wharton	TX	Simoneaux B	03/23/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	TAM 110	
5007.1	MNPSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalean	
5007.2	MNPSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalean	
008.1	MBDSD	Uvalde	Uvalde	TX	Simoneaux B	03/24/2021	1,3,,17,B,10,14a,39	TAM 110	
5008.2	MBDSD	Uvalde	Uvalde	TX	Simoneaux B	03/24/2021	1,3,,17,B,10,14a,39	TAM 110	
5008.3	MBDSD	Uvalde	Uvalde	TX	Simoneaux B	03/24/2021	1,3,,17,B,10,14a,39	TAM 110	
5010.1	MBDSD	College Station	Brazos	TX	Simoneaux B	03/31/2021	1,3,,17,B,10,14a,39	Unk	
5010.2	MPPSD	College Station	Brazos	TX	Simoneaux B	03/31/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Unk	
5011.1	MBDSD	College Station	Brazos	TX	Simoneaux B	03/31/2021	1,3,,17,B,10,14a,39	Unk	
5011.2	MNPSD	College Station	Brazos	TX	Simoneaux B	03/31/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Unk	
5012.1	MBDSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,,17,B,10,14a,39		spreader blend
5012.2	MBDSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,,17,B,10,14a,39		spreader blend
5012.3	MBDSD	Castroville	Bexar	TX	Simoneaux B	03/24/2021	1,3,,17,B,10,14a,39		spreader blend
5013.1	MNPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Scout 66	
5013.2	MBDSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,,17,B,10,14a,39	Scout 66	
5014.1	TNBJG	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,2a,2c,3,9,24,,10,28,39	Jagalene	
5014.2	MNPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalene	
5015.1	MNPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 107	
5016.1	MNPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Kharkof	
5016.2	MNPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Kharkof	
5017.1	MPPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	TAM 110	
5017.2	MPPSD	College Station	Brazos	TX	Simoneaux B	04/01/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	TAM 110	
5018.1	MNPSD	Thrall	Williamson	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalene	
5018.2	MNPSD	Thrall	Williamson	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalene	
5018.3	MNPSD	Thrall	Williamson	TX	Simoneaux B	04/01/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagalene	
5019.1	MJBJG	Thrall	Williamson	TX	Simoneaux B	04/01/2021	1,3,16,24,,10,14a,28	TAM 110	
5019.2	MJBJG	Thrall	Williamson	TX	Simoneaux B	04/01/2021	1,3,16,24,,10,14a,28	TAM 110	
5020.1	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 111	

Table 3. Information on individual collections and race designations of derived leaf rust isolates.

COLLECTION / ISOLATE	RACE	CITY	COUNTY	STATE	COLLECTOR	COLLECTION DATE	VIRULENCE FORMULA	CULTIVAR	COMMENT
5020.2	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 111	
5021.1	MPPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	TAM 204	
5021.2	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 204	
5021.3	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 204	
5022.1	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 101	
5022.2	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 101	
5023.1	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Smiths Gold	
5023.2	MPPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Smiths Gold	
5024.1	MBDSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,,17,B,10,14a,39	TAM 305	
5024.3	MNPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,3ka,17,30,B,10,14a,39	TAM 305	
5025.1	MPPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Jagalene	
5025.2	MPPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Jagalene	
5025.3	MPPSD	Castroville	Bexar	TX	Simoneaux B	04/06/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Jagalene	
5026.1	MPPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Jagalene	Lr24
5027.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Avery	
5027.2	MPPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Avery	
5028.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	LCS Chrome	
5029.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	LCS Link	
5030.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Zenda	
5030.2	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Zenda	
5031.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Lakin/Guller T10R20 P1	VS
5031.2	MPPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Lakin/Guller T10R20 P1	VS
5032.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	LCS Yeti	
5032.2	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	LCS Yeti	
5032.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	LCS Yeti	
5033.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	WB Grainfield	
5033.2	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	WB Grainfield	
5034.1	TCTLB		Riley	KS	Bowden B	04/16/2021	1,2a,2c,3,26,3ka,11,17,30,B,,"	KS89180B	Rare Race Lr26
5034.2	MPPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	KS89180B	Rare Race Lr26
5035.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	SY Monument	
5035.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	SY Monument	
5036.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Bentley	Lr21
5036.2	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Bentley	Lr21
5037.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Larry	
5037.2	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Larry	
5038.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Smith's Gold	
5038.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Smith's Gold	
5040.1	MCTNB		Riley	KS	Bowden B	04/16/2021	1,3,26,3ka,11,17,30,B,14a	Pioneer 25R77	
5040.2	MBTNB		Riley	KS	Bowden B	04/16/2021	1,3,,3ka,11,17,30,B,14a	Pioneer 25R77	
5041.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Bob Dole	Rare Race
5041.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Bob Dole	Rare Race
5042.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Lakin	Susceptible No significant R-genes
5042.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Lakin	Susceptible No significant R-genes
5043.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Jagger	
5043.2	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	Jagger	
5043.3	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Jagger	
5044.1	MLPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,3ka,17,30,B,10,14a,39	Eastwood	
5044.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Eastwood	
5045.1	MPPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	T158	
5045.2	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	T158	
5046.1	MBDSD		Riley	KS	Bowden B	04/16/2021	1,3,,17,B,10,14a,39	Fuller	Castroville
5047.1	MNPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,3ka,17,30,B,10,14a,39	McNair 701	Castroville
5047.2	MLPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,3ka,17,30,B,10,14a,39	McNair 701	Castroville
5047.3	MPPSD		Riley	KS	Bowden B	04/16/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	McNair 701	Castroville
5048.1	MCTNB	Painter	Accomack	VA	Santantonio N	05/12/2021	1,3,26,3ka,11,17,30,B,14a	Massey	
5048.2	MCTNB	Painter	Accomack	VA	Santantonio N	05/12/2021	1,3,26,3ka,11,17,30,B,14a	Massey	
5049.1	TDPSB	Tiffin	Seneca	OH	Olson E	05/26/2021	1,2a,2c,3,24,3ka,17,30,B,10,14a		
5049.2	TCTNB	Tiffin	Seneca	OH	Olson E	05/26/2021	1,2a,2c,3,26,3ka,11,17,30,B,14a		
5049.3	TFTSB	Tiffin	Seneca	OH	Olson E	05/26/2021	1,2a,2c,3,24,26,3ka,11,17,30,B,10,14a		
5050.1	MNPSD	Lahoma	Major	OK	Hunger B	05/14/2021	1,3,9,24,3ka,17,30,B,10,14a,39	LCS Julep	
5050.2	MNPSD	Lahoma	Major	OK	Hunger B	05/14/2021	1,3,9,24,3ka,17,30,B,10,14a,39	LCS Julep	
5051.1	MNPSD	Lahoma	Major	OK	Hunger B	05/14/2021	1,3,9,24,3ka,17,30,B,10,14a,39	LCS Revere	
5051.2	MNPSD	Lahoma	Major	OK	Hunger B	05/14/2021	1,3,9,24,3ka,17,30,B,10,14a,39	LCS Revere	
5052.1	MNPSD		Lancaster	NE	Wegulo S	06/02/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5052.2	MNPSD		Lancaster	NE	Wegulo S	06/02/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5052.3	MNPSD		Lancaster	NE	Wegulo S	06/02/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5053.1	TCJTB	Warsaw	Richmond	VA	Santantonio N	05/25/2021	1,2a,2c,3,26,11,17,B,10,14a,18	Massey	Collected from Virginia Official Variety Trial
5053.2	TCJTB	Warsaw	Richmond	VA	Santantonio N	05/25/2021	1,2a,2c,3,26,11,17,B,10,14a,18	Massey	Collected from Virginia Official Variety Trial

Table 3. Information on individual collections and race designations of derived leaf rust isolates.

COLLECTION / ISOLATE	RACE	CITY	COUNTY	STATE	COLLECTOR	COLLECTION DATE	VIRULENCE FORMULA	CULTIVAR	COMMENT
5054.1	MBTNB	Clarksville	Howard	MD	Rawat N	06/08/2021	1,3,,3ka,11,17,30.B,14a		
5055.1	MCTNB	Clarksville	Howard	MD	Rawat N	06/08/2021	1,3,26,3ka,11,17,30.B,14a		
5055.2	MCTNB	Clarksville	Howard	MD	Rawat N	06/08/2021	1,3,26,3ka,11,17,30.B,14a		
5055.3	MCTNB	Clarksville	Howard	MD	Rawat N	06/08/2021	1,3,26,3ka,11,17,30.B,14a		
5056.1	TBTNB	Wye Island	Queen Anne's	MD	Rawat N	06/08/2021	1,2a,2c,3,,3ka,11,17,30.B,14a		
5056.2	TBTNB	Wye Island	Queen Anne's	MD	Rawat N	06/08/2021	1,2a,2c,3,,3ka,11,17,30.B,14a		
5059.2	MPPSD	Williamson	Pike	GA	Mergoum M	05/18/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		
5061.1	MPPSD	Plains	Sumter	GA	Mergoum M	05/20/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		
5061.1	MPPSD	Plains	Sumter	GA	Mergoum M	05/20/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		
5061.2	MPPSD	Plains	Sumter	GA	Mergoum M	05/20/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		
5065.1	MBDSD	Kingman	Kingman	KS	DeWolf E	05/27/2021	1,3,,17.B,10,14a,39	T-158	
5065.2	MBDSD	Kingman	Kingman	KS	DeWolf E	05/27/2021	1,3,,17.B,10,14a,39	T-158	
5068.1	MNPSD	Hutchinson	Reno	KS	DeWolf E	05/27/2021	1,3,9,24,3ka,17,30.B,10,14a,39		
5068.3	MNPSD	Hutchinson	Reno	KS	DeWolf E	05/27/2021	1,3,9,24,3ka,17,30.B,10,14a,39		
5069.1	MPPSD	Hutchinson	Reno	KS	DeWolf E	05/27/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		
5069.2	MPPSD	Hutchinson	Reno	KS	DeWolf E	05/27/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		
5070.1	MPPSD	pratt	Pratt	KS	DeWolf E	05/27/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		Trace after fungicide
5070.2	MPPSD	pratt	Pratt	KS	DeWolf E	05/27/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		Trace after fungicide
5070.3	MPPSD	pratt	Pratt	KS	DeWolf E	05/27/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39		Trace after fungicide
5071.1	MPPSD	Ashland	Clark	KS	DeWolf E	06/08/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39	Everest	
5071.2	MNPSD	Ashland	Clark	KS	DeWolf E	06/08/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Everest	
5071.3	MNPSD	Ashland	Clark	KS	DeWolf E	06/08/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Everest	
5072.1	MNPSD	Belleville	Republic	KS	DeWolf E	06/09/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Rock Star	
5072.2	MNPSD	Belleville	Republic	KS	DeWolf E	06/09/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Rock Star	
5072.3	MPPSD	Belleville	Republic	KS	DeWolf E	06/09/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39	Rock Star	
5076.1	TNBJS	St Paul	Ramsey	MN	Kolmer J	06/25/2021	1,2a,2c,3,9,24,,10,14a,21,28,39		
5076.2	MNPSD	St Paul	Ramsey	MN	Kolmer J	06/25/2021	1,3,9,24,3ka,17,30.B,10,14a,39		
5076.3	MNPSD	St Paul	Ramsey	MN	Kolmer J	06/25/2021	1,3,9,24,3ka,17,30.B,10,14a,39		
5078.1	MBDSD	Dakota Lakes	Hughes	SD	Byamukama E	06/24/2021	1,3,,17.B,10,14a,39		
5078.2	MNPSD	Dakota Lakes	Hughes	SD	Byamukama E	06/24/2021	1,3,9,24,3ka,17,30.B,10,14a,39		
5078.3	MNPSD	Dakota Lakes	Hughes	SD	Byamukama E	06/24/2021	1,3,9,24,3ka,17,30.B,10,14a,39		
5079.1	MBDSD	Volga	Brookings	SD	Byamukama E	06/28/2021	1,3,,17.B,10,14a,39	Whistler	
5079.2	MBDSD	Volga	Brookings	SD	Byamukama E	06/28/2021	1,3,,17.B,10,14a,39	Whistler	
5079.3	MBDSD	Volga	Brookings	SD	Byamukama E	06/28/2021	1,3,,17.B,10,14a,39	Whistler	
5080.1	MNPSD	Rosemount	Dakota	MN	Kolmer J	07/06/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Morocco	
5080.2	MNPSD	Rosemount	Dakota	MN	Kolmer J	07/06/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Morocco	
5082	5082.1	MBTNB	Waseca	MN	Kolmer J	07/06/2021	1,3,,3ka,11,17,30.B,14a	Morocco	
5082.2	MBTNB	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,3,,3ka,11,17,30.B,14a	Morocco	
5083.1	MBTNB	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,3,,3ka,11,17,30.B,14a	Morocco	
5083.3	MNPSD	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Morocco	
5084.1	TBTNB	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,2a,2c,3,,3ka,11,17,30.B,10,14a	Morocco	
5084.2	TBTNB	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,2a,2c,3,,3ka,11,17,30.B,10,14a	Morocco	
5085.1	MPPSD	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39	Morocco	
5085.2	TBTNB	Waseca	Waseca	MN	Kolmer J	07/06/2021	1,2a,2c,3,,3ka,11,17,30.B,10,14a	Morocco	
5086.1	TCTSB	Ithaca	Tompkins	NY	Bergstrom G	07/01/2021	1,2a,2c,3,26,3ka,11,17,30.B,10,14a	NY 11013-10-15-1312	
5086.2	MPPSD	Ithaca	Tompkins	NY	Bergstrom G	07/01/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39	NY 11013-10-15-1312	
5086.3	MPPSD	Ithaca	Tompkins	NY	Bergstrom G	07/01/2021	1,3,9,24,26,3ka,17,30.B,10,14a,39	NY 11013-10-15-1312	
5088.1	TCTSB	Ithaca	Tompkins	NY	Bergstrom G	07/01/2021	1,2a,2c,3,26,3ka,11,17,30.B,10,14a	Erie	
5089.1	MCTNB	Ithaca	Tompkins	NY	Bergstrom G	07/01/2021	1,3,26,3ka,11,17,30.B,14a	Medina	
5089.2	MCQHB	Ithaca	Tompkins	NY	Bergstrom G	07/01/2021	1,3,26,3ka,11,10,18	Medina	
5090.1	MBDSD	Lamberton	Redwood	MN	Anderson J	07/09/2021	1,3,,17.B,10,14a,39	Morocco	
5090.2	MBDSD	Lamberton	Redwood	MN	Anderson J	07/09/2021	1,3,,17.B,10,14a,39	Morocco	
5091.1	MBDSD	Lamberton	Redwood	MN	Anderson J	07/09/2021	1,3,,17.B,10,14a,39	Morocco	
5091.2	MBDSD	Lamberton	Redwood	MN	Anderson J	07/09/2021	1,3,,17.B,10,14a,39	Morocco	
5092.1	MNPSD	Lamberton	Redwood	MN	Caspers R	07/12/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Morocco	
5093.1	TBBGS	Rosemount	Dakota	MN	Caspers R	07/13/2021	1,2a,2c,3,,10,21,28,39		Spreader Rows
5093.2	TBBGS	Rosemount	Dakota	MN	Caspers R	07/13/2021	1,2a,2c,3,,10,21,28,39		Spreader Rows
5094.1	MNPSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30.B,10,14a,39	Morocco	
5094.2	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39	Morocco	
5095.1	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39	Morocco	
5095.2	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39	Morocco	
5095.3	MCTNB	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,26,3ka,11,17,30.B,14a	Morocco	
5096.1	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39		Spring wheat
5096.2	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39		Spring wheat
5096.3	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39		Spring wheat
5097		Crookston	Polk	MN	Kolmer J	07/20/2021		Morocco	
5097.1	MJMIG	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,16,24,3ka,30,10,14a,28	Morocco	
5097.2	MJMIG	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,16,24,3ka,30,10,14a,28	Morocco	
5098.1	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39	Morocco	
5098.2	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39	Morocco	
5098.3	MBDSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,,17.B,10,14a,39	Morocco	



Table 3. Information on individual collections and race designations of derived leaf rust isolates.

COLLECTION / ISOLATE	RACE	CITY	COUNTY	STATE	COLLECTOR	COLLECTION DATE	VIRULENCE FORMULA	CULTIVAR	COMMENT
5099.1	MPPSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Morocco	
5099.2	MPPSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Morocco	
5099.3	MPPSD	Crookston	Polk	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39	Morocco	
5100.1	MPPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39		
5100.2	MPPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39		
5100.3	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5101.1	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5101.2	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5103.1	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39		
5104.1	MPPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39		
5105.1	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5105.2	MBDSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,,17,B,10,14a,39		
5106.1	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5107.1	MNPSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5107.2	MBDSD	Casselton	Cass	MN	Kolmer J	07/20/2021	1,3,,17,B,10,14a,39		
5108.1	MNPSD	Morris	Stevens	MN	Curt R.	07/21/2021	1,3,9,24,3ka,17,30,B,10,14a,39		a lot of leaves
5108.2	MNPSD	Morris	Stevens	MN	Curt R	07/21/2021	1,3,9,24,3ka,17,30,B,10,14a,39		a lot of leaves
5108.3	PBDQJ	Morris	Stevens	MN	Curt R	07/21/2021	1,2c,3,,17,B,10,28,39		a lot of leaves
5110.1	LCDSG	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,26,17,B,10,14a,28	Breeding Line SW16030-1	
5110.2	MCDSG	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,3,26,17,B,10,14a,28	Breeding Line SW16030-1	
5110.3	MCDSG	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,3,26,17,B,10,14a,28	Breeding Line SW16030-1	
5111.1	MNPSD	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,3,9,24,3ka,17,30,B,10,14a,39		
5111.2	MPPSD	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39		
5111.3	MPPSD	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,3,9,24,26,3ka,17,30,B,10,14a,39		
5113.1	TCRKG	Mt. Vernon	Skagit	WA	Wang M	06/29/2021	1,2a,2c,3,26,3ka,11,30,10,14a,18,28		
5115.1	MJBIG	St Paul	Ramsey	MN	Kolmer J	07/09/2021	1,3,16,24,,10,14a,28		
5115.1	MJBIG	St Paul	Ramsey	MN	Kolmer J	07/09/2021	1,3,16,24,,10,14a,28		
5116.1	MNPSD	St Paul	Ramsey	MN	Kolmer J	08/11/2021	1,3,9,24,3ka,17,30,B,10,14a,39	RB07	
5116.2	MNPSD	St Paul	Ramsey	MN	Kolmer J	08/11/2021	1,3,9,24,3ka,17,30,B,10,14a,39	RB07	
5116.3	MNPSD	St Paul	Ramsey	MN	Kolmer J	08/11/2021	1,3,9,24,3ka,17,30,B,10,14a,39	RB07	
5117.1	TFTSB	Williamson	Pike	GA		05/14/2021	1,2a,2c,3,24,26,3ka,11,17,30,B,10,14a		Sample is in plastic tube
5117.2	MNPSD	Williamson	Pike	GA		05/14/2021	1,3,9,24,3ka,17,30,B,10,14a,39		Sample is in plastic tube

**Table 4.** Hard red winter and spring wheat cultivars grown in 2021 (+ indicates that the cultivar was resistant to all isolates tested).

Oklahoma	Kansas	Nebraska	Minnesota	North Dakota
Gallagher <i>Lr26</i> 10.9%	SY Monument 9.4%	SY Monument 14.2%	WB9590 18.0%	SY Ingmar <i>Lr21</i> 13.2%
Smith's Gold <i>Lr34 Lr37 Lr77</i> 9.2%	WB Grainfield <i>Lr39</i> 5.5%	Husker Genetics: Settler CL <i>Lr11</i> 8.5%	SY Valda + 12.8%	SY Valda + 9.5%
Doublestop CL Plus No <i>Lr</i> gene 8.3%	Zenda <i>Lr37</i> 4.7%	Husker Genetics: Ruth <i>Lr37</i> 7.3%	Linkert <i>Lr16 Lr23 Lr34</i> 11.9%	WB 9590 7.5%
Iba <i>Lr37 Lr34</i> 3.1%	T158 <i>Lr37 Lr39</i> 3.1%	WB-GrainField <i>Lr39</i> 6.8%	WB9479 <i>Lr21</i> 10.27%	AP Murdock <i>Lr21</i> + 4.7%
Winterhawk <i>Lr39</i> 3.0%	Joe <i>Lr21</i> 2.8%	SY Wolverine 6.7%	MN Torgy <i>Lr16</i> 9.67%	Glenn <i>Lr21</i> 4.4%
Green Hammer 2.8%	Winterhawk <i>Lr39</i> 2.7%	Brawl CL Plus <i>Lr14a Lr34</i> 6.5%	AP Murdock <i>Lr21</i> 8.4%	Faller <i>Lr21</i> 4.2%
WB4515 2.4%	Bob Dole <i>Lr37 Lr39</i> 2.4%	LCS Link 4.7%	Shelly <i>Lr21</i> 4.15%	Shelly <i>Lr21</i> 3.3%
SY Monument 2.3%	LCS Chrome <i>Lr37 Lr39</i> 2.4%	WB4304 3.4%	MN Washburn <i>Lr16</i> 4.0%	Bolles + 3.0%
Bentley <i>Lr21 Lr39</i> 2.1%	TAM 114 2.4%	Husker Genetics: Robidoux 3.3%	WB Mayville 3.06%	ND Vitpro + 2.9%
TAM112 <i>Lr39</i> 1.7%	Everest 1.9%	AP503 CL2 3.0%	SY Ingmar + 1.65%	CP3530- <i>Lr21</i> 2.7%

## **SOUTH CAROLINA**

### **CLEMSON UNIVERSITY**

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

### ***Transcriptomic and proteomics studies in common wheat for grain quality traits and Fusarium head blight resistance.***

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Common wheat is an essential nutritional source in the United States and worldwide. Global wheat production averages around 765 million tons per year, with Americans consuming 4% of the total annually (FAO 2020; USDA 2021). As the population continues to grow, the demand for wheat is increasing, but wheat yields have flatlined over the last 20 years (Schauberger et al. 2018). Additionally, wheat gluten proteins, primarily associated with end-use performance, were identified to be responsible for many foodborne disorders (Rustgi et al. 2019; Brouns et al. 2019). Plant processes, such as wheat grain development, can be examined to combat stagnating yields and improve nutritional quality and safety, and

offer a better understanding of these processes so that grain yield, end-use performance, nutritional quality, and safety can be optimized to meet the growing need for nutritious and safe grains.

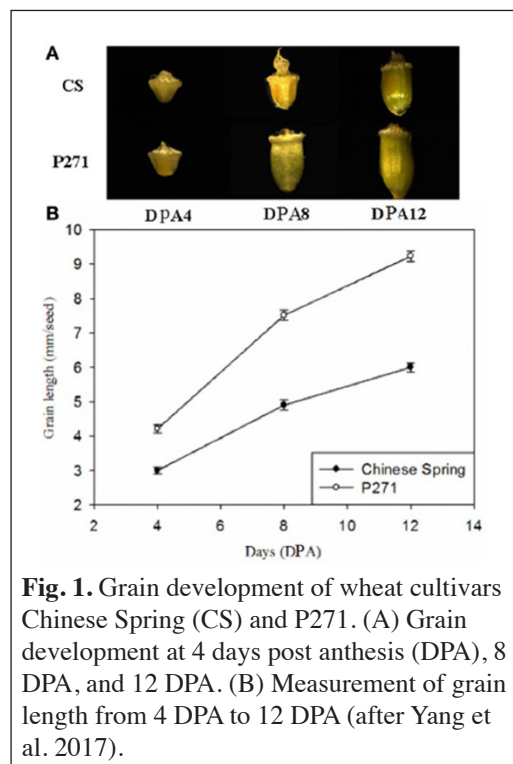
Wheat grain development is an intricate process that consists of three developmental stages: cellularization, grain filling, and maturation (Nadaud et al. 2010). During the first stage, the fundamental grain structures develop (Sabelli and Larkins, 2009). Indeed, 80% of the final grain size is decided during this developmental stage due to the cell divisions in the endosperm and proliferation of the resulting cells (Brocklehurst 1977; Laudencia-Chingcuanco et al. 2007; Sabelli and Larkins 2009; Nadaud et al. 2010). Approximately 12 days after anthesis, grain development transitions into its second stage, grain filling. Lasting approximately two weeks, during this phase, the grain begins to accumulate storage proteins and carbohydrates, and grain weight increases twofold. Twenty-eight days post-anthesis, grain filling begins to stagnate and is complete after 35 days. During the third stage, around 42 days after anthesis, the grain begins to dry and reaches its final weight (Shewry et al. 2012).

Another critical factor affecting wheat grain quality, yield, nutritional properties, and safety is *Fusarium* head blight (FHB) or scab. This disease is widespread and causes massive reductions in yield, grain quality, and safety. Unfortunately, there is limited understanding of the FHB resistance mechanism, demanding a detailed proteomics-based investigation of differences between FHB susceptible and resistant wheat cultivars after artificial *Fusarium* inoculation.

Proteomics and transcriptomics can offer important insight into the molecular mechanisms behind wheat grain development and defense. Proteomics has been utilized to observe the effects of abiotic stressors, including drought, heat, salinity, and biotic stressors such as insects and fungal pathogens (Peng et al. 2009; Ford et al. 2011; Eldakak et al. 2018; Lavergne et al. 2020; Chunduri et al. 2021). Utilizing transcriptomics in addition to proteomics allows for a greater understanding of the transcriptional and translational modifications that take place during the wheat grain development. Previously, these studies in wheat were limited as they only analyzed one genotype of wheat or did not compare wheat genotypes with different grain characteristics such as large and small-sized grains and differences in the level of FHB resistance.

**Variation in the protein accumulation patterns during early grain development of large and small-seeded wheat cultivars.** To analyze metabolic differences between small and large grain wheat, the cultivars P271 and Chinese Spring (CS) were used as model genotypes (Fig. 1A). P271 demonstrates a larger grain size from 4 to 12 DPA (Fig. 1B) than that of CS, and the two genotypes also have embryological developmental differences as CS endosperm cellularization was nearly completed at 8 DPA, whereas P271 endosperm cellularization was not completed until four days later at 12 DPA. The CS endosperm was sickle-shaped at 8 DPA and, in its development, crushed the integuments and nucellus and filled all space within the pericarp. P271, on the other hand, displayed a kidney-like shaped endosperm at 8 DPA, and its endosperm did not enlarge and occupy the pericarp until after 8 DPA.

To further study the underlying metabolic mechanisms that led to these developmental differences, iTRAQ (isobaric tags for relative and absolute quantitation) quantitative proteome characterization approach was utilized at three grain development time points (4 DPA, 8 DPA, and 12 DPA). 3,678 proteins were identified in both cultivars, of which 130 proteins displayed at least a two-fold difference in expression between the two cultivars, and 306 differentially expressed proteins (DEPs) were found in the developmental stage comparisons. Twelve of these proteins were found to express solely in CS with seven upregulated and five downregulated genes, while two proteins expressed only in P271 with both proteins upregulated. 91 of the 130 DEPs detected in the comparison of CS to P271 showed upregulation at least at one developmental time point, whereas the remaining were downregulated at least at one developmental stage.



**Fig. 1.** Grain development of wheat cultivars Chinese Spring (CS) and P271. (A) Grain development at 4 days post anthesis (DPA), 8 DPA, and 12 DPA. (B) Measurement of grain length from 4 DPA to 12 DPA (after Yang et al. 2017).

Gene ontology enrichment analysis of the DEPs comparing the two wheat cultivars at different developmental stages showed at 4 vs. 8 DPA, most of the proteins belonging to the classification of biological process. Chinese Spring displayed more upregulated genes compared to P271 in the following classifications: biosynthetic process, lipid metabolic process, and small molecule metabolic process, but having more downregulation in catabolic processes, photosynthesis, carbohydrate metabolic process, and generation of precursor metabolites and energy. In proteins categorized in the cellular component category, more DEPs were found to be downregulated than upregulated, with CS having more downregulated DEPs in the subcategories of thylakoid, plastid, and protein complex, whereas those of P271 fell into the subcategories of chromosome, plasma membrane, protein complex, and nucleus. In the molecular function category, the DEPs followed a similar trend, with more DEPs being downregulated than upregulated, with the DEPs being categorized as ion binding and oxidoreductase activity.

In a comparison of both CS and P271 at 12 vs. 8 DPA, DEPs falling under carbohydrate metabolic process were more upregulated in CS, and similar numbers of DEPs fell in the subcategory biosynthetic process were downregulated in both cultivars. P271 possessed more DEPs in the cellular component category falling in the subcategories protein complex, chromosome, mitochondrion, nucleus, and intracellular exhibiting downregulation. However, in P271, not all DEPs categorized as intracellular, cytoplasm, nucleus, and protein complex were downregulated as some also displayed upregulation. More upregulated DEPs in CS fall in the subcategories extracellular region, extracellular space, and endoplasmic reticulum. In the analysis of the DEPs falling under the molecular function category, they followed a similar trend to the 4 vs. 8 DPA results, as most DEPs were found to have a role in ion binding and oxidoreductase activity.

A Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis found that most DEPs belong to the categories of carbon metabolism, protein processing in the endoplasmic reticulum, amino acid biosynthesis, and carbon fixation in photosynthetic organisms. At 12 DPA vs. 8 DPA, P271 accumulated more proteins in the categories of starch and sucrose metabolism, amino sugar and nucleotide sugar metabolism, and protein processing in the endoplasmic reticulum. The differences in protein accumulation of these proteins could be responsible for explaining why there are such developmental differences between the large grain wheat, P271, and the smaller grain wheat, CS, as sucrose metabolism and starch biosynthesis play an important role in grain development in cereals (Zhang et al. 2021).

#### **Variation in the transcription patterns during early grain development of large and small-seeded wheat varieties.**

Transcriptional analysis offers additional useful information into the mechanism driving early grain development. Insight is gained through the use of microarrays and RNA sequencing, which gives details on gene expression, determining which genes could play important roles in determining grain size and quality (Laudencia-Chinguanco et al. 2006, 2007; Wan et al. 2008; Pfeifer et al. 2014; Rangan et al. 2017; Ramirez-Gonzalez et al. 2018). To further examine the differences in large grain and small grain wheat, the cultivars used in the above-mentioned proteomics study (P271 and CS) were analyzed for their transcription patterns. Using RNA sequencing and STEM software, a comparison was performed of the differentially expressed genes (DEGs) between the large grain wheat (P271) and the smaller grain size wheat (CS) followed by gene ontology category enrichment and KEGG pathway enrichment.

Chinese Spring DEGs were over-represented in the profiles at 8 DPA and both P271 and CS genes displayed two main expression patterns: consistent downregulation and consistent expression succeeded by down-regulation. However, the two cultivars demonstrate these expression patterns at different time points in their grain development. CS also had a third, but less common expression pattern, where downregulation was followed by a constant gene expression.

In gene ontology analysis, genes were grouped into three distinct categories: biological processes, cellular component, and molecular function. For genes belonging to the biological processes category, at 4, 8, and 12 DPA for both cultivars, the majority belonged to cellular process and metabolic process. When comparing the two cultivars against one another, P271 had more genes involved in cellular and metabolic processes downregulated at 4 and 8 DPA and upregulated at 12 DPA. In regard to DEGs categorized in the cellular component category, the majority of the DEGs belonged to the subcategories organelle, cell, and cell part at all three developmental time points (4, 8, and 12 DPA). P271 possessed more genes displaying downregulation at 4 DPA than CS while also having more genes upregulated at 8 and 12 DPA. DEGs grouped into the category molecular function mostly belonged to the subcategories binding and catalytic activity at all three developmental time points. Both subcategories had similar behavior between the P271 and CS as more genes were downregulated at 4 and 8 DPA while more genes were upregulated at 12 DPA.

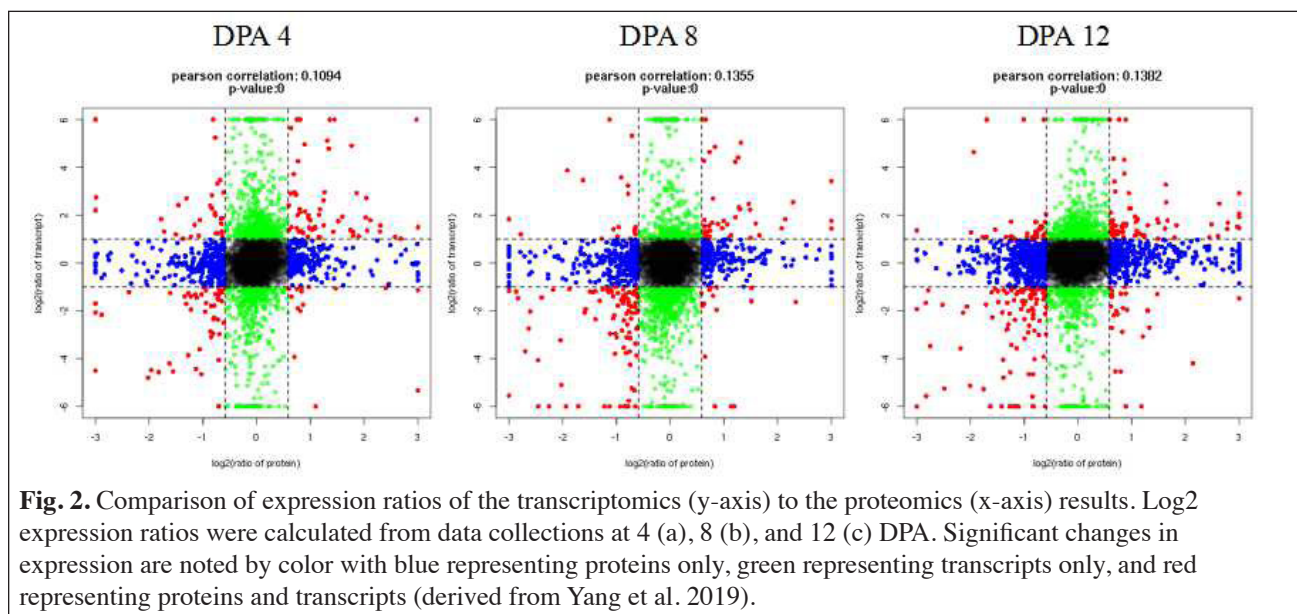
KEGG pathway enrichment analysis at 4 DPA between CS and P271 found that there were more genes involved in the processes of starch and sucrose metabolism, amino acid biosynthesis, and plant-pathogen interaction. At 8 DPA,



there were more genes active in phenylpropanoid biosynthesis, plant hormone signal transduction in addition to starch and sucrose metabolism, and plant-pathogen interaction-related genes that were also active at 4 DPA. Furthermore, in the comparison of the two cultivars at 12 DPA, genes were found to be involved in the following processes: pyrimidine metabolism, ribosome biogenesis, purine metabolism, spliceosome, starch, and sucrose metabolism, and plant hormone signal transduction.

**Correspondence between the transcriptomic and proteomic data during early grain development in common wheat.** The information gained from transcriptomics and proteomics studies sheds light on the developmental differences and pathways involved in early grain development between large and small grain wheat cultivars; however, there may be other factors that participate in controlling protein accumulation other than simply gene expression. Further comparison utilizing the same samples of CS and P271 allowed determining the relationship between transcription and translation in early wheat grain development and offered the ability to detect the effect of outside influencers on the post-transcriptional regulation.

At the three different developmental stages (4 DPA, 8 DPA, and 12 DPA), 5468, 5526, and 4964 sequences displayed correspondence between the proteomics and transcriptomics analysis. As demonstrated in Fig. 2, correlation testing of the mRNA:protein ratios revealed an insignificant relationship between the two, but there are some correlating data points that hint at the correspondence between transcript accumulation and protein abundance. Data points existed that did not correspond between transcript accumulation and protein abundance, which suggests that post-transcriptional regulation occurred. This has not been previously reported in studies examining transcription or protein accumulation during wheat grain development.



In a comparison of transcription versus protein accumulation at the three developmental points, the larger grain cultivar, P271, had higher expression levels of genes related to starch and sucrose metabolism when compared to the smaller grain cultivar; however, the abundance of the corresponding proteins was low. Intriguingly, the opposite observation was noticed at 12 DPA, where a higher abundance of protein related to starch and sucrose metabolism was recorded, but the expression level of the related genes was low.

**Genomic distribution of differentially expressed genes/proteins contributing to the early grain development in common wheat.** Differentially expressed genes/proteins were then mapped to determine their location within the wheat genome to further examine which chromosomes played a major role in the early grain development of common wheat. Continuing the comparison of the large grain cultivar, P271, to the smaller grain cultivar, CS, the majority of the DEGs/DEPs mapped to the A and B subgenomes in wheat, with the A subgenome possessing more than the expected number of DEGs/DEPs at 4 DPA and 8 DPA, respectively. 12 DPA had contrasting results where the B sub-genome possessed more DEGs/DEPs than expected. Furthermore, grouping homeologous chromosomes together found that at 4 DPA, groups

3 and 6 chromosomes contained the most DEGs/DEPs, at 8 DPA, groups 1, 3, and 4 chromosomes contained the most DEGs/DEPs, and at 12 DPA, groups 1 and 5 chromosomes contained the most DEGs/DEPs. Further examination at the individual chromosome level found that chromosomes 1A, 4B, and 5B possessed the largest number of DEGs/DEPs at all time periods tested. Chromosomes 3A, 3B, 4A, and 6A also contained large numbers of DEGs/DEPs at time periods 4 DPA and 8 DPA, whereas chromosomes 1B and 1D contained a large number of DEGs/DEPs at 8 DPA and 12 DPA. Other chromosomes of interest include those that only mapped DEGs/DEPs at one time period, which includes chromosome 6D at 4 DPA, chromosomes 2A and 7D at 8 DPA, and 2B at 12 DPA.

Examination of the distributions of the DEGs/DEPs within the regions of the individual chromosomes found that at 4 DPA majority mapped to the centromeric and pericentromeric regions, while at 8 DPA and 12 DPA, there was a much more even distribution of the DEGs/DEPs. Homeologous genes were also found in 14 instances at specific developmental points, with genes expressed at the same developmental point indicating cumulative expression while expression at different developmental points indicates sub-functionalization. Of 221 localized DEGs/DEPs, 24 overlapped with known quantitative trait loci for grain characteristics such as thousand-grain weight, grain width, and grain thickness.

**Differences in the protein accumulation pattern of Fusarium head blight-resistant and susceptible wheat genotypes.** In addition to aiding the understanding of early grain development, proteomics was utilized to determine protein accumulation patterns for other beneficial traits, including Fusarium head blight resistance. Fusarium head blight (FHB) can have a devastating effect on wheat yields, reducing grain quality and can lead to the accumulation of mycotoxins (Bottalico and Perrone 2002; Eldakak et al. 2018).

Wheat cultivars Xinong 538, resistant to FHB, and Zhoumai 18, susceptible to FHB, were used as model genotypes in proteomics analysis using iTRAQ-labeling-based mass spectrometry. 13,669 unique proteins were identified between the two cultivars, with 1,034 proteins displaying reduced accumulation and 1,471 showing increased accumulation in Xinong 538. In Zhoumai 18, 392 proteins showed reduced accumulation, and 495 showed upregulation.

Gene ontology studies categorized differentially accumulated proteins into three distinct categories: biological process, cellular component, and molecular function. In the biological process category, the majority of proteins fell into the subcategories metabolic process, single-organism process, and cellular process, with Xinong 538 possessing more differentially accumulated proteins in each of the three subcategories than Zhoumai 18. In the cellular component category, DAPs were enriched in the subcategories cell, cell membrane, and organelle, with both genotypes displaying the enrichment. Enrichment also occurred in both cultivars in the molecular function category 'binding'.

The Kyoto Encyclopedia of Genes and Genomes analysis provided additional details regarding the number of proteins involved in different metabolic pathways. Enrichment of DAPs occurred in categories such as metabolic pathways, biosynthesis of antibiotics, biosynthesis of secondary metabolites, phenylpropanoid biosynthesis, biosynthesis of amino acids, carbon metabolism, ribosome, and microbial metabolism in diverse environments, with Xinong 538 showing three times more enrichment in these pathways than Zhoumai 18. Enrichment in oxidative phosphorylation and protein processing in the endoplasmic reticulum were exclusive to Xinong 538, although enrichment in photosynthesis and carbon fixation in photosynthetic organisms was exclusive to Zhoumai 18. These findings support earlier studies where proteins involved in host defense were found to be highly expressed after inoculation with *F. graminearum* (Eldakak et al. 2018; Fabre et al. 2019).

In the case of FHB resistance, protein accumulation had a direct correspondence with mRNA accumulation as four selected genes, which concur FHB defense (Chitinase IV, Thaumatin-like 1, PR1.1, and PR1.2) had increased accumulation of both mRNA and protein in the resistant Xinong 538 cultivar after inoculation with *F. graminearum* (Anand et al. 2003; Mackintosh et al. 2007; Geddes et al. 2008).

**Protein profiling of the wheat DNAM population (core collection) for reduced gluten content.** The seed storage proteins, precisely gluten in wheat grains, determine end-use performance and cause celiac disease and gluten allergy in sensitive individuals. Celiac disease affects >1.4% of the global population (Singh et al. 2018). Currently, there is no widely available therapy for those suffering from these conditions; thus, they must abstain from consuming products containing gluten (Rustgi et al. 2019). One strategy for alleviating this problem for gluten-sensitive individuals is by producing wheat grains reduced in immunogenic proteins. Of the three subgenomes of hexaploid wheat the D subgenome has been found to possess the highest number of epitopes recognized by the immune system of predisposed individuals (Spaenij-Dekking et al. 2005). We intend to identify genotypes with reduced content of immunogenic proteins using a D-genome,

nested association mapping population (DNAM) derived from crosses between common wheat line KS05HW14-3 and eight *Aegilops tauschii* donors. The objective of creating this population was to develop more genetic diversity within the D subgenome of common wheat. We are currently screening a DNAM core collection (Strauss et al. 2020) to identify lines completely lacking or accumulating the reduced quantity of immunogenic gluten proteins. Additionally, we intend to decipher the genetic regulation of immunogenic gluten protein accumulation in wheat grains via protein quantity loci mapping using this population. Information from these experiments will be used to further breeding programs to develop reduced immunogenic wheat varieties for celiac patients.

Together this research aims to improve wheat grain quality and gain further understanding of the mechanisms responsible for increased yields, increased disease resistance, and reduced immunogenicity. With a growing global population, greater knowledge of the genes that control these traits could play a valuable role in keeping up with a growing demand for wheat as consumption increases.

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### ***2021 Wheat Production in the Commonwealth of Virginia.***

**Growing Season and Production.** Autumn 2020 had near-normal temperatures and significant rainfall in many areas of the Commonwealth. Some farmers took advantage of favorable weather and by the end of September, 19% of the intended wheat acres had been seeded compared to the 5-year average of 9%. Wet conditions persisted with 20% of the state having ‘surplus’ soil moisture in late October. By 8 November, 66% of wheat acres were planted, exactly matching the 5-year average. Temperatures in late November were above normal, with a little less rain in some areas, but more than 10% of intended acres were still not planted due to wet soils. For the 2020 calendar year, Richmond received 15 more inches of rainfall than the long-term average. Wet weather persisted in many areas in January and February, delaying nitrogen fertilizer applications on many fields and leaving many fields with dead spots due to standing water. This resulted in only 26% of the crop rated good or excellent in late February. Wet weather and warm temperatures were the norm in March and crop condition improved to 39% of the crop rated good or excellent. The weather pattern persisted into mid-April. Seven percent of the crop had headed by 18 April, compared to the 5-year average of 11% by this date. Wheat condition improved through early May with heading still 13% behind average date. May was warm and dry for most areas with over half the state reporting soil moisture deficits. On 13 June, 52% of the wheat crop was rated good or excellent. By this date, 18% of wheat acres were harvested, which was behind the normal pace. The Virginia field office of USDA’s National Agricultural Statistics Service estimated that Virginia planted 220,00 acres (89,100 hectares) of wheat in 2020 of which 125,000 acres (50,585 hectares) was harvested by July of 2021. Virginia produced  $8.04 \times 10^6$  bushels (219,000 metric ton) of wheat in 2021 and the average yield was 67 bu/acre (4505.8 kg/ha).

**Disease incidence and severity.** Disease pressure was almost completely absent across most of Commonwealth of Virginia. Across six locations evaluated in the Official Variety Trial, no significant disease was observed during flowering and early grain fill, with the exception of barley yellow dwarf virus symptoms, which averaged a 1.7 severity score on a

0–9 scale (with 0 being no disease and 9 being very severe disease). Some regions, including the Northern Neck experienced leaf rust pressure very late in the grain fill period (average score of 1.4 on a 0–9 scale), but was unlikely to have significantly affected yield so late in the season.

**State cultivar tests.** Wheat trials were planted in seven-inch rows at Blackstone, Orange, Holland, Painter, and Shenandoah Valley. They were planted in six-inch rows at Blacksburg and Warsaw. The no-till locations (Holland and Shenandoah Valley) were planted at 48 seeds per square foot. All other locations were planted at 44 seeds per square foot. Selecting the best wheat cultivars is challenging but becomes easier with adequate information on performance over multiple environments. Past seasons across Virginia have provided the opportunity to evaluate day length sensitivity, spring freeze damage, glume blotch, scab (*Fusarium* head blight), and general plant health. Many newer wheat varieties and lines performed well in all environments tested. The future for wheat cultivars adapted to Virginia conditions is very positive. Dr. Nicholas Santantonio, Virginia Tech’s small grains breeder, has many lines starting with ‘VA’ shown in the by- and over-location tables that are in the top-yielding group and that display good disease resistance. The released cultivars that yielded significantly higher than the statewide mean in 2021, in descending yield order, were Dyna-Gro 9002, AgriMAXX 514, USG 3451, USG 3472, Cropland 8045, MAS#86, Dyna-Gro 9120, DynaGro Laverne, MBX 120, USG 3329, Dyna-Gro Shirley, Dyna-Gro 9172, Southern Harvest 9520, and Hilliard. USG 3451; Dyna-Gro 9120 also had test weight that was significantly higher than the mean of all lines tested. Average yield of all lines tested in 2020–21 was 81.9 bu/acre, down 7.3 bu/acres from 2019-20. Released lines with yields higher than the 3-year statewide mean, in descending yield order, were SY Viper, USG 3329, Pioneer 26R59, MAS #86, and Featherstone 125. SY Viper and Featherstone 125 also had test weight that was significantly higher than the mean of all lines tested over the 3 years. Producers who grow large acreages of wheat should plant two or more cultivars having significantly different maturity dates in order to ensure harvest of high-quality grain having high test weight and no sprouting. In Virginia, it is typical for sporadic or consistent rain showers to interrupt harvest. These wetting and drying cycles and subsequent delays can significantly reduce grain test weight and quality. Growers can circumvent this problem by planting cultivars that differ significantly in maturity. Early maturing cultivars often can be harvested first and prior to significant rain showers, and later maturing cultivars harvested subsequently will suffer less damage and losses in test weight and quality due to exposure to such a rain event.

**Newly released cultivars:** No new wheat cultivars were released by the Virginia Agricultural Experiment Station in 2021, but several were staged for release the following year.

**Virginia Wheat Yield Contest Results** (<http://www.viriniagrains.com/yield/yieldcontests/>) (Table 1).

Yield rank	Wheat class	Grower	Farm	County	Yield (bu/ac)	Yield (kg/ha)
1	SRW	Guy Cochenour	GG Farms	Shenandoah	120.6	8,110.4
2	SRW	Shane Richman	Haynie Farms	Shenandoah	112.9	7,592.5
3	SRW	Justin Welch	Welch Farms	Northumberland	110.2	7,411.0
1	HRW	Joe Gray	Herren Farm LLX	Culpeper	105.8	7,115.1

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## **WASHINGTON**

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[www.wsu.edu/~wwql/php/index.php](http://www.wsu.edu/~wwql/php/index.php)

Alecia Kiszonas, Mary Baldrige, Gail Peden, William Kelley, Shelle Lensen, Eric Wegner, Janet Luna, Stacey Sykes, Judene McLane, Robin Saam, Kelly Leonard, Susan Conrad, Sintayehu Daba, Katrina Johnson, Megan Russo, Daniel Zborowski, Mylea Harlan, Gabriely Alfaro, and Francesco Camerlengo.

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.

Kiszonas leads 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, legumes, super soft wheat, grain flavor, and Falling Number.

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## ITEMS FROM URUGUAY

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***Untapping the blast resistance from the D-subgenome progenitor of wheat.***

Paula Silva; Lidia Calderon (Unidad de Mejoramiento de Trigo, Asociación de Productores de Oleaginosas y Trigo (AN-APO), Santa Cruz de la Sierra, Bolivia); Liangliang Gao, John Raupp, Gioavana Cruppe, and Barbara Valent (Department of Plant Pathology, Kansas State University, Manhattan, Kansas, USA); Open Wild Wheat Consortium (<https://openwildwheat.org>); and Jesse Poland (Center for Desert Agriculture, King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia).

Wheat resistance has been significantly improved through the identification, introgression, and deployment of novel genes from different wild relatives. An example of an economically important trait for which the cultivated bread wheat germplasm lacks diversity is wheat head blast (WHB). Therefore, identifying new resistance genes is of top priority to broaden the available genetic resources against WHB. In this study, we hypothesized that, *Aegilops tauschii* is an unexploited source of genes for resistance to WHB that could be utilized for breeding. The objectives were to characterize the level of resistance to WHB across a diverse panel of *Ae. tauschii* and to identify genomic regions associated with resistance. We evaluated a panel of 226 accessions under controlled conditions and combined this data with  $3 \times 10^6$  SNP markers to run a genome-wide association mapping analysis. We were able to identify resistant accessions from both lineages, with most of the resistant accessions belonging to L2. WHB resistance mapped to chromosome 7DL at 626 Mb, where three candidate genes are annotated. Both lineages shared the same resistant haplotype, which suggests that the same gene is controlling WHB resistance. This is the first report of genomic regions from *Ae. tauschii* associated with resistance to WHB. Resistant accessions identified here could be utilized to introduce WHB resistance into the wheat primary pool. However, further research is needed to understand the various mechanisms of this resistance. Qualitative resistance to WHB available in the current wheat gene pool is limited, therefore, continuing this search using other species related to wheat and different isolates will be crucial to broadening the resistance genes available to introgress into wheat germplasm.

***Dissecting wheat curl mite resistance in bread wheat.***

Paula Silva, Liangliang Gao and John Raupp (Department of Plant Pathology and Wheat Genetics Resource Center, Kansas State University, Manhattan, KS 66506, USA), OWWC (<https://openwildwheat.org>), and Jesse Poland (Center for Desert Agriculture, King Abdullah University of Science and Technology (KAUST), Thuwal 23955, Saudi Arabia).

Wheat curl mite (WCM) is a threatening pest for wheat, mainly by vectoring several viral diseases, such as wheat streak mosaic virus. To date, only five resistance genes have been identified, and three of them, *Cmc1*, *Cmc4*, and *CmcTAM112*, were donated by different accessions of *Aegilops tauschii*, the donor of the wheat D-subgenome. Moreover, the three genes were transferred to very similar regions on chromosome 6DS in wheat. Here we postulate that resistance genes *Cmc1*, *Cmc4*, and *CmcTAM112* are allelic forms of the same gene; which can be inferred based on haplotype compositions around the resistance locus. Our objective was to elucidate the genetic relationship between the three resistance genes. We evaluated the haplotype sequence for the *Ae. tauschii* donors of the resistance genes *Cmc4* and *CmcTAM112*, and resistant wheat lines carrying either *Cmc1*, *Cmc4*, or *CmcTAM112*. We found that the three genes share the same resistant haplotype despite being from different lineages and carrying introgressions from different sources. This result strongly supports that *Cmc1*, *Cmc4*, and *CmcTAM112* are all the same gene with different names. Furthermore, we demonstrated that identification and utilization of a resistance gene from a different genetic source (e.g., different subspecies in *Ae. tauschii*) is not sufficient to consider that the gene is truly novel. In this example with WCM resistance, although *Cmc1*, *Cmc4*, and *CmcTAM112* were introgressed from completely different *Ae. tauschii* sources, they were indeed the same locus due to a previously undiscovered ancient admixture between the subspecies. Detailed genetic characterization of a resistance locus is, therefore, needed to truly conclude the identity and relationship of individual genes. Overall,

these results contribute to better understand the genetic basis of WCM resistance and highlight the necessity of screening other potential sources of resistance to broaden the available genes to breed wheat against WCM.

## 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
698615 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-K-ABD-1	United States	Ohio
698616 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-K-ABD-2	United States	Ohio
698617 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-K-ABD-3	United States	Ohio
698618 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-K-ABD-4	United States	Ohio
698619 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-K-ABD-5	United States	Ohio
698620 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-W-ABD-1	United States	Ohio
698621 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-W-ABD-2	United States	Ohio
698622 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-W-ABD-3	United States	Ohio
698623 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-W-ABD-4	United States	Ohio
698624 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SWQL-W-ABD-5	United States	Ohio
698692 PVP	<i>X Triticosecale</i> spp.	UC-Atrea	United States	California
698693 PVP	<i>X Triticosecale</i> spp.	UC-Bopak	United States	California
698800 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Yecora Rojo-515	United States	California
698810	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos-Wapo-A1b	United States	California
698811	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos-Vrt2-null	United States	California
698812	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos-vrn1 vrn2-null	United States	California
698813	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos-svp1-null	United States	California
698814	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos-ful2-null	United States	California
698815	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos-ful3-null	United States	California
698826 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	161616E392726	United States	Georgia
698827 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GA-16E55	United States	Georgia
698828 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	161616LE182725	United States	Georgia
699003 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KS Hamilton	United States	Kansas
699047	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N-1 (NIL w/Fhb1)	United States	Minnesota
699048	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N-2 (NIL w/o Fhb1)	United States	Minnesota
699049	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N-38 (NIL w/Fhb1)	United States	Minnesota
699050	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	N-37 (NIL w/o Fhb1)	United States	Minnesota
699051	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	W-7 (NIL w/Fhb1)	United States	Minnesota
699052	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	W-5 (NIL w/o Fhb1)	United States	Minnesota
699053	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	W-9 (NIL w/Fhb1)	United States	Minnesota

**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
699054	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	W-8 (NIL w/o Fhb1)	United States	Minnesota
699056 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	122015W	United States	Iowa
699057 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	AP Roadrunner	United States	Iowa
699060 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KWS Sunset	Germany	Niedersachsen
699061 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Delta Grow 1800	United States	Arkansas
699107	<i>Triticum turgidum</i> subsp. <i>durum</i>	Kronos FT-A2 A10 allele	United States	California
699109 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Runner	United States	Colorado
699110 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	VI Presto CL+	United States	Colorado
699111 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	VI Voodoo CL+	United States	Colorado
699112 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	VI Shock	United States	Colorado
699114 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KS Hatchett	United States	Kansas
699115 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	AM Cartwright	United States	Kansas
699116 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Milestone	United States	Montana
699237 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Kivari AX	United States	Colorado
699241 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Piranha CL+	United States	Washington
699242 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Balance	United States	Washington
699243 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Sockeye CL+	United States	Washington
699244 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	SD Andes	United States	South Dakota
699246	<i>X Triticosecale</i> spp.	W1411 (+2J1d)	United States	North Dakota
699247	<i>X Triticosecale</i> spp.	W1412G (+3J1d)	United States	North Dakota
699248	<i>X Triticosecale</i> spp.	W1414 (+1J1d)	United States	North Dakota
699249	<i>X Triticosecale</i> spp.	W1415G (+4J2d)	United States	North Dakota
699250	<i>X Triticosecale</i> spp.	W1416G (+5J1d)	United States	North Dakota
699251	<i>X Triticosecale</i> spp.	W1417 (+7J2d)	United States	North Dakota
699252	<i>X Triticosecale</i> spp.	W1441G (+4J1d)	United States	North Dakota
699253	<i>X Triticosecale</i> spp.	W1445G (+2J2d)	United States	North Dakota
699254	<i>X Triticosecale</i> spp.	W1447 (7J1d)	United States	North Dakota
699255	<i>X Triticosecale</i> spp.	W1449 (+6J1d)	United States	North Dakota
699256	<i>X Triticosecale</i> spp.	W1460G (+6J2d)	United States	North Dakota
699308 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	ND Stanley	United States	North Dakota
699329 PVP	<i>X Triticosecale</i> spp.	Outlaw	Canada	Ontario
699379 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Epoch	United States	Nebraska
699380 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NW13493	United States	Nebraska
699398 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	High Country	United States	North Carolina
699472 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PBLP40B	United States	Iowa
699473 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PCMK57B	United States	Iowa
699474 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PDRR94B	United States	Iowa
699475 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PTAR09B	United States	Iowa
699476 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PWEN66B	United States	Iowa
699477 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PYSM29B	United States	Iowa
699478 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PZUD06B	United States	Iowa
699479 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	TW Elite	United States	Colorado
699480 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	TW Olympic	United States	Colorado
699481 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	CAG Justify	United States	Colorado
699482 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	CAG Reckless	United States	Colorado
699483 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MS Cobra	United States	Colorado
699484 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Dual	United States	Colorado
699485 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Ascent	United States	Colorado
699643 PVP	<i>X Triticosecale</i> spp.	APB298	United States	Arizona



**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
699644 PVP	<i>X Triticosecale</i> spp.	APB308	United States	Arizona
699670 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PASS54B	United States	Iowa
699671 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PBTLO6B	United States	Iowa
699672 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PDKD09B	United States	Iowa
699673 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PDLPO0B	United States	Iowa
699674 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PDUA86B	United States	Iowa
699675 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PEMZ97B	United States	Iowa
699676 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PFEZ17B	United States	Iowa
699677 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PHHY42	United States	Iowa
699678 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PJNF94B	United States	Iowa
699679 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PLJW60B	United States	Iowa
699680 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PMBN59B	United States	Iowa
699681 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PPNE55B	United States	Iowa
699682 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PPWU07B	United States	Iowa
699683 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PQAJ29B	United States	Iowa
699684 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PQAN73B	United States	Iowa
699685 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PQTB00B	United States	Iowa
699686 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PRSU04B	United States	Iowa
699687 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PRUL80B	United States	Iowa
699688 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PSFG91B	United States	Iowa
699689 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PSMQ37B	United States	Iowa
699690 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PSRG14	United States	Iowa
699691 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PTSW65	United States	Iowa
699692 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PVLC66B	United States	Iowa
699693 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PWEF05B	United States	Iowa
699694 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PYPU95B	United States	Iowa
699695 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PZDF21B	United States	Iowa
699697 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PGNQ06B	United States	Iowa
699698 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PKJH92B	United States	Iowa
699699 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PLSK70B	United States	Iowa
699700 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PUMH97B	United States	Iowa
699701 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PWGL11B	United States	Iowa
699702 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	6PWML76B	United States	Iowa
699708 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	TX-EL2	United States	Texas
699796 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9215	United States	Minnesota
699797 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB9516	United States	Minnesota
699798 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB6211CLP	United States	Minnesota
699799 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB7313	United States	Minnesota
699800 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB4510CLP	United States	Minnesota
699801 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB4619	United States	Minnesota
699802 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	WB4511	United States	Minnesota
699898 PR	<i>Triticum turgidum</i> subsp. <i>durum</i>	Faraj	Morocco	Casablanca-Settat
699925 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	CDC Defy	Canada	Saskatchewan
699926 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	ND Heron	United States	North Dakota
699953 PVP	<i>Secale cereale</i>	NF95319B	United States	Oklahoma
699957 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	MT Sidney	United States	Montana
699960 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Cameo	United States	Washington
699984	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Doris	United States	Washington
699985	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Ruth	United States	Washington
699986	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Eileen	United States	Washington

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

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
699987	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Skagit 455-17E	United States	Washington
699988	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Wolfe	United States	Washington
699989	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Skagit 1622	United States	Washington
699990	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Skagit 1685	United States	Washington
700011 JPR	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	GA09436-16LE12	United States	Georgia
700014 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	Hedge CL+	United States	Washington
700116 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KWS316	Germany	Niedersachsen
700117 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	DE2201291	Germany	Niedersachsen
700118 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	DE2201263	Germany	Niedersachsen
700119 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	KWS317	Germany	Niedersachsen
700311 PVP	<i>X Triticosecale</i> spp.	Hyton	Canada	Ontario
700315 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Dagger AX	United States	Colorado
700316 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Eclipse AX	United States	Colorado
700317 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Hydra AX	United States	Colorado
700318 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Jefe	United States	Colorado
700319 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Kraken AX	United States	Colorado
700320 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LCS Mani AX	United States	Colorado
700321 PVP	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LSC Sol AX	United States	Colorado
700335	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	NC13-20076	United States	North Carolina
700336	<i>Triticum aestivum</i> subsp. <i>aestivum</i>	LA03136E71	United States	Louisiana

**V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2022 SUPPLEMENT**

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The most recent version of the Catalogue, compiled for the 13<sup>th</sup> International Wheat Genetics Symposium held in Yokohama, Japan, is available on the Komugi (<http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp>) and GrainGenes (<http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/>) websites. Supplements 2014, 2015, 2016, 2017, 2018, 2019, 2020, and 2021 also are available at those sites as well as the *Annual Wheat Newsletter*.

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

## Morphological and Physiological Traits

### 1. Gross Morphology: Spike characteristics

#### 1.5. Elongated glume

**PI.** Syn *VRT-A2* (VEGETATIVE TO REPRODUCTIVE TRANSITION 2) orthologue of *OsMADS55* {11606, 11587}. *Traes7A026175200*.

**PI.** Add: 7AS {11606, 11587}. **i:** NILs developed in {11606, 11587}.

**i:** Paragon derivative {11606}.

**itv:** NILs developed in {11587}

**tv:** *T. petropavlovskyi* {add: 11587}; tall and dwarf (with *Rht22*) Polish wheat accessions from Xinjiang {11587}. According to {11606} *T. petropavlovskyi* is hexaploid.

**ma:** Located between SSR markers *XP25* (128.79 MB) and *XP87* (128.92) in CDSREFSeq\_v1 {11587}.

**c:** An insertion in intron 1 causes alternate splicing and >50-fold up-regulation of the *PI* allele affecting kernel length, glume length, and flowering date through the brassinosteroid pathway {11587}. The *VRT-A2a* allele {11606} is present in Chinese Spring and other non-long-glume tetraploid and hexaploid accessions. The *VRT-A2b* in long-glume accessions has a 160-bp sequence replacing a 563-bp sequence in intron 1 in all *T. polonicum*, *T. petrapavlovkyi* and hexaploid Arrancada landraces {11606}. Loss-of-function mutations in both *VRT2* homoeologs in tetraploid wheat delay heading time, reduce plant height, and increase number of spikelets per spike {11607}.

**6. Awnedness****6.1. Dominant inhibitors of awns****6.1.2. Tipped 1.**

**B1.** *TraesCS5A02G542800* (*b1* allele), annotated as a C2H2 zinc finger gene with an EAR domain (11570, 11571, 11581, 11582, 11596). Located in the terminal region of chromosome 5A that originated from homoeologous group 4 {11571}. Expression of *TraesCS5A02G542800* was higher in awnless genotypes {11571, 11581, 11582}.

**B1.** *ALI-1* {11581}. **tv:** Glossy Huguenot {11570}.

**c:** Functionally confirmed by transforming awned Kennong 199 with a 2,017-bp fragment containing *TraesCS5A02G542800* and UTRs from YMZ {11581}.

Associated with increased number of spikelets per spike and decreased kernel size in a survey of global bread wheat germplasm {11571}. Associated with lower grain length and 1,000-kernel weight {11581}.

**b1.** *ali-1* {11581}. **v2:** Chinese Spring *B2 Hd* {1293}.

At end of awn section add: A GWAS of 364 wheat accessions identified 26 loci associated with awn length {11581}.

**18. Dormancy (seed)**

Add: to the introductory sentences: 'For a review of genes involved in PHS see {11569}.

**18.3. Preharvest sprouting*****PHS1.***

***Phs1.*** Add synonyms: *Phs-A1* {11546}; *TaMKK-A* {11546}.

Genotypes with and without favourable haplotypes are discussed in {11546}.

According to {11547} red grain color increases the time to dormancy release and has a cumulative effect when combined with other dormancy genes not associated with grain color.

Add at end of section: For a review of Preharvest Sprouting see {11595}.

**44. Height****44.3. Reduced height*****RHT22***

***Rht22.*** **tv:** Add: Ailanmoi {11587}.

**XX. Hybrid Weakness****Hybrid necrosis**

***NE1.*** **ma:** *Nwu\_5B-4137* – 0.2 cM – *NE1* – 0.3 cM – *Nwu\_5B\_4114* at 383.30 – 388.01 Mb in CS RefSeq 1.0 {11594}.

**52. Lesion Mimicry**

Add introductory sentence: Lesion mimic phenotypes are characterized by spontaneous hypersensitivity not unlike disease resistance. Lesions are often not produced when leaf sectors are protected from light, and disease levels on mutant individuals may be lower than on non-mutant sibs.

Lesion phenotype caused by complementary recessive alleles.

***LM1* and *LM2.***

***LM1*** {11572}. 3BS {11572}.

**ma:** *Xwmc674-3B* – 1.2 cM – *LM1* – 3.8 cM – *Xbarc133/Xbarc147-3B* {11572}.

***lm1*** {11572}. **v:** Zaosui 30 *Lm2* {11572}.

***LM2*** {11572}. 4BL {11572}.

**ma:** *Xgwm513-4B* – 1.5 cM – *LM2* – 2.9 cM – *Xksum154-4B* {11572}.

***lm2*** {11572}. **v:** Yanzhan 1 *Lm1* {11572}.

Lesion phenotypes caused by single genes

**LM3** {11573}. 3BL {11573}.

**ma:** Mapped to a 3 cM proximal region of chromosome 3BL {11573}.

**Lm3** {11573}. Partially dominant. **v:** Line Lm3 {11573}.

The mutant phenotype appeared in an F<sub>1</sub> plant of cross Line 3-1/Jing 411. The plant was then backcrossed six times with Line 3-1 and the selected line was named Lm3.

**LM4** {11577}. 2DS {11577}.

**ma:** Fine mapped within a 8.06 cM interval flanked by *Xgwm210-2D* and *Xgwm455-2D* using specifically developed markers *m4\_01\_cib* and *lm4\_02\_cib* {11577}.

**Lm4** Normal allele. Recessive.

**lm4** {11577}. The allele named *lm4* and conferring the lesion phenotype was described as dominant {11577}.

This lesion mutant appeared in a Yanzhan 1/Neixiang 188 RIL population in which the segregation of mutant versus normal phenotype was 1:1.

**LM5.** Semi-dominant. 2AL {11576}.

**Lm5** {11576}. **v:** MC21, an EMS-induced mutant in Chuannong 16 {11576}.

**ma:** *KASP-4211* (630.3 Mbp) – 0.6 cM – *Lm5* – 3.7 cM – *KASP5353* (703.53 Mbp) {11576}.

### 30. Glume Color and Awn Color

#### 30.1. Red (brown/bronze/black) glumes

**RG-B1.**

**Rg-B1a.** *TraesCS1B02G005200.*

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

**c:** Encodes an R2R3-MYB transcription factor {11538}. *TraesJAG1B01G000800* and *TraesNOR1B01G001100* in red glume Jagger and Norin 40, respectively, carried the same *Rg-B1b\_h1* sequence; haplotype comparisons revealed that a specific group of MYB alleles was conserved in red glume genotypes {11538}.

### XX. Red Seed Color

**R-A1.**

**R-A1b.** *Tamyb10-A1* {10107}. **c:** GenBank AB191458.

**R-B1.**

**R-B1b.** *Tamyb-10-B1* {10107}. **c:** GenBank AB191459.

**R-D1.**

**R-D1b.** *Tamyb10-D1* {10107}. **c:** GenBank AB19160.

According to {11547}, red grain color increases the time to dormancy release and has a cumulative effect when combined with other dormancy genes not associated with grain color.

### 81. Tiller Inhibition

**TIN4.** 2DL {11574, 11575}.

**Tin4** {11575}. *QLtn.sicau-2D* {11574}. Low tillering.

**i:** H461/Chuannong 16 NIL7B {11575}.

**v:** H461 {11574, 11575}.

**tin4.** High tillering. **i:** H461/Chuannong 16 NIL7A {11575}.

**v:** Chuannong 16 {11574, 11575}.



**84. Yield and Yield Components****84.7. Spikelet number/spike****FT2 Flowering Locus 2**

Loss-of-function mutations in FT2 increased spikelet number per spike but reduced but reduced fertility {11604}.

**FT-A2.** *TraesCS3A02G143100.* 3AL {11605}.

A natural mutation causing an aspartic acid (**v:** Pavon; **tv:** Kronos) to alanine (**v:** Chinese Spring; Berkut) change at position 10 (D10A) in FT-A2 was associated with significant increases in SNS and grain number per spike with no negative effect on fertility {11605}.

**WAPO1****WAPO-A1**

Add comment: *WAPO-A1* is the causal gene for *QSNS.ucw-7A* {11383} that also affects grain number per spike and spike yield {11603}.

**SVPI and VRT2**

Loss-of-function mutations of both homoeologs in *SVPI* (*TraesCS6A02G313800* and *TraesCS6B02G343900*) and *VRT2* (*TraesCS7A02G175200* and *TraesCS7B02G080300*) in tetraploid wheat increase number of spikelets per spike, delay heading time and reduce plant height {11607}.

**Disease/Pest Reaction****90. Reaction to *Blumeria graminis* DC.****PM21.**

**Pm21.** Following the existing chromosome identification add: T6AL·6AS-6VS {11578}.

**PM24.****Pm24.**

**pm24.** *TraesCS1D02G058900* {11414}.

The same candidate gene was predicted for *PmDTM* in Datoumai (11556), but according to their results Chiyacao, Hulou, and Datoumai showed differential responses to an array of *Bgt* isolates {11414}.

**PM60.**

**Pm60** ex *T. urartu*.

**Pm60** ex *T. turgidum* subsp. *dicoccoides* {11551}. *TRIDC7AG077150.*

*MLIW72* {10545}, *MLIW172* {11095}, *PmG16* {10886, 11551}.

**i:** WEW G18-6 / LDN RIL 154 {11551}; G18-16 {10886, 11551}.

**v:** Ruta {11551}. **ma:** *Xuhw386-7A* – 0.3 cM – *Pm60* – 1.4 cM – *Xuhw-7A* {11551}.

The cloned *M60* sequences from the diploid and tetraploid sources differed by 8 SNP that changed 6 amino acids {11551}.

**PM69.**

**Pm69** {11541}. *PmG3M* {11302}. 6BL {11302}. **bin:** 6BL-0.7-1.00.

**tv:** *T. turgidum* subsp. *dicoccoides* G-305-3M {11302} TD116180 (University of Haifa Wild Cereal Gene Bank), CGN19852 (Netherlands Centre for Genetic Resources) {11541}.

**ma:** *Xgpw7262-6B* – 6.9 cM – *PM69* (*PmG3M*) – 4.5 cM – *Xedm149-6B* {11302}.

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

- MIWE74** {11589}. 2BS {11589}. v: WE74 {11589}.  
**tv:** *T. turgidum* subsp. *dicoccoides* G-748-M {11589}.  
**ma:** Mapped to a 799.9 kb region corresponding to physical region 25.48-26.28 in CHr2\_Zavitan v2.0 (26.59-27.01 in IWGSC RefSeq v1.0) {11589}. The relationship to *Pm26* and *MIWI70* was not established {11589}.
- PmHHXM** {11565}. 4AL {11565}. v: Honghuaxiaomai {11565}.  
**ma:** Located in a 1.77 Mb (0.18 cM) region flanked by *Xkasp475200* and *Xhnu522* {11565}.
- PmKN0816** {11598}. 2BL {11598}. v: KN0816 {11598}.  
**ma:** Mapped to a region of chromosome carrying *Pm6*, *Pm33*, *Pm51*, *Pm64* and *PmQ* but distinguished from each other by specificity {11598}.
- Pm6S'** {11597}. Derived from *Ae. longissima*. 6A and 6B {11597}.  
**ad:** CS + 6S'#3 TA7548 {11597}.  
**v:** T27 (Ti6AS·6AL-6S'#3-6AL) {11597}; R43 (T6BS·6BL-6S'#3'#3 {11597}.  
**al:** *Ae. longissima* TA1910 {11597}.  
**ma:** Mapped to a distal 6S'#3 interval of 42.8 Mb flanked by markers *Ael58410* and *Ael5799* {11597}.
- Pm6S'* conferred resistance to 28 of 30 Chinese *Bgt* isolates {11597}.

**89. Reaction to *Bipolaris sorokiniana*****SB4.**

- Sb4** {11592}. 4BL {11592}. v: Line7H9094 {11592}.  
**ma:** *YK12831* – 1.18 cM – *SB4/YK12828* – 0.01 cM – *YK13104* {11592}.
- Line 7H909 was selected from a segregating F<sub>4</sub> line from a cross of resistant cultivars GY17 and Zhongyu1211 {11592}.

**96. Reaction to *Fusarium* spp.****96.1. Disease: Fusarium head blight**

**Glenn (R) / MN00261-4 (S):** RIL population: three of 15 QTL for FHB response and heading date were stable and explained >10% of the phenotypic variation; these were located on chromosome arms 5BL, 6BS (possibly *Fhb2*) and 7AS {11568}.

**96.2. Disease: crown rot**

**UC1110 / PI 610750:** RIL population: Three QTL had an additive effect: *QFCR.heau-6A* ( $R^2 = 0.078 - 0.102$ ) from UC1110; and *QFCR.heau-2A* ( $R^2 = 0.052 - 0.070$ ) and *QFCR.heau-2D* ( $R^2 = 0.072 - 0.093$ ) from PI 610750 {11548}.

**105. Reaction to *Puccinia graminis* Pers.****SR9.**

- Sr9e.** *SrKn* {11590}. v: Line Td31-5R PI700734 {11514, 11590}.  
**tv:** Svevo {11590}.  
**tv2:** Kronos *Sr13* {11590}.  
**ma:** *SrKn* was mapped to a 0.29 cM region flanked by *pku4856F<sub>2</sub>R<sub>2</sub>* and *pku4917F<sub>3</sub>R<sub>3</sub>* {11590}.

A completely revised *SR13* listing is provided.

- SR13** **ma:** *Xwmc59-6A* – 5.7 cM – *Sr13* {10607}; *CD926040* – *Sr13* – *BE471213* {10777}; *CD926040* – *SR13* – *BE471213* {10777}; Markers *Xgwm427-6A* and *AFSr13S* (proximal) and *Xdupw-6A* (distal) showed variable but close (<10 cM) linkage with *SR13* in six durum crosses – these markers were variously applicable across durum

backgrounds, but only *Xgwm427-6A* was variable in a range of hexaploid derivatives with *Sr13* likely originating from a single source {11146}.

- c:** *Sr13* was identified as a CC-NBS-LRR gene with three resistance haplotypes in two specificities {11217}; now four resistance haplotypes and four specificities {11584}.

***Sr13*** {674}.

***Sr13a*** {674, 11217, 11584}. 6AL {929}.

**bin:** 6AL-8.

- i:** Khapstein /9\*LMPG {685, 11217}; Khapstein / 10\*Marquis *Sr7b* {686}; Sr13/9\*LMPG {685}.

**v2:** Khapstein *Sr7a Sr14* {674}; Machete *Sr2* {10607}.

**itv:** Rusty-KL-B {11584}; Rusty-KL-C {22044}.

**tv:** Cando {11584}; Durox {11584}; Grenora {11584}; Kronos PI 576168 {11217}; Lakota {11584}; Maier {11217}; Mountrail {11584}; Renville {11217}; Strongfield ..... {11584}; Transend {11584}; Wells {11584}.

**tv2:** Khapli *Sr7a Sr14* {674}.

**c:** KY825225 (Resistance haplotype R1) {11217}.

***Sr13b*** {11217, 11584}. **itv:** Im-C2 {11584}; Im-7B {11584}; Rusty-14803 {11584}.

**tv:** Ben {11584}; Botno {11584}; Calvin {11584}; Carpio {11584}; D99656 {11217}; D15143 {11584}; Joppa {11584}; Kofa PI 584336 {10777, 11217}; Lebsock {11584}; Leeds *Sr92 Sr8b* {11584}; Lloyd {11584}; Medora PI 496260 {10777, 11217}, CIttr 7777 {11584}; Munich {11584}; ND Grano {11584}; ND Riveland {11584}; Pierce {11584}; Rugby {11584}; Sceptre {10777, 11584}; Svevo {11584}; *T. turgidum* subsp. *carthlicum* PI 387696 {11584}; *T. turgidum* subsp. *polonicum* CIttr 14803 {11584}; Tioga {11584}; Vic {11584}; Ward {11584}.

**c:** GenBank KY225226 (Resistance haplotype R2) {11217}.

***Sr13c*** {11584}. **itv:** 8155-B2 {11584}; 8155-C2 {11584}; Rusty-SR464-C1 {11584}; ST464-C1 {10473, 11584}.

**tv:** Alkabo {11584}; Altar 84 {11584}; CIttr 7771 {11584}; D101073 {11584}; Langdon {11217, 11584}; PI 352548 {11584}; ST464 *Sr9e* {10473, 11584}.

**c:** GenBank KY924305 (Resistance haplotype R3 {11217}.

***Sr13d*** {11584}. **itv:** CAT-A1 {11584}.

**tv:** Camadi Abdu Tipo #103 {22044}.

**c:** GenBank MW033594 (Resistance haplotype R4 {11584}.

**Unspecified allele** {11280}. **tv:** PI192051 {11280}.

The identities of alleles of many of the *Sr13* genotypes listed under **tv:** were based on specific marker sequences (11584); some entries are likely to carry additional resistance genes.

Haplotypes of other germplasm previously listed are unknown: **v2:** French Peace *Sr7a Sr9a*{680}. **tv2:** Arrivato *Sr8b Sr9e* {10607}.

A resistance gene in Khapstein/9\*LMPG and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However, the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance locus mapped in {10778} could not be *SR13*.

**SR22.**

**SR22b.** **i:** Add: PI 700735 and reference {11514} to current entry.

**SR27.**

**Sr27.** **c:** Encodes an NLR with closest similarity to *Sr13* among cloned wheat *Sr* alleles {11561}.

**SR38.**

**Sr38.** **v:** Add: CDS Stanley {11579}; Mace {11579}; SY Mattis {11579}.

**SR63.**

**Sr63** {11554}. Adult plant resistance. *QSrGH.cs-2AL* {11554}.2AL {11554}.  
**tv:** GH/M14 RIL49 XXXXX {11554}; GH/M14 RIL188 AUSXXXX {11554}.  
**tv2:** Glossy Huguenot *Sr58* (syn *QSrGH.cs-1BL*) AUS2499 {11554}.  
**ma:** IWA200-KASP\_32429 – 2.7 cM – *Sr63* – 3.0 cM – IWB4881-2AL {11554}.

**Sr8155B1** {22040}.

Recessive. 6AS {11580}.  
**v:** Choteau / Mountrail Der. SXD 43 PI 681713 {11580}; Marruecos\*2/Citr 8155 {22040}.  
**tv:** Alkabo 11580}; Renville {11580}.  
**tv2:** Grenora *Sr13* {11580}; Munich *Sr13* {11580}.  
**ma:** Co-segregation with *KASP\_6AS\_IWB10558* {11580}.

Also predicted in durum accessions Belzer, Dilse, Lloyd, Divide, and Montrail {11580}.

**106. Reaction to *Puccinia striiformis* Westend.****106.1. Designated genes for resistance to stripe rust****YR17.**

**Yr17.** **v:** Add: CDS Stanley {11579}; Mace {11579}; SY Mattis {11579}.

**YR27. *TraesKAR2B01G0121530LC*.**

**Yr27.** Add synonym: *QYr.sgi-2B.I* {10184, 11232}.  
**v:** Avocet 2B (= AvocetS + *QYr.sgi-2B.I*) {11593}.  
**v2:** Kariaga *Yr18* {11593}.  
**ma:** A *Yr27*-specific molecular marker was based on Asn 895 found only in *Yr27* {11593}.  
**c:** *Yr27* is an allele at the *LR13/NE2* locus {11593}.

**YR29.**

**Yr29.** **tv:** Add: Stewart {11542}.  
*Yr29* is a frequent gene in durum wheat ({11542}and references therein).

**YR34.**

**Yr34.** **ma:** Add: *Yr34* is in a 5AS.5AL-5A<sup>m</sup>L translocation segment that is present in genotypes Arina*Lr-For* and SY Mattis in the Wheat10+ Genome panel {11602}.

**YR40.**

**Yr40.** **v:** Add: TA56501 {11553}. **ad:** TA7659 {11553}.  
 Add note: Line TA5601 carries an estimated 5% of 5M<sup>s</sup>; and TA5602, 20% {11553}. Genetic analysis of the segment in TA5602 indicated terminal replacement of 9.4 Mb in chromosome 5D and that *Yr40* is 12.4 cM proximal to *Lr57* {11553}.

**YR70.**

**Yr70.**  
 Add note: The introgression carrying the *Ae. umbellulata* segment replacing terminal chromosome arm 5DS was 9.47 Mb with the break point between *TraesCS5D02G1600* and *TraesCS5G02G20010* {11552}. Independent mutations indicated that *Yr70* differed from *Lr76* {11552}.

**YR78.**

**Yr78.** **v:** Add: Cadenza {11591}; Lancer {11591}; Spelt PI 190962 {11591}.  
**ma:** *Yr78* was mapped to a 0.05 cM interval including the un-assembled *NOR-B2* locus on chromosome 6BS (RefSeq v1.1 0 region between 101,735,482 and 112,897,900 bp) {11591}.  
 Add note: According to {11174} *Yr78* is identical to *QYr.wgp-6BS.I* in Stephens {10602} and *QYr.sun-6B* in Janz {10751}.

**YR84.**

**Yr84** {11585}. *YrPI487260* {11585}. 1BS {11585}  
**v:** Ruta\*2 / PI487260 {11585}.  
**tv:** *T. turgidum* subsp. *dicoccoides* PI 487260 {11585}.  
**ma:** Located at 9.65–11.99 Mb *YR84* is proximal to *Yr10* (0–1.4 Mb) and distal to *YR15* (98 Mb) {11585} in the Zavitan v2 assembly (11585).

*Yr84* confers resistance to all *Pst* pathotypes thus far tested and is described as incompletely dominant. Other named *YR* loci in chromosome 1B are proximal to *YR15* on located in arm 1BL. The low infection type is ; (fleck) to ;1 on a 0–4 scale. *Yr84* therefore varies from other permanently named *Yr* genes in the region by location, specificity and dominance.

**106.2. Temporarily designated genes for resistance to stripe rust**

**YrAS2388.** (= *Yr28*). **v:** KS91WGRC11 {11599}.  
**ma:** KASP markers were developed in {11566}.

**YrPak** {11543}. 5BS {11543}. **v:** PI 1388231 {11543}.  
**ma:** *sunKASP\_338* – 3.3 cM – *YrPak* – 3.5 cM – *sumKASP\_341* {11543}.

PI 1388231 also carried two genes for adult plant resistance, one of which was positive with *Lr46* marker *Lr46\_SN-PIG22* {11543}.

**YrZH22** {11563}. 4BL {11563}. **v:** Zhoumai 22 {11563}.  
**ma:** *XWGGBI33* – 3.29 cM – *YrGH22* – 2.63 cM – *XWGGBI46* {11563}.

*YrZH22* could not be distinguished from *Yr50* based on map location.

**106.3. Stripe rust QTL**

**Avocet S (S) / Eltan (MR):** RIL population: Three QTL for seedling reaction located on chromosome arms 2BS, 4AL, and 5BS (minor) and two addition QTL for APR identified on chromosome arms 6AS and 7BL {11560}. A significant increase in the disease response of Eltan was associated with races virulent on Eltan seedlings.

**Avocet S (S) / Qinnong 142 (R):** RIL population: Two QTL for seedling resistance to race CYR23 on chromosome arms 1DL and 4AL. These genes were not effective against races used in the field where APR was controlled by QTL on chromosome arms 1BL (*QYrqin.nwafu-1BL*: probably *Yr29*), 6BS (*QYrqin.nwafu-6BS*, possibly *Yr78*); 2AL (*QYrqin.nwafu-2AL*) and 2BL (*QYrqin.nwafu-2BL*) {11559}.

**Chuanmai 42 (variable) / Chuanmai 55 (R):** RIL population: Two QTL on chromosomes 1B and 2A were derived from CH55 and a less effective QTL on chromosome 7B was from CH42 {11558}. The chromosome 1B QTL was postulated to be *Yr29*. CH42 carries *Yr24* and CH55 carries the T1BL·1RS (*Yr9*) translocation and 5TB·7B reciprocal translocation; neither – neither gene was effective in this study {11558}.

**Guangtougoumai (R) / Avocet S (S):** RIL population. *QYr.GTM-5DL* accounted for 22–44% of the phenotypic variation across three sites (11562).

**Mianyang351-15 (R) / Zhengzhou 5389 (R):** RIL population: Seven QTL were located on chromosome arms 1BL (*Yr29*), 2AS (*Yr17* or another gene), 2DS, 3AS, 3DS, and 7BL (possibly associated with *Lr68*) {11545}.

**Mingxian 169 / P10090.** *QYr.nwafu-6A* (syn *YrPI0090* for adult-plant resistance reduced stripe rust severity by a mean 14.8%. Located in the chromosome 6A centromeric region and flanked by *Ax94460938* and *Ax710585473*, a 3.5-cM region corresponding to physical interval 107.1–446.5 Mb {11555}.

**Stewart (R) / Banshi.** Durum,  $F_5$  and  $F_7$  populations: *Yr29* and *QYr-3BL* ( $r^2 = 0.045$ ); the latter was in the vicinity of *Yr80* with *kIWA6221* as the nearest marker {11542}.

**Thatcher (S) / Hong Qimai (R) and Luke (MR) / AQ24788-83 (R):** RIL populations: *QYr.cau-2AL*, more effective than *Yr18*, accounted for up to 52% of the phenotypic variation {11564}.



**Svevo (R) / Zavitan (MS)**. Tetraploid, RIL population tested in Israel and China. Nine QTL for APR; eight from Svevo and one from Zavitan, the most effective of which was *QYrsv.swust-1BL.1* {11557}. This QTL overlapped the *Yr29* region and Svevo was positive for the *Yr29* marker.

### 107. Reaction to *Puccinia triticina*

#### 107.1. Genes for resistance

##### **LR13.**

**Lr13.** c: Add: *Lr13* is an allele of the *YR27/NE2* locus {11593}.

##### **LR14.**

**Lr14a.** i: Arina *LrFor* {11549}. v2: Forno *Lr34 Lr75* {11549}.

c: *Lr14a* encodes a membrane-localized protein with 12 ankyrin repeats and structural similarity to  $\text{Ca}^{2+}$ -permeable non-selective cation channels {11549}. GenBank MT 123593.

Add note: Based on sequence *Lr14a* was identified in a few spelt (e.g. PI 190962) and a few wild emmer accessions {11549}.

##### **Lr14b.**

Add note: A marker based on the *Lr14a* sequence failed to amplify a product in the Tc+14b NIL {11549}.

##### **LR23.**

**Lr23.** v: BT-Schomburhk {11601}.

tv: Gaza {11601}; Tamoroi {11601}.

ma: SSR and KASP markers were developed in {11601}.

##### **LR17.**

**Lr17a.** v: Add: CDS Stanley {11579}; Mace {11579}; SY Mattis {11579}.

##### **LR36.**

**Lr36.** ma: *Xcfd13-6* – 5.2 cM – *Lr36* – 3.8 cM – *Xgwm88-6B* {11588}.

Since *Lr36* is located in an alien segment these markers likely map the boundaries.

##### **LR42.**

*AET1Gv20040300*

ma: Flanked by *pC43* and *pC50* at 8.65 Mb and 8.77 Mb, respectively (*Aet 4.0*) {11599}.

##### **Lr42.**

v: Add: KS93U50 {11599}.

c: CC-NB-ARC structure {11599}.

##### **lr42.**

c: The *lr42* allele has fewer LRR repeats {11599}.

Marker *Pc50*, 46 kb from *lr42* was recommended for MAS although additional gene-based markers were identified {11599}.

According to {11599} *Lr42* was present in >1,000 CIMMYT lines.

##### **LR47.**

**Lr47.** Add note: KASP markers for detection of *Lr47* are reported in {11544}.

##### **LR57.**

**Lr57.** v: Add: TA56501 {11553}.

Add note: Line TA5601 carries an estimated 5% of 5M<sup>e</sup>; and TA5602, 20% {11553}. Genetic analysis of the segment in TA5602 indicated terminal replacement of 9.4 Mb in chr 5D and that *Lr57* is 12.4 cM distal to *Yr40* {11553}.

##### **LR76.**

**Lr76.** Add note: The introgression carrying the *Ae. umbellulata* segment replacing terminal Chr. 5DS was 9.47 Mb with the break point between *TraesCS5D02G1600* and *TraesCS5G02G20010* {11552}. Independent mutations indicated that *Lr76* and *Yr70* were different genes {11552}.

**LR81.**

**Lr81** {11583}. *Lr470121* {11583}. 2AS {11583}. **bin:** 2AS-0.78–1.00.  
**v:** RIL 92 {11583}.  
**v2:** PI 470121 *Lr34* {11583}.  
**ma:** *Xwmc827-2A* – 9.4 cM – *Xstars-KASP320* – 0.5 cM – *LR81* – 0.2 cM – *Xstars-KASP323* – 5.3 cM – *Xwmc296-2A* {11583}.

**LR82.**

**Lr82** {11586}. *LrAW2* {11586}. Recessive. 2BL {11586}.  
**v:** Aus27352 {11586}.  
**ma:** *KASP\_22131* – 0.8 cM – *Lr82* – 1.2 cM – *KASP\_11333* {11586}.

**107.3. QTL for reaction to *P. triticina***

**Bairds (R) / Atred#1:** RIL population: Four QTL for APR, including *Lr46*, *QLr.cim-5BL* and *QLR.cim-6BL* from Bairds and *QL.cim-2Bc* from Atred#1 {11600}.

Tetraploid wheat

**Mianyang351-15 (R) / Zhengzhou 5389 (R):** RIL population: four QTL were located on chromosome arms 1BL (*Lr46*), 2AS (*Yr37*), 2DS, and 7BL (*Lr68*) {11545}.

Complex Resistance

Carberry. *Lr21 Lr16 Lr23 Lr34 Lr46* {11567}.

**XXX. Reaction to *Sitobiplosis mosellana* (Gehin)****SM1.**

**Sm1.** **v:** Add: CDC Landmark {11579}; Paragon {11579}; Unity {11579}.  
**ma:** KASP marker developed in {11579}.  
**c:** Gene candidate with NB-ARC-LRR-kinase-MSP structure {11579}.

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**VI. ABBREVIATIONS AND SYNONYMS USED IN THIS VOLUME.****PLANT DISEASES, PESTS, AND PATHOGENS:**

**BYDV** = barley yellow dwarf virus  
**BMV** = barley mosaic virus  
**CCN** = cereal cyst nematode, *Heterodera avenae*  
**FHB** = Fusarium head blight  
**RWA** = Russian wheat aphid  
**SBMV** = soilborne mosaic virus  
**SLB** = Septoria leaf blotch  
**TMV** = *Triticum* mosaic virus  
**WDF** = wheat dwarf mosaic  
**WSBMV** = wheat soilborne mosaic virus  
**WSMV** = wheat streak mosaic virus  
**WSSMV** = wheat spindle streak mosaic 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* = *Septoria 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. *armeniicum* = *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 bessarabicum*

*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

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**UNITS OF MEASUREMENT:**

**bp** = base pairs  
**bu** = bushels  
**cM** = centimorgan  
**ha** = hectares  
**kDa** = kiloDaltons  
**m<sup>2</sup>** = square meters  
**m<sup>3</sup>** = 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** = quantitative 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 tagged 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 69 MANUSCRIPT GUIDELINES.**

The required format for Volume 69 of the *Annual Wheat Newsletter* will be similar to previous editions edited from Kansas State University.

**CONTRIBUTIONS MAY INCLUDE:**

- Current activities on your projects.
- New cultivars and germ plasm released.
- Special reports of particular interest, new ideas, etc., normally not acceptable for scientific journals.
- A list of recent publications.
- News: new positions, advancements, retirements, necrology.
- Wheat stocks; lines for distribution, special equipment, computer software, breeding procedures, techniques, etc.

**FORMATTING & SUBMITTING MANUSCRIPTS:**

Follow the format in previous volumes of the *Newsletter* in coordinating and preparing your contribution, particularly for state, station, contributor names, and headings. Use Microsoft Word™ or send an RTF file that can be converted. Please include a separate jpg, gif, or equivalent file of any graphic in the contribution. Submit by email to [jraupp@ksu.edu](mailto:jraupp@ksu.edu).

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The *Annual Wheat Newsletter* also will continue to be available (Vol. 37–68) through the Internet on Grain-Genes, the USDA–ARS Wheat Database at <http://wheat.pw.usda.gov/ggpages/awn/>.