ANNUAL WHEAT NEWSLETTER

Volume 55

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IN DEDICATION TO DR. HARRY C. YOUNG, JR.

Harry C. Young, Jr., professor emeritus in the Department of Plant Pathology at Oklahoma State University, passed away 22 February, 2009, in Wichita, KS, at the age of 90. Young grew up in Wooster, OH, where he attended public schools and obtained a B.S. in botany from The Ohio State University in 1940. He was awarded an M.S. degree in plant pathology in March 1943 and Ph.D. in plant pathology and plant breeding from the University of Minnesota in June 1949. Young began his career at Oklahoma State University in 1950, where he spent his entire career and retired in 1982.

Young was a U.S. Army Air Corps Captain during WWII and served from 1943–46. He was trained as a photography analyst and, later, was a Technical Supply Officer for the 379th Fighter Squadron, 362nd Group, Fighter Command, 9th Air Force in the European Theater.

Young made notable contributions in plant pathology research and in training graduate students, several of whom have made significant contributions to the science of plant pathology. Young's area of research included developing disease-control programs involving the diseases of fruit nursery stock, small and coarse grain cereals, and turfgrasses; the population dynamics of combinations of genes for pathogenicity in the wheat leaf rust fungus, *Puccinia triticina*; the specifics of disease progress of stalk rot of maize caused by *Diploidia zeae*; and disease-monitoring programs, especially for diseases of wheat, oats, triticale, and barley. He served on several committees of the American Phytopathological Society including Plant Disease Detection, Disease Management, Epidemiology, Disease Loss Appraisal, Disease and Pathogen Physiology, and International Cooperation.

Young conducted two special research projects of particular interest to him. One was the role of the alternate host in the pathogenic variability of the wheat leaf rust pathogen. This study was conducted at the University of Minnesota and supported by a sabbactical Leave from Oklahoma State University, a John Simon Guggenheim Memorial Foundation Fellowship, and a grant by the U.S. Department of Agriculture in 1961–62. Second was the comparison of variability in pathogenicity of wheat leaf rust populations in the presence of two different alternate hosts of the pathogen (species of the genera *Thalictrum* and *Anchusa*) and in the absence of any alternate host. This study was conducted at the Estacao Agronomica Nacional, Oeiras, Portugal, and was supported by a Fulbright Hayes Senior Post Doctorial Fellowship and a grant from the Fundacao Caluste Gulbenkian de Lisboa in 1969–70.

Young's three major avocations in life were golf, light plane flying, and skiing. The former led to intensive study of disease and disease control of turfgrass pathogens, particularly in bent grass greens. He was a member of the Oklahoma Golf Course Superintendents and the Oklahoma Turfgrass Research Foundation, providing them with disease control counsel throughout much of his career until he retired in 1982. He continued playing golf after his 90th birthday. His private plane flying greatly enhanced his supervision of State and Regional research plots and in visiting research stations in the southern Great Plains. He continued flying until about age 87. His desire to ski resulted in him and wife Joan, married since 1943, moving to Pagosa Springs in the southern mountains of Colorado after retirement.

REPORT FROM WHEAT CROP GERMPLASM COMMITTEE
Thursday, 8 January, 2009.
San Diego, CA, USA.

Present: Harold Bockelman, Dave Matthews, Tom Payne, Kim Campbell, Dave Marshall, Anne Marie Thro, Giles Waines, and Daren Coppock.

Introductions.

Report from National Small Grains Germplasm Collection. Update on wheat resources in NSGC, including new PI assignments and the Wheat CAP populations. Several new accessions were assigned PI numbers this year. Many are PVPd lines from the U.S. and also landraces from Tajikistan, wild wheats from Turkey, and winter durums from OSU. WheatCAPs mapping populations are coming in and have been assigned GSTR numbers. GSTR is a prefix for Genetic Stock, *Triticum*. GSTR accessions are maintained and distributed but not regenerated.

The total size of the collection is now over 135,000, including over 65,000 *Triticum* sp. The size of collection is an issue to be aware of because maintenance and regeneration costs increase. No action needed at this point but the committee needs to continue to function to determine priorities.

Defining the gaps in the collection and priorities for future acquisitions. There continues to be some funding for collecting trips. Some *Aegilops* species are missing. There is a fair collection of *Aegilops* that have never been assigned PI numbers.

Some geographic areas are under-represented. Iran, top of Zagros mountains, especially for *T. urartu*. There is quite a bit of germ plasm available that was collected from Iranian valleys but not from Iranian mountains. It is a difficult place in which to collect; even the Iranians are not keen on going there. Armenia. Giles collected some *Ae. tauschii*, and *T. monococcum* last year with funding from California sources. Giles has been asked to go back to Armenia through the American University of Armenia.

Recently the collection has been able to collect and deposit material from various countries in Central Asia because of joint collecting trips with ICARDA. This was formerly a gap.

Weedy ryes are not well represented in either the U.S. or CIMMYT germ plasm collections and would be easily collected, likely from Turkey.

Some discussion of how to access germ plasm from Iraq. Iraq is working on Ug99 and the CIMMYT–ICARDA wheat program has a reasonable amount of collaboration.

Need to identify gaps. One method of doing this is to look at a species/geographic matrix. This can be done on a limited basis currently, but will be greatly facilitated in the new GRIN because of the GIS capabilities.

Action: Need to identify vulnerable collections of individual researchers, for example that of Giles Waines, etc. that might become threatened due to retirement, changes in priorities, or changes in funding. Also need to get an inventory of genetic stock collections (Lukazewski and Sears collection in Missouri) and develop plan for maintenance and distribution.

Update on evaluations and future priorities.

Ug99. The NSGC is involved with Ug99 work through stem rust screening in Kenya. Part of the collection is being screened in Kenya every year with lines that are prescreened at Aberdeen using local races; susceptible lines are not sent. The data is not in GRIN at this point; but still being characterized.

Dave Marshall has been summarizing data on U.S. cultivars and experimental lines (not necessarily collections). There is some resistance, particularly in winter wheat. Commercially grown wheat, especially spring types, have a pretty high level of vulnerability.

Giles recommended that we evaluate roots. We do not have descriptors for wheat roots. Roots are important for drought and root disease tolerance.

Action: Anne Marie will attempt to organize a paper session on root health for the CSSA meetings in 2010.

Heat tolerance. Need suggestions on how to measure this trait? Heat tolerance in India and Sudan needed at germination. Effect of heat stress on photosynthesis (Zoran Ristic); Tony Hall is writing a new review of heat tolerance.

Wheat blast. A new disease identified in Uruguay and southern Brazil; similar to rice blast. CIMMYT is keeping an eye on this to see how much of a threat it will be.

Other threats. Russian Wheat Aphid is one of best characterized. Leaf rust, much of the data was collected years ago. Stripe rust data is relatively recent. Stem rust data is currently being collected. Did a lot of work with Hessian fly in the past. Characterization of plant, spike, and seed descriptors is continuing at Aberdeen.

Characterization of quality traits is missing. We have discussed doing single-kernel characterization. There are some good molecular tools for characterization of quality traits. Molecular characterization is starting and we should have more data in the next 5 years, at least on the core.

Deposit of protected materials. The NPGS will handle materials protected by PVP and by other MTAs. A voucher sample is required to be sent to the National Lab at Ft. Collins in two cases:

- when PVP is applied for and
- when material is registered in the CSSA *Journal of Plant Registrations* (JPR).

The NPGS maintains both voucher samples but assigns the same PI number to both.

The originator is responsible for distribution for 5 years after a JPR registration or for the life of the protection (up to 20 years) if PVPd or protected in some other manner. GRIN shows that it exists but must be requested from breeder. After 5 years, or, if protected, after protection expires (max 20 years), the voucher sample is split and sent to the field station (the NSGC) for maintenance and distribution. Dave Ellis and Jeff Pederson, editor of JPR, worked to make sure that protected lines can be registered.

Action: Kim will write a short summary of these policies for CSSA news.

New material coming into the U.S.

CIMMYT nurseries; facilitating the exchange of CIMMYT materials, especially winter wheat nurseries from CIMMYT–Turkey. Update on what has happened with APHIS since last year. APHIS–PPQ has agreed to work with Jim Peterson and the ARS, Dave Marshall, and Harold Bockelman. Dave Marshall facilitated a risk assessment for Turkey. The germ plasm is treated as a USDA project because of the urgency of Ug99. International nurseries from Turkey are coming in through the USDA–Aberdeen; Blair Goates travels to Corvallis to inspect. Thanks to Davis Marshall and Kay Simmons for working this out.

The primary CIMMYT nurseries coming in are increased under quarantine at Corvallis, OR (winter), and at Stillwater, OK (winter and spring). Within the U.S., the FAWWON is distributed by Jim Peterson and several spring nurseries including the stem rust nursery are distributed by Art Klatt. Some national disease recovery money was made available to Art Klatt to continue. Some breeders go to him all the time; other programs do not know about it. Some people get the material themselves from CIMMYT and do not go through Art or Jim. In general, CIMMYT sends seed

to whoever asks. Many breeders are informed through Ug99. Much of the communication is done through regional nurseries.

CIMMYT is concerned because they do not get any data back from U.S. collaborators. The data window for a particular CIMMYT International nursery is 2 years. Australia and Ethiopia are in the same situation because quarantine tends to break information flow. Australia recognized this because they were a black hole in terms of data (U.S. is also). Australia initiated the 'CAGE', the CIMMYT–Australia Germplasm Enhancement Program; a suite of projects funded by GRDC to promote uptake of CIMMYT germ plasm by Australian breeding programs. CAGE pools information that the Australians collect and also are a resources for germ plasm.

New international nursery. The International Adaptation Trial (IAT) is distributed by the University of Queensland, Australia. They had probe genotypes for root problems (micronutrients and root diseases). Used strategically in Australia. Perhaps the U.S. can collaborate or start an additional nursery adapted to U.S., because the CIMMYT nursery is spring wheat.

Action: Ask U.S. Regional Nursery collaborators to remind people to send data back to CIMMYT from the international nurseries and remind people to contact Art Klatt or Jim Peterson if they are interested in particular nurseries.

Germ plasm bank at CIMMYT (Tom Payne). There are about 144,000 accessions in the germ plasm bank. In 2008, CIMMYT management allotted 300,000 for capital upgrade of seed processing. Three automated dishwashers, modified for seed washing in sodium hypochlorite, were purchased. An automated, seed-packaging unit was purchased from ZingPack (Cleveland) to increase flow-through. The entire wheat gene bank is being bar coded and will be finished by May. The collection is housed in two separate chambers, a base collection and an active collection. David Bonnet was hired recently as a prebreeder.

Yue Jin has been evaluating international nurseries for resistance to stem rust and perhaps just sending data back to Ravi. CIMMYT has good contacts with USDA germ plasm system.

International Treaty. The President has signed the treaty but it is up to the Senate to ratify. Primarily applies to new material that will come into the CIMMYT germ plasm bank but not to existing material. Does not have so much bearing on what we do with collections at this point. Applies to new material entered into the collection. June Blaylock at ARS that is working out how to deal with this. Dave Ellis said that at present, U.S. recipients would not get the SMTA for existing germ plasm, but germ plasm that is newly acquired would fall under the SMTA.

New. GRIN. Development is funded through Global Crop Diversity Trust to provide software for any germ plasm collection and can run on different platforms, is in five languages, and will include GIS data. Customers want maps so that they can do geographic analysis. A selection tool will be used to select germ plasm in order to know where it came from and can be overlaid with information about soil or climate.

A project with IRRI to georeference and double check all the latitude and longitude data. Andy Jarvis at CIAT is working on software to use the georeference data and species or herbaria information to predict where species will grow and look at gene bank accessions to see if we have sampled there and determine gaps.

Grin is considered good by those who know how to use it, but many customers are not happy. The major goal of this new GRIN is user friendliness. The beta edition will be evaluated soon. Pete Cyr at the USGS Plant Introduction Station at Ames is the main contact.

Recommendation from committee to journals. Action: When germ plasm that is not patented or otherwise protected is used to support the science reported in refereed journal articles, we recommend that the germ plasm be deposited into a publicly available reference collection, or, at least made available to other researchers. For example, when a gene is named, the germ plasm in which it was first discovered should be deposited into a germ plasm bank so that others can access that germ plasm to do allelism tests (Dave Marshall).

Request suggestions for new committee members. We need seven representatives to provide geographical representation and to include industry, CIMMYT, Canada, Mexico (not CIMMYT), rye, and triticale.

2010 meeting date. Meet with the NWIC in Orlando, FL.

MINUTES OF THE NATIONAL WHEAT IMPROVEMENT COMMITTEE (NWIC) MEETING.
9 January, 2009.
San Diego, CA, USA.

Attendees: C.J. Peterson (chair), R.A. Graybosch (secretary), C.A. Griffey, T. Payne, J. Rudd, D. Marshall, H. Bockelman, James Anderson, R. Zemetra, B. Bahm, A.M. Thro, L. Talbert, F. Dowell, S. Haley, Joe Anderson, T. Bartram, R. Bowden, D. Worrall, B. Carver, K. Simmons, K. Garland-Campbell, D. Coppock, S. Chao, J. Nelson, G. Cisar, R. Ward, M. Pumphrey, D. Matthews, K. Kahn, M. Bonman, and J. St. John.

Informational items.

National Association of Wheat Growers (NAWG). It was noted the position of NAWG Science & Technology Advisor presently is vacant. This position holds voting membership on the NWIC. A motion was passed to allow NAWG to appoint an individual to represent their interests, with full voting privileges, at future NWIC meetings, until this position is filled once again.

The following individuals, agencies/organizations provided funding or research updates to the Committee.

National Association of Wheat Growers
USDA–ARS
USDA–CSREES
CIMMYT
The Bill & Melinda Gates Foundation
Annual Wheat Newsletter (Brett Carver, Oklahoma State University)
NWIC Wheat Genomics Subcommittee (Jim Anderson, University of Minnesota)
Graingenes (Dave Matthews, USDA–ARS)
Wheat Germplasm Committee (Kim Garland-Campbell, USDA–ARS). It was noted some new individuals are needed for this committee.

Rust reports.

Durable Rust Resistance in Wheat Project. The DRRW Project announced the launch of the 'Rustopedia' (http://www.rustopedia.org/traction/permalink/Resources262), an online resource for scientists, policymakers, donors, and others interested in the wheat rusts.

David Marshall, USDA–ARS, Raleigh, NC, provided an update on the rust screening nurseries sponsored by USDA and established in coöperation with CIMMYT in Kenya. The intent of the nurseries is to screen germ plasm for response to Ug99 stem rust. Only about 5% of tested U.S. cultivars carry resistance. M. Bonman, USDA–ARS, Aberdeen, ID, noted the National Small Grains Collection is conducting a preliminary screen of materials for resistance to Ug99.

Carl Griffey, Virginia Polytechnic Institute and State University, and K. Garland-Campbell, USDA–ARS, reported on the status of stripe (yellow) rust and leaf (brown) rust. It was noted that leaf rust still is the predominant rust causing yield losses in the U.S. Stripe rust continues to effect production, but races tend to be more stable than those causing leaf rust.

Research initiatives.

The NWIC supports ongoing research efforts in the following areas. The committee voted this year to support all efforts equally, without assigning priorities. All were deemed of critical importance to U.S. and world wheat production.

Cereal Rust Initiative
Small Grains Genotyping Labs
Food Security/Wheat Quality Initiative
Aberdeen Small Grains Research Enhancement
Karnal Bunt Research Initiative

Future meetings.

The next meeting of the National Wheat Improvement Committee was set for 10 December, 2009, in Orlando, FL.

A Joint Congress: Hard Winter Wheat Workers Workshop and the National Wheat Genomics Workshop, 7–10 March, 2010, Lincoln, NE (http://conferences.unl.edu/wheat).

WHEAT WORKER'S CODE OF ETHICS

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

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

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

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

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

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

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December 2008.

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New SynOp International Triticeae Mapping Initiative (ITMI) population seed increase.

To: Members of the Wheat Research Community

From: Cal Qualset (coqualset@ucdavis.edu) and Mark Sorrells (mes12@cornell.edu).

We are in the process of a field seed increase at Davis, CA, of about 2,000 lines of two new populations constructed using the same parents (Synthetic W7984 and Opata 85) as the original ITMI mapping population. One is a doubled haploid (designated SynOp-DH) and the other is an RIL (designated SynOp-RIL) population described below. We need funds to complete the work and are sending the following request to state Wheat Commissions or Committees. We will also send this to various corporations and international contacts. Because you may be asked by potential donors about the relevance of the populations, we wanted to inform the wheat research community of its imminent availability and provide information about them.

There has been considerable interest by researchers to receive these new populations, and we are doing a one-time seed increase so that everyone can receive the same seed source and so that future large-scale seed increases will not be necessary. I hope you will help promote this effort by indicating your support for it to potential donors. If your own program can assist financially, we would greatly appreciate hearing from you. Harvest will begin about 15 June. Come on over! We have sickles. Feel free to send this information to others or contribute in other ways. Thank you.

Genetic stocks for wheat breeding and genomics research. Reconstruction of the SynOp (ITMI) mapping population 'Synthetic Wheat W7984 / Opata M85'.

In the early days of RFLP mapping, scientists of the ITMI developed an RIL population from a synthetic wheat, *Ae. tauschii* [DD] x Altar durum [AABB] hybridized with Opata M85 [AABBDD] bread wheat. This population, contrary to many wheat hybrid populations, had high variation [polymorphism] for DNA sequences and, therefore, was very useful for constructing a DNA molecular linkage map for wheat. The population included 150 RILs and was, and still is, widely used for mapping important traits of wheat. The population was initially distributed globally by M.E. Sorrells, Cornell University, where the first linkage map was developed. The population has been maintained and advanced several generations at the University of California, Davis, by C.O. Qualset and P.E. McGuire. The RILs have been distributed to more than 25 researchers and more than 20 papers have been published on genetics of wheat quality, kernel hardness, threshability, disease resistance, flowering time, and several morphological traits.

This population has proved valuable for initial mapping of traits, but the population is too small for detailed mapping and to aid in gene discovery. Requests have been received for a larger population of RILs of this useful population. Hence, the population has been reconstructed with a new cross having the same parents and advanced to near-homozygosity by J.P. Gustafson, USDA, Columbia, MO, and M.E. Sorrells, Cornell University. In addition, Daryl Somers, formerly of Canada Food and Agriculture, Winnipeg, Manitoba, produced doubled haploid (DH) lines that each have complete homozygosity. The reconstructed populations now includes about 1,700 new F_2-derived RILs (SynOp-RIL) and 200 DH lines (SynOp-RIL).

This population is public domain and will be distributed to all scientists who request seed. The intention is to provide 10 seeds of each line so that researchers can grow sufficient plants to extract DNA or grow additional plants to meet their research needs. We are now engaged in the seed increase phase. The objective now is to produce sufficient seed of each line for distribution to all qualified research scientists who request seed for the next 10 years. Because the lines from this cross vary so widely in many traits, including vernalization requirement, it is essential that the materials be grown at a site where all of the lines will produce at least 100 grams of seed. Northern California provides such an environment with autumn planting. C.O. Qualset at the University of California, Davis, has agreed to conduct this seed increase planting and to collect data on several traits to characterize each inbred line. The lines were planted in November 2008 and will be harvested in June 2009. Qualset is a retired professor and founding coördinator of ITMI, a position he held for 12 years and is available, without cost, to carry out this activity. However, there are expenses for the culture of the field plots, harvesting, seed cleaning and packaging, and distribution of the seeds for which no funds are available.

We are requesting your organization to assist with meeting these costs, estimated to be $10,000. A donation of any amount would be appreciated. We hope you can participate in this effort, and, of course, your organization would be welcome to receive seed for your research.

Funds may be transferred by check to C.O. Qualset payable to the Regents of the University of California. Acknowledgement of receipt of tax deductible donation will be made.

Thank you for your consideration.

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Advancements towards sequencing the bread wheat genome: An update of the projects of the International Wheat Genome Sequencing Consortium.

Kellye Eversole, IWGSC, Eversole Associates, 5207 Wyoming Road, Bethesda, MD 20816, USA.

Genome sequences hold the key for understanding the molecular basis of phenotypic traits and variation. Although the sequencing of model plant genomes, such as *Arabidopsis thaliana* and rice, has revolutionized our understanding of plant biology over the past 10 years, it has not translated efficiently into crop improvement for maize, wheat, or barley. At the same time, comparative genomic studies have revealed the limits of conservation between rice and the other cereal genomes; thereby necessitating the development of genomic resources and programs for maize, sorghum, wheat, and barley to serve as the foundation for future genome sequencing and the acceleration of genomic-based improvement of these essential crops. Despite the recognition that genome sequencing is critical for crop improvement, the size and complexity of the Triticeae genomes has been perceived as an obstacle for the efficient development of genome sequencing projects. Thus, genomics and its application to the production of wheat has lagged behind advances in other cereal crops, such as rice, sorghum, and maize. Today, wheat is the last major crop for which no genome sequencing effort is underway. Recently, however, technological advances offer the prospects of tractable large-scale programs that can deliver much-needed genomic resources for wheat.

In November 2003, a USDA–NSF-funded international workshop of wheat geneticists and sequencing specialists identified the first objectives towards sequencing the hexaploid wheat genome, i.e., physical mapping and assessment of sequencing strategies (Gill et al. 2004). To capitalize on the momentum of this workshop, the International Wheat Genome Sequencing Consortium (IWGSC, http://www.wheatgenome.org) was established in January 2005 with the goal of coördinating the international effort to build the foundation for and leading the effort to sequence the bread wheat genome.

As an international industry, academic, and governmental agency collaboration, the IWGSC is committed to providing wheat breeders and industry state-of-the-art tools and technologies that enable profitability throughout the wheat industry. The consortium is governed by a coördinating committee, comprised of scientific and financial contributors, who support sequencing the bread wheat genome, and an executive director (K. Eversole) supported by six co-chairs from Europe (C. Feuillet, France, and B. Keller, Switzerland), Australia (R. Appels), the USA (J. Dvorak and B. Gill), and Japan (Y. Ogihara). General membership in the consortium is open to anyone and business meetings are open to the public. Business meetings and workshops or coördinating committee meetings are held in conjunction with most major international plant genomics meetings.

To ensure the rapid delivery of tools to breeders, the IWGSC identifies short-term and long-term strategic goals, advocates for sequencing the wheat genome, coördinates international scientific efforts to build resources for wheat, develops and assists in the development of project proposals, and secures funding for collaborative efforts aimed at meeting identified goals. By implementing a milestone-based strategy, the consortium delivers products and tools while working towards the ultimate goal of a sequenced bread wheat genome. This overall strategy ensures the immediate availability of significant outputs for wheat breeders and the wheat industry at large in parallel to continued advancements in basic research on the wheat genome.

Projects coördinated and endorsed by the IWGSC fall within two broad categories: physical mapping (construction of physical maps for the D genome of *Ae. tauschii* and for the hexaploid wheat genome) and sequencing (the development of the resources necessary for sequencing and the testing of technologies to determine the best method for sequencing). The following provides an update of the IWGSC projects.

Physical mapping.

To provide the greatest resources to enhance wheat production and also advancing our basic understanding of the hexaploid wheat genome, the first priorities for the consortium are to establish a physical map of the 21 hexaploid wheat chromosomes and to complete the physical map of *Ae. tauschii*. This will facilitate the map-based isolation of the hundreds of genes and QTL for traits of agronomic importance as well as delivering 'perfect' markers for wheat breeding.

At the same time, the physical map will provide the substrate for sequencing the wheat genome regardless of the ultimate sequencing strategy selected.

In August 2006, the IWGSC road map for physical mapping projects was established and agreed upon by the IWGSC coördinating committee at the ITMI meeting in Victor Harbour, Australia. This road map includes the completion of a physical map of the D genome of the wild diploid *Ae. tauschii,* as a framework for the construction of the physical maps for the seven chromosomes of the D genome of hexaploid wheat. The IWGSC also aims to complete the maps of the homoeologous A and B chromosomes. The D-genome project was initiated six years ago (http://wheat.pw.usda.gov/PhysicalMapping/) and has established efficient protocols and software to perform BAC fingerprinting and contig assembly (Luo et al. 2003). These protocols are being used now for the hexaploid wheat genome project. Funding from the US National Science Foundation has been provided recently to complete the D-genome physical mapping project (PI, J. Dvorak, University of Californai, Davis, CA, USA).

The construction of physical maps in hexaploid wheat is performed with a chromosome-specific strategy that has been pioneered in Europe by the Institute of Experimental Botany in the Czech Republic and the INRA in France. This approach relies on the recent improvement of chromosome sorting and BAC library construction technologies that allowed the construction of chromosome-specific BAC libraries (Dolezel et al. 2007). The first BAC library already has been used successfully in a pilot project to establish a chromosome landing ready physical map of chromosome 3B, the largest wheat chromosome (3X the rice genome) (PI, C. Feuillet; INRA, France) and was published in 2008 (Paux et al. 2008).

The successful pilot project to develop a physical map on chromosome 3B of Chinese Spring by a single laboratory has opened up the route for the international collaborative effort on the 20 remaining chromosomes of hexaploid wheat. During the past two years, physical mapping projects for additional chromosomes have been initiated and physical mapping and sequencing project leaders have been secured for all of the bread wheat chromosomes. A summary of the status of the physical mapping projects follows and an illustration of the current status of the Chinese Spring physical mapping projects is provided in Fig. 1.

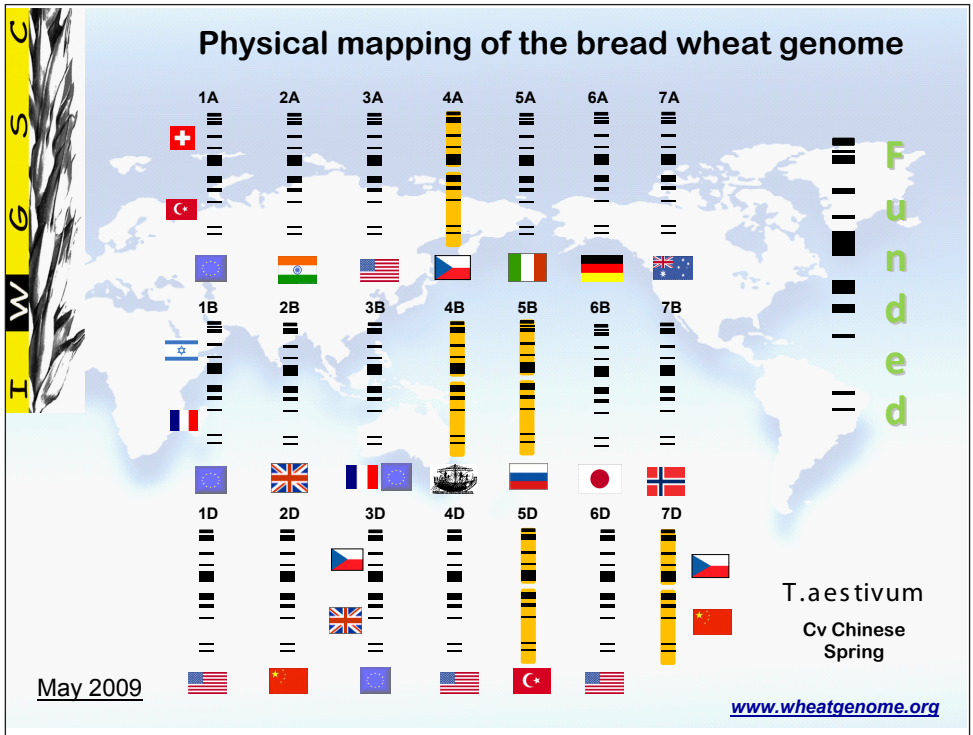

Fig. 1. Project leadership status for chromosome-based physical maps of bread wheat.

IWGSC physical mapping projects.

1. Completed projects

- 3B — Led by C. Feuillet (INRA, France), this has served as the pilot project for developing the first physical map of a flow-sorted chromosome. After a first 9.6X chromosome landing ready physical map (Paux et al. 2008), the project was completed in the framework of the EU FP7 project TriticeaeGenome to an 18X sequence-ready physical map of chromosome 3B of Chinese Spring. The 3B physical map can be found at http://urgi.versailles.inra.fr/gbrowse/cgi-bin/gbrowse/Wheat_FPC/.

2. Funded projects

- 1A, 1B, 3D, (3Bv2) — TriticeaeGenome project funded by the EU Commission under FP7 and coördinated by C. Feuillet (INRA, France) with 17 EU partners. This European project will complete the physical maps of group 1 and 3 chromosomes in wheat (and barley). Map-based cloning of targeted QTL, molecular breeding, and bioinformatics platforms will be developed within the framework of this project as well.
- 1, 4, and 6D of hexaploid wheat and all of *Ae. tauschii* — D-genome project led by J. Dvorak (UC, Davis), B. Gill (KSU), and O. Anderson (USDA–ARS). This project, funded by the US. National Science Foundation, will complete the *Ae. tauschii* physical map and physical maps of chromosomes 1, 4, and 6 of the D genome of Chinese Spring.
- 2AL — Led by K. Singh (Punjab Agricultural University, India). This project for the construction of the physical map of the long arm of chromosome 2A is funded by the Department of Biotechnology of the Indian Ministry of Science and Technology.
- 2D — Led by J. Jia (KL-CGB, CAAS, China) and funded by the CAAS (Chinese Academy of Agricultural Sciences). This project will develop a physical map of chromosome 2D.
- 3AS/3AL — Led by B. Gill (KSU, USA) and funded by the USDA (CSREE–NRI). These projects are developing anchored physical maps of the short and long arms of chromosome 3A.
- 4A – Led by J. Dolezel (Institute of Experimental Botany, Czech Republic). This project resulted in the construction of a BAC library and funding is being sought for physical mapping.
- 5A — Led by L. Cattivelli (Experimental Institute for Cereal Research, Italy) and funded by the Agricultural Research Council of Italy. This project will develop a physical map of chromosome 5A.
- 5B — Led by E. Salina (Institute of Cytology & Genetics, Russia). This project, developed in collaboration with European and U.S. partners, will construct the physical map of chromosome 5B of Chinese Spring. A 2- year grant was approved by the INRA–RFBR (Russian Foundation for Basic Research) for developing markers and genetic maps that will be needed for anchoring. Other grants will be submitted to funding agencies in 2009-2010 for the construction of the 5B BAC library and for fingerprinting.
- 7DS — Led by J. Dolezel (IEB, Olomouc, Czech Republic), this project to construct the physical map of chromosome 7DS has received funding for the construction of the BAC library and fingerprinting has been achieved. A proposal is pending for funds for the anchoring of the map.
- 7DL — This project is led by S. Weining (Northwest A&F University, Yangling, Shaanxi, China), R. Appels (Murdoch University, Perth, Australia), and J. Dolezel (IEB, Olomouc, Czech Republic). Funding for the BAC library was provided by the Czech Science Foundation. Northwest A&F University has provided funding for fingerprinting and anchoring for the completion of the 7DL physical map.
- Radiation hybrid mapping — Led by S. Kianian (North Dakota State University, Fargo, ND, USA) and funded by the U.S. National Science Foundation, this project will develop high-resolution, RH physical maps that will be used to anchor existing bacterial artificial chromosome (BAC) contigs and clones for the D-genome of hexaploid wheat. Other panels are under development for the other chromosomes such as for 3B (Paux et al, 2008).

3. Projects under development.

- 2B — Led by M. Bevan (JIC, UK), this project will develop the physical map of chromosome 2B of Chinese spring and will be submitted to funding agencies in late 2009 or in 2010.
- 4B — Led by M. Nachit (ICARDA, Syria) and D. Habash (Rothamstead Research, UK), the development of the physical map of chromosome 4B will be included in the proposed *4Phoenicia* project that will build scientific capabilities for the Mediterranean region to underpin wheat genomics for sustainable agriculture.
- 5D — Led by H. Budak (Sabanci University, Turkey), this project to establish a physical map of chromosome 5D of Chinese spring is under development and will be submitted to funding agencies in 2009.
- 6A — Led by T. Schnurbush (IPK Gatersleben, Germany), this project will construct the physical map of chromosome 6A.
- 6B — Led by Y. Ogihara (Kyoto University, Japan), this project will establish the physical map of chromosome 6A.
- 7A — Led by R. Appels (Murdoch University, Perth, Australia), this project will establish the physical map of chromosome 7A of Chinese Spring.
- 7B — Led by O. Olsen (Norwegian University of Life Sciences, Aas, Norway and Hedmark University College in Hamar, Norway). A proposal to construct the physical map of chromosome 7B is being finalized for submission to regional and national public/private entities.

Sequencing.

In the past few years, there has been an exponential growth in the number of sequencing strategies and the rhythm at which the technologies are evolving. For the first time, the possibility to sequence the hexaploid wheat genome at a reasonable cost appears to be within reach. To begin to assess how these new technologies can be applied efficiently to the wheat genome in a manner that will deliver high quality reference genome sequences that can be readily exploited by breeders to accelerate crop improvement, the IWGSC was joined by the International Barley Sequencing Consortium in hosting a workshop in September 2008 in Evry, France.

The primary workshop goal was to develop strategic road maps for sequencing the wheat and barley genomes in the next few years. The workshop brought together international experts in the human and agriculturally-important genome sequencing projects, developers of genome sequencing technologies, scientists with extensive knowledge of the structure and organization of the wheat and barley genomes, representatives of international genome sequencing centers interested in *de novo* sequencing of plant species, as well as representatives of governmental funding agencies. At the workshop, a consensus was reached on a two-phase sequencing strategy:

Phase 1: Obtaining a good quality sequence that can be used as soon as possible to develop tools for breeding and that represents a platform for phase 2. Establish pilot sequencing projects on chromosomes 3B of wheat to establish the most cost effective approaches for the wheat genome. Roche 454 Titanium and Illumina Solexa technologies should be tested separately and in combination on sorted chromosomes and on the minimal tiling paths. Furthermore, the potential utility of WGS paired-end datasets on the diverse next generation sequencing platforms in pilot projects should be explored. Such datasets are needed to train algorithms for Triticeae genome characteristics and advance the approach. At the same time, such data will deliver 'gene-catalog' sequence datasets that complement EST resources for marker and breeding-tool development.

Phase 2: Achieving high quality 'gold standard' sequences that will enable all functional and structural analyses of the two genomes.

The full workshop report can be found on the IWGSC website at (http://www.wheatgenome.org/documents).

A number of projects are currently underway to evaluate the feasibility of using new sequencing technologies to accelerate marker development and reduce MTP sequencing cost while maintaining quality and without losing access to the non genic but yet relevant sequences. The following provides a summary of specific IWGSC sequencing projects.

IWGSC sequencing projects.

1. *Chromosome sequencing. 3BSEQ* — Led by C. Feuillet (INRA, Clermont-Ferrand, France), this project entitled 'Sequencing, Annotation, and Characterization of the Bread Wheat Chromosome 3B' (3BSEQ) has been submitted to the French ANR Plant Biotech Flagship Project Call 2009. The 3BSeq project aims at obtaining an annotated sequence of the largest bread wheat chromosome, chromosome 3B, and at exploiting this knowledge to develop tiling arrays of the 3B gene space for further functional and structural characterizations. The project will take advantage of the potential offered by the next generation sequencing and array technologies to develop an original strategy and deliver a high quality draft sequence of the chromosome.

2. *Sequencing of megabase-sized contigs on chromosome 3B.*

- C. Feuillet, (INRA France): Two projects (supported by the ANR-Genoplante and the Genoscope) to sequence more than 20 Mb of BAC contigs distributed in different regions of chromosome 3B have been completed and a publication is forthcoming.
- R. Appels (Murdoch University, Australia): Sequencing of two Mb-sized contigs located on chromosome 3BS (supported by GRDC) has been completed, and a publication is forthcoming.

3. *3AS sample sequencing project* — Led by B. Gill (KSU, USA) and funded by the USDA (CSREES-NRI), this project will generate 18.4 Mb of sequence from the chromosome 3AS BAC libraries, sequence 48 targeted BAC clones, and BAC end sequence 10,000 random clones. The second sequencing component of this project is to compare the 3AS BAC sequences with sequences from homoeologous chromosome arm 3BS.

4. Mining the allohexaploid wheat genome for useful sequence polymorphisms — Led by K. Edwards (University of Bristol, UK) and funded by the Biotechnology and Biological Sciences Research Council (BBSRC), this project will use next generation sequencing to identify sequence differences in the genomes of five key cultivars and explore ways to sequence the wheat genome.

Bioinformatics.

Broad bioinformatics capabilities will be necessary to annotate the sequence and to ensure the greatest utility of data for breeders. To coördinate the manual and automated annotation of the wheat genome, the IWGSC established an annotation working group in 2006 that was expanded subsequently to include all of the Triticeae. The Group is chaired by P. Leroy (INRA, Clermont-Ferrand, France) and T. Wicker (University of Zurich, Switzerland).

During 2006 and 2007, the Triticeae Annotation Working Group developed annotation guidelines (http://www.wheatgenome.org/tools). In 2007, a semi-automated annotation pipeline, TriAnnot (http://urgi.versailles.inra.fr/projects/TriAnnot/), was developed and continues to be improved. The IWGSC coördinated a Bioinformatics Tool Workshop that was held in January 2009 in conjunction with the XVII Plant and Animal Genome conference in San Diego, California. The agenda and links to speaker abstracts can be found on the PAG website (http://www.intl-pag.org/17/17-iwgsc2.html). Under the coördination of D. Matthews (USDA–ARS, Cornell University, Ithaca, NY, USA), GrainGenes has established an IWGSC GrainGenes BAC repository for annotated genome sequences (http://www.tritgenome.org/tawg/). New sequencing technologies, full-length cDNA sequences, and deep transcriptome sequencing will be essential resources for annotation and the IWGSC supports projects to develop these resources.

The major challenge for all genome-sequencing projects is developing bioinformatics capabilities for exploitation of the sequence. During the IWGSC–IBSC workshop on sequencing technologies, it became clear that bioinformatics capacities needed to be developed well in advance of the availability of the sequence. The workshop participants agreed that we need to develop a centralized database that will extend the Ensembl platform to plants and that we had to develop a mechanism for obtaining ongoing feedback from the sequence users. The IWGSC goals for bioinformatics, thus, include the development of a publicly available, centralized, comprehensive database that integrates annotation and other available biological data, including comparative genomics, variation, and regulatory data.

Next steps and future meetings.

During the next year, the IWGSC will continue to seek funding for the development of physical maps and sequencing of all of the chromosomes of hexaploid wheat to ensure that the entire wheat industry can begin to exploit rapidly genomic information while efforts are underway to obtain a complete sequence of bread wheat. Concurrently, the IWGSC will continue to explore the feasibility of using the new sequencing technologies for the construction of physical maps and for sequencing the bread wheat genome and may organize another sequencing technologies workshop in 2010. The IWGSC will expand its efforts in bioinformatics to ensure the development of a centralized database and to coordinate the various bioinformatic tools and resources that will be established through the individual physical mapping and sequencing projects. The IWGSC is exploring the possibility of organizing a workshop to develop a road map for the establishment of bioinformatics capabilities in late 2009 or 2010.

The IWGSC will hold a coördinating committee meeting in conjunction with the ITMI meeting in Clermont-Ferrand, France, in August 2009. In January 2010, the IWGSC will host a workshop and an open business meeting at the Plant and Animal Genome Conference in San Diego, California and may organize another annotation workshop. Meeting information as well as general information will be available at the IWGSC website (http://www.wheatgenome.org).

Finally, as more and more resources for breeders are becoming available through the IWGSC projects, a concerted effort is underway now to increase significantly the active industry involvement in the consortium. Six breeding companies now sponsor the consortium in addition to the public and grower organizations (Fig. 2, p. 16). The IWGSC is working with industry to identify chromosomal regions of importance for early, targeted sequencing and deep sequencing. Additionally, the IWGSC encourages all physical mapping and sequencing projects to include isolation of genes and QTL underlying industry-identified key traits in wheat.

With the completion of the first physical map of a bread wheat chromosome, funding in place for physical maps of 10 other chromosomes and the entire *Ae. tauschii* genome, the submission of the first proposal to sequence a wheat chromosome, and the rapid development of new sequencing technologies, the IWGSC goal of obtaining a first draft sequence of the wheat genome is within reach.

Fig. 2. Sponsors of the IWGSC.

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II. NATIONAL WHEAT GENOMICS CONFERENCE

2008 National Wheat Genomics Conference

1–2 December, 2008.
Indianapolis, IN, USA.

Update on the NWIC Subcommittee on Wheat Genomics.

Eduard Akhunov was elected as the new university representative. The current subcommittee membership is listed in the table below. Please do not hesitate to contact any of us on issues that you think will be important for the subcomittee to discuss. Information about the committee can be found at: http://wheat.pw.usda.gov/NWIC/

Role (term duration)	Name	E-mail
Chair (2009)	Stephen Baenziger	Pbaenziger1@unl.edu
NWIC Representative (2009)	Jim Anderson	ander319@umn.edu
Industry/Nonprofit Representative (2010)	Rollie Sears	rollin.sears@syngenta.com
Industry/Nonprofit Representative (2011)	Jay Romsa	jay.romsa@genmills.com
University Representative (2011)	Eduard Akhunov	eakhunov@ksu.edu
University Representative (2010)	Mark Sorrells	mes12@cornell.edu
USDA Representative (2010)	Olin Anderson	oanderson@pw.usda.gov
USDA Representative (2011)	Justin Faris	justin.faris@ars.usda.gov
At-large Representative (2009)	Ed Souza	souza.6@osu.edu
IWGSC (ex officio)	Kellye Eversole	eversole@eversoleassociates.com

The subcommittee will meet annually, but the next meeting of the whole community will be every other year beginning in 2010. **Mark your calendars:** A Joint Congress, combining the Hard Winter Wheat Workers Regional Workshop and The National Wheat Genomics Workshop, will be held 7–10 March, 2010, at the Embassy Suites, Lincoln, NE.

Finally, the summarized results of the second national survey of genomics priorities for wheat which was undertaken by The National Wheat Improvement Committee (NWIC) Subcommittee on Wheat Genomics. The full survey results are attached below and can be found at: http://wheat.pw.usda.gov/NWIC/WheatResPrioritiesSum08F.pdf.

The survey was distributed at the second annual National Wheat Genomics Conference (approximately 65 researchers attended) and by a directed e-mail solicitation so that those unable to attend the meeting could share their views and have input. Every effort was made to insure the survey was widely distributed among the U.S. wheat research community. At the annual meeting, the main theme was wheat genomics and aspects of wheat research related to genomics. Briefly summarized the research priorities are to

1) expand molecular mapping of economically important traits,
2) increase molecular marker development to better cover the wheat genome,
3) develop a physical map of the hexaploid wheat genome,
4) improve ease-of-use and interoperability of wheat-related databases, and
5) exploit functional genomics to understand gene expression and gene networks.

If you have any questions concerning the survey, please do not hesitate to ask. Also please share this survey with whomever you think would appreciate knowing these results. The results of the survey have also been included in The 'NWIC/NAWG Research Priorities for FY10' booklet, which is posted at http://cropandsoil.oregonstate.edu/wheat/reports/NWIC/index.htm.

In the NWIC/NAWG Research Priorities for FY10, they state 'The NWIC and NAWG support the goal of advancing wheat genomics to serve as the foundation for basic research and provide the tools for improving food, fuel, and crop yields in a changing environment. We support increased funding of these efforts through collaborative national research grants, such as those sponsored by USDA–NIFA Agriculture and Food Research Initiative and the National Science Foundation.'

In 2006, the NWIC authorized the formation of a Subcommittee for Wheat Genomics, comprised of seven elected members, representing university and USDA–ARS researchers, industry, and nonprofit agencies. The goal of the Subcommittee for Wheat Genomics is to facilitate communication among U.S. researchers, assess national genomics research needs and goals, develop strategies and organize research efforts, facilitate communication with national granting agencies and participation in international initiatives, and advocate for funding of wheat genomics research at the national level.

Guiding principles.

- Wheat is the ideal model species for studying polyploid genome evolution and trait variation because of the unmatched complement of aneuploid genetics stocks, natural diversity, and wide adaptation.
- Public wheat breeding and research is critical to U.S. agriculture because three quarters of all wheat cultivars were developed by public wheat breeders.
- The open exchange and publication of wheat research contributes to the rapid advancement of new scientific knowledge for improvement of wheat and other crops.
- The study of polyploidy genetics and gene expression will provide key information about how genes and alleles interact in a polyploid genome.
- Wheat research has led to novel discoveries in the genetics and biology of vernalization, genetic control of chromosome behavior, and end-product quality.
- Wheat cytogenetics has made major contributions and continues to provide novel genetics stocks and other tools for understanding mechanisms of chromosome pairing and for chromosome manipulation.'

National Wheat Improvement Committee Subcommittee on Wheat Genomics.

4–6 December, 2008.
Indianapolis, IN, USA.

Executive Summary – The future of wheat genomics research in the United States. The National Wheat Improvement Committee (NWIC) Subcommittee on Wheat Genomics held their second annual meeting, The National Wheat Genomics Conference (NWGC). The purposes of the meeting were to provide a venue for U.S. wheat workers to learn of current endeavors in U.S. wheat genomics and related research and to provide a forum to foster interaction, discussion, and collaboration among wheat scientists. The meeting also provided the opportunity to formulate and communicate the future research needs of the U.S. wheat-genomics community. Although the main theme of the conference was wheat genomics, the session topics and presentations encompassed other aspects of wheat research related to genomics. To guide strategic planning, key speakers relating to critical research topics important for the future of wheat improvement were invited to give presentations. These research topics were considered relative to the overarching goal of understanding the genetic basis of traits in wheat. The research topics listed below, and the prioritized research necessary to achieve the goal of advancing wheat genomics, serve as the foundation for basic research and provide the tools for improving food, fuel, and crop yields in a changing environment. Based on surveys distributed at the conference and a directed e-mail solicitation, the **top five wheat genomics research priorities are**

1) increased support for mapping traits of economic importance for molecular breeding,
2) more molecular markers,
3) a physical map of hexaploid wheat genome,
4) improved ease of use and interoperability of wheat-related databases, and
5) to study functional genomics to understand gene expression and gene networks.

Recently funded projects that were listed in past surveys. Complete, anchored physical map of *Ae. tauschii* (highest priority in 2007) and wheat radiation hybrid mapping to initiate genome sequencing.

Key research topics that define our research goals and priorities.

- Wheat is the ideal model species for studying polyploidy genome evolution and trait variation because of the unmatched complement of aneuploid genetics stocks, natural diversity, and wide adaptation.
- Public wheat breeding and research is critical to U.S. agriculture because three quarters of all wheat varieties were developed by public wheat breeders.
- The open exchange and publication of wheat research contributes to the rapid advancement of new scientific knowledge for improvement of wheat and other crops.
- The study of polyploidy genetics and gene expression will provide key information about how genes and alleles interact in a polyploid genome.
- Wheat research has led to novel discoveries in the genetics and biology of vernalization, genetic control of chromosome behavior, and end-product quality.
- Wheat is well situated to continue as a leading model for comparative genomics and genome evolution.
- Wheat cytogenetics has made major contributions and continues to provide novel genetics stocks and other tools for understanding mechanisms of chromosome pairing and for chromosome manipulation.

Community resources will help achieve our research goals. To advance these research areas, community resources must be created or strengthened. The questionnaire below was distributed to attendees of the Wheat Genomics Conference and also sent to U.S. wheat researchers by e-mail to develop a consensus of priorities among wheat researchers in the U.S.

Prioritize general community needs (1 = highest rank; rank up to five topics).

_____ Centralized catalog of genomics resources available to the community
_____ Increased support for mapping traits of economic importance for molecular breeding
_____ Improved doubled haploid technology
_____ Enhanced quantitative genetics methods and tools
_____ Improved ease of use and interoperability of wheat-related databases
_____ Complete genome sequence of *Aegilops tauschii*
_____ Physical map of hexaploid wheat genome
_____ Genome sequence of hexaploid wheat gene space, potentially linked to the genetic map
_____ Draft BAC sequences for the entire hexaploid wheat genome
_____ Full-length wheat cDNA collection (sequences and clone access)
_____ Functional genomics studies to understand gene expression and gene networks
_____ More molecular marker development including SNPs and SSRs
_____ Improved wheat transformation methods
_____ TILLING populations and services for different classes of wheat
_____ A second BAC library for hexaploid wheat genome
_____ Other _____

Response to questionnaire. Forty-one responses were received. The rank is based on the number of scores a topic received (count) as well as the average score. The index was calculated as 'count /average score', thus, the index reflects both average score and the number of times the topic was selected as a priority . Topics are shown in the original order that they appeared on the survey.

Rank	Count	Average	Index	Topic
11	10	2.9	3.4	Centralized catalog of genomics resources available to the community
1	27	2.2	12.2	Increased support for mapping traits of economic importance for molecular breeding
8	13	3.4	3.8	Improved doubled-haploid technology
13	10	3.4	2.9	Enhanced quantitative genetics methods and tools
4	18	2.8	6.5	Improved ease of use and interoperability of wheat-related databases
6	14	2.7	5.2	Complete genome sequence of *Aegilops tauschii*

Rank	Count	Average	Index	Topic
3	17	2.1	8.0	Physical map of hexaploid wheat genome
9	13	3.4	3.8	Genome sequence of hexaploid wheat gene space, potentially linked to the genetic map
14	5	4.2	1.2	Draft BAC sequences for the entire hexaploid wheat genome
7	14	3.4	4.2	Full-length wheat cDNA collection (sequences and clone access)
5	18	3.2	5.7	Functional genomics studies to understand gene expression and gene networks
2	22	2.6	8.5	More molecular marker development including SNPs and SSRs
10	14	3.7	3.8	Improved wheat transformation methods
12	12	4.0	3.0	TILLING populations and services for different classes of wheat

Other Topics written on the surveys.

3 – A second BAC library for hexaploid wheat genome
5 – Need for a regional, perhaps USDA operated facilities for production of doubled haploids and transformation
1 – Wheat small-RNA targeting libraries
1 – Improved markers for end-use quality traits
2 – VIGS, transformation, and RNAi-related research
3 – Bioinformatics tools so breeders can properly integrate marker information in a molecular breeding strategy

Assessment of 2008 survey results. The results of this survey differed substantially from the 2007 survey. The highest priority was for a new topic that was suggested in the 'Other' category in last year's survey. That topic was 'Increased support for mapping traits of economic importance for molecular breeding', which was likely influenced by the Wheat CAP project which is ending in 2009. 'More molecular marker development' moved up to second and 'Physical map of hexaploid wheat genome' dropped to third. 'Improved ease of use and interoperability of wheat-related databases' remained in fourth place. 'Functional genomics studies to understand gene expression and gene networks' was ranked fifth, whereas the fifth topic last year, 'Full-length wheat cDNA collection', dropped to seventh.

Wheat researchers who responded to this year's surveys placed a high priority on the use of molecular markers for mapping economic traits in wheat and new marker development is essential for that activity. Wheat genomics researchers also recognize the value of physical maps. A physical map for *Ae. tauschii* was the highest priority last year, and it was funded by NSF. A physical map of hexaploid wheat was second last year and third this year. Wheat-related databases have ranked high in all of our surveys, because they are recognized as an essential tool for all wheat research. The lowest ranking topics were quite different from last year. Last year, the three lowest priority topics were si(micro) RNA collection, improved coördination of RFPs from NSF and the USDA, and improved wheat-transformation methods. This year, the three lowest priority topics were draft BAC sequences for the hexaploid wheat genome, enhanced quantitative genetics methods, and TILLING populations and services. Five respondents wrote in 'Facilities for production of doubled haploids and transformation. Of the 14 topics, sequencing priorities ranked 6, 7, and 9, almost identical to 2007. These results reflect a very strong and pressing need for marker resources, online databases, and physical maps relating to positional cloning, mapping traits, and marker-assisted selection as compared to genome sequencing, transformation, and TILLING population research. The success of the Wheat CAP project has clearly had an impact on the priority topics in this survey compared to 2007.

SPEAKER AND POSTER ABSTRACTS – NATIONAL WHEAT GENOMICS CONFERENCE

5–6 December, 2008.
Indianapolis, IN, USA.

Note: Speaker abstracts are followed by the poster abstracts.

Accessing the barley genome.

Timothy J. Close, Department of Botany & Plant Sciences, University of California, Riverside, CA 92521, USA.

Assemblies of nearly 500,000 barley ESTs from a range of barley genotypes have been used to define more than 13,000 single nucleotide polymorphisms (SNPs). From these and several hundred SNPs from other sources, three pilot Illumina, GoldenGate assays were developed to test 4,596 SNPs for high-throughput genotyping. Two production-scale GoldenGate assays, BOPA1 and BOPA2, were developed from 3,072 of the tested SNPs and deployed within the USDA BarleyCAP (http://barleycap.cfans.umn.edu/) and UK AGOUEB (http://barleygenetics.net/lukesite/html/agoueb/guide_to_illumina_genotyping.htm) projects, and throughout the barley community. A barley consensus genetic linkage map composed of 2,943 SNPs was produced using data from four doubled-haploid mapping populations. An estimated two-thirds of all gene-bearing BACs in a Morex library were identified with ~12,500 overgo probes, increasing the compiled number of gene-positive BACs to 83,831 clones. High-information-content fingerprinting was applied to these BACs, yielding 1,700 Mb of gene-bearing BAC contigs, available at http://phymap.plantsciences.ucdavis.edu:8080/barley/. Combinatorial pools of part of the minimal tiling path (MTP) were applied to BOPA1 and BOPA2, anchoring 1,319 MTP BACs to 1,150 SNP loci representing 1,079 unique genes. Several groups have established TILLING populations, and a large portion of existing mutant and germ plasm collections are in the process of being analyzed using the barley GoldenGate assays. The SNP-based genetic map, with barley/rice synteny displays and information on gene-BAC relationships, is available through HarvEST:Barley for Windows (http://harvest.ucr.edu) or online (www.harvest-web.org). Work is underway in Europe to fully sequence thousands of gene-bearing BACs, create a physical map of the entire barley genome, and generate several 100,000 BAC-end sequences, which is intended to thoroughly relate the barley physical map to reference genomes. A whole-genome sequencing strategy is in a formative stage under the auspices of the International Barley Sequencing Consortium (http://barleygenome.org/) in coördination with the International Wheat Genome Sequencing Consortium (www.wheatgenome.org). As the density of information increases, it becomes ever easier to relate barley to wheat genomes, thus, the vision of barley as a genome model for wheat is becoming a reality.

Phenotyping for physiological breeding and gene discovery in wheat.

Matthew Reynolds [1,2], Yann Manes [1], and Peter Langridge [2].

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Approaches that can be used to increase rates of genetic gains in stress breeding include (i) strategic, trait-based crossing to combine complementary traits in progeny, (ii) high-throughput phenotyping and genotyping to enrich for desirable alleles in early generations, and (iii) exploring genetic resources to broaden the genetic base. Using a combination of the above approaches, CIMMYT has released drought-adapted germ plasm that shows superior expression of a range of complementary physiological traits deriving from both conventional sources and landraces and wild relatives. New genetic technologies are expected to further accelerate the potential for genetic gains, however, one of the current bottlenecks is precision phenotyping. For gene discovery within mapping populations, high-throughput phenotyping techniques such as thermal imaging for canopy temperature and spectral reflectance for ground cover and stem carbohydrates permit large numbers of genotypes to be screened with high efficiency. Confounding factors still need to be resolved in studies where genes of major effect are not controlled. Major genes not only affect the crop's morphology but also may lead to interactions between phenology and, for example, availability of soil water at key growth stages. These factors may cause QTL to be falsely identified and complice the already difficult challenge of dissecting 'genotype x environment' interaction. New generations of mapping populations are being developed that contrast in drought-adaptive traits but not in flowering time or height. However, progeny of bi-parental crosses still encompass the problem that transgressive segregation of parental alleles usually result in some agronomically inferior genotypes and, therefore, alleles long since excluded in plant breeding may mask more subtle effects. Association genetics provides a potential alternative where genetically diverse but elite cultivars can be used for gene discovery.

Evolution of wheat genomes.

P. Gornicki [1], D. Chalupska [1], H.Y. Lee [1], J.D. Faris [2], A. Evrard [1], B. Chalhoub [3], and R. Haselkorn [1].

[1]–Department of Molecular Genetics and Cell Biology, University of Chicago, IL, USA; [2] USDA–ARS Cereal Crops Unit, Northern Crop Science Laboratory, Fargo, ND 58105, USA; and [3] Laboratory of Genome Organization, URGV-INRA, 91057 Evry Cedex, France.

The DNA sequences of wheat A, B, and D *Acc* homoeoloci were analyzed with a view to understanding the evolution of the *Acc-1* and *Acc-2* genes and the origin and evolution of the three genomes in modern hexaploid wheat. The 2.3–2.4 million years ago (MYA) divergence time calculated for the three homoeologous chromosomes, based on coding and intron sequences of the *Acc-1* genes, is at the low end of other estimates. Our clock was calibrated using 60 MYA for the divergence between wheat and maize. On the same time scale, wheat diverged from barley and rice 11.6 MYA and 50 MYA, respectively, based on sequences of *Acc* and other genes. The regions flanking the *Acc* genes are not conserved between the A, B, and D genomes, but they are conserved among them. Substitution rates in intergenic regions consisting primarily of repetitive sequences vary substantially along the loci and are, on average, 3.5-fold higher than the *Acc* intron substitution rates. The composition of the *Acc* homoeoloci suggests haplotype divergence exceeding 0.5 MYA, in some cases. Such variation might result in a significant overestimate of the time since tetraploid wheat formation, which occurred no more than 0.5 MYA.

Sequence and assembly of the maize B73 genome.

The Maize Genome Sequencing Consortium. Genome Sequencing Center, Washington University School of Medicine, St. Louis, MO 63108, USA; Arizona Genomics Institute, University of Arizona, Tucson, AZ 85721, USA; Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA; and Iowa State University, Ames, IA 50011, USA.

The Maize Genome Sequencing Consortium was launched with a three-year grant to produce the sequence of the maize (B73) genome. We recently completed the sequencing of 16,600 BAC clones that correspond to a minimal tiling path for the genome. These clones represent a near complete genome sequence of maize with unique regions brought to finished quality. This sequence, accessible via GenBank and, of most relevance to cereal geneticists, via a Genome Browser (maizesequence.org), provides a more refined view of the maize genome. In this presentation, we will describe the methods used to select and produce the draft sequence and annotations, as well as efforts being conducted during the third year of the project to improve and annotate the maize genome sequence.

Characterizing the wheat genome by random BAC and sample sequencing.

Phillip SanMiguel [1], Katrien M. Devos [2], Xiangyang Xu [2], A. Costa de Oliveira [3], J. Estill [3], M. Estep [3], and J.L. Bennetzen [3].

[1] Agricultural Genomics Center, Purdue University, West Lafayette, IN 47907, USA; [2] Departments of Crop and Soil Sciences and Plant Biology, University of Georgia, Athens, GA 30602; and [3] the Department of Genetics, University of Georgia, Athens, GA 30602, USA.

The genome structure of the hexaploid wheat cultivar, Chinese Spring (CS), was assayed using several, random-sequencing techniques, including sequencing randomly chosen BACs as well as performing random shotgun Sanger and Next Generation sequencing runs. Twenty-four million bases (9.5X average coverage) of sequence from 220 randomly chosen BACs were generated. More than 10,000 Sanger sequencing reads from the clones of random-sheared genomic DNA produced nearly 8 million bases of sequence. A trial, Applied Biosystems SOLiD run yielded 200 million 35-base reads of which roughly 3 billion bases appear high quality. Furthermore, >190 of the BACs have been successfully mapped using a repeat-junction amplification method on deletion line genomic DNA. Annotation of the first 66 BACs has uncovered 76 confirmed gene homologies, suggesting that there are about 180,000 genes and pseudogenes in CS wheat. Preliminary gene distribution analysis found that 30 of the 66 BACs contained no confirmed genes. These annotation results suggest that one would need to sequence 53% of the CS genome to find 100% of the genes, 49% to find 95% of the genes, or 15% to find 50% of the genes. As expected, the majority of the sequence found in the wheat genome derives from long, terminal repeat (LTR) retrotransposons.

Genetic regulation of tillering.

Gary J. Muehlbauer. Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN 55108, USA.

The activity of the shoot apical and axillary meristems largely determines above ground plant architecture. In wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.), tillers develop from axillary meristems in the leaf axil. The number of vigorous tillers with spikes determines the overall grain yield. The overall objectives of this work are to understand the genetics of tillering in the Triticeae. In barley, we have characterized the low-tillering mutants *uniculm2* (*cul2*), *uniculm4* (*cul4*), *low number of tillers* (*lnt*), and *absent lower laterals* (*als*). We used histological approaches to examine the morphology of axillary meristems in the mutants. RNA profiling was used to identify candidate genes for the mutants and physiological processes that are unique to the mutants. Our double-mutant analysis indicates that at least two pathways are involved in tillering. We also identified and characterized a *suppressor of uniculm2* (*suc2*) mutant that, in combination with c*ul2*, exhibits tillering. In wheat, we developed transgenic wheat expressing the maize *teosinte branched1* (*tb1*) gene. These plants exhibit reduced tiller and spike number, an increase in the number of spikelets and leaves, and a reduction in height compared to wildtype control plants. These results demonstrate that overexpression of the maize *tb1* gene results in reduced tillering in wheat. Decreased tiller number in the transgenic wheat plants is due to the restriction of the outgrowth of the tiller buds. Increased expression of the *tb1* gene in maize, rice, and *Arabidopsis* also results in plants that exhibit reduced branching, indicating that increased expression of *tb1* is a general mechanism that plants use to repress branching.

Genetic regulation of developmental phases in winter wheat.

Yihua Chen, Brett Carver, Shuwen Wang, Shuanghe Cao, and Liuling Yan. Plant and Soil Sciences, Oklahoma State University, Stillwater, OK 74078, USA.

The orderly development and growth of winter wheat through its life cycle can be dissected into several phases based on morphological, physiological, or agronomic traits. In the present study, the developmental process was characterized at three stages, initial internode length at stem elongation, heading date, and physiological maturity. These traits were mapped in a population of recombinant inbred lines (RILs) generated from a cross between two winter wheat cultivars, Jagger and 2174. The variation in the developmental process was found to be controlled by three major QTL, each tightly associated with a known flowering gene, *VRN-A1* on chromosome 5A, *PPD-D1* on chromosome 2D, and *VRN-D3* on chromosome 7D. On the basis of the average contributions of these candidate genes for QTL to the total phenotypic variation (R^2) over three years, *VRN-A1*, *PPD-D1*, and *VRN-D3* were found to have the most significant effect on stem elongation, heading date, and physiological maturity, respectively, and all of them also had durable effects on other developmental traits characterized at different stages. Whereas the Jagger *VRN-A1* and *VRN-D3* alleles promoted the developmental process, the Jagger *VRN-D1* allele delayed the developmental process due to its sensitivity to photoperiod. No direct interactions were found between these genes, but the combination of their alleles and effect durations determined various developmental phases in winter wheat.

Syntenic relationship of the wheat greenbug-resistance gene Gb3 region with rice and Brachypodium distachyon.

Perumal Azhaguvel [1], Jackie C. Rudd [1], Yaqin Ma [2], Ming-Cheng Luo [2], Yiqun Weng [1, 3].

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The greenbug, *Schizaphis graminum* (Rondani), is an important aphid pest of small-grain crops in many parts of the world. A single dominant gene, *Gb3* that originated from *Ae. tauschii*, has been deployed in the hard winter wheat cultivars TAM 110 and TAM 112 and has provided consistent and durable resistance against prevailing greenbug biotypes. Previously, we mapped *Gb3* in the recombination-rich, telemetric bin of wheat chromosome arm 7DL. In the present study, high-resolution, subgenome mapping was carried out using an F_2 segregating population of *Ae. tauschii* and two hexaploid populations. Molecular markers were developed by exploring the Triticeae ESTs and the syntenic relationships among wheat, rice, and *B. distachyon* in the *Gb3* region. The *Brachypodium* sequences in super contig_0 aligned with Triticeae ESTs were thoroughly examined. A high degree of colinearity between the wheat 7DL distal bin and the *Brachypodium* super contig_0 was observed. Total of 70 *Gb3*-linked markers were mapped in the *Ae. tauschii* population, of which 21 were based on wheat–*Brachypodium* colinearity. Markers closely linked with *Gb3* were used to screen *Ae. tauschii* and wheat 7DL-specific BAC libraries. BAC contigs were constructed with markers flanking *Gb3*. Fifteen *Ae. tauschii* BAC-end sequence-based markers were fine mapped in a *Gb3* window of 3.0 cM. This research demonstrates the value of publicly available resources such as the wheat D-genome mapping database ((http://wheat.pw.usda.gov/PhysicalMapping/), the rice database (http://wheat.tigr.org/tdb/e2k1/tae1/index.shtml), and the *B. distachyon* database (http://www.brachypodium.org).

The concurrence of Stagonospora nodorum blotch resistance with host-selective toxin insensitivity in tetraploid wheat.

Chenggen Chu [1], Timothy L. Friesen [2], Shiaoman Chao [2], Justin D. Faris [2], and Steven S. Xu [2].

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Resistance to Stagonospora nodorum blotch (SNB) in hexaploid wheat (*Triticum aestivum* L.) is associated with insensitivity to host-selective toxins (HSTs) produced by the pathogen. In this research, we evaluated the association between HST insensitivity and SNB resistance in tetraploid wheat (*T. turgidum* L.). Two natural populations consisting of 172 wild emmer (*T. turgidum* subsp. *dicoccoides*) accessions and 206 cultivated tetraploid wheat accessions, including *T. turgidum* subsps. *carthlicum, polonicum*, *turgidum*, *dicoccum*, and *turanicum*, were inoculated with a mixture of three *S. nodorum* isolates and infiltrated with purified SnToxA and crude culture filtrate of isolate Sn2000KO6-1 (an isolate with a disrupted *ToxA* gene). The associations between SNB resistance and insensitivity to SnToxA and Sn2000KO6-1 were 43% and 30%, respectively. To further investigate the correlation between SNB resistance and insensitivity to specific HSTs, a doubled-haploid (DH) population consisting of 146 lines was developed from the cross between the SNB-susceptible durum cultivar Lebsock and the SNB-resistant *T. turgidum* subsp. *carthlicum* accession PI 94749. Genetic linkage maps constructed in this population spanned 2,036.7 cM and consisted of 283 markers that covered all 14 chromosomes. We inoculated the population with the *S. nodorum* isolates Sn2000 and LDNSn4 to evaluate the development of SNB. We also infiltrated the population with the purified HSTs SnToxA and SnTox3 and with crude culture filtrate from isolates LDNSn4 and Sn2000KO6-1 to evaluate reaction to the HSTs and identify the corresponding host genes conferring sensitivity. QTL analysis revealed that genomic regions on chromosome arms 2BS, 4BS, and 5BL governed resistance to isolate Sn2000, and loci on chromosome arms 2BS, 3AS, 5BS, and 5BL conferred resistance to isolate LDNSn4. The effects of the 5BS and 5BL QTL were due to the underlying toxin sensitivity loci *Snn3* and *Tsn1,* which confer sensitivity to the previously characterized toxins SnTox3 and SnToxA, respectively. No evidence for a host-toxin interaction associated with the 3AS QTL was found, but the effects of the 2BS and 4BS QTL were due to novel host-toxin interactions that have not been previously reported. Therefore, these results led to the identification of two new *S. nodorum* HSTs and their corresponding host sensitivity genes, and they demonstrate that these novel host-toxin interactions, along with previously characterized host-toxin interactions, play important roles in the development of SNB in this population. This research indicates that host-toxin interactions in the wheat-*S. nodorum* pathosystem are major disease conferring factors in tetraploid wheat, just as they are in hexaploid wheat.positional cloning of two host-sensitivity genes: *Tsn1* on 5BL and *Snn1* on 1BS. Toward the map-based cloning of *Tsn1* on chromosome 5B, we sequenced and assembled chromosome 5A and 5B BAC contigs spanning the gene. Evaluation of gene content and micro-colinearity between the orthologous regions of 5A, 5B, and rice chromosome 9 indicated the 5A region and rice share a higher level of micro-colinearity than the 5B region does with rice due to the presence of numerous transpositions, deletions, and rearrangements present in the wheat 5B region. In addition, the 5B *Tsn1* candidate region is nearly four times larger than the corresponding region of 5A due to the presence of additional genes and transposable elements. At least ten genes exist within the 350-kb *Tsn1* candidate-gene region, and they are currently being validated by comparative sequence analysis of *Tsn1*-disrupted mutants and virus-induced gene silencing. An important applied by-product of this research is the development of efficient PCR-based markers for *Tsn1*, which are being used to introgress SnToxA insensitivity into adapted germ plasm. Overall, this research demonstrates the potential of the wheat–*S. nodorum* pathosystem to be an excellent toxin-based inverse gene-for-gene model.

Comparative analysis of transcripts associated to all-stage resistance and adult-plant resistance to stripe rust in wheat.

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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is a destructive disease of wheat worldwide. Genetic resistance is the preferred method for controlling stripe rust, of which two major types are race-specific and race-nonspecific resistance. Race-specific resistance includes the qualitatively inherited all-stage resistance, controlled by single major resistance (*R*) genes. Conversely, adult-plant resistance is race nonspecific, inherited quantitatively, and durable. Previously, we characterized the gene-expression signatures involved in *Yr5*-controlled all-stage resistance and *Yr39*-controlled adult-plant resistance using the Affymetrix Wheat GeneChip. For this study, we designed and constructed custom oligonucleotide microarrays containing probes for the 116 and 207 transcripts that we had found important for the *Yr5* and *Yr39* resistance responses, respectively. We used this custom microarray to profile the resistance responses of eight wheat genotypes with all-stage resistance (*Yr1*, *Yr5*, *Yr7*, *Yr8*, *Yr9*, *Yr10*, *Yr15*, and *Yr17*) and five genotypes with adult-plant resistance (*Yr18*, *Yr29*, *Yr36*, *Yr39*, and the adult-plant resistance gene in the *Yr8* line). The aim of this analysis was to identify common and unique gene-expression signatures involved in the two types of resistance, which were used to infer information regarding the general pathways involved in all-stage resistance and adult-plant resistance.

Balance and dosage interdependence of homoeolog gene expression in polyploid wheat.

Jasdeep S. Mutti and Kulvinder S. Gill. Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA.

Gene duplication by polyploidy (homoeologues) or other means (paralogues) is a prominent feature of angiosperm evolution. We studied gene expression among three homoeologues of hexaploid wheat that evolved from a common progenitor about 3 million years ago (MYA) and came into a common nucleus at different times, ~0.5 and 0.01 MYA. Gene expression corresponding to each homoeologue was identified by sequence comparison of cultivar Chinese Spring ESTs, and the results were confirmed by SSCP analysis of RNA using nullisomic-tetrasomic lines. Of the 632 genes analyzed, 58% were expressed from all three homoeologues, 33% from two, and only 9% were expressed from one of the three homoeologues. The largest percentage of genes (14%) were expressed in the anthers and the least (7%) were expressed in pistils. The highest number of homoeologues/gene were expressed in the roots (1.72 out of three homoeologues), and the lowest number were expressed from the anthers (1.03 out of three homoeologues). In general, the proportion of expressed copies decreased with an increase in homoeologue copy number. The most significant observation was that homoeologues for 87% of the genes showed different expression patterns in different tissues and, thus, have likely evolved different gene expression controls. About 30% of the genes showed dosage dependence as the expression of homoeologues changed in response to changes in structural copy number.

QTL analysis of germination heat sensitivity in winter wheat.

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Winter wheat is usually planted in early September in the southern Great Plains to increase forage production for the purpose of cattle grazing. As a negative consequence of early planting, wheat seed may exhibit secondary dormancy under the hotter soil conditions typically encountered in early September. Poor emergence and stand establishment of extremely sensitive cultivars may result in significant forage yield reduction of about 50%. This phenomenon is termed germination heat sensitivity (GHS) or thermodormancy. Evaluation of breeding material is difficult because of unpredictable weather conditions at planting and the continuous decrease in heat sensitivity during seed storage. The environment of the maternal plant in which seed production occurs also may confound differences in GHS. In this study, 94 recombinant inbred lines (RILs) derived from two local cultivars, Intrada (HW) and Cimarron (HRW), were used to map QTL controlling GHS. Seed samples were collected in years 2006 and 2007 from both the field and greenhouse and stored at room temperature until the end of August. Germination rates were investigated in growth chambers at two temperature regimes, 35/27ºC day/night to test GHS, and constant 24ºC as control. At 24ºC, all RILs showed germination rates exceeding 90%, indicating that primary dormancy had been released at test time. Two major QTL were detected on chromosomes 3AS and 4AL. The locus *QGhs.osu-3A* was tightly linked with SSR marker BARC310, explaining 11–24% of the phenotypic variance. *QGhs.osu-4A* was located between *Xgwm637* and *Xwmc513*, accounting for 19–58% of the phenotypic variance. SNP marker BF474615 indicated that this locus was adjacent to the deletion bin 4AL13-0.59-0.66. There was significant epistatic interaction between the two QTL. Strong 'QTL × environment' interaction implied that the seed-storage condition and test time had large effects on expression of GHS. The coincidence of markers for GHS and preharvest sprouting tolerance suggested that they might share common points in their regulatory pathways, which might be reactivated by heat stress. In addition, phenotypic data and mapping results both confirmed that seed color had no association with GHS.

Association mapping of quantitative trait loci resistant to aluminum toxicity in U.S. winter wheat.

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Aluminum (Al) toxicity is a major constraint for wheat production in acid soils worldwide. To date, three QTL for Al resistance have been mapped through linkage mapping. To validate these mapped QTL and identify new QTL for Al resistance from U.S. wheat breeding lines, association mapping was conducted using 211 simple-sequence repeat (SSR) markers covering the 21 wheat chromosomes and 205 U.S. elite, winter wheat breeding lines, including 119 hard red winter wheat (HRWW), 21 hard white winter wheat (HWWW), and 65 soft red winter wheat (SRWW) from four U.S. wheat regional nurseries. On average, one SSR amplified 8.4 alleles across the 205 lines, ranging from 2 to 24. The 205 lines were divided into six subpopulations including four hard winter wheat (HWW) subpopulations and two soft winter wheat (SWW) subpopulations, on the basis of 1,770 alleles analyzed by the Structure2.0 software. Among the four HWW subpopulations, subpopulation 1, mainly from Oklahoma and Kansas, showed a higher level of Al tolerance than the other three subpopulations, with an average field score of 1.62 on a 0–5 scale. Two SWW subpopulations had a high level of Al tolerance with average field Al scores of 1.38 and 1.67. Genome-wide association analysis identified at least four significant regions that were associated with Al resistance, and three were reported previously by linkage mapping. Analysis of linkage disequilibrium indicated that markers in the 4DL major QTL region were closely linked and good markers for marker-assisted selection. Another major QTL on 3BL, identified from the Chinese landrace FSW in our lab, also showed a high association with Al tolerance ($P<0.01$) in U.S. winter wheat lines. A minor QTL in the 2AS region also was validated in the association analysis, but an additional QTL with a large effect on Al resistance was identified in the association mapping study. In addition to the three mapped QTL, a new locus on 2DL also displayed a significant effect on Al resistance. Markers identified in this study will be useful for marker-assisted selection in U.S. winter wheat breeding programs.

Structural and functional genomics: resources and uses related to quality.

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The applications of genomics to wheat quality are only now starting to be realized, and a review of current and projected future bioinformatics resources will include examples of contributions of genomics to understanding and improving wheat quality. Such examples will involve structural genomics to understand the chromosome organization of wheat quality loci, use of ESTs to gain structural and functional insights into gene structure and expression, uses and limitations of array platforms, and the development of markers for high-throughput mappings. Projections on the ongoing change in DNA sequencing capacity will be reviewed, along with issues related to data load, such as problems associated with single experiments producing gigabytes of data. How such data can be stored, accessed, analyzed, and useful information extracted will become increasing problematical.

Identifying quantitative end-use quality traits through marker-trait associations.

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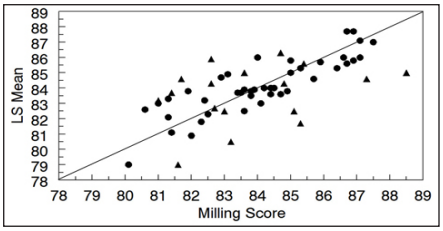
End-use quality traits (grain, milling, and baking) are generally expensive and difficult to measure. We are in the process of estimating phenotypic trait values for a wide range of Pacific Northwest wheat genotypes, including soft white spring, winter, and club; hard red winter and spring; and hard white winter and spring. Phase 2 of the research will attempt to associate molecular markers with quantitative variation in end-use quality phenotypes.

We currently have assembled four large data sets derived from a long-term (~10 years) study known as the 'G&E' (Genotype and Environment). The G&E study utilizes grain samples produced from the Washington State University Cereal Variety Testing Program, a multi-location replicated trial of advanced breeding lines and current cultivars. The G&E uses single-rep grain samples from 4–6 locations each year. Most lines and cultivars are included in the study for three years; long-term checks are included for the entire life of the program. The four nurseries are soft spring, soft winter, hard spring, and hard winter. For soft spring, the long-term checks are Alpowa and Zak and for soft white winter, they are Eltan, Madsen, Stephens, Hiller, and Rely. The soft spring data set is comprised of approximately 340 samples; the soft winter set has about 970 samples. The traits under study are grain yield, test weight, grain protein, NIR grain hardness, SKCS single kernel hardness, weight and size and their standard deviations, break flour yield, flour yield, milling score, flour ash, flour protein, Mixograph water absorption, flour SDS sedimentation volume, flour-swelling volume, rapid ViscoAnalyzer peak hot paste viscosity, cookie diameter, sponge cake volume, and polyphenol oxidase L-DOPA absorbance. Currently, the issue at hand is to determine what the best estimate is for each genotype's phenotype. The first two approaches involve i) simple calculations of arithmetic means and ii) calculation of least squares means. The latter has the advantage of accommodating year-to-year variation to adjust the marginal means. As an example, differences between means and LS means for milling score ranged from -2.0 to +1.1 (soft winter) and -3.3 to +3.6 (soft spring) and for cookie diameter -0.14 to +0.13 (soft winter) and -0.17 to +0.11 (soft spring) (see figure at right). Overall means for milling score for soft winter and spring wheats were 84.1 and 83.7, respectively. Cookie diameters of 9.37 and 9.47 cm diameter were obatined for soft winter and spring wheats, respectively.



Mapping phenotypic and gene expression QTL related to preharvest sprouting resistance in white winter wheat.

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The premature germination of seeds before harvest, known as preharvest sprouting (PHS), is a serious problem in all wheat growing regions of the world. In order to determine genetic control of PHS resistance in white winter wheat from the relatively uncharacterized United States germ plasm, a doubled-haploid population consisting of 209 lines from a cross between the PHS-resistant cultivar Cayuga and the PHS-susceptible cultivar Caledonia was used for composite interval QTL mapping (CIM) of the PHS trait and gene expression at physiological maturity. A total of 16 environments were used to detect 15 different PHS QTL including a major QTL, *QPhs.cnl-2B.1*, that was significant in all environments tested and explained from 5% to 31% of the trait variation in a given environment. Three other QTL, *QPhs.cnl-2D.1*, *QPhs.cnl-3D.1*, and *QPhs.cnl-6D.1*, were detected in six, four, and ten environments, respectively. Gene expression levels in mature embryo tissue were measured using a >17,000 feature, long-oligonucleotide microarray. Composite interval analysis revealed 2,729 eQTL from 1,700 genes distributed across the genome. Significant eQTL clusters were observed on several chromosomes. Of the 2,729 eQTL, 117 were found to overlap with the previously defined PHS QTL. The eQTL that overlapped with PHS QTL were tested for correlation with the PHS trait using the Pearson product moment correlation in R. Those genes with eQTL that collocated with PHS QTL and were significantly correlated with the PHS trait were considered good candidates for being involved in PHS and seed dormancy. This study provides valuable information for marker-assisted breeding for PHS resistance, future haplotyping studies, candidate gene analysis, and research into seed dormancy.

Poster 1. Molecular characterization of the chromosomal region harboring the Hessian fly resistance genes H32 and H26 in wheat.

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Hessian fly [*Mayetiola destructor* (Say)] is one of the most important insect pests that attack wheat. A total of 32 genes conditioning resistance to Hessian fly have been identified in wheat (*Triticum aestivum* L.) and its relatives. Two resistance genes, *H32* and *H26*, derived from *Ae. tauschii*, were mapped to the long arm of chromosome 3D and reside within the deletion bin 3DL3-0.81-1.00. The objective of this study was to determine the physical and genetic relationships between these two Hessian fly resistance genes. *H32* was previously mapped in the ITMI population and *H26* in an F_2 population. Fourteen, EST-derived, STS markers flanking the *H26* locus were assigned to the linkage map of *H32* in the ITMI population. Two of the STS markers, *Xrwgs10* and *Xrwgs11*, were found to flank the *H32* locus with a genetic distance of 0.5 cM on both sides. *Xrwgs10* is 3.2 cM distal to *H26* and *Xrwgs11* is 1.0 cM proximal to *H26* on the genetic map of *H26*. Another STS marker, *Xrwgs12*, which is 1.0 cM proximal to *H26*, co-segregated with *H32* in the ITMI population. Integrative analysis of these two genetic maps suggests that *H32* and *H26* are likely allelic or closely linked. STS markers closely linked to the Hessian fly gene (or genes) will be useful for marker-assisted selection in wheat germ plasm development and breeding.

Poster 2. Association analysis of soft wheat quality traits in eastern U.S. soft winter wheat.

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Soft wheat quality is highly heritable, controlled by multiple loci, and has been mapped in a number of bi-parental crosses. We expanded the mapping information determining soft wheat quality by using association analysis between genetic markers and quality phenotyping in 187 soft winter wheat cultivars from the eastern U.S. Quality samples were obtained from 2007 production environments in Ohio, Indiana, New York, and Virginia. Samples were milled at the USDA–ARS Soft Wheat Quality Laboratory, and flour was evaluated using the solvent retention capacity test (AACC Method 56-11) and the sugar snap cookie method (AACC Method 10-52). Results from the genetic marker analysis indentify a region of chromosome 2B associated with a complex set of milling traits, likely controlled at multiple, linked loci. These traits are best marked by the microsatellite primers, BARC98, GWM429, and BARC010. Genetic markers specific to the high-molecular-weight glutenin locus, *Glu1D*, identified the Dx5 allele associated with coarser flour texture. Association analysis for quality traits in this population should prove useful for identifying new markers for agronomically important traits.

Poster 3. Genome-wide identification of the quantitative trait loci associated with end-use quality of bread wheat grown under drought conditions.

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Improving the end-use quality of bread wheat is a major target for many breeding programs. The process can be accelerated by using molecular markers tightly linked to the genes controlling the end-use quality. This study was conducted to identify qualitative trait loci (QTL) related to grain quality (grain hardness, kernel weight, and kernel diameter), flour quality (flour protein content, flour yield, and flour paste viscosity), mixing quality (mixing peak time and height, mixing tolerance, and mixing absorption), and baking quality (SDS-sedimentation (SED)). A population of 180 recombinant inbred lines was generated from a cross between Rio Blanco, a hard white winter cultivar, and IDO444, a hard red winter wheat line. The two parents have same glutenin subunits on chromosomes 1A (2*) and 1D (5+10) but have different subunits on 1B (7+8 and 13+16), and a different GBSS locus on 4A. The end-use quality of each line was evaluated separately from seed samples harvested from two dryland locations, Rockland and Arbon in southern Idaho in 2006–07. A total of 438 marker loci were mapped on the 20 linkage groups, except chromosome 1D, with the total map length spanning 3,051 cM. Overall, 53 QTL (LOD > 2.5) with various significances were detected on 15 chromosomes, and 20 manifested in both locations. The most significant QTL associated with flour viscosity was identified and located on chromosome 4A and explained over 60% of phenotypic variation. Our results confirmed that end-use quality is a complex trait that was affected by various loci on multiple chromosomes. The novel QTL and tightly linked markers identified in this study provided very useful information for improving the end-use quality of bread wheat.

Poster 4. Differential gene expression in wheat under long-term, post-anthesis heat stress using microarray and real-time PCR techniques.

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Long-term, post-anthesis, high temperature stress is one of the major limiting factors for wheat production globally, including the southern Great Plains areas in U.S. The objectives of the research were to study the differential gene expression in heat-tolerant and heat-sensitive wheat lines at long-term, high temperature stress. The plants were grown in optimum conditions in a growth chamber. In the expression study, the plants were exposed to stress after flowering by gradually increasing the temperature from 20/15°C to 36/30°C day/night in 4 days with 80% relative humidity and 16/8 hours daylight to simulate natural conditions. Leaf tissue was collected from both heat-treated and control plants at 4, 7, and 10 days. The microarray gene expression study was performed by using an Affymetrix gene chip array at only the 4- and 7-day sampling dates. A total of 337 and 228 genes were up-regulated at day 4 and day 7, respectively. In tolerant lines, 41 genes were up-regulated at both dates, whereas in the sensitive lines, 917 and 1,045 genes were up-regulated at day 4 and day 7, respectively, with a common expression of 236 genes. The putative functions of the ESTs were predicted by BLASTX. The differentially expressed genes were broadly classified according to their function. In the tolerant lines, protein synthesis-, transcription factor-, cell wall synthesis-, signaling-, photosynthesis-, and oxyreductase genes were expressed higher under stress conditions. On the other hand, genes related to cell wall degradation, senescence, metabolism, and stress had higher expression in the heat-sensitive lines. The differential expression of 14 selected transcripts was studied by real-time PCR of tolerant and sensitive lines and their parents under stress and optimum conditions. Results from real-time PCR confirmed their differential expression. The differential expression of those genes may be attributed to genotypic variations in response to heat stress.

Poster 5. Single nucleotide polymorphism markers for Fusarium head blight resistance in wheat.

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Fusarium head blight (FHB) is a devastating disease in humid and semihumid wheat-growing regions of the world. The quantitative trait locus (QTL) on 3BS (*Fhb1*) of Sumai 3 and Ning 7840 has been identified to have the largest effect on FHB resistance. Simple-sequence repeat (SSR) markers flanking the *Fhb1* are identified. These SSR markers have been widely used for marker-assisted screening of *Fhb1*. However, the SSR markers flank a relatively large chromosome region of the QTL and more closely linked markers to the QTL may improve selection efficiency. The rich sources of wheat expressed-sequence tags (ESTs) and the abundance of single nucleotide polymorphism (SNP) markers makes SNPs ideal markers for fine mapping. We developed SNP markers based on wheat ESTs that mapped to the 3BS QTL region. A total of 15 SNPs were identified between Ning 7840 and Clark (FHB-susceptible) based on sequence analysis of three different ESTs. SNP primers were designed and the single-base extension method was used to analyze the SNPs in 125 'Ning 7840/Clark' recombinant inbred lines. Three SNP markers mapped between *Xgwm533* and *Xgwm493*. Two of them, *Xsnp-21-1* and *Xsnp–20-1a*, have higher coefficient of determination (R^2) than *Xgwm533* and should be good markers for marker-assisted selection of the *Fhb1* QTL in breeding programs.

Poster 6. Discovery and mapping of single-feature polymorphisms in wheat using Affymetrix arrays.

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Affymetrix arrays have been used to discover single feature polymorphisms (SFPs) in several crop species. To demonstrate the utility of the Affymetrix GeneChip® Wheat Genome Arrays in SFP discovery and mapping in wheat (*Triticum aestivum* L.), complimentary RNAs synthesized from mRNA isolated from seedlings of 71 F_{8-12} recombinant inbred lines (RILs) from the cross 'Ning 7840/Clark' were hybridized to the Affymetrix array. SFP prediction on the array data followed the method of Kirst et al. A total of 955 SFPs were selected and combined with simple-sequence repeat (SSR) data for mapping. A high-density, genetic map consisting of 923 SFPs and 269 SSR markers and covering a genetic distance of 1,944 cM was constructed with 877 SFPs assigned to 21 chromosomes. The SFPs were distributed randomly within a chromosome and effectively filled gaps between SSRs but were unevenly distributed among the different genomes. The B genome had the most SFPs and the D genome the least. Map positions of a selected set of SFPs were validated by SNaPshot analysis and comparison with previous EST physical mapping data. Results indicate that the Affymetrix array is a cost-effective platform for SFP discovery and mapping using RILs. The new map will be an important source of markers for detecting quantitative trait loci and high-resolution mapping.

Poster 7. New wheat data in GrainGenes.

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Several wheat maps have been added to GrainGenes this year. A durum map, 'Kofa/UC1113', containing SSR and SNP markers, was submitted from the Wheat CAP project. A dozen more maps from this project are expected in the next year. Another tetraploid map, 'Langdon/*T. turgidum* subsp. *dicoccoides* G18-16', containing SSR and DArT markers, was obtained from Peleg et al. (Tzion Fahima). A bread wheat map, 'Nanda 2419/Wangshuibai', was obtained from Zhengqiang Ma; in addition to the MAG markers (expressed STSs and SSRs) that were placed on this map, data on a total of 2,500 MAG markers was added to the database.

The NSF-sponsored, D-genome, physical mapping project has anchored many BACs to genetically mapped markers. Now, several GrainGenes maps display the positions of these BACs relative to loci on chromosomes 1–7D, which is the beginning of an integrated physical/genetic map for wheat.

Poster 8. Saturation mapping of scab resistance QTL in Ernie and application to marker-assisted breeding.

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Fusarium head blight (FHB) is caused mainly by *Fusarium graminearum* in wheat and results in significant yield and quality losses in humid and warm areas of the world. QTL for scab resistance have been mapped in exotic and native sources. However, only a few QTL have been widely deployed in breeding programs using marker-assisted selection due to the lack of diagnostic and tightly linked markers for most QTL. Four major QTL for type-II resistance were previously mapped on chromosomes 5A, 4B, 3BS, and 2B of Ernie. A set of 243 'Ernie/MO94-317' RILs were evaluated in inoculated, mist-irrigated, scab nurseries at Columbia, MO, and Blacksburg, VA. The 4B QTL region was associated with field FHB severity (R^2=4.2%), index (R^2=4.4%), kernel quality assessed as 100-grain weight (R^2=8.0%), and Fusarium-damaged kernels (FDK, R^2=6.2%). The awn-inhibitor gene B_1 is associated with field FHB incidence (R^2=4.5%) and index (R^2=5.3%) in the Virginia test and with FHB severity (R^2=4.2%) in the Missouri test. Another QTL associated with 100-grain weight is on chromosome 2DS (R^2=12.4%). One minor QTL for FDK (R^2=4.3%) on chromosome 5A is separate from the major QTL for type-II resistance and the B_1 gene. Tightly linked markers are being used for marker-assisted selection in breeding populations for the four QTL in Ernie and the two major QTL on chromosomes 3BS and 6B of Sumai 3, which will facilitate the pyramiding of various QTL for FHB resistance using marker-assisted selection in cultivar development. This material is based upon work supported by the U.S. Department of Agriculture under Agreement No. 59-0790-4-102. This is a coöperative project with the U.S. Wheat & Barley Scab Initiative.

Poster 9. Map-based cloning of the fungal toxin sensitivity gene Tsn1 in wheat.

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The wheat *Tsn1* gene on wheat chromosome arm 5BL confers sensitivity to the host-selective proteinaceous toxins Ptr ToxA and SnToxA produced by the pathogenic fungi *Pyrenophora tritici-repentis* and *Stagonospora nodorum*, respectively. Compatible *Tsn1*-ToxA interactions lead to extensive cell death and disease susceptibility. We employed a map-based strategy combined with haplotype analysis of natural populations to delineate the *Tsn1* candidate region to a 120-kb segment containing five genes. Comparative sequence analysis of multiple independent EMS-induced ToxA-insensitive mutants revealed that *Tsn1* is a member of the NBS-LRR class of disease resistance genes but, in this case, it confers susceptibility. Evaluation of the level of microcolinearity between the orthologous regions of wheat chromosomes 5A and 5B, *Brachypodium*, and rice indicated that the 5A region, *Brachypodium*, and rice share a higher level of microcolinearity than the 5B region does due to the presence of numerous transpositions, deletions, and rearrangements present in the wheat 5B region. *Tsn1* lies on a 100-kb, chromosome 5B-specific insertion that is specific to ToxA-sensitive genotypes. Homoeoalleles of *Tsn1* do not exist on chromosomes 5A and 5D, and recessive *tsn1* alleles are rare because ToxA-insensitivity is usually conferred by the null allele on 5B. Phylogenetic analysis indicated that *Tsn1* is related to other NBS-LRR proteins encoded by toxin sensitivity genes and several rust resistance genes from other grasses. The isolation of *Tsn1* will allow us to decipher the molecular interactions and mechanisms associated with the wheat-*P. tritici-repentis* and wheat-*S. nodorum* pathosystems.

Poster 10. BIBAC library and physical map construction of the Puccinia triticina pathotype PRTUS3.

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Leaf rust is the most common and one of the most important cereal diseases of the world. Current leaf rust control has consisted of breeding for resistant cultivars by identifying Lr genes in the host. These cultivars quickly become susceptible to infection due to the tremendous extant genetic diversity of the pathogen that allows it to overcome resistant cultivars in 2–4 years. Development of alternate methods of control are limited, because little is known about the *Puccinia* genome and plant-pathogen interaction. Construction of a genome-wide physical map is important in order to fully understand the infection mechanism of the pathogen and its interaction with the host. In an effort to discover more about the genetic potential of leaf rust in terms of AVR and VIR gene regulation and create novel plant resistance breeding strategies in the future, we have proposed to study the pathogen's genome by constructing a BIBAC library and a physical map of the pathogen. The BIBAC library is being constructed from pathotype PRTUS 3, which has AVR-1 disrupted using T-DNA mutagenesis via particle bombardment. The characterization of the AVR-1 in the BIBAC library will serve as a point of reference for cloning heterologous AVR and VIR genes, and defining their regulation and mode of inheritance and recombination.

Poster 11. Defining the pleiotropic nature of heat-tolerance QTL controlling end-use quality and yield stability during reproductive-stage heat stress in wheat (Triticum aestivum).

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High temperature during reproductive development is a major factor limiting wheat production and end-use quality in the southern Great Plains and in many other environments worldwide. We have initiated a project to integrate genotypic (QTL), multiple phenotypic, and transcript level data to identify genes controlling reproductive-stage heat tolerance in wheat. Heat tolerance is defined here as the maintenance of yield and end-use quality during reproductive-stage heat stress. Efforts have initially focused on building recombinant inbred lines (RILs), collecting RIL morphological and yield response data from field and controlled environment studies, and mapping QTL linked to reproductive-stage heat tolerance. Our mapping has, to date, focused particularly on yield maintenance QTL. Given the importance and known sensitivity to heat stress, QTL associated with end-use quality maintenance were mapped in correlation with yield maintenance QTL to determine the collective pleiotropic effects of heat-tolerance QTL. Mapping of end-use quality QTL was done by SDS sedimentation of grain from each RIL harvested in both growth chamber- and field-imposed heat stress experiments. The hard white spring wheat Halberd was used as the source of heat tolerance. Two populations were used; one consisted of 64 F_6 'Halberd/Cutter' and the other a population of 120 'Halberd/Karl 92' F_6 RILs. Each population was grown under both heat stress and control conditions in the field and greenhouse. Heat stress in the greenhouse was applied by a 3-day treatment of 38°C applied 10 days after pollination. Quality results were analyzed for their relation to mapped yield-maintenance, heat-tolerance QTL. The resulting map will allow us to determine whether grain quality traits and yield-maintenance QTL segregate together or independently from heat-tolerance QTL. An improved understanding of the correlation between end-use quality and yield-stability QTL (heat tolerance) during reproductive-stage heat stress will aid in breeding plants possessing both attributes using marker-assisted selection and in basic research aimed at defining the molecular basis of heat tolerance.

Poster 12. Molecular detection of QTL associated with adult-plant resistance to powdery mildew in two soft red winter wheat populations.

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The soft red winter wheat cultivars Massey and USG3209 contain adult-plant resistance (APR) to powdery mildew (PM), which is caused by the fungual pathogen *Blumeria graminis* f. sp. *tritici*. Quantitative trait loci (QTL) analyses were completed using composite interval mapping on two different recombinant inbred line populations, 'Becker/Massey' (B/M) and 'USG3209/Jaypee' (U/J). Genotypic data were collected using 589 diversity-arrary technology (DArT) markers and 10 microsatellite markers on 152 individuals from the B/M population and 363 DArT markers, three single-nucleotide polymorphism, and 225 microsatellite markers on 130 individuals from the U/J population. Powdery mildew phenotypic data were collected in 16 environments for the U/J population and in four environments for the B/M population. Significant QTL conferring APR to PM were identified on chromosomes 2A, 2B, and 1B in both populations. Additional data including yield, leaf rust resistance, milling and baking quality, height, and heading date have been collected on the U/J population for use in the Wheat CAP project. Several significant QTL have been identified for these additional traits in the U/J population. Updated genetic linkage maps from both populations have been produced.

Poster 13. Moving Bdv2, conferring resistance to yellow dwarf disease, from chromosome 7D to chromosome 7A or 7B in wheat.

Kristen Rinehart [1], Herb Ohm [1], and Joe Anderson [1, 2].

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Yellow dwarf (YD) disease caused by the luteoviruses BYDV and CYDV is one of the most prevalent and devastating viral diseases affecting wheat yields. The viruses are transmitted to wheat plants by aphids (*Rhopalosiphum padi*). Partial resistance to YD occurs in wheat (*Triticum aestivum* L.). The highly effective resistance genes *Bdv2* and *Bdv3* have been transferred to wheat from a related grass species, *Thinopyrum intermedium*. *Bdv2*, from chromosome 7ST, and *Bdv3*, from chromosome 7E, were, respectively, introgressed into wheat on a chromosome segment that replaced the distal half of chromosome arm 7DL. In order to combine *Bdv2* and *Bdv3* in wheat, one of the two genes must be moved to another homoeologous chromosome, 7A or 7B. The objective of this research is to move *Bdv2* to chromosome 7A or 7B in wheat. A wheat line containing *Bdv2* was crossed with the Chinese Spring lines N7D–T7A and N7D–T7B. The resulting F_1 plants were then crossed with the Chinese Spring *Ph1b* deletion line to encourage homoeologous chromosome pairing between T7DS·7DL-7ST and 7A or between T7DS·7DL-7ST and 7B. F_2 plants identified by DNA marker genotyping as homozygous for the *Ph1b* deletion and heterozygous for *Bdv2* were harvested. The F_3 seedlings were exposed to viruliferous *R. padi* aphids, and an ELISA test was performed to determine the virus titer. Plants with low virus titer are being screened with markers associated with *Bdv2* and markers mapped to chromosome 7AL or 7BL. Plants in which *Bdv2* is present and markers on 7AL or 7BL are absent are likely recombinants in which *Bdv2* was moved to 7A or 7B.

Poster 14. QTL validation for agronomic traits on chromosome 3A of hexaploid wheat using recombinant-inbred chromosome lines.

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A study of chromosome substitution lines between two hard red winter wheat cultivars Wichita (WI) and Cheyenne (CNN), showed that chromosome 3A from WI increased grain yield by 15 to 20% when placed in the CNN background, whereas the reciprocal substitution line with CNN chromosome 3A in a WI background decreased grain yield by 15 to 20%. Follow-up research was conducted to determine the trait variation caused by chromosome 3A by creating 98 recombinant inbred chromosome lines (RICLs) in the Cheyenne background where the RICLs involved chromosome 3A of both cultivars. In the CNN(RICL3A) population, QTL were detected for seven of the eight agronomic traits studied. A major, grain yield QTL detected in the combined analysis explained 28% of the phenotypic variance, and the substitution of the WI allele for a CNN allele increased grain yield by 66 kg/ha. The WI(RICL3A) population (the RICLs involve WI and CNN chromosome 3A in WI background) were used to validate the QTL detected in the CNN(RICL3A). Effectively, WI(RICL3A) are the mirror population to the previously studied CNN(RICL3A). The objectives of this study were to (1) identify and map QTL for eight agronomic traits on chromosome 3A in individual environments and combined across environments, (2) evaluate 'QTL x environment' interaction (QEI) by comparing the consistency of QTL detected in individual environments and, (3) compare the QTL detected in this study to those obtained in the CNN(RICL3A). A population of 90 WI(RICLs3A), developed through a doubled-haploid (DH) system from a cross between WI and chromosome substitution line WI(CNN3A), were used to investigate the QTL for grain yield and its components traits and were planted in Lincoln, Mead, and North Platte, NE, during the 2007–08 cropping season. QTL were detected for anthesis date, plant height, grain yield, grain volume weight, and 1,000-kernel weight. A grain yield QTL detected at Lincoln and in the combined analysis explained 17% of the phenotypic variance, and the substitution of a CNN allele for a WI allele decreased grain yield by 118 kg/ha. This grain yield QTL was the major grain yield QTL detected in the CNN(RICL3A) population and was at a similar position. In addition to grain yield, grain volume weight and 1,000-kernel weight QTL were detected in the combined analysis that explained 38% and 14% of the phenotypic variance, respectively. The first year results of this study indicated the possibility of detecting most of the major chromosome 3A QTL reported in the previous CNN(RICL3A) studies using a different background. The WI 3A alleles in a previous CNN(RICL3A) study showed an increased in grain yield and yield components traits and, as expected, the CNN 3A alleles in the this WI(RICL3A) study has a decreased effect on grain yield and yield components traits. The unique opportunity of using chromosome substitution lines provides a chance for examining the effects of QTL on a single chromosome. The use of RICLs from a reciprocal substitution also will avoid the limitation of a one-way chromosome substitution in determining the interactions between chromosomes.

Poster 15. Wheat lectins: A key defense strategy against Hessian fly attack.

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The Hessian fly [*Mayetiola destructor* (Say)] is one of the most destructive pests of wheat (*Triticum aestivum* L.) worldwide. The wheat–Hessian fly interaction operates in a gene-for-gene manner and can be classified as exhibiting incompatible (resistant plant) or compatible (susceptible plant) interactions. Virulent larvae cause stunting and yield loss in susceptible plants, whereas avirulent larvae die within a few days of the infestation. The resistant plants show little sign of stress or yield loss, suggesting an energy-efficient active defense at the molecular and physiological levels. To unravel the molecular mechanisms operating during compatible and incompatible interactions, we employed a transcriptomics approach utilizing various tools such as differential display, Curagen Gene-Calling, and the Affymetrix GeneChip Wheat genome array to identify unique and novel genes that are differentially expressed in these interactions. Our studies revealed the accumulation of transcripts belonging to a prominent class of genes encoding lectins in the resistant plants. Plant lectins, also referred to as agglutinins, are a heterogenous group of proteins that are able to reversibly bind simple sugars and/or complex carbohydrates and have been implicated in defense against pests and pathogens. The lectins identified in the wheat plants could be grouped into several categories such as the jacalin-related lectins (*Hfr-1*, *Wci-1*, Horcolin), chitin-binding lectins (*Hfr-3*, WGA), and others. Quantitative, real-time PCR studies indicated a strong accumulation of transcripts of some lectin genes in the resistant plants and positively correlated with increased protein levels as assessed by immunodetection. Further functional characterization of one of the lectins, HFR-1, revealed its antifeedant and insecticidal properties leading to detrimental effects on related dipteran larvae. Hessian fly larval behavioral studies showed that avirulent Hessian fly larvae on resistant plants exhibited prolonged searching and writhing behaviors as they unsuccessfully attempted to establish feeding sites. The rapid accumulation of HFR-1 and other lectins indicates an early defense response to Hessian fly larval attack and correlates well with the behavior of the avirulent larvae on the wheat plants. The predominant mode of action seems to be contributing to conditions that starve the avirulent larvae, leading to antibiosis. Our results open up potential applications in engineering transgenic wheat plant lines over-expressing lectins that will confer resistance against this and other devastating insect pests.

Poster 16. Lesion mimic associates with adult-plant resistance to leaf rust in wheat.

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Lesion mimic (LM) symptoms that resemble plant disease symptoms in the absence of pathogen infection may confer enhanced disease resistance to a wide range of pathogens. Wheat line Ning7840 shows LM symptoms at heading that resemble flecking symptoms of initial leaf rust infection and adult-plant resistance (APR) to leaf rust. The gene responsible for LM, designated as *lm*, was a recessive gene from a natural mutation and was located on the proximal region of chromosome 1BL within deletion bin C1BL6-0.32 using a population of 179 recombinant inbred lines (RIL) derived from the cross 'Ning7840/Chokwang'. Ning7840 has the short arm of chromosome 1R from the rye T1B°·1R translocation, therefore, carries *Lr26*. To identify the gene for APR to leaf rust and understand the relationship between *lm* and APR, the RIL population was infected with the isolate PRTUS55, an isolate virulent to *Lr26*, at anthesis in greenhouse experiments. The result showed that *lm* was associated with APR to rust, and the lines with the LM phenotype had a significantly higher level of resistance than those non-LM lines across all experiments. Composite interval mapping consistently detected a QTL, *Qlr.pser.1B,* for APR on chromosome 1BL. *Qlr.pser.1B* co-segregated with *lm* and explained 61.0% of phenotypic variation for leaf rust resistance in two greenhouse experiments. An additional QTL was detected on chromosome 7DS and coincided with the marker for an APR gene *Lr34* (csLV-Lr34). A significant interaction was observed between *lm* and *Lr34*. A combination of the two genes significantly reduced both rust area and infection type. The gene *lm* may have pleiotropic effect on APR by limiting the growth and development of fungi in wheat leaf tissue.

Poster 17. Molecular mapping of the stem rust resistance gene Sr6 on chromosome 2DS in wheat.

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The stem rust resistance gene *Sr6* confers a high level of resistance against a wide range of stem rust races in North America. The expression of *Sr6* resistance is influenced by temperature, light intensity, and genetic background of the recipient genotype. Here, we report the identification of molecular markers linked to *Sr6* on the short arm of chromosome 2D in two mapping populations. One population of 136 F_2s and their $F_{2:3}$ families from the cross 'Chinese Spring/ISr6-Ra' and 140 recombinant-inbred lines from the cross 'MN98550/MN99394' were screened for stem rust reaction in the seedling stage. In both populations, resistance to stem rust was conferred by a single gene that was postulated to be *Sr6* based on parental reaction to *Puccinia graminis* f. sp. *tritici* races. In the Chinese Spring population, a bulked segregant analysis was used to screen 418 SSR markers that covered the entire genome of wheat. Four markers, *Xwmc453*, *Xcfd43*, *Xcfd77*, and *Xgwm484*, were mapped within a chromosome region that spanned 9.7 cM. The closest markers, *Xwmc453* and *Xcfd43,* were linked to *Sr6* at distances of 1.1 cM and 1.5 cM, respectively. In the 'MN99394/MN98550' population, these four markers spanned 6.4 cM, and the closest markers, *Xcfd43* and *Xwmc453*, were 1.3 cM and 1.7 cM away from *Sr6*, respectively. The closest markers identified in both populations proved to be useful for marker-assisted selection of *Sr6*.

Poster 18. Leaf epicuticular wax improves heat tolerance in wheat.

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[1] Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843, USA and [2] Institute of General and Physical Chemistry, Belgrade, Serbia.

We are investigating the role of leaf epicuticular wax as a heat-avoidance mechanism in wheat. Higher epicuticular wax deposition in the leaf increases reflectance and may help to reduce leaf temperature, stomatal conductance, and improve water-use efficiency. Thirteen adapted cultivars of wheat were grown in the greenhouse. The wheat lines were subjected to a heat treatment under well-watered conditions at 10 DAP for 2 days at 38°C/20°C day/night temperatures. Leaf reflectance was measured with a Unispec spectral analysis system and leaf epicuticular wax was quantified at 10 DAP, 12 DAP, and 15 DAP. Leaf temperatures and stomatal conductance were recorded at midday during the heat treatment. Yield data from the wheat cultivars also were recorded. Statistical analyses indicate that the leaf epicuticular wax content is correlated significantly to improved temperature depression, reduced stomatal conductance, and yield stability parameters. Although some cultivars increase wax deposition and reflectance during heat treatment, no statistically significant increase in reflectance was observed nor were the two traits correlated. Continued statistical analysis may resolve this issue. Although stomatal conductance was negatively correlated with epicuticular wax content, like wax, it too also is positively correlated with temperature. From the correlation studies conducted so far, we may conclude that leaf epicuticular waxes may play a more efficient role in reducing leaf temperatures and improving heat tolerance in terms of yield stability in wheat, as apposed to increasing stomatal conductance and water loss. On going studies will identify QTL regulating leaf epicuticular wax accumulation in wheat and integrate this map with ongoing mapping studies that are defining QTL regulating reproductive-stage heat tolerance in terms of yield and end-use quality stability.

Poster 19. A point mutation demonstrating the pleiotropic effects of the domestication gene Q in hexaploid wheat.

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The *Q* gene is a major domestication gene in wheat because it confers the free-threshing character and pleiotropically influences many other domestication-related traits. The *Q* gene has been isolated and identified as a member of the APETALA2 (AP2) family of transcription factors. In this study, we created an ethyl methanesulfonate (EMS)-induced, *Q*-disrupted mutant in the *Triticum aestivum* subsp. *aestivum* cultivar Bobwhite (BW) to evaluate the function and pleiotropic effects of *Q*. Sequence analysis of the mutant revealed a point mutation within the first AP2 domain of the coding region. Relative quantitative (RQ)-PCR analysis indicated the level of *Q* transcription in the mutant was significantly reduced compared to the wild type. Comparison of wild-type BW and the mutant indicated that *Q* influences plant height, spike-emergence time, spike shape, rachis disarticulation, glume toughness, and threshability, which was consistent with previous reports. In addition, the *Q*-disrupted mutant also had fewer tillers and spikelets, which resulted in decreased yield compared to wild-type BW. Cell morphology observations of the rachis and glumes revealed major differences in cell shape, arrangement and density, and abscission zone formation between the mutant and the wild type, which provides explanations for the underlying biological differences in glume architecture and threshability. These results indicated that the mutation that gave rise to the *Q* gene not only allowed for the domestication of wheat, which contributed substantially to the rise of modern civilization, but it also contributed to increased yield and agronomic performance, further substantiating *Q* as a 'super' gene.

ITEMS FROM ARGENTINA

CORDOBA NATIONAL UNIVERSITY
College of Agriculture, P.O. Box 509, 5000 Córdoba, Argentina.

Application of exogenous hormones in wheat.

R.H. Maich, F. Ripoll, H. Sosa, and M.J. Tello.

This study measured the effect of foliar applications (exogenous) of hormones and/or hormonal cofactors on yield and its components in rain-fed, cultivated wheat. Univariate statistical analysis (ANOVA) showed no significant differences between treatments for any of the characters analyzed. Treatment with cytokinins, gibberellins, and indole butyric acid (5) differed from the other treatments, including the control test (1; Fig. 1).

The antagonism between cytokinins and ABA in maintaining open, or closed, stomata in order to facilitate gas exchange was apparently attenuated with the application of exogenous cytokinins, gibberellic, and indole butyric acids. However, the higher biomass production achieved and number of seed did not make a difference in terms of yield. The severe water stress before and during grain filling generated a reduced movement of resources and diminishing dry matter partitioning (lower harvest index and seed weight).

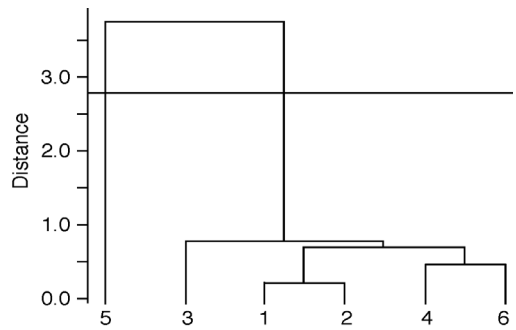

Fig. 1. Dendrogram of treatments; 1, control; 2, antioxidant; 3, micronutrients (B, Mo, and Co); 4, micronutrients (B, Cu, Mo, and Zn); 5, cytokinins, gibberellins, and indole butyric acid; 6, cytokinins.

Maintaining grain yield potential with higher stubble production in rain-fed wheat.

G.A. Piacenza and R.H. Maich.

This study compared stubble and grain production of commercial and experimental lines of bread wheat cultivated under rain-fed conditions. The differents genotypes were grouped according to phenology. Three trials were performed using completely randomized experimental designs. The material was sown under notill practices at three sowing dates in May 2008. At flowering, genotypes with longer biological cycles showed a water deficit of 84%, intermediate types were at 74%, and shorter types 75%. Grain yield fluctuated between 1.6 ton/ha and 2.9 ton/ha. Both commercial and experimental lines were situated in the top of the ranking for grain production. However, taking into account stubble production, the experimental lines performed better than the commercial wheats. Plant breeding conducted under rain-fed conditions in the central, semiarid region of Argentina generated new genotypes with grain yield similar to that of most cultivars, but with a stubble production around one to two tons more. Taking into account the limited water resources of the region and in order to reduce evaporation and increase efective precipitation, these new genotypes make a more sustainable system than the wheat–soybean rotation.

ITEMS FROM BRAZIL

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

Wheat in Brazil – 2008 crop year.

Eduardo Caierão.

In the 2008 crop year, Brazilian wheat production was about 6 x 10^6 tons (Conab 2009), which is enough to supply only 50% of the domestic demand. This deficit in production makes Brazil one of the world's largest wheat importers. The south region, comprised of the states of Rio Grande do Sul, Santa Catarina, and Paraná, accounts for 95% of the national production. Nonetheless, due to the characteristics of the cultivation system utilized, average grain yield is not the highest in the country. The best figures are observed in the southeast region, where some irrigated areas bring the average up (Table 1).

Table 1. Cultivated area, total production, and grain yield of wheat in Brazil in 2008 (Source: CONAB 2009).

Region	Area (ha x 1,000)	Production (t x 1,000)	Grain yield (kg/ha)
North	—	—	—
Northeast	—	—	—
Central-west	68.2	167.0	2,449.0
Southeast	100.0	265.1	2,654.0
South	2,256.0	5,598.1	2,482.0
Brazil	**2,424.1**	**6,030.8**	**2,488.0**

In 2008, the area planted to wheat was 31% larger than that of the previous crop year. Furthermore, total production and average grain yield/hectare achieved in 2008 were 47% and 12% larger than those of 2007, respectively.

In 2009, the wheat supply in Brazil will be turbulent. The 2008 year crop in Argentina, on which Brazil is highly dependant, had significant losses due to drought, which caused a reduction of about 8 x 10^6 tons in total production. Thus, supply in Brazil will probably not be enough to satisfy the demand, and Brazilian mills might have to procure wheat in the American and European markets.

Reference.

CONAB. 2009. Companhia Nacional de Abastecimento. Central de Informações Agropecuárias/Grãos/Trigo. Disponível em: http://www.conab.gov.br/conabweb/index.php?PAG=131.

Qualitative evolution of Brazilian wheat.

Eduardo Caierão, Pedro Luiz Scheeren, and Márcio Sóe Silva.

The quality profile of Brazilian wheat varies according to the region where it is produced. The southern region is characterized by the cultivation of soft wheat cultivars, and the south-central and central regions are marked by the production of bread wheat. Although this trend is kept in the quality profile of newly released wheat cultivars, the number of cultivars and the magnitude of gluten strength have increased substantially, regardless of cultivation region.

This qualitative evolution has been achieved thanks to research efforts, especially in the genetic improvement field, which is responsible for the triumph over severe biotic and abiotic stresses. In southern Brazil, for example, the greatest obstacle is the high rainfall during harvest months, which favors preharvest sprouting, leaf rust, and Fusarium head blight. In the south-central and central regions, excessive heat, water deficiency, and wheat blast (*Pyricularia grisea*) are the main limiting factors.

For sake of illustration of the challenges that must be overcome by wheat improvement programs in southern Brazil, the Canadian consultant Samborski, during a visit to EMBRAPA in the 1970s said that in Rio Grande do Sul State

"wheat is grown against God's will". In this report, three surveys that represent the evolution in the quality profile of Brazilian wheat for gluten strength will be presented.

Survey 1. In 2008, the J. Macêdo Mill, through its consultant Reino Pecala Rae, published the profile of gluten strength (W) for the six most planted cultivars in the state of Paraná in 1998–99 and 2004–06. In the 1998–99 period, the six most planted cultivars represented 75.3% of the total cultivated area and had a weighted mean W value of 293 × 10^{-4}J. In the 2004–06 period, another six cultivars took 76.6% of the area and the weighted mean of gluten strength was 343 × 10^{-4}J (Table 2). The absolute difference in W between assessment periods was 50 points.

Table 2. Gluten strength of the six most cultivated cultivars in Paraná State in 1998–99 and 2004–06 (% = cultivated area; W = gluten strength; Source: J. Macêdo Mill, 2008).

1998–99			2004–06		
Cultivar	**%**	**W**	**Cultivar**	**%**	**W**
OR 1	19.1	280	CD104	30.0	364
Iapar 53	15.8	306	BRS 208	16.5	275
BR 18	14.2	324	BRX 220	16.0	340
Ocepar 16	10.4	266	IPR 85	6.5	365
Ocepar 22	9.8	271	CD 111	4.6	500
Ocepar 21	6.0	309	Supera	3.0	234
Total	75.3	293	Total	76.6	343

Survey 2. Apassul is the Seed Producers Association of the Rio Grande do Sul state and publishes yearly the percentage of wheat available for planting according to the certification and inspection system. In a survey for the 2003–07 period, the percent area planted to cultivars with gluten strength below 180 × 10^{-4}J dropped consistently, reaching 45% in 2007. On the other hand, the percentage of available seed with gluten strength above 180 × 10^{-4}J has increased, reaching 55% in 2007 (Fig. 1).

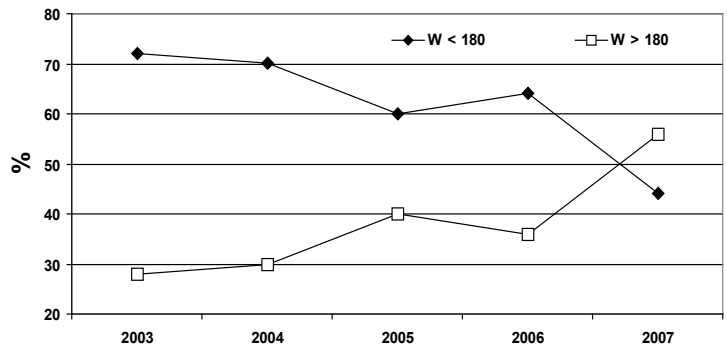

Fig. 1. Evolution of the percent seed availability for the 10 most planted wheat cultivars in crop years 2003 through 2007 in Rio Grande do Sul state of Brazil according to Gluten Strength (W × 10^{-4}J). Source: Apassul, 2008.

Although these data are not scientific, the results observed are at commercial scale and indicate a trend in the qualitative evolution of wheat in the state of Rio Grande do Sul, which is usually considered to be of too low quality for bread. The continuous effort by Embrapa towards wheat improvement, together with the support of other public and private institutions such as Fundacep, OR Seeds, Fepagro, and Coodetec, have contributed to the establishment of this panorama. However, if this trend is lined up with the domestic demand (70% bread wheat, strong gluten and 30% soft wheat, weak gluten), the availability of weak wheat, suitable for biscuit production, probably will soon become limited. Considering this situation, Embrapa has kept a partnership with some biscuit companies, anticipating possible gaps in the supply of weak wheat with homogeneity and identity.

Survey 3. The third survey was performed by the J. Macêdo Mill in 1998–99 and 2004–06. In this study, the gluten strength of samples received by the mill from Brazil's Rio Grande do Sul and Paraná states and Argentina were assessed. While the percentage of samples with gluten strength above 250 × 10^{-4} J increased for wheats of Brazilian origin (from 0 to 10% in Rio Grande do Sul and from 53 to 57% in Paraná, they decreased for wheats of Argentinian origin (from 69 to 31%; Fig. 2, p. 44).

The percentage of samples with gluten strength below 200 × 10^{-4}J also attests to the qualitative evolution towards stronger wheats in Brazil. In Rio Grand do Sul, the percentage dropped from 95% to 71% and, in Paraná, from 18% to 8%. In Argentina, the percentage of soft wheats increased from 4% to 33%. This decrease in the number of strong wheat samples received by the J. Macêdo Mill is due to the introduction of Baguette wheat, featuring high grain yield potential with lower gluten strength, in Argentina.

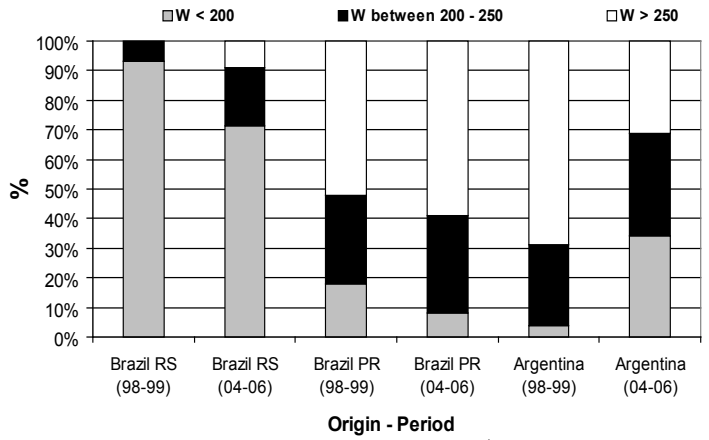

Fig. 2. Evolution of gluten strength (W × 10^{-4}J) in samples received by the J. Macêdo Mill in Brazil, coming from Argentina and Brazil (Rio Grande du Sul (RS) and Paraná (PR) States) in 1998–99 and 2004–06 (Source: J. Macêdo Mill, 2007).

The quality of Brazilian wheat has significantly increased in the last few years. Nevertheless, cultivar mixtures and the varying features of Brazilian wheats is still a challenge that should be overcome in order to increase the value of this cereal.

Embrapa's share in the Brazilian wheat seed market (2000–08).

Eduardo Caierão, Márcio Sóe Silva, and Pedro Luiz Scheeren.

Since its founding in the mid-1970s, Embrapa has worked on wheat genetic improvement, aiming at developing more and more productive cultivars with better tolerance/resistance to biotic and abiotic stresses, aligned with the quality profile demanded by industry and consumers. In almost 40 years of existence, more than 100 cultivars have been made available to farmers, many of which have had a remarkable importance in the recent history of the Brazilian wheat crop and were the most grown cultivars in their time. For example, in the state of Rio Grande do Sul, the most grown cultivars were CNT 10 (1982), CNT 8 (1985–87), Wheat BR 23 (1990–94), Embrapa 16 (1995–98), BRS 49 (2000), and BRS 179 (2002–03). The genealogy of the cultivars released during these years that became market leaders is described in Table 3.

Table 3. The genealogy of Embrapa cultivars that became market leaders in the Brazilian state of Rio Grande do Sul.

Cultivar	Year	Pedigree
CNT 10	1982	IAS 46/IAS 49//IAS 46/Tokai 66
CNT 8	1985–87	IAS 20/ND 81
Wheat BR 23*	1990–94	Corre Caminos/Alondra Sib/3/IAS 54-20/Cotiporã//CNT 8
Embrapa 16	1995–98	Hulha Negra/CNT 7//Amigo/CNT 7
BRS 49	2000	BR 35/PF 83619//PF 858/PF 8550
BRS 179	2002–03	BR 35/PF 8596/3/PF 772003*2/PF 813//F 83899

Table 4. Participation of public and private institutions in the wheat seed market (%) in the Brazilian state of Rio Grande do Sul from 2002 to 2008.

Breeder	Profile	2002	2003	2004	2005	2006	2007	2008
Coodetec	Public/Private	1	1.5	4	5	4	3	5
Embrapa	Public	35	45	44	40	23	11	14
Fepagro	Public	1	0.5	0	1	0	0	0
Fundacep	Public/Private	48	37	23	18	33	37	48
OR Seeds	Private	14	16	27	35	40	47	32
Other	—	1	0	2	1	0	2	1
Totals	Public	36	45.5	44	41	23	11	14
	Public/Private	49	38.5	27	23	37	40	53
	Private	14	16	27	35	40	47	32
	Others	1	0	2	1	0	2	1

Historically, Embrapa has played a significant role in the Brazilian wheat seed market, whether for the market share it has held or for setting the standards for the market as a whole (in economic and technical aspects). Beginning in 1997 with the implementation of the Cultivar Protection Law for the wheat crop, other plant-improvement companies have grown, especially because of the possibility of charging royalties for marketed seed and because of the importance of wheat in Brazil. The wheat seed market shares in Brazil, for the states of Rio Grande do Sul and Paraná, are presented and the aggregation, according to the company profile (public or private) (Table 4 and Table 5, p. 45).

Table 5. Participation of public and private institutions in the wheat seed market (%) in the Brazilian state of Paraná from 2000 to 2008.

Breeder	Profile	2000	2001	2002	2003	2004	2005	2006	2007	2008
Coodetec	Public/Private	14	14	26	28	31	46	41	34	35
Embrapa	Public	23	27	24	16	22	23	33	44	48
Iapar	Public	38	37	30	30	27	18	10	8	8
OR Seeds	Private	21	14	17	23	18	13	15	13	6
Other	—	4	8	3	3	2	0	1	1	2
Totals	Public	61	64	54	46	49	41	43	52	56
	Public/Private	14	14	26	28	31	46	41	34	35
	Private	21	14	17	23	18	13	15	13	5
	Others	4	8	3	3	2	0	1	1	2

In Rio Grande do Sul, Embrapa was the market leader in 2003, 2004, and 2005, but its participation has decreased drastically, down to 14% of the market share in 2008. From 2005 to 2008, Fundacep increased its participation, growing from 18% to 48%. The participation of public companies was once larger, especially in 2002, 2003, and 2004. In 2007, an equilibrium between the participation of public and private companies was achieved (Table 4, p. 44).

In Paraná, the current participation of Embrapa in the wheat seed market is highly significant, having reached its highest rate in nearly 10 years (55%). On the other hand, the participation of Iapar (a traditional breeder in the state) has abruptly dropped since 2000, reaching only 7% in 2008. Coodetec, which led the market in 2004, 2005, and 2006, also has shown a reduction in its participation in the last 2 years. The participation of OR Seeds in the Paraná market is rather modest and achieved its highest rate (23%) in 2003 (Table 5).

ITEMS FROM THE PEOPLES REPUBLIC OF CHINA

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Characterization of low-molecular-weight glutenin subunit Glu-B3 genes and the development of STS markers in common wheat.

To characterize the LMW-GS genes at the *Glu-B3* locus, gene-specific PCR primers were designed to amplify eight near-isogenic lines and Cheyenne with different *Glu-B3* alleles (*a*, *b*, *c*, *d*, *e*, *f*, *g*, *h*, and *i*) defined by protein electrophoretic mobility. The complete coding regions of four *Glu-B3* genes with the complete coding sequence were obtained and designated as *GluB3-1*, *GluB3-2*, *GluB3-3*, and *GluB3-4*. Ten allele-specific PCR markers designed from SNPs present in the sequenced variants discriminated the *Glu-B3* proteins of electrophoretic mobility alleles *a*, *b*, *c*, *d*, *e*, *f*, *g*, *h*, and *i*. These markers were validated on 161 wheat cultivars and advanced lines with different *Glu-B3* alleles, thus confirming that the markers can be used in marker-assisted breeding for wheat grain processing quality.

Characterization of novel LMW-GS genes at the Glu-D3 locus on chromosome 1D in Aegilops tauschii.

The objectives of this study were to clarify the relationship between LMW-GS *Glu-D3* gene of *Ae. tauschii* registered in GenBank and the six *Glu-D3* genes, including 12 allelic variants of common wheat characterized in our previous studies, and identify novel *Glu-D3* genes and haplotypes from *Ae. tauschii* using gene-specific PCR amplification. By searching

the NCBI database, 13 LMW-GS genes/pseudogenes of *Ae. tauschii* were retrieved and classified into five gene families based on their nucleotide similarity with the six *Glu-D3* genes of common wheat. Of these, four *Ae. tauschii* genes *AY585350*, *AY585354*, *AY585355*, and *AY585356* matched to *GluD3-4*, *GluD3-5*, *GluD3-1*, and *GluD3-2* of common wheat, respectively, and one pseudogene *AY585351* matched to *GluD3-6*; none matched to *GluD3-3*. In order to identify the *Glu-D3* genes from *Ae. tauschii* corresponding to *GluD3-3* and *GluD3-6* of common wheat, gene-specific primers were developed to amplify 8-18 *Ae. tauschii* entries. As a result, two novel *Glu-D3* genes, designated *GluDt3-3* and *GluDt3-6*, were identified. *GluDt3-3* showed seven allelic variants or haplotypes at the DNA level in eight *Ae. tauschii* entries, designated as *GluDt3-31*, *GluDt3-32*, *GluDt3-33*, *GluDt3-34*, *GluDt3-35*, *GluDt3-36*, and *GluDt3-37*. Two to eight SNPs were found among the seven haplotypes and 1–4 amino acid substitutions among the deduced peptides. Multiple-sequence alignments showed that the DNA similarity was 99.6–99.9% among the seven *GluDt3-3* haplotypes, and 99.4–99.7% between these haplotypes and those of common wheat *GluD3-3* gene. *GluDt3-6* presented seven haplotypes in 18 *Ae. tauschii* entries, designated as *GluDt3-61*, *GluDt3-62*, *GluDt3-63*, *GluDt3-64*, *GluDt3-65*, *GluDt3-66*, and *GluDt3-67*. *GluDt3-61*, from *Ae. tauschii* entry Ae38, was the only one haplotype with complete coding sequence, and the other six were all pseudogenes. Compared with *GluD3-6* gene of common wheat, *GluDt3-61* exhibited a 3-bp insertion, a 42-bp deletion, and 11 base substitutions, leading to a glutamine insertion in position 52, a 14 amino acid deletion in position 84–97, and 10 amino acid mutations in its deduced peptide. *GluDt3-62* and *GluDt3-63* showed a 6-bp insertion, a 24-bp deletion, and a 15–21 base substitution in the coding region, of which a nonsense mutation from C to T at position 622 resulted in pseudogenes. *GluDt3-64* had five base substitutions, including a nonsense mutation at the position 742. *GluDt3-65*, *GluDt3-66*, and *GluDt3-67* all had a base deletion at position 247, as well as 7–8 base substitutions, which resulted in frameshift mutations in the three haplotypes. These results indicated that *Ae. tauschii* also contains six *Glu-D3* genes, and their allelic variants are even richer than those in common wheat.

Allelic variation at the Glu-D3 locus in Chinese bread wheat and effects on dough properties, pan bread, and noodle qualities.

Glutenin subunit alleles at the *Glu-D3* locus and their effects on dough properties, pan bread, and dry white Chinese noodle (DWCN) qualities were investigated using 106 winter and facultative wheat cultivars and advanced lines. Allele *Glu-D3c* (42.5%) was the most frequent glutenin subunit, followed by *Glu-D3b* (25.5%) and *Glu-D3a* (23.6%). *Glu-D3d* and *Glu-D3f* occurred in only three and six cultivars, respectively. The effect of *Glu-D3* was significant for DWCN quality, accounting for up to 16% of the variation, but there were no significant differences between individual *Glu-D3* alleles on dough properties and qualities of DWCN and pan bread. Interaction effects '*Glu-A1* × *Glu-D3*' and '*Glu-B1* × *Glu-D3*' were significant for DWCN quality and loaf volume. More work is needed to understand the effects of *Glu-D3* variation on the determination of dough properties and end-use quality.

Characterization of a phytoene synthase 1 gene (Psy1) located on common wheat chromosome 7A and development of a functional marker.

Phytoene synthase (Psy), a critical enzyme in the carotenoid biosynthetic pathway, demonstrated high association with the yellow pigment (YP) content in wheat grain. Characterization of Psy genes and the development of functional markers for them are of importance for marker-assisted selection in wheat breeding. We characterized the full-length genomic DNA sequence of a Psy gene (*Psy-A1*) located on chromosome 7A by *in silico* cloning and experimental validation. The cloned *Psy-A1* comprises six exons and five introns, 4,175 bp in total, and an ORF of 1,284 bp, encoding a Psy precursor peptide of 428 amino acids with a calculated molecular weight of ~47.7 kD. A co-dominant marker, YP7A, was developed based on polymorphisms of two haplotypes of *Psy-A1*, yielding 194-bp and 231-bp fragments in cultivars with high and low YP content, respectively. The marker YP7A was mapped on chromosome 7AL using a RIL population from cross 'PH82-2/Neixing 188', and a set of Chinese Spring nullisomic-tetrasomic lines and ditelosomic line 7AS. *Psy-A1*, co-segregating with the STS marker YP7A, was linked to SSR marker *Xwmc809* on chromosome 7AL with a genetic distance of 5.8 cM, and explained 20–28% of the phenotypic variance for YP content across three environments. A total of 217 Chinese wheat cultivars and advanced lines were used to validate the association between the polymorphic band pattern and grain YP content. The results showed that the functional marker YP7A was closely related to grain YP content and, therefore, could be used in wheat-breeding programs targeting of YP content for various wheat-based products.

Cloning and phylogenetic analysis of polyphenol oxidase genes in common wheat and related species.

Cloning and phylogenetic analysis of polyphenol oxidase (PPO) genes in common wheat and its relatives would greatly advance the understanding of molecular mechanisms of grain PPO activity. Six wheat relative species, including *T. urartu*, *T. monococcum* subsps. *monococcum* and *aegilopoides*, *T. turgidum* subsps. *dicoccoides* and *durum,* and *Ae. tauschii*, were sampled to isolate new alleles at *Ppo-A1* and *Ppo-D1* loci corresponding to common wheat PPO genes,. Seven new alleles were identified from these species, which were designated as *Ppo-A1c* (from *T. urartu*), *Ppo-A1d* (*T. monococcum* subsp. *aegilopoides*), Ppo-A1e (*T. monococcum* subsp. *monococcum* and *T. turgidum* subsp. *durum*), *Ppo-A1f* (*T. turgidum* subsp. *dicoccoides*), *Ppo-A1g* (*T. turgidum* subsp. *durum*), and *Ppo-D1c* and *Ppo-D1d* (*Ae. tauschii*). Five out of the seven alleles detected in the wheat relatives contained an open reading frame (ORF) of 1,731 bp encoding a polypeptide of 577 residues, which is the same as those of *Ppo-A1* and *Ppo-D1* genes in common wheat, whereas the full-length ORF of the allele *Ppo-A1g* from *T. turgidum* subsp. *durum* was not obtained, and a 73-bp deletion occurred in the third exon of *Ppo-D1d*, an allele from *Ae. tauschii*, resulting in a shorter polypeptide of 466 amino acids. The 191-bp insertion in the first intron reported previously in common wheat was also found in *T. turgidum* subsp. *dicoccoides* lines, implying that more than one tetraploid wheat lines may be involved in the origination of common wheat. Phylogenetic trees were constructed using the genomic DNA sequences of the seven alleles, together with four from common wheat and four partial PPO gene sequences deposited in GenBank. The genome tribe A was divided into two clusters, one of which contained *Ppo-A1d* and *Ppo-A1e*, and the other included the remaining five alleles at the *Ppo-A1* locus. The alleles from different clusters showed high sequence divergences, indicated by dozens of SNPs and five to six InDels. The genome tribe D comprised the alleles *Ppo-D1a*, *Ppo-D1c*, *Ppo-D1d*, and *Ppo-D1b*, and the former three were clustered together, showing significant sequence divergence from *Ppo-D1b*.

Association between percent SDS-unextractable polymeric protein (%UPP) and end-use quality in Chinese bread wheat cultivars.

The effect of genotype and environment on the size distribution of polymeric proteins was studied in two trials, Trial I with 33 spring cultivars and Trial II with 21 winter cultivars sown in four environments in the northwestern China spring wheat region and northern winter wheat region, respectively. The association between quantity and size distribution of polymeric protein and dough properties (both trials), and northern-style Chinese steamed-bread (CSB) (Trial I) and pan bread (Trial II) qualities also were investigated. In Trial I, all protein attributes, i.e., flour protein content, SDS-extractable polymeric protein in the flour (EPP), SDS-unextractable polymeric protein in the flour (UPP), and percent UPP in total polymeric protein (%UPP), were largely determined by environment, whereas variation in dough strength resulted from variation in UPP and %UPP across environments. In Trial II, EPP was largely determined by environment, and UPP and %UPP were largely determined by genotype. These differences might result from different levels of protein content and dough strength in the two trials. EPP was positively correlated with dough extensibility and was generally negatively correlated with dough stability and maximum resistance in both trials. However, %UPP was significantly positively correlated with dough stability and maximum resistance and end-use quality in both trials. In Trial I, the correlation coefficients between %UPP and maximum resistance and CSB score were 0.90 and 0.71, respectively, whereas in Trial II, the correlation coefficients between %UPP and maximum resistance and pan bread score were 0.96 and 0.87, respectively. Therefore, selection for high %UPP together with high-quality-glutenin subunits should lead to improved dough strength and end-use quality in Chinese wheats.

Molecular characterization of Pina and Pinb allelic variations in Xinjiang landraces and commercial wheat cultivars.

Our objective was to characterize allelic variations at the *Pina* and *Pinb* loci in Xinjiang wheat germ plasm for further understanding the mechanisms involved in endosperm texture formation and the status of grain texture in Chinese bread wheat. A total of 291 wheat cultivars, including 56 landraces, and 95 introduced and 140 locally improved cultivars, grown in Xinjiang, were used for SKCS measurement and molecular characterization. Among the harvested grain samples, 185 (63.6%), 40 (13.7%), and 66 (22.7%) were classified as hard, mixed, and soft, respectively. Eight different genotypes for the *Pina* and *Pinb* loci were identified, including seven previously reported genotypes, i.e., *Pina-D1a*/*Pinb-D1a*, *Pina-D1a*/*Pinb-D1b*, *Pina-D1b*/*Pinb-D1a*, *Pina-D1a*/*Pinb-D1p*, *Pina-D1a*/*Pinb-D1q*, *Pina-D1a*/*Pinb-D1aa*,

Pina-D1a/*Pinb-D1ab*, and a novel *Pinb* allele, *Pinb-D1ac*. This new allele, detected in the local landrace Kashibaipi and Red Star (from Russia) had a double mutation at the 257th (G to A substitution) and 382nd (C to T substitution) nucleotide positions of the coding region. *Pina-D1b*, *Pinb-D1b*, and *Pinb-D1p* were the most common alleles in Xinjiang wheat germ plasm, with frequencies of 14.3%, 38.1%, and 28.6% in hard textured landraces, 25.5%, 56.9%, and 11.8% in hard introduced cultivars, and 24.8%, 47.8%, and 26.5% in hard locally improved cultivars, respectively. The restriction enzymes *Apa*I, *Sap*I, *Bst*XI, and *Sfa*NI were used to identify *Pinb-D1ab* or *Pinb-D1ac*, *Pinb-D1b*, *Pinb-D1e*, and *Pinb-Dg,* respectively, by digesting PCR products of the *Pinb* gene. The unique grain hardness distribution in Xinjiang bread wheat and the CAPs markers for identification of the *Pinb* alleles provided useful information for breeding wheat cultivars with optimum grain textures.

HarvestPlus wheat.

A study of the effects of processing method including pan bread, steamed bread, and Chinese dry white noodles on mineral element including Fe, Zn, and P concentrations has been completed. High and significant processing and genotype effects on all the traits were found, with processing method contributing the largest for concentration of K, whereas the other traits were influenced mainly by genotype. Genotype, environment, and their interactions all had highly significant effects on all mineral element concentrations and kernel characteristic traits including 1,000-kernel weight and protein content.

Distribution of the photoperiod insensitive Ppd-D1a allele in Chinese wheat cultivars.

Photoperiod response is of great importance for optimal adaptation of bread wheat cultivars to specific environments, and variation is commonly associated with allelic differences at the *Ppd-D1* locus on chromosome 2D. A total of 926 Chinese wheat landraces and improved cultivars collected from nine wheat-growing zones were tested for their genotypes at the *Ppd-D1* locus using allele-specific markers. The average frequency of the photoperiod-insensitive *Ppd-D1a* allele was 66.0%, with frequencies of 38.6% and 90.6% in landraces and improved cultivars, respectively. However, the *Ppd-D1a* allele was present in all improved cultivars released after 1970, except for spring wheats in high latitude northwestern China and winter wheats in Gansu and Xinjiang. The presence of the *Ppd-D1a* allele in landraces and improved cultivars increased gradually from north to south, illustrating the relationship between photoperiod response and environment. *Ppd-D1a* in Chinese wheats is derived from three sources, the Japanese landrace Akagomughi and the Chinese landraces Mazhamai and Youzimai. The current information is important for understanding the broad adaptation of improved Chinese wheat cultivars.

Resistance to rusts and powdery mildew.

Stem rust. In total, 134 differential cultivars were sown in 29 locations, and stem rust only was observed in Guizhou and Keshan. Twe;ve differential cultivars from North America were used to characterize races of 52 Chinese stem rust samples,and the frequencies of major races CFM, CFR, MFM, and MFC were 50.0%, 15.4%, 15.4%, and 11.5%, respectively. Three dominant, Chinese races, 21C3CTH, 21C3CFH, and 34MKG, were used to characterize the resistance of 367 Chinese advanced lines and 131 CIMMYT lines (first stem rust nursery) giving 92 and 310 resistant genotypes, respectively.

Six Australian races were used to identified the stem rust resistance genes in 70 Chinese wheat cultivars, and *Sr5*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr9g*, *Sr10*, *Sr18*, *Sr21*, *Sr23*, *Sr24*, *Sr31*, and *Sr38* were present in 43 genotypes; 11 genotypes conferred resistance to *Sr31*. Molecular markers for *Sr24*, *Sr31*, and *Sr38* were used to confirm the results from gene postulations and indicated that the data from molecular marker shares 90% agreement with gene postulation.

More than 300 Chinese cultivars were sent to Kenya for screening to Ug99. Four cultivars from the Sichuan Province were identified to be MR in Kenya in 2007, and a 5-ha seed increase/pilot plot per cultivar for three cultivars will be sown in October 2008. A total of 380 Chinese cultivars, including the those with an MR response identified in the 2007 season in Kenya, were sent to Kenya for field testing. The first Stem Rust Resistance Nursery and 60 Stem Rust Resistance Materials for China and Turkey were increased and distributed to 16 Chinese institutes. Forty key

agronomic parents from five representative institutes were sent to Cornell University. A stem rust workshop was held in June, with 35 participants from 25 institutes. Five Chinese scientists attended the Ug99 Rust Workshop in Australia.

Molecular mapping of leaf rust resistance gene LrZH84 in Chinese wheat line Zhou 8425B.

With the objectives of identifying and mapping new genes for resistance to leaf rust, F_1 and F_2 plants and F_3 lines from a cross between resistant line Zhou 8425B and susceptible line Chinese Spring were inoculated with Chinese *P. triticina* races THTT and MBHP in the greenhouse. A total of 793 pairs of SSR primers were used to test the parents and resistant and susceptible bulks. Seven polymorphic, chromosome-1B markers were used for genotyping the F_2 and F_3 populations. Zhou 8425B carried a single dominant resistance gene, temporarily designated *LrZH84*, linked to SSR markers *Xgwm582-1B* and *Xbarc8-1B* with genetic distances of 3.9 cM and 5.2 cM, respectively. The *Xbarc8* allele co-segregated with *Lr26* in the F_3 population. The *Xgwm582* allele associated with *LrZH84* was identified as a wheat gene and shown to be present in the Predgornaia 2 parent of Zhou 8425B. The seedling reaction pattern of *LrZH84* was different from those of lines with *Lr26*, *Lr33*, *Lr44*, and *Lr46*, all of which are located in chromosome 1B. We concluded that *LrZH84* is likely to be a new leaf rust-resistance gene.

A novel homeobox-like gene associated with reaction to stripe rust and powdery mildew in common wheat.

Stripe rust and powdery mildew, caused by *P. striiformis* f. sp. *tritici* and *B. graminis* f. sp. *tritici*, respectively, are severe diseases in wheat worldwide. In our study, differential amplification of a 201-bp cDNA fragment was obtained in a cDNA-AFLP analysis between near-isogenic lines Yr10NIL and Avocet S, inoculated with *P. striiformis* f. sp. *tritici* race CYR29. A full-length cDNA (1,357 bp) of a homeobox-like gene, TaHLRG (GenBank accession EU385606), was obtained in common wheat based on the sequence of GenBank accession AW448633 with high similarity to the above fragment. The genomic DNA sequence (2,396 bp) of TaHLRG contains three exons and two introns. TaHLRG appeared to be a novel homeobox-like gene, encoding a protein with a predicted 66-amino-acid homeobox domain and was involved in race-specific responses to stripe rust in real-time quantitative PCR analyses with Yr9NIL, Yr10NIL, and Avocet S. TaHLRG also was associated with adult-plant resistance to stripe rust and powdery mildew based on the field trials of doubled haploid lines derived from the cross 'Bainong 64/Jingshuang 16' and two $F_{2:3}$ populations from the crosses 'Lumai 21/Jingshuang 16' and 'Strampelli/Huixianhong'. A functional marker, THR1, was developed based on the sequence of TaHLRG and located on chromosome 6A using a set of Chinese Spring nulli-tetrasomic lines.

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Development and characterization of wheat–alien chromosome lines.

Alien chromosome lines between wheat and seven alien species including *Haynaldia villosa, Leymus racemosus, Roegneria kamoji, R. ciliaris, Secale cereale, Hordeum californicum, and Thinopyrum bessarabicum* have been developed and characterized by chromosome C-banding, in situ hybridization, and molecular marker analysis.

The powdery mildew-resistance gene *Pm21* of *H. villosa* was located on chromosome arm 6VS and a T6VS·6AL translocation was developed and is now widely used in breeding programs in China. Ten cultivars, including Nannong 9918, Neimai 8~10, Shimai14, and Shimai15, with high yield and good disease resistance have been developed and released. The yellow mosaic virus disease resistance gene of *H. villosa* was located on the short arm of chromosome 4V and a translocation line T4VS·4AL has been developed.

Three *T. aestivum–L. racemosus* addition lines with Fusarium head bright resistance were developed. The FHB-resistance genes were mapped to chromosomes 5Lr#1, 7Lr#1, and Lr#7. More than ten *T.aestivum–L. racemosus* translocation lines involving chromosomes 5Lr#1, 7Lr#1, and Lr#7 with FHB resistance have been developed. An FHB-resistance gene on chromosome 7Lr#1 was named as *Fhb3*. A *T. aestivum–R. kamoji* translocation line with FHB resistance has been developed, and the FHB-resistance gene was mapped to chromosomes 1Rk#1. A total of 10 *T. aestivum–R. ciliaris* alien addition lines have been developed. An FHB-resistance gene was mapped to chromosome 2Rc. Addition, substitution, and translocation alien chromosome lines of *T. aestivum–H. californicum* and *T. aestivum–Th. bessarabicum* have been developed. Chromosome 5J and 3J of *Th. bessarabicum* might contain salt tolerance gene(s).

Mass production of wheat–Haynaldia villosa translocation lines by irradiation of a Triticum turgidum subsp. durum–H. villosa amphiploid.

Haynaldia villosa possesses many important agronomic traits and is a useful gene resource for wheat improvement. In order to develop more wheat–*H. villosa* translocations involving different chromosomes and chromosome segments of *H. villosa*, a *T. turgidum* subsp. *durum–H. villosa* amphiploid was irradiated with ^{60}Co γ-rays. Pollen collected from the spikes 1, 2, and 3 day after irradiation was pollinated to emasculated spikes of common wheat cultivar Chinese Spring. Genomic *in situ* hybridization was used to identify wheat–*H. villosa* chromosome translocations in the M1. The transmission of the identified translocation chromosomes was analyzed in the following BC_1, BC_2, and BC_3 generations. An efficient method for inducing wheat–*H. villosa* chromosomal translocations has been established. A number of intergeneric translocations between *T. turgidum* subsp. *durum* and *H. villosa* have been identified. This provides a new strategy for rapid mass production of wheat-alien chromosomal translocations, especially terminal translocations that is more important for wheat improvement.

Inducing chromosome translocations with small alien segments by irradiating mature female gametes of whole-arm translocation lines.

The development of translocations with small alien chromosome segments, especially interstitial translocation, will be helpful for better utilization and cytology-based physical mapping of alien useful genes. The *T. aestivum–H. villosa* T6VS·6AL translocation line carries the powdery mildew resistance gene *Pm21*. In order to create small chromosome segment translocation lines of 6VS, the female gametes of wheat–*H. villosa* T6VS·6AL translocation line were irradiated

by ^{60}Co-γ ray before flowering. Anthers were removed from the irradiated florets on the same day and the florets were pollinated with normal fresh pollens of *T. aestivum* cv. Chinese Spring. Genomic *in situ* hybridization (GISH) on preparations of root-tip cells at mitosis metaphase was used to detect chromosome structural changes with small segments of 6VS. More than 20 new translocations and deletions involved in different regions of chromosome 6VS have been obtained. Several intercalary translocations with powdery mildew resistance gene *Pm21* have been developed. Irradiating mature female gametes of whole arm translocation is a new and highly efficient approach for creation of small segment chromosome structural changes, especially for interstitial translocations.

Cloning and transfer of powdery mildew resistance gene.

A microarray analysis using the barley Affymetrix Gene-Chip was conducted to clone candidate genes of *Pm21*. A full length candidate clone has been identified. The candidate gene was transformed into a wheat variety Yangmai 158, which is susceptible to powdery mildew, using a shot-gun method. The transgenic plants showed high powdery mildew resistance, indicating its good compensation function.

ITEMS FROM CROATIA

BC INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS
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Preliminary testing of the new Bc winter wheat lines for resistance to Fusarium head blight (Fusarium graminearum Schw.).

Slobodan Tomasović, Branko Palaveršić, Rade Mlinar, Ivica Ikić, and Tomislav Ivanušić.

Diseases caused by fungi of the genus *Fusarium* spp. inflict heavy damages in many wheat-growing regions world wide. Fungi of the genus *Fusarium* produce micotoxins (DON and ZEN) that have harmful effect on health of humans and domestic animals. The spread of this disease is the result of intensive growth of semidwarf wheat cultivars in the narrow maize–wheat rotation. Among the measures of control of this disease, breeding for resistance is one of the most important. Development of reliable techniques for artificial inoculation is a prerequisite for wheat breeding for disease resistance to be able to test a large number of materials in the breeding process. Every year about 1,000 wheat genotypes are tested under conditions of artificial inoculation with *F. graminearum* at the Bc Institute. The hightest yielding and most resistant lines with other good agronomic traits were screened in preliminary trials to be tested in exact trial (Fig. 1). In a trial with four replications in Botinec in 2008, the 25 highest yielding winter wheat lines were planted with artificial inoculation with *F. graminearum* (Fig. 2, p. 52). These investigations compared resistance to Fusarium head blight of the wheat lines from the exact trial with the resistance scores of the lines from preliminary trials in 2007. Significant differences in levels of resistance among the tested wheat lines were obtained in the 2008 trial. Visual rating of infection (VRI) ranged from 0.58 to 47.81. The most resistant lines were Bc 14 (3.71), Bc 12 (3.85), and Bc 1 (8.25), followed by

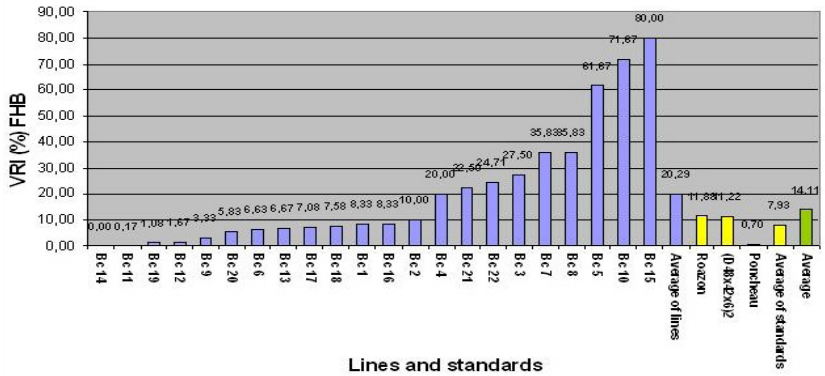

Fig. 1. Resistance to Fusarium head blight in 22 new Bc winter wheat lines in comparison with standards. Results are from preliminary trials screened after artificial infection, Botinec 2007.

Table 1. Bc winter wheat lines from exact cultivar trials with a high level of resistance to Fusarium head blight after artificial infection in comparison with standard cultivars, Botinec 2008.

Line	Fuarium head blight – visual rating of infection (%)
Bc 14	3.71 **
Bc 12	3.85 **
Bc 1	8.25 *
Bc 18	13.77 *
Bc 17	14.27 *
Bc 9	14.44 *
Average	9.71
Standards	
Roazon	14.89 *
(D48x42x6)2	6.75 **
Poncheau	0.58 **
Average of standards	7.41
Average	8.56

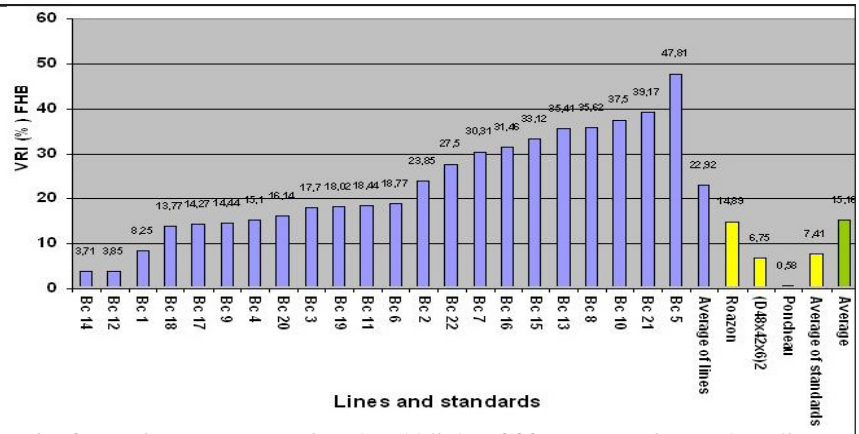

Fig. 2. Resistance to Fusarium head blight of 22 new Bc winter wheat lines in comparison with standards in exact cultivar trials after artificial infection, Botinec 2008.

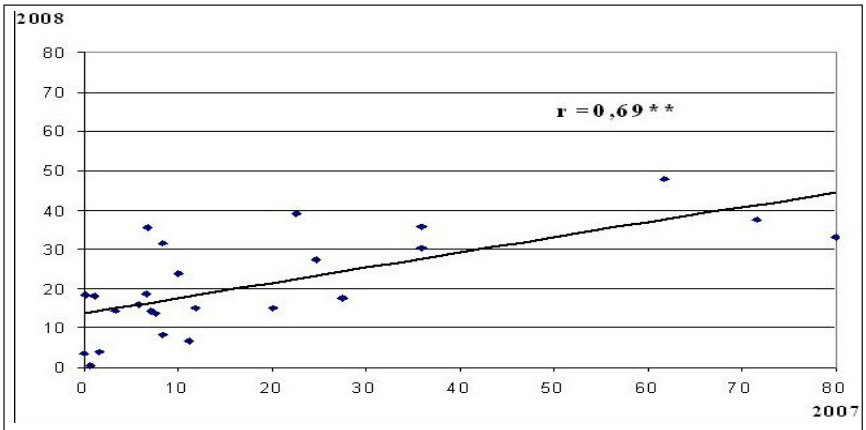

Fig. 3. Correlation between 22 Bc winter wheat lines and three standards for resistance to Fusarium head blight. Tested in preliminary investigations and in exact cultivar trials after artificial infection, Botinec 2007 and 2008.

Bc 18 (13.77), Bc 17 (14.27), and Bc 9 (14.44) (Table 1). A strong correlation between wheat lines of resistance to Fusarium head blight in the exact trial and in preliminary investigations (r = 0.69) was obtained, which proves the reliability of the preliminary results (Fig. 3). The artificial inoculation technique and evaluation of Fusarium head blight using VRI was suitable for testing a large number of wheat lines.

Acknowledgement. These results are from the scientific project 'Breeding wheat for yield, quality and resistance to Fusarium head blight, 106-1780691-2155' partially supported by the Croatian Ministry of Science, Education and Sports and represents a complementary part of program No. 1780691 (Research and improvement of genetic traits of field crops).

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ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK
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A. Börner, E.K. Khlestkina, B. Kobiljski, U. Kumar, S. Landjeva, U. Lohwasser, M. Nagel, S. Navakode, M.A. Rehman Arif, M.S. Röder, A. Weidner, L.Q. Xia, and K. Zaynali Nezhad.

Molecular linkage map of durum wheat.

A molecular (SSR marker) map of a durum wheat population is under development. The mapping population consists of 114 RILs and was developed at ICARDA be crossing Omrabi 5, a drought-tolerant cultivar, with Belikh 2, a heat- and salt-tolerant cultivar. As a prerequisite for the map construction, the parental screening was carried out with 224 Gatersleben wheat microsatellite (GWM) markers of which 114 were polymorphic between the parents. The B genome revealed a higher polymorphism rate (53%) compared to the A genome (47%). The population genotyping is in progress. In parallel, the lines will be phenotyped for abiotic stress response.

Molecular linkage map of bread wheat.

A new, SSR-based genetic linkage map of bread wheat based on 143 F_2 individuals derived from an intraspecific cross between Gatersleben gene bank accessions TRI 11712 and TRI 105, two winter wheat accessions from Pakistan and Sweden, respectively, was constructed. The parental lines were analyzed with more than 600 SSR primer pairs. Out of 600 SSRs tested for polymorphism, 17 (2.6%) did not show amplification (null) in both the parents. Overall, 350 SSR primer pairs were polymorphic and 272 were applied for population genotyping, which yielded 308 polymorphic loci and 288 of these mapped on 19 linkage groups with a total map length of 2,681 cM. The average of chromosome length was 141 cM and the average number of loci per chromosome 15; an average of one locus per each 9.3 cM on this map. Chromosomes 6D and 4D failed to generate proper maps because of the low amount of detected polymorphism. Less loci were mapped to the D genome (21.5%) compared to those on the A (36.9%) or B (41.6%) genomes. More important, this map contained 66 new loci. The described linkage map could be useful to enrich the consensus bread wheat genetic map by incorporating the 66 new loci.

Stable, across-environment QTL.

The International Triticeae Mapping Initiative (ITMI) RIL population was used to detect QTL underlying key agronomic characters in bread wheat. Trait measurements were taken from five independent field experiments performed in Serbia. Stable, across-environment QTL involved in the determination of heading/flowering time and ear morphology (length)/ grain yield were detected on chromosome arms 2DS and 4AL, respectively. These map locations are consistent with those obtained where the same population has been grown in contrasting geographical sites in Germany or Russia. However, as a result of 'QTL x environment' interactions, not all these QTL are expressed in all environments. Nevertheless, the (pleiotropic) effect on ear morphology (length) appears to be expressed in almost all environments and, so, represents a high value target for wheat improvement.

Anthocyanin pigmentation genes on homoeologous group-7 chromosomes.

Three bread wheat crosses 'Saratovskaya 29/Yanetzkis Probat', 'Chinese Spring–Hope 7B DS)/TRI 2732' and 'Golubka/ Novosibirskaya 67' were used for microsatellite-based mapping of genes determining anthocyanin pigmentation of anthers (*Pan-D1*), culm (*Pc-A1*, *Pc-B1*, and *Pc-D1*), leaf sheaths (*Pls-A1* and *Pls-B1*), and leaf blades (*Plb-A1*, *Plb-B1*,

and *Plb-D1*). The clustering of these genes with previously mapped *Rc-1* genes for red coleoptile on chromosomes 7AS, 7BS, and 7DS was shown. In addition, a set of 37 wheat cultivars and introgression lines was analyzed for presence of anthocyanin pigment on different plant organs. A significant correlation has been found between presence of anthocyanin on coleoptile and culm, coleoptile and leaf blade, coleoptile and anther, and anther and leaf blade.

Anthocyanin pigmentation in durum wheat.

Analyzing the F_2 population of a cross between the two durum wheat IPK genebank accessions, TRI 15744 and TRI 2719, a novel gene was described and mapped in wheat that controls anthocyanin pigmentation of the glume and was designated *Pg* (purple glume). This gene was mapped close to one of the two complementary dominant genes controlling anthocyanin pigmentation of the pericarp (gene *Pp3*) in the centromere region of chromosome 2A, whereas another *Pp* gene (*Pp1*) was mapped on the short arm of chromosome 7B, near the gene *Pc* controlling anthocyanin pigmentation of the culm and co-segregating with *Pls* (purple leaf sheath) and *Plb* (purple leaf blade). On the basis of the mapping results, the *Pp3*, *Pc*, *Pls*, and *Plb* genes of durum wheat were regarded as allelic to the bread wheat *Pp3*, *Pc-B1*, *Pls-B1*, and *Plb-B1* loci, respectively, whereas allelism of *Pp1* of *T. turdigum* subsp. *durum* and *T. aestivum* remains disputed, because this *Pp* gene was mapped in the former on the short arm and in the latter on the long arm of chromosome 7B.

Glume coloration.

An allelism test has confirmed that chromosome 1A genes for red and black glume coloration are allelic. Similarly, we showed that chromosome 1D genes for smokey-grey and red glume coloration also are allelic. Consensus maps of chromosomes 1A and 1D, carrying loci *Rg-A1* and *Rg-D1*, respectively, were derived from the mapping data obtained previously. The gliadin-specific microsatellite marker MW1B002 was mapped to chromosome 1B, 2 cM proximal from gene *Rg-B1*. Co-distribution of red glume coloration with specific alleles of locus MW1B002 was found in Russian, Albanian, Indian, and Nepal bread wheat collections.

Preharvest sprouting / dormancy.

In order to compare QTL data of wheat and rye for preharvest sprouting and dormancy the results from the ITMI population were checked against results from disomic wheat–rye addition lines. For wheat, a major QTL could be found on chromosome 4AL for both traits. In a first test with wheat–rye addition lines, chromosome 7R could be identified for these traits. In replications with wheat (Chinese Spring)–rye (Imperial) and wheat (Chinese Spring)–rye (King II) addition lines of chromosome 7R, 7RS, and 7RL, the important region for preharvest sprouting and dormancy, could be localized on chromosome 7RL, on one hand, and on chromosome 7RS, on the other hand. Looking for homologous regions between wheat and rye chromosome, 7RS has a relationship with chromosome 4 of wheat; chromosome 7RL provides no comparability with the wheat results.

Leaf rust and powdery mildew resistance derived from Aegilops markgrafii.

Introgression lines resistant to either powdery mildew or leaf rust and derived from the cross of the wheat cultivar Alcedo and *Ae. markgrafii* accession S740-69, which are susceptible and resistant to both diseases, respectively, were used in a complex crossing program. The aims were the combination of both resistances in one genotype and the identification of the gene(s), which are responsible for powdery mildew resistance regarding number and location.

The F_2 generations originating from a cross between six powdery mildew-resistant introgression lines with the same leaf rust-resistant line were tested at the seedling stage (Ann Wheat Newslett 54:48 2008) and investigated at adult-plant stage for both diseases. Segregation analyses for the inheritance of powdery mildew resistance resulted in two recessive genes for four of the six F_2 progenies. The remaining two F_2 progenies were characterized by two dominant, resistance genes. The leaf rust resistance was inherited by two dominant genes across all F_2 generations.

Only four of the five F_2 progenies from the cross of different powdery mildew introgression lines with the susceptible wheat cultivar Kanzler were grown in the same experimental field described above. According to the segrega-

tion analyses, the powdery mildew resistance was inherited by at least one dominant gene and some minor factors except for one line with three recessive genes.

Information from monosomic analyses was used to start the localization of the powdery mildew resistance genes within the introgression lines. Chromosomes 1A, 7A, and 6D were identified to have main effects with respect to powdery mildew resistance. Therefore, a total of 42 wheat SSR markers distributed over these three chromosomes were selected to detect polymorphisms between the crossing parents and introgression lines. Between the parental lines, 64% of polymorphism was detected. Depending from the introgression line, 6 to 10 SSR markers were finally suitable to detect DNA fragments from the *Ae. markgrafii* parent.

Septoria tritici blotch resistance from Triticum aestivum subsp. spelta.

A new source of resistance to *Septoria tritici* blotch has been mapped on chromosome 7D of *T. aestivum* subsp. *spelta*. A microsatellite-based genetic map was constructed from a set of 87 DH lines bred from the cross between Chinese Spring and a Chinese Spring-based line carrying chromosome 7D from spelt wheat. Two regions of the chromosome were associated with pathogen isolate-specific QTL expressed at both the seedling and the adult-plant stage. One of these may be allelic to the major resistance gene *Stb4* present in the bread wheat cultivar Tadinia.

Seed longevity.

Germination tests were performed on wheat accessions stored in the cold store of the germ plasm bank of IPK Gatersleben to investigate the intraspecific variability of seed longevity. The material originated from various parts of Asian, European, and American continents. In total, 213 accessions were analyzed consisting of 193 hexaploids, 18 tetraploids, and two diploids. The accessions were harvested in 1974 and stored in glass jars at 0±1°C and 8±2% seed moisture content. Initial germination data were available from 1977. Germination rates were high, having a mean of 87.04 ± 9.04%. The average decreased after 34 years of storage to 56.15 ± 23.03%. There was a clear increase in variation. Although 14 accession showed germination rates < 10%, other accessions kept high germinabilities with 68 > 70% and 24 > 80%. The loss of viability detected was independent from origin, growth type (spring/winter habit), and ploidy level of the germ plasm. Because the accessions investigated come from a seed multiplication performed in the same year (1974), at the same place (experimental fields, IPK Gatersleben), handled the same way during/after harvest (threshing and cleaning), and stored under identical conditions in one and the same cold chamber in glass jars, the differences in germinability discovered in the present study must be due to genetic variation in seed longevity.

Mapping the trait for seed vigor in the D genome.

A QTL analysis was performed with a set of 85 bread wheat lines containing homozygous introgressions of the *Ae. tauschii* D genome to identify chromosome regions associated with seed vigor. To assess seed vigor traits, measurements on a range of the germination characteristics were obtained for germination percentage on first (day 4) and final (day 8), mean germination time, mean germination rate, and the coefficient of germination synchrony. All trait measurements were obtained on the bases of 1-mm root protrusion and normal seedling development in fresh seeds (controls) and in seeds subjected to accelerated ageing (AA). The latter involved seed treatment with high temperature and high humidity to mimic natural ageing after prolonged storage. As an estimate of seed longevity, a seed vigor index was determined for all the traits as a ratio of the AA trait and the control trait values.

A total of 53 significant QTL (LOD > 3.0) were detected in clusters on chromosomes 1D (19), 5D (16), 7D (16), and 2D (2), individually explaining 16 to 37 % of the phenotypic variation. Most of the QTL controlling different vigor traits were located on overlapping regions. In controls, the majority of the QTL (25 out of 29) were identified on chromosomes 7D (16) and 1D (9). Following AA, almost all detected QTL were located on chromosome 5D (7 out of 8). Chromosomes 1D (9 QTL) and 5D (7) harbored all detected QTL for vigor indexes.

A wide region close to the centromere of chromosome 1D contributed to the genetic variation in the germination timing, rate, and synchrony both in controls and the corresponding vigor indexes. A broad region in the 5D long arm involving seven QTL affected the post-AA final germination percentage and the corresponding vigor index. A cluster of

QTL in the proximal part of 7D short arm affected the first count germination percentage, timing, and rate of development of normal seedlings in the controls.

In the controls, the wild donor alleles were associated with earlier germination and more synchronized development of normal seedlings. The wild, donor alleles decreased the germination percentage in both controls and AA, and reduced the vigor indexes.

Spot blotch resistance.

Spot blotch is a destructive disease of wheat in warm and humid wheat growing regions of the world. To identify the QTL for spot blotch resistance, an intervarietal mapping population in the form of RILs was developed from the cross 'Yangmai 6 (a Chinese source of resistance)/Sonalika (a spot blotch susceptible cultivar)'. Using SSR markers, four QTL, designated as *QSb.bhu-2A, QSb.bhu-2B, QSb.bhu-5B*, and *QSb.bhu-6D*, were identified. These QTL together contributed up to 63.1% of phenotypic variation. Two QTL on chromosomes 2B and 5B with major effects were consistent over 3 years. Two additional RI populations ('Ning 8201/Sonalika' and 'Chirya 3/Sonalika') also were investigated for the QTL analysis. Four QTL were identified on the chromosomes 2AS, 2BS, 5BL, and 7DS and explained 61.9% of phenotypic variation in a simultaneous fit. In the third cross ('Chirya 3/Sonalika'), the F_7 and F_8 populations were evaluated for 2 years. The selected chromosomes of this population were analyzed for the presence of QTL, and four were identified on chromosomes 2AS, 2BS, 2DS, and 7DS. The QTL identified in the 'Chirya 3/Sonalika' population explained 34.4% of phenotypic variation in a simultaneous fit. All QTL alleles for reduced disease severity were derived from the respective resistant parent in all mapping population.

Stay-green trait.

The stay-green (SG) trait is delayed senescence. Leaves remain green even after the seed has reached chemical maturity and is considered an important trait that allows a plant to retain their leaves in active photosynthetic states. The parents of the mapping population 'Chirya 3/Sonalika' differed in respect to stay-green trait. Therefore, this population was segregating for the stay-green trait, and we identified a QTL on the short arm of chromosome 1A that explained up to 19% of the phenotypic variation. This population will be analyzed with more microsatellite markers covering all chromosomes to identify more QTL for stay green.

Viviparous-1 gene associated with preharvest sprouting tolerance in European wheat cultivars.

Preharvest sprouting reduces the quality of wheat and the economic value of the grain. In this study, we determined the diversity of *Vp-1B* alleles in 490 accessions of European winter wheat cultivars by using the STS marker *Vp1B3* to provide basic information for the breeder for the production of improved PHS-tolerant cultivars. Four alleles of *Vp-1B* were found in the wheat cultivars tested, three of which (*Vp-1Ba*, *Vp-1Bb*, and *Vp-1Bc*) had previously been identified in Chinese wheat cultivars. The fourth was a new allele that had a 25-bp deletion in the third intron region, compared with the nucleotide sequence of *Vp-1Ba*, and was designated as *Vp-1Bd*. The list of tested cultivars can be found at: http://pgrc.ipk-gatersleben.de/viviparous

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ITEMS FROM HUNGARY

AGRICULTURAL RESEARCH INSTITUTE OF THE HUNGARIAN ACADEMY OF SCIENCES
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Wheat season. The 2007–08 season was favorable for the winter cereals. The winter was milder than average, and neither real drought or heat stress, nor severe disease attack endangered the good yield. National wheat average reached 5.02 t/ha, that was the highest yield in the last 5 years. Quality of wheat harvested before mid July was very good, than the long rainy period reduced the quality in some regions.

Breeding.

Z. Bedö, L. Láng, O. Veisz, G. Vida, M. Rakszegi, K. Mészáros, and S. Bencze.

Breeding. Two winter wheat cultivars were registered in Hungary in 2008; the winter wheats Mv Toborzo, Mv Marsall, Mv Suba, Mv Kolo, Mv Beres, and the winter durum Mv Makaroni were registered in Kosovo.

Mv Bodri (Mv 18-05) is an early maturing short straw cultivar with high yield potential, selected from the cross 'GT6687-12R/ERYT162'. The frost resistance level determined in phytotron tests is very good. Mv Bodri has average protein content, with good gluten quality. The HMW-glutenin composition is 1, 7+9, 5+10, and the cultivar does not carry the T1B·1R translocation. Mv Bodri is moderately resistant to powdery mildew and leaf rust and resistant to stem rust.

Mv Toldi (Mv 19-05) is an early maturing, top quality wheat. The head type is awned, the plant height is optimal (95-100 cm), with good lodging resistance. mv Toldi has good frost tolerance and winter hardiness. The cultivar was selected from the cross 'Mironovskaya-Ostistaya/Atay85//Alfold'. Mv Toldi has high gluten content and very good baking quality; the dough strength and stability, especially, are excellent. The HMW composition is 2*, 7+9, 5+10.

Disease resistance studies.

Marker-assisted selection. Within the framework of international projects (Bioexploit-EU FP6 and NAP-BIO-NEWSEED), molecular marker-assisted selection is being used to incorporate known resistance genes (*Lr9, Lr24, Lr25, Lr29, Lr37*, and *Lr47*) into four Martonvásár cultivars (Mv Emma, Mv Madrigál, Mv Magvas, and Mv Pálma). The presence of the resistance genes is detected using public PCR-based (STS and SCAR) markers in various backcross generations.

Effective *Lr* genes. The degree of infection exhibited by genotypes carrying known leaf rust resistance genes was tested in artificially inoculated nursery. Genes *Lr9, Lr19, Lr24, Lr25, Lr28, Lr29, Lr35, Lr37,* and *Lr47* continued to provide effective protection against leaf rust in Martonvásár in 2008.

Powdery mildew race survey. Powdery mildew isolates collected in the Martonvásár area were used to determine the race composition of the pathogen population, the degree of virulence, and the efficiency of known resistance genes. The races dominant in 2008 (and their frequency) were 51 (43.5%), 76 (25.8%), and 77 (9.7%). The virulence complexity in the pathogen population was calculated as 6.18, which was higher than in any previous year. Almost complete protection against the tested wheat powdery mildew isolates was provided by the resistance gene combination *Pm4a+* (Khapli).

Abiotic stress resistance studies. Work has begun on the collection of genetic materials and the development of various types of population for an analysis of the genetic regulation of heat tolerance. Wheat cultivars with various types of ad-

aptation were identified in preliminary studies, after which a cross was made between the heat-tolerant, drought-sensitive cultivar Mv Magma and the heat-sensitive, drought-tolerant cultivar Plainsman V. Homozygous lines were developed either from anther culture or using the SSD method. A total of 11,424 anthers were cultured from the 'Plainsman V/Mv Magma' cross (STR3 line), 39.3% plants of which were successfully regenerated, with 12.4% green plant regeneration. At present, 222 DH_0 plants of microspore origin are being raised from this line in the phytotron. In the case of the 'Mv Magma/Plainsman V' cross, 6,250 anthers were cultured. The plant regeneration ratio was 28.3%, and the green plant regeneration ratio 11%. A total of 281 plants have been planted out from this cross.

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Department of Plant Genetic Resources and Organic Breeding.

M. Molnár-Láng, G. Kovács, É. Szakács, A. Schneider, I. Molnár, and A. Sepsi.

Characterization of a leaf rust-resistant wheat–*Thinopyrum ponticum* partial amphiploid BE-1 using sequential multicolor GISH and FISH. *In situ* hybridization (multicolor GISH and FISH) was used to characterize the genomic composition of the wheat–*Th. ponticum* partial amphiploid BE-1. The amphiploid is a high-protein line having resistance to leaf rust and powdery mildew and has a total of 56 chromosomes per cell. Multicolor GISH using J-, A-, and D-genomic probes showed 16 chromosomes originating from *Th. ponticum* and 14 A-genome, 14 B-genome, and 12 D-genome chromosomes. Six of the *Th. ponticum* chromosomes carried segments different from the J genome in their centromeric regions. We demonstrated that these alien chromosome segments did not originate from the A, B, or D genomes of wheat, so the translocation chromosomes were considered to be J^s-type chromosomes carrying segments similar to the S genome near the centromeres. Rearrangements between the A and D genomes of wheat were detected. FISH, using Afa family, pSc119.2, and pTa71 probes, allowed the identification of all the wheat chromosomes present and the determination of the chromosomes involved in the translocations. The 4A and 7A chromosomes were identified as being involved in intergenomic translocations. The replaced wheat chromosome was identified as 7D. The localization of these repetitive DNA clones on the *Th. ponticum* chromosomes of the amphiploid was described in the present study. On the basis of their multicolor FISH patterns, the alien chromosomes could be arranged in eight pairs and could also be differentiated unequivocally from each other.

Polymorphism analysis using 1RS-specific molecular markers in rye cultivars of various origin. Six different 1RS-specific molecular markers (RMS13, Bmac213, GPI, 5S, SCM9, and IAG95) were tested in 20 rye cultivars of various origin. The aim of the experiments was to choose rye cultivars which give polymorphic PCR products with these 1RS-specific markers compared to the wheat cultivar Mv Magdaléna, which contains the T1BL·1RS translocation. The polymorphic rye cultivars can be presumed to differ from the T1BL·1RS translocation originating from the Petkus rye cultivar and will hopefully carry effective resistance genes that can be incorporated into the T1BL·1RS translocation in wheat. Twenty rye cultivars (at least two plants/cultivar) were analyzed with these markers. Of the 52 rye samples analyzed, three plants were polymorphic, one (Kisvárdai Alacsony from Hungary) for the 5S marker, one (Kriszta from Hungary) for the RMS13 marker, and one (Porto from Portugal) for the SCM9 marker. The polymorphic plants were grown to maturity in the phytotron.

Fluorescent *in situ* hybridization polymorphism on the 1RS chromosome arms of cultivated *Secale cereale* species. The study was focused on the selection of *S. cereale* cultivars of different geographic origin showing polymorphism detectable by FISH on their 1RS chromosome arms. One perennial and four annual genotypes were tested. FISH with the DNA probes pSc119.2 and $(AAC)_5$. The pSc119.2 probe gave hybridization signals different from that of the rye 'Petkus' on the 1RS arms of all five rye cultivars examined. Differences were manifested mainly in the intensity of the labelling, but the complete lack of FISH signals and double signals were also observed. The other chromosomes of the five rye cultivars could also be identified, and polymorphism for both DNA probes was detected on them.

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Genetic and physiological studies.

A. Vágújfalvi, A. Soltész, I. Vashegyi, G. Kocsy, and G. Galiba.

Verification of candidate genes for wheat frost tolerance by transformation. *Cbf* genes are the most likely candidate genes for frost tolerance in cereals. Recently, we proved that out of the 13 *Cbf* genes encoded in the wheat genome, *Cbf14* and *Cbf15* are the most important in the control of low temperature tolerance in wheat. In a collaborative work with Dr. Wendy Harwood (Department of Crop Genetics, John Innes Centre, Norwich UK), barley plants were transformed with these candidate genes via an *Agrobacterium*-mediated transformation method. The presence of the transgene was confirmed by PCR. Transgenic lines will be tested for improved abiotic stress tolerance.

Identification and characterization of stress-responsive candidate genes in wheat. A wheat oligonucleotide microarray (15,000 oligos) was developed in a collaboration with the Biological Research Center in Szeged (Dr. János Györgyey). Cold-hardened wheat genotypes with different freezing tolerance were compared for the selection of cold-responsive genes which may be involved in the hardening process. The earlier identified cold-responsive candidate genes were further characterized. Their expression was examined following various abiotic stress treatments in different organs.

Publications.

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Cell Biology Department.

B. Barnabás, K. Jäger, H. Ambrus, and A. Fábián.

Cryopreservation of wheat gametic cells. The cryopreservation method of wheat egg cells using a simple one-step vitrification procedure was elaborated. The procedure involved loading the cells with 25% of a vitrification solution, dehydration, droplet vitrification, and storage in liquid nitrogen, unloading, and rehydration of the cells. Supplementation with 120 mM ascorbic acid significantly increased the proportion of viable egg cells after de- and rehydration. During the early phase of rehydration, ascorbic acid reduced the probability of membrane damage caused by rapid water uptake. Maintaining the temperature of the cells at 0°C during the de- and rehydration processes increased cell survival by 29%. Wheat egg cells dehydrated and vitrified in vitrification solution VS4A, consisting of 30% glycerol, 10% sucrose, 120 mM ascorbic acid, and 5% propylene glycol, subsequently thawed, unloaded in BVSA, and rehydrated, showed post-thaw cell viability of 12.7%.

Abiotic stress tolerance. The effects of meiotic water deficit and combined heat and drought stress were studied on microsporogenesis and fertility of wheat. Among normal pollen, 12% of the drought-stressed, tolerant Plainsman V and

34% of the sensitive Cappelle Desprez pollen were arrested at early stages of gametogenesis. Drought stress manifested in significant reduction of the mean fertility in both sensitive (41%) and tolerant (33%) genotypes. Combined stress applied during meiosis among developmental arrests caused serious morphological anomalies in the sensitive genotype. When plants of the Planisman V were subjected to simultaneous drought and heat, an additional 24% significant decrease occurred in the ratio of normal pollen. The fertility of the basal part of the spikes was similar to the control in both genotypes, but the seed set in the middle and on the top of the spikes decreased significantly as a consequence of combined drought and heat stress.

Wheat plants of drought-tolerant Plainsman V and drought-sensitive Cappelle Desprez genotypes were subjected to drought and combined drought and elevated, 34/24ºC day/night temperature at three various phases of reproductive development; at meiosis, from the 1st to the 5th day after pollination; and from the 5th to the 9th day of seed development. After seed maturation, the germination frequency of the grains was calculated, and the seminal root number of the seedlings was determined. Neither of the stress treatments affected the germination percentage of the genotypes significantly. Neither of the treatments reduced the number of seminal roots in the case of the tolerant genotype. However, in the sensitive cultivar, the ratio of seedlings with only one root increased to 42% after drought stress applied 5–9 days after pollination (DAP). In this genotype, the combined stress increased the proportion of one-rooted seedlings up to 56% and 78% when applied during 1–5 DAP and 5–9 DAP, respectively.

Cytological alterations caused by aluminum (Al) were examined in anther cultures of the commercial wheat Mv Pálma, and the efficiency of in vitro selection was demonstrated. Although the anther walls retarded the appearance of toxicity symptoms, cytological changes similar to those observed in root cells were detected in the microspores. The severity of Al toxicity and the efficiency of selection depended on the Al concentration and the mode of treatment. Single Al treatments (0.6 and, especially, 1.6 mM) gave DH lines with increased Al tolerance. Repeated Al treatment severely inhibited the cell division of the microspores, and it was lethal even at a concentration as low as 0.6 mM. The results show that microspore embryogenesis can be exploited for studying the cytological effect of Al and for increasing the Al tolerance of wheat.

Paraquat and cold tolerance of DH maize plants selected and regenerated from microspores using paraquat as ROS progenitor were compared to those of a nonselected DH line and the original hybrid. Three of five paraquat-tolerant DH lines possess higher cold tolerance than the control DH line and the original hybrid during the germination period. On the other hand, plants exposed to low-temperature stress (8°C) at the early autotrophic phase of developments resulted in a higher cold tolerance in all of the five paraquat-selected DH lines. The results demonstrated that the microspore-selected DH lines using paraquat as a ROS progenitor resulted not only in higher tolerance against the paraquat-mediated oxidative damage but helped in the protection against the low-temperature stress.

Embryo development in wheat. Currently, great interest is shown in understanding the process of embryogenesis and, due to the relative inaccessibility of these structures *in planta*, extended studies are carried out in various *in vitro* systems. Embryos developing *in vitro* closely followed the morphology of their *in planta* counterparts, and their cell types and tissues also were similar, demonstrating the applicability of the present culture system for studying the process of zygotic embryogenesis. However, some important differences also were detected in the case of *in vitro* development; the disturbance of or lack of initial polarity led to changes in the division symmetry of the zygotes and subsequently to the formation of uniform cells in the globular structures. Presumably, differences between the *in vitro* and *in planta* environments resulted in a lower level of differentiation and maturation in *in vitro* embryos and in abundant starch and protein accumulation in the scutellum.

Publications.

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ITEMS FROM INDIA

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Current activities: Improvement of wheat quality and rust resistance in Indian wheat.

B.K. Das and S.G. Bhagwat.

Improvement of wheat for quality in an Indian wheat background is being carried out by using HMW-glutenin subunits as a selection criterion. The rust resistance genes *Sr31/Lr26/Yr9* and *Sr26*, *Sr24/Lr24* are being combined with high yielding ability and specific HMW subunits. Selected lines from several intervarietal crosses in different generations (F_2, F_3, and F_4) are being evaluated.

Radiation-induced mutations in wheat.

S.G. Bhagwat, B.K. Das, and S. Bakshi.

Earlier, the cultivar C306, known for its good chapati-making quality was treated with gamma rays, and mutants with early flowering were isolated in the M_2 generation. The parent showed anthesis in about 75 days, whereas the mutants showed anthesis in 50 to 63 days. Seven mutant lines were analysed for quality traits. Grain-protein content ranged from 11.9 to 14.9% compared to 13.1% in the parent. SDS-PAGE of total grain protein showed that the mutants had an unaltered HMW-glutenin subunit pattern. Rheological properties estimated using a Brabender Farinograph showed that the mutant lines had comparable water absorption, dough-development time, dough stability, degree of softening, and quality number. The early mutants are being carried forward.

MP3054 and Hindi 62 were treated earlier with gamma rays. M_2-generation plants were grown in 2008-09. Plants that flowered early and had reduced culm length were identified as mutants and harvested individually.

A bread wheat genetic stock with morphological markers for dark glumes, hairy glumes, hairy leaf, purple culm, and red grain was mutagenized with gamma rays. In the M_2 generation, plants with altered morphology were identified and individually harvested. The M_3 was grown as plant-to-row progeny. Although variations for the extent of glume pigmentation or hairiness, spike morphology, and culm length were observed, lines were found to segregate for the mutant traits.

Validation and marker-assisted selection for rust resistance and quality-related genes in Indian wheat.

B.K. Das and S.G. Bhagwat.

Validation of SCAR marker $SCS1302_{609}$ for gene *Sr24*. Molecular markers developed for traits such as disease resistance using a specific genotype may not necessarily work in others. Hence, validating markers in diverse genotypes is important. In this study, marker $SCS1302_{609}$ (Gupta et al. 2006) reported for *Lr24/Sr24* was validated by analyzing

wheat genotypes/cultivars with wide genetic background and also in segregating populations. PCR conditions were optimized by gradient PCR at different temperatures (60.3°C, 61.1°C, 61.9°C, 62.3°C, and 63°C). The optimum annealing temperature was found to be at 61°C. Forty-one wheat genotypes were screened using the primers for SCAR marker $SCS1302_{609}$. The genotypes with *Sr24* yielded a 607-bp band. Wheat genotypes that were reported to carry other *Sr* genes, i.e., *Sr31*, *Sr26,* and also noncarriers of *Sr24^,* did not amplify this marker, indicating that SCAR marker $SCS1309_{609}$ was specific only to gene *Sr24* in the Indian wheat genotypes/cultivars.

SCAR marker analysis in segregating populations. The SCAR marker $SCS1302_{609}$ also was validated by analyzing two segregating populations (Kalyansona/Vaishali and Kalyansona/Vidisha). The genotypes (RR, Rr, and rr) of individual plants in the F_2 generation were identified by scoring the rust reaction of respective F_3 progenies. Analysis of DNA from these plants using marker $SCS1302_{609}$ showed that, out of the 52 resistant plants, 51 amplified the SCAR marker and one failed to amplify. Of the 21 susceptible plants, 19 did not amplify the marker and two showed amplification. This result deviated from the expected 9:3:3:1 (Res/+:Res/–:Sus/+:Sus/–) ratio for independent assortment between the stem rust-resistance locus *Sr24* and the SCAR marker. Three recombinants were observed in the F_2 population. Using MAPMAKER (version 3.0), the distance between $SCS1302_{609}$ and the *Sr24* locus was estimated to be 4.3 cM.

Similarly, an F_2 population from the cross 'Kalyansona/Vidisha' was screened for rust reaction and the presence of marker $SCS1302_{609}$. A total of 18 plants were screened in the F_2 generation for their phenotype. Of the 14 F_2 plants with a resistant phenotype, five were confirmed to be homozygous and nine were confirmed to be heterozygous based on the phenotypes of their progenies in the F_3 generation, and four F_2 plants were found to be homozygous for a susceptible reaction. All the resistant plants showed amplification of the SCAR marker. All five susceptible plants did not amplify this marker. The marker, therefore, was found to be suitable for screening *Sr24* in early generation material.

Marker-assisted breeding to combe rust resistance genes *Sr24* and *Sr31* and *Glu-D1d* (coding for HMW-glutenin subunits 5+10) is underway in a cross between FLW-2 and Kite. In the F_2 generation, ~220 plants are being analyzed using SCAR markers. Plants with both rust-resistance genes and *Glu-D1d* will be selected and advanced.

Marker-assisted backcrossing. To transfer *Sr24* and *Glu-D1d* into HD2189, marker-assisted backcross breeding (MAB) is being carried out. Thirty BC_3F_1 plants were grown, and DNA from leaves of 4-week-old individual plants was extracted and screened using SCAR markers for the two genes. In the winter of 2008–09, seven plants with both markers were identified. Backcrosses were made using the HD2189 recurrent parent and carriers of both the markers.

Genotyping of an RIL population for variation at the Xgwm261 locus.

S. Bakshi and S.G. Bhagwat.

A 192-bp allele at the *Xgwm261* microsatellite locus is known for its association with reduced height gene *Rht8* in hexaploid wheat. Indian wheat cultivars showed a predominance of 165-bp, 174-bp, and 192-bp alleles at this locus. In our earlier analysis of Indian wheat cultivars, the 192-bp allele at the *Xgwm261* locus did not show association with height reduction at the Trombay location, which is a warm environment. An RIL population of 139 lines derived from the two cultivars Sonalika (165 bp) and Kalyansona (192 bp) was assayed for polymorphism at the *Xgwm261* locus. The RIL segregation fit a 1:1 ratio for the presence of 165-bp and 192-bp alleles. These RILs were grown in the field at Trombay during the winter of 2008–09, and data for phenotypic traits of culm length (cm), spike length, spikelet number, and flag-leaf blade area (cm) were recorded. Plant growth was affected by heat stress during the season. Further analysis is in progress.

Genetic relationships among bread wheat genotypes with different seedling thermotolerance using parentage analysis, SSRs, and agronomic data.

Heat stress affects the productivity of wheat in many wheat-growing regions of India. The tolerance of wheat plants to higher than optimum temperature varies at different plant-growth stages. Seedling thermotolerance was assessed among 56 genotypes using membrane thermostability (MTS) and triphenyl tetrachloride tests (TTC). Twenty genotypes with varying thermotolerance were selected and grown in heat stressed and non-heat stressed environments to evaluate their phenotypic performance. Parentage data were used to find the degree of relationship among these genotypes. The

genotypes also were subjected to an SSR analysis to find molecular similarities among the genotypes. Further analysis is underway to deduce the genetic relationships and commonalities based on quantitative, parentage, and SSR data.

Wheat tissue culture.

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Calli were induced from scutellum-supported embryos of immature seeds in three lines of *T. turgidum* subsp. *dicoccum*, two cultivars of *T. aestivum* subsp. *aestivum*, and two experimental stocks with the sphaerococcum trait. Differences in growth rates of the calli from different cultivars were observed. Calli from experimental stocks carrying the sphaerococcum trait were smaller than the rest. Calli obtained from the scutellum-supported embryos of mature seeds in four cultivars of *T. aestivum* subsp. *aestivum* and the two experimental stocks showed that the growth rate of the calli from experimental stocks carrying sphaerococcum trait were significantly lower.

Calli obtained from scutellum-supported embryos of immature seeds were irradiated with gamma rays. Three days after irradiation, the calli were assayed using TTC (2,3,5-triphenyl tertazolium chloride). At 50 Gy, the reduction in TTC values for Unnath C306 (*T. aestivum* subsp. *aestivum*) was 9% and for DDK1029 (*T. turgidum* subsp. *dicoccum*) was 1%. A 65% and 68% decrease in the TTC value of Unnath C306 and DDK1029, respectively, were observed after a 500-Gy treatment.

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Development and use of molecular markers for wheat genomics and breeding

Construction of framework linkage map(s) using trait-specific, intervarietal RIL populations. Three framework linkage maps using three mapping populations have been prepared in our laboratory for QTL interval mapping of various

agronomically important traits. These three mapping populations originally were prepared for the following three traits: (i) grain protein content (GPC); (ii) preharvest-sprouting tolerance (PHST), and (iii) grain weight (GW).

Framework linkage maps of GPC, PHST, and GW populations. Previously, we prepared a framework linkage map for the GPC population using 171 SSR markers. The map spanned a genetic distance of 3,272.4 cM and had large gaps in certain regions, which adversely affected the precision of QTL mapping studies. In view of this, a total of 47 markers were added to the existing framework map of the GPC population making the total number of markers in the map 217. The map now spans a total genetic distance of 3,868 cM.

For the PHST population, the genetic map that was prepared consisted of 214 loci (198 SSR, 5 AFLP, and 11 SAMPL loci) that were distributed on all 21 wheat chromosomes with an average of 10.19 loci/chromosome. The map spanned a genetic distance of 3,972 cM. Of the total mapped loci, a maximum of 77 loci were mapped to the A genome (11 loci/chromosome), followed by 73 loci to the B genome (10.42 loci per chromosome), and 64 loci to the D genome (9.14 loci/chromosome).

For the GW population, a total of 294 loci, including 194 SSR, 86 AFLP, and 14 SAMPL loci, were mapped on all the 21 chromosomes of wheat genome (average 14 loci/chromosome) covering a map length of 5,211 cM. SSRs were more abundant in the A genome (110 SSR loci with an average of 15.7 loci per chromosome) than either the B (103 SSR loci with an average of 14.7 SSR per chromosome) or D genomes (81 SSRs with an average of 11.57 SSR per chromosome).

QTL analysis for grain weight and related kernel traits in bread wheat. Kernel size and shape are important traits in bread wheat because of their relationship with yield and milling quality. For the genome-wide genetic dissection of some kernel traits in bread wheat (kernel size including 1,000-kernel weight (GW) and kernel shape), an intervarietal RIL mapping population derived from the cross 'Rye Selection 111/Chinese Spring' was used. Kernels from Rye Selection 111 are larger than kernels from Chinese Spring in all dimensions. The two parental genotypes and RILs were evaluated in six environments for GW; for other traits (kernel length, width, volume, projection area, vertical perimeter, and horizontal axis proportion), the data was recorded over three environments. Digital image analysis was used for recording the data. Using genotypic and phenotypic data, genome-wide, single-locus QTL analysis (involving inclusive composite interval mapping (ICIM)) and two-locus QTL analysis (involving QTLNetwork) were used to identify the main effect QTL (M-QTL), epistatic QTL (E-QTL), and 'QTL × environment' interactions (QE and QQE). Single-locus QTL analysis for GW revealed a total of 11 QTL (including four major and stable QTL). Threshold LOD scores (3.95 to 32.0) were used to score QTL that contributed significantly to the phenotypic variation (PV = 4.37% to 82.0% per QTL). Similarly, for other related traits, a total of 45 QTL were identified (ranging from four for the vertical perimeter to 13 for kernel length) above threshold LOD values (2.52 to 9.27), which contributed significantly to phenotypic variation (PV = 6.97 for kernel length to 29.87 for projection area). Among the above QTL for GW and related traits, 11 were found to control more than one trait (including four for GW) and were, therefore, considered as pleiotropic/coincident QTL. A two-locus QTL analysis for GW resolved a total of 24 QTL, which included three M-QTL (also detected by single-locus analysis) and 21 E-QTL involved in 12 digenic QQ interactions. Similarly for other traits, a total of 35 QTL including seven M-QTL (five of the seven also were detected through ICIM) and 28 E-QTL involved in 15 digenic QQ and two QQE interactions were detected. The molecular markers linked with the major/coincident QTL for GW and other traits may prove useful in marker-assisted selection for the development of improved bread wheat cultivars.

QTL analyses for grain color and preharvest sprouting. Using the GPC population, single- and two-locus QTL analyses resolved a total of 11 QTL for PHS and 12 QTL for GC. These QTL included both the main-effect QTL (M-QTL; seven for PHS and six for GC) and epistatic QTL (E-QTL; four for PHS and six for GC). The MQTL explained a greater proportion of phenotypic variation (PV) than the E-QTL for both the traits. Four QTL for each of the two traits were co-localized, whereas the remaining M-QTL and E-QTL were unique for each of the two traits. Of all the QTL, one major QTL each for PHS and GC are of interest for breeding PHS-tolerant, white-grained, bread wheat genotypes. The major QTL for PHS, which is independent of grain color, was located on chromosome arm 6AL and explained up to 29.47% PV, whereas the major QTL for GC, co-localized with a minor QTL for PHS, was located on chromosome arm 3BL and explained up to 36.18% PV. Physical mapping placed the QTL for PHS within the 53% proximal region of 6AL, whereas the QTL for GC was placed within 19% of the distal region of 3BL. Comparative genomic analysis also identified 5.47 Mb and 1.63 Mb rice genomic regions, which are orthologous to the wheat genomic regions containing the major QTL for PHS and GC, respectively. SSR markers flanking the major QTL for PHS and GC may be used in wheat-breeding programs aimed at developing PHS-tolerant, white-grained wheat genotypes through MAS. Further-

more, the information gained from physical and comparative mapping may be used in the future for fine mapping and map-based cloning of the above two major QTL.

Genetic diversity and population structure analysis among Indian bread wheat cultivars. As a first step towards association mapping in wheat, we carried out genetic diversity and structure analyses in a collection of 263 Indian wheat cultivars (45 developed during before the Green Revolution and 218 developed during thew post-Green Revolution period) that were released over a period of ~100 years (1910 to 2006). For this purpose, we used a set of 42 SSR markers, one from each arm of the 21 individual chromosomes. The above 42 SSRs had a total of 294 alleles (mean 7.0; range 2–14/SSRs), which included 101 (34.35 %) rare alleles occurring at a frequency of <5%. The average number of alleles/locus (5.91 vs. 5.74) and the estimates of genetic diversity (0.65 vs. 0.61) in the cultivars belonging to pre-and post-Green Revolution periods did not differ significantly indicating that the Green Revolution did not lead to any loss of genetic diversity. The model-based *Structure* analysis identified a total of 14 subpopulations including two subpopulations predominantly comprising cultivars from the pre-Green Revolution period and 12 subpopulations mostly comprising cultivars from post-Green Revolution period.

Introgression of QTL for GPC using MAS. Ten F_1 hybrids were derived from the crosses of each of the 10 elite, Indian, bread wheat genotypes with a high GPC donor genotypes and Yecora Rojo, carrying a major QTL for GPC (*GPC-B1*). The F_1 hybrids were backcrossed with the respective elite recipient parental genotype and the BC_1F_1 plants were raised either in off-season nursery at National Phytotron Facility, IARI, New Delhi during 2004–05 or in the rabi season 2005–06 at the Research Farm of CCS University, Meerut. From the BC_1F_1 onwards, MAS (foreground and background selection) was exercised for three successive backcross generations for the rapid introgression of high GPC QTL and reconstruction of the recipient genotypes. The foreground selection for *GPC-B1* QTL was carried out using STS marker *Xuhw89*, which is tightly linked (0.1 cM) to the *GPC-B1* QTL. Background selection for the recovery of the recurrent parent genotype was carried out using 35 SSRs (representing 52 polymorphic loci) and 12 AFLP primer combinations (889 polymorphic AFLP loci). In each of the 10 BC_3F_1 populations, 2–5 positive plants carrying *GPC-B1* QTL showing higher GPC (up to 1.72% higher than the recipient genotypes) and high genomic similarity (up to 100%) with the recipient parental genotype were selected. In the BC_3F_2 generation, progenies of the six crosses could be advanced in National Phytotron Facility at IARI during the off-season 2006–07, and the BC_3F_3 seed from 29 plants homozygous for the GPC-B1 QTL (identified following foreground selection) was obtained. Using BC_3F_3 seed, 29 BC_3F_3 progenies (belonging to six crosses) were evaluated in five replications at the Research Farm of CCS University, Meerut, during the rabi season 2007–08. Out of these progenies, 17 progenies showed significantly higher GPC (1.08 to 2.51%) over their respective recipient parent genotypes. These progenies with significantly higher GPC did not show any adverse effect of increased GPC on tiller number, spike traits, and 1,000-kernel weight, although some of these progenies did show reduction in plant height. The 17 progenies (BC_3F_4) with significantly higher GPC were evaluated in 2-m single-row plots in five replications at each of the three different locations (Meerut, Pantnagar, and Ludhiana) during the rabi season 2008–09 and the data on six agronomic traits (plant height, spike length, number of spikelets/spike, number of seeds/spike, seed weight/spike, and 1,000-kernel weight) were recorded. Out the above 17 BC_3F_4 progenies, 10 BC_3F_4 progenies were evaluated in separate yield trail in 2-m^2 plots in three replications at Meerut during 2008–09. The data were recorded on grain yield and six agronomic traits. Efforts are underway to record the data on GPC of all the progenies in both the trials. Superior BC_3F_4 progenies will be identified after complete data on all the traits is obtained. In addition to the above, BC_3F_2 progenies of the nine crosses (including four crosses involving the recipient genotypes that were not involved in the above BC_3F_4 progenies) were evaluated at the Research Farm of CCS University, Meerut, during the rabi-season 2007–08. Following foreground selection, 99 plants homozygous for the *GPC-B1* QTL were selected and their progenies (BC_3F_3) were evaluated in 2-m, single row plots in five replications during the rabi season 2008–09 at the Research Farm of CCS University, Meerut. Data were recorded on six agronomic traits (plant height, spike length, number of spikelets/spike, number of seeds/spike, seed weight/spike, and 1,000-kernel weight) on these progenies. Data on GPC will be recorded soon. The BC_3F_3 progenies showing significantly higher GPC and high genomic similarity with the recipient parent genotypes will be evaluated in the future in replicated/multilocation trials for GPC and yield-related traits.

Marker-assisted selection for preharvest sprouting tolerance and leaf rust resistance in bread wheat. In wheat, preharvest sprouting and susceptibility to leaf rust are two major problems that lead to the degradation of grain quality associated with significant losses in yield. We earlier identified a major QTL (*QPhs.ccsu-3A.1*) on chromosome 3A that explained >70% phenotypic variation for PHST across a number of environments. The desirable allele of this QTL was introgressed through MAS into the elite, but PHS susceptible, amber-grained wheat cultivar HD2329 carrying alien leaf rust-resistance genes (*Lr24* + *Lr28*). In each of the backcross generation, foreground selection was exercised using

flanking markers (gwm155 and wmc153), and background selection was performed using 52 polymorphic SSR loci (distributed on all the 21 bread wheat chromosomes) and 146 AFLP loci. In the BC_3F_1, the desirable alleles of the two leaf rust-resistance genes *Lr24* and *Lr28* also were tracked using linked SCAR markers. The reconstituted plants, exhibiting upto 93.4 3% genetic similarity with the recipient parent, were selfed to obtain homozygous plants in the BC_3F_2, which were further evaluated in the BC_3F_3. Seven lines with pyramided PHST QTL and Lr genes exhibited high level of PHS tolerance (PHS score 2–4) and resistance against leaf rust under artificial conditions. The present work demonstrates successful application of marker-assisted selection for targeted pyramiding of QTL/genes for more than one trait into an improved wheat cultivar.

Introgression of QTL for GW using MAS. Crosses involving 10 elite Indian bread wheat genotypes as recipient parents and the genotype Rye Selection 111 (RS111) as a donor parent were attempted during the off-season 2005–06 in the Phytotron Facility at IARI, New Delhi ,and the F_1 seed was collected. These F_1s were raised during the rabi season 2006–07 and were backcrossed with their respective recurrent parents to obtain the BC_1F_1 seed. A total of 470 BC_1F_1 seeds belonging to five crosses [RS111/HD2329, PBW343 (*Lr9*)/RS111, HI977/RS111, K9107/RS111, and RAJ3765/RS111] were obtained. Using above seed material, ~259 BC_1F_1 plants were raised during rabi 2007–08. Following foreground selection, 27 positive plants for markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for GW on chromosome 1A), 127 positive plants for the marker *Xwmc24*, and 57 positive plants for the marker *Xwmc59* were selected. The selected BC_1F_1 plants were backcrossed with their respective recurrent parents and BC_2F_1 seeds was obtained, which were used to raise BC_2F_1 progenies in the field during the rabi season 2008–09. Following foreground selection, three positive plants for both the markers *Xwmc24* and *Xwmc59* (associated with two separate QTL for GW on chromosome 1A) involving recipient genotype PBW343 (*Lr9*), 142 positive plants for the marker *Xwmc24* involving recipient genotypes PBW343 (*Lr9*), K9107 and Raj3765, and 18 positive plants for the marker *Xwmc59* involving recipient genotype PBW343 (*Lr9*) were selected. The selected plants were backcrossed with their respective recurrent parents to obtain BC_3F_1 seed, which will be used to raise BC_3F_1 progenies during 2009–10 rabi season.

Orthology between genomes of *Brachypodium*, wheat, and rice. Comparative sequence analysis of 3,818 *Brachypodium* EST (bEST) contigs and 3,792 physically mapped wheat EST (wEST) contigs revealed that as many as 449 bEST contigs were orthologous to 1,154 wEST loci that were bin-mapped on all the 21 wheat chromosomes. Similarly, 743 bEST contigs were orthologous to specific rice-genome sequences distributed on all the 12 rice chromosomes. As many as 183 bEST contigs were orthologous to both wheat and rice genome sequences, which harbored as many as 17 SSRs conserved across the three species. Primers developed for 12 of these 17 conserved SSRs were used for a wet-lab experiment, which resolved relatively high level of conservation among the genomes of *Brachypodium*, wheat, and rice. The study thus confirmed that *Brachypodium* is a better model than rice for analysis of the genomes of temperate cereals like wheat and barley. The whole-genome sequence of *Brachypodium*, which should become available in the near future, will further facilitate greatly the studies involving comparative genomics of cereals.

Analysis of host–pathogen interaction in leaf rust-infected bread wheat. One major objective in wheat-breeding programs is the development of leaf rust-resistant cultivars. However, for the long-term, effective management of resistance against this disease, the molecular basis of disease resistance and the host-pathogen interaction should be known. For the above purposes, we have attempted both *in silico* and wet-lab approaches to study transcriptome analysis.

In silico study. Transcript based UniGene sets provide great potential to identifying the differentially expressed genes upon infection with leaf rust in bread wheat. Three, wheat cDNA libraries containing ~51,000 ESTs were utilized in the present study. The first cDNA library of the uninfected, disease-resistant Thatcher wheat stock (background gene *Lr10*) contained 22,803 ESTs. The second cDNA library of an infected, disease-resistant Thatcher wheat (background gene *Lr10*) contained 22,740 ESTs, and the third cDNA library of an infected, disease-resistant Thatcher wheat stock (background gene *Lr1*) contained 6,698 ESTs. Using the ESTs belonging to the three libraries, digital gene-expression analysis was conducted with the help of Digital Differential Display (DDD) program available at NCBI. Using this approach, a total of 68 differentially expressed UniGenes were identified, which formed three major clusters, each cluster representing a different class of genes including biotic and abiotic stress responsive genes as well as regulatory genes.

Wet-lab study. For transcriptome analysis of seedling resistance provided by the gene *Lr28*, total RNA was isolated from seven-day-old seedlings of each of the resistant (HD2329 + *Lr28*) and susceptible (HD2329) wheat stocks (a) before inoculation, i.e., at 0 h; (b) at 48 h, 96 h, and 168 h after inoculation with leaf rust pathogen race 77-5; and (c) at 168 h after the mock inoculation. Using the above RNA samples, high-quality cDNA samples were obtained. These cDNA samples were utilized to study the transcript derived fragments (TDFs) following cDNA–AFLP analysis using 17

*Eco*RI+3/*Mse*I+3 γP^{32} labeled primer combinations. Following cDNA-AFLP analysis, over-expressed TDFs in the resistant host following pathogen inoculation are being cloned and sequenced for their functional analysis.

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Preservation of wheat and barley germ plasm under natural storage conditions.

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We preserved seeds of wheat and barley germ plasm for long periods under the natural conditions of Dalang Maidan in the Lahaul Valley to reduce the exorbitant costs of installation and maintenance of artificial and conditioned storage rooms for germ plasm preservation. We also aimed to develop a standby repository for valuable Indian wheat and barley germ plasm presently being maintained in artificial storage rooms at the NBPGR, New Delhi, and DWR, Karnal. Accidental lapses leading to complete seed lethalities in these storerooms always loom large owing to unexpected human error, natural calamities, or electrical failure.

For every 1% decrease in seed moisture and 10°F in storage temperature, the life of seed is doubled (Harrington and Douglas 1970). Therefore, an attempt was made to store wheat and barley germ plasm under natural conditions characterized with low humidity and low temperature year round, at the Regional Station, Directorate of Wheat Research (ICAR), Dalang Maidan, in district Lahaul Spiti (Himachakl Pradesh). This station is located at approximately 32°.21' north latitude and 77°.14' longitude and is about 6-km upstream from the point of origin of the Chenab River, on the banks of the Chandra River at an altitude of approximately 3,300 M (10,000 ft) above mean sea level. This place is located at a very high altitude and enjoys a temperate-dry climate with an average annual rainfall of 250 mm. The area is covered with snow for about 5 months; from December to April.

Temperatures above 20°C during the summer months are a rare phenomenon, even at lower elevations. Records of the natural temperature and relative humidity (monthly means) pertaining to the room used to store the experimental seeds were maintained. The mean monthly temperature inside the storage room varied within a range of –20–20°C, and humidity levels were not above 60% during the 10-year span of the experiment (Table 1, p. 72).

Routinely during the last decade, new germ plasm accessions developed under national wheat program (All India Coordinated Wheat & Barley Improvement Programs) and those collected from international sources are packed in alkathane pouches, arranged together in plastic trays, and stacked in steel boxes at room temperature. This experiment

was initiated in 1997. The oldest seed lot available now is 10-years old and was tested for viability by germination tests. Because the number of lines stored during 1997 at this station was large, the viability test were restricted to 60 bread, 20 durum, 10 dicoccum, and 10 barley lines. In each case, seeds were kept on a wet filter paper sheet in a Petri plate with the lid covered with another piece of wet filter paper. Petri plates with seeds were incubated at room temperature. Percent germination, total normal seedlings, and time to achieve 25% germination were compared to that for 1-year-old seeds to evaluate viability of stored seed. Straight-growing, greenish white seedlings with well-formed roots were treated as normal, while those with a curved appearance, thin texture, and brownish color were treated as abnormal. In each case, 300 grains were examined. Data were pooled for all accessions within the same crop. A mean value and standard deviation of the accessions within the same crop were calcualted.

Table 1. Temperature (°C) and relative humidity (% RH) records of the seed storage site at Dalang Maidan, India.

Month		1997	1998	1999	2000	2001	2002	2003	2004	2005	2006
January	°C	-19	-16	-18	-22	-21	-17	-20	-19	-23	-16
	RH	45	42	43	45	47	42	43	45	43	45
February	°C	-5	-8	-4	-2	-7	-5	-8	-4	-8	-5
	RH	48	49	48	47	43	46	45	46	43	46
March	°C	2	4	4	2	3	6	5	3	2	5
	RH	51	52	54	53	52	52	53	54	54	54
April	°C	9	8	9	9	8	9	6	9	8	7
	RH	56	55	54	58	57	52	56	54	55	53
May	°C	11	13	11	11	12	14	12	11	12	13
	RH	51	52	51	52	54	53	52	51	52	50
June	°C	17	16	18	20	21	21	18	19	18	20
	RH	49	51	52	51	52	55	49	50	51	51
July	°C	22	21	20	23	23	24	23	23	22	21
	RH	58	56	59	54	58	56	56	54	55	56
August	°C	24	23	23	21	19	23	24	23	24	23
	RH	59	53	58	58	54	48	58	56	58	57
September	°C	18	17	18	17	16	18	18	17	18	19
	RH	49	46	49	45	48	42	46	47	47	48
October	°C	11	13	12	13	14	15	12	13	14	12
	RH	44	45	43	42	45	42	43	44	43	42
November	°C	6	5	8	9	11	10	11	12	8	9
	RH	41	42	41	42	40	42	41	40	42	43
December	°C	2	3	3	4	5	3	2	2	3	4
	RH	42	43	42	41	43	42	42	41	41	40

Barley and dicoccum wheat retained germination ability to a greater extent than the durum and bread wheats after storage under natural conditions at Dalang for 10 years (Fig. 1). Also noteworthy is that these crops represented two different groups. The first group, consisting of barley and dicoccum wheat, exhibited germination above 60%, whereas the group of durum and bread wheat were below 60%. Such a grouping also was supported in the counts made for normal vs. abnormal seedlings produced by the germinated seeds (Fig. 2). The another criterion used to assess the viability of 10-year-old seed was the time needed for 25% germination compared to

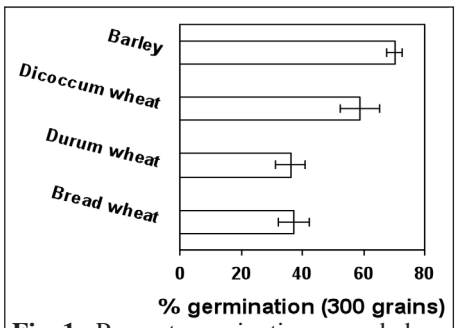

Fig. 1. Percent germination recorded in wheat and barley seeds after storage under the natural conditions for 10 years at Dalang Maidan, India.

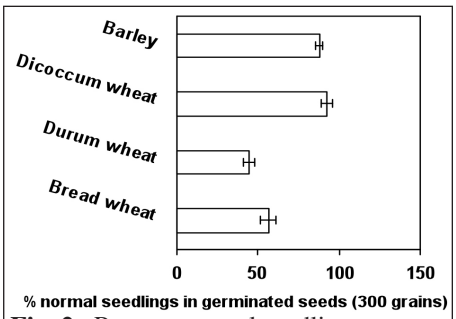

Fig. 2. Percent normal seedlings obtained in germinated seeds of wheat and barley after storage under the natural conditions for 10 years at Dalang Maidan, India.

that for 1-year-old seed of the same crop. All crops except dicoccum wheat experienced an adverse effect from 10 years of storage on the time needed to achieve 25% germination (Fig. 3). The duration was the greatest for bread wheat (72 hours) followed by durum wheat (48 hours) and barley (24 hours).

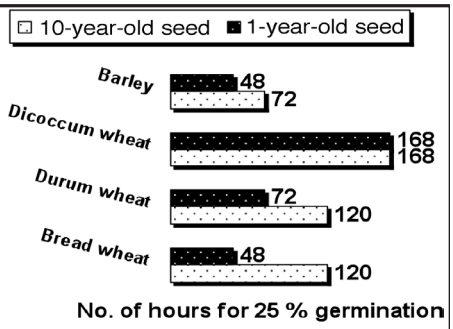

Fig. 3. Time needed for 25% germination of wheat and barley seed after storage under natural conditions for 10 years at Dalang Maidan, India.

From these observations, we conclude that wheat and barley germ plasm can be stored safely at least for 10 years under the natural conditions that prevail at Dalang Maidan, India (monthly mean temperature -20–20°C and mean RH below 60 %). Justice and Bass (1978) reported for wheat a relative storability index of 2 (50% of the seed are expected to germinate after 3–5 years of storage). Our investigations showed that seed germinated normally after 10 years of storage (more than 25% in each case) and in terms of germ plasm maintenance, without spending exorbitant prices to construct and run artificial storage systems. Furthermore, we also concluded that barley and dicoccum seed can withstand long-term storage effects better than bread and durum wheat. However, that dicoccum and barley seed exhibits greater viability compared to bread and durum wheats after 10-years of storage needs further investigations. Seeds of other Gramineae species are known to survive under storage for more than 10 years (Pristley 1986), and we expect that it might prove true for wheat and barley stored under the natural conditions of Dalang Maidan.

Summary. New germ plasm accessions in wheat and barley result from the programs engaged with prebreeding, natural exploration, introductions, and breeding. Due to the scarcity of land at research farms, growing enormous numbers of new accessions every year for maintenance may not be possible. Alternatively, these germ plasm collections may be maintained as seed under storage systems. Conventionally, germ plasm is preserved for long periods in artificially erected storerooms that need huge monetary investments for development and maintenance. Moreover, such structures are prone to accidental handling and unreliable electric supply, which may lead to lethality of valuable stocks. The natural preservation facility available at Dalang Maidan, Regional Station, Directorate of Wheat Research (ICAR) in the Lahaul Valley is envisaged as a potential alternative to unreliable and expensive artificial storage systems. The 10-year-old seed of wheat and barley stored at this station were tested for their viability using a seed-germination test. All seeds were found to have maintained their viability. The dicoccum and barley lines maintained their viability more efficiently than the bread and durum wheats.

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Effect of subculturing on infection potential of Tilletia indica, the incitant of Karnal bunt of wheat.

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Abstract. Karnal bunt resistance in wheat breeding lines was tested by artificial inoculation of emerging spikes with secondary sporidia raised on growth media. The sporidial cultures were maintained through subculturing with weekly transfers. A significant reduction in the production of primary and secondary sporidia was observed in the 2nd, 3rd, 4th, and 5th descendant cultures (DC2, DC3, DC4, and DC5) compared to the parental culture (PC). The budding potential of the primary sporidia to secondary sporidia and self-budding in the secondary sporidia tended to decrease with weekly transfers during subculturing. Secondary sporidia harvested from the cultures were inoculated onto the susceptible wheat cultivar HD 2009 at growth stage Z 49 (emerging spike) for evaluating the infection potential of the parental and descendent cultures (PC and DC). We found that disease severity was reduced significantly in spikes inoculated with descendant cultures compared to the parental culture.

Karnal bunt (KB) of wheat was first reported from northern India by Mitra (1931). The disease is distributed over all of northwest India in an endemic form and occurs in traces over a larger part of south Asia (Warham 1986). Besides India and Pakistan, KB is reported from other countries such as Nepal (Singh et al. 1989), Iraq (CMI 1989), Mexico (Duran 1972), the U.S. (Ykema et al. 1996), and South Africa (Crous et al. 2001). Karnal bunt impairs the quality of wheat-based products and reduces seed germination (Mehdi et al. 1973; Bedi and Meeta 1981; Bansal et al. 1984). The disease also poses serious implications for international trade and exchange of wheat germ plasm in view of the pathogen's migration into new areas (Royer and Ritter 1988). This disease is known to hamper the export of wheat from India because of stringent quarantine restrictions posed by several importing countries as a preventive measure to avoid entry of KB into their territory (Nagarajan et al. 1997).

Cultivation of resistant cultivars offers the best promise for an economical and environmentally safe management of this disease. Resistance to KB in cultivars during their breeding is evaluated by artificial infection tests (Gill et al. 1993). These tests involve inoculation of secondary sporidial suspension of *T. indica* with the help of a hypodermic syringe into the emerging spike at growth stage Z 49 of wheat crop (Aujla et al. 1987). An inoculum density of 10,000 secondary sporidia/mL of water is required for successful creation of artificial epiphytotics of KB (Gill et al. 1993). Sporidial inoculum is prepared by making a water suspension of the sporidia harvested from culture slants maintained for longer periods (Munjal 1974; Dhiman and Bedi 1983). Sporulating mycelium is abundant at 18°C for up to 7 days (the surface of the medium fully occupied by shiny white mycelium; Fig. 4, top left), then gradually deteriorating leading to desiccation (Fig. 4, top right). Therefore, the mycelium needs to be transferred to new agar slants to remain viable and sporulating. Fresh mycelial cultures are initiated from teliospores in December in order to have an adequate amount of inoculum for the large number of breeding populations in February of the next year, when test entries are at growth-stage Z 49. The cultures are transferred at least five times, to fresh potato dextrose yeast extract medium (PDYEA), to maintain their viability before their use as inoculum during the middle of February (average temperature 18–22°C). The effect of repeated transfers of sporidial cultures to fresh growth media on their viability and ability to produce secondary sporidia (responsible for infection) is reported here.

Fig. 4. Mycelium of *Tilletia indica*: fresh and viable (upper left), old and desiccated (upper right); allantoid or secondary (curved) and filiform or primary (thread like) sporidia budding into secondary sporidia (lower).

Materials and methods. Teliospores were germinated at 12°C over a thin layer of 2% agar in a Petri plate after extracting from punctured sorus of an infected kernel. Mycelial cultures were initiated 6, 5, 4, 3, 2, and 1 weeks prior to the onset of growth stage Z 49 in the KB-susceptible wheat cultivar Arjun (HD 2009) by incubating germinated teliospores on the slants of PDYEA at 18°C. On successive transfers to new slants at 7-day intervals, the cultures initiated 6, 5, 4, 3, and 2 weeks attained the 5th, 4th, 3rd, 2nd, and 1st descendant generation, respectively at the onset of growth stage Z 49 in HD 2009. At the time of inoculation, cultures transferred for 5, 4, 3, 2, and 1 times were available. A sporulating culture also was initiated one week before onset of growth stage Z 49 in HD 2009 and was designated as the parent culture (PC) and inoculated without any transfer to serve as a control. The descendent cultures (DC) obtained after the 1st, 2nd, 3rd, 4th, and 5th transfers were designated DC1, DC2, DC3, DC4, and DC5, respectively. The parental and descendant cultures were examined for production of primary and secondary sporidia in actual and budding states (Fig. 4, bottom). One mL of distilled water was poured onto the slant followed by vigorous shaking. Simultaneously, 1 mL of sporidial suspension was mounted on a slide. Six slants were observed in each case and five slides/slant were prepared. Enumeration of sporidia was made in one microscopic field (400X) randomly focused on each slide. The data were subjected to an analysis of standard deviation about the mean. Microsporidia harvested from the PC and DCs were inoculated on the spikes of susceptible wheat cultivar HD 2009 at stage Z 49 (Zadoks et al. 1974) following the methods of Aujla et al. (1987). Each culture was inoculated on nine spikes. The percent coefficient of infection (CI) was calculated individually for each spike after harvest (Aujla et al. 1989). The KB severity of nine spikes was recorded as percent CI, and the data were subjected to an analysis of standard deviation about the mean.

Results and discussion. The PC and their respective DCs up to the fifth generation were examined for their potential to produce primary and secondary sporidia in the actual and budding states. Production of primary and secondary sporidia remained equal between the PC and the DC1. However, a significant reduction in the sporidia count was noted in the 2nd, 3rd, 4th, and 5th DCs compared to the parental cultures. A gradual decrease occurred in sporidia production after from the DC2 to the DC5 generation (Figs. 5A and B, p. 75). Primary and secondary sporidia showing budding to pro-

duce more secondary sporidia (Figs. 5C and D) were at the maximum in the PC, DC1, and DC2 cultures for primary and the PC and DC1 for the secondary without any significant difference. However, budding was reduced significantly in the DC3, DC4, and DC5 for primary sporidia and the DC2, DC3, DC4, and DC5 for secondary sporidia compared to that in the PC (Figs. 5C and D).

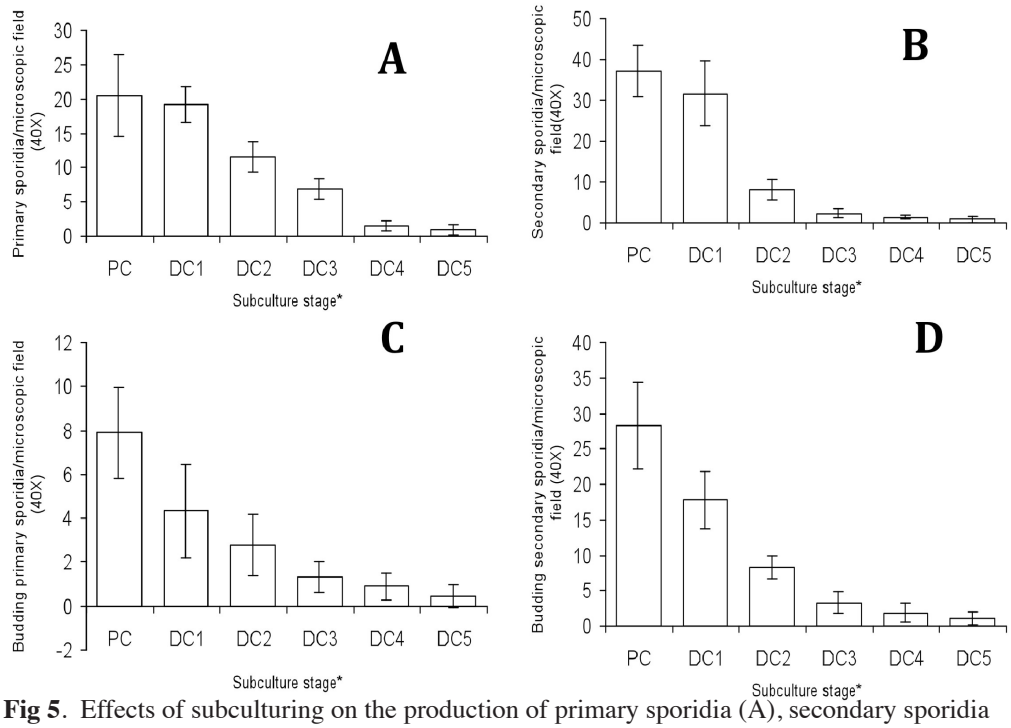

Fig 5. Effects of subculturing on the production of primary sporidia (A), secondary sporidia (B), budding primary sporidia (C), and budding secondary sporidia (D). PC, parent culture obtained from germinated teliospores; DC1, descendant culture generation 1, obtained after subculturing the PC; DC2, descendant culture generation 1 obtained after subculturing the DC1; DC3, descendant culture generation 1 obtained after subculturing the DC2; DC4, descendant culture generation 1 obtained after subculturing the DC3; and DC5, descendant culture generation 1 obtained after subculturing the DC4.

The infection potential of the PC, DC1, DC2, DC3, DC4, and DC5 also was evaluated by inoculating a spore suspension onto spikes of the KB-susceptible HD 2009 at growth stage Z 49. The PC and DC1 inflicted the maximum disease severity without any significant differences (Fig. 6), but disease severity was reduced significantly in spikes inoculated with DC2, DC3, DC4, and DC5.

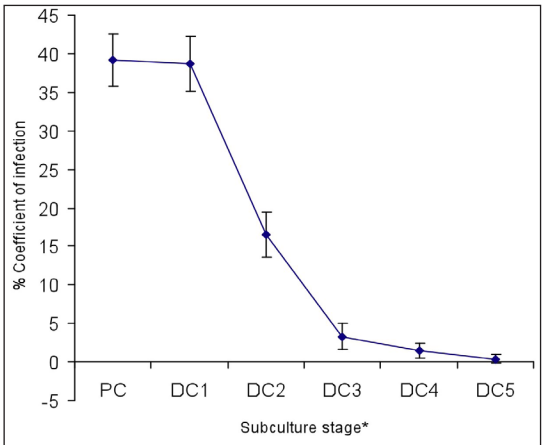

Fig. 6. The effect of subculturing on the infection potential of *T. indica* on the susceptible wheat cultivar HD 2009. See Fig. 2 for description of abbreviations.

Like other major diseases of wheat, evaluating resistance to KB during breeding of a cultivar is an essential practice in Indian wheat programs (Gill and Aujla 1986). Before their release to farmers, wheat cultivars are evaluated in the Karnal Bunt Screening Nursery (KBSN) under artificial and natural conditions (Nagarajan et al. 1997) for resistance in multilocation nurseries at KB hot spots. All popular cultivars now grown in KB-effected areas of northwest India were either rated free of disease or resistant/tolerant based on a percent coefficient of infection below 5 during the artificially inoculated KBSN tests. However, none of the cultivars maintained resistance when cultivated in farmer fields in northwest India. The field susceptibility of the cultivars may be attributed to inadvertent recording of disease escapes, less disease pressure, or a higher level of resistance under artificial testing. Use of inadequate inoculum may be one of the several reasons contributing to a disease escape or less disease pressuer. To ensure ample availability of inoculum at the onset of the critical susceptibility stage Z 49 (Zadoks et al. 1974), a common practice uses cultures initiated in December for inoculations in February and frequent transfer (at least weekly) to fresh growth medium to avoid desiccation. Therefore, fifth generation cultures are inoculated for creation of artificial epidemics.

This study compared the infection potential of cultures originating from teliospores and those obtained as successive descendants after transfer into fresh growth media. The criteria for assessing the infection potential of the cultures was estimated using the secondary sporidia either as such or through the production of primary sporidia that contribute to inoculum potential by producing secondary sporidia through the process of budding (Gill et al. 1993). The budding state was used in the case of secondary sporidia, because it is a natural phenomenon for the mass multiplication of secondary sporidia (Holton 1949; Krishna and Singh 1982, 1983; Aujla et al. 1988).

Secondary sporidia are best produced by PCs that are freshly isolated from the teliospore (Fig. 5B, p. 75). Their transfer to fresh growth medium, if required for the purpose of avoiding desiccation, has no significant impact on their potential to produce secondary sporidia. The same case is true for primary sporidia. The budding potential of sporidia also was the best in the PC and DC1 for secondary sporidia and the PC through the DC2 for primary (Fig. 5C and D, p. 75). The effectiveness of inoculum potential of the PC and DC1 was supported further by the significantly higher severity of disease they caused in spikes of the susceptible HD 2009 compared to other descendant cultures (Fig. 6, p. 75). KB symptoms did not appear in spikes inoculated with cultures obtained after fourth subculturing. The percent CI was reduced significantly from 37.60 to 15.80 in spikes inoculated with cultures resulting from the second transfer (Fig. 6, p. 75).

Based on these findings, we suggest that for satisfactory creation of artificial epidemics of Karnal bunt, inoculating test materials with cultures obtained directly from teliospores or from their first descendant cultures is important.

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Genetic analysis of Karnal bunt (Tilletia indica) resistance in bread wheat.

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Abstract. Karnal bunt of wheat caused by *Neovossia indica* (Mitra) Mundkur (Syn. *Tilletia indica*) has serious implications for the international trade of commercial grain and exchange of wheat germ plasm. In this study, generation mean analysis was carried out on six generations in six crosses of bread wheat to study the genetics of Karnal bunt resistance. A scaling test indicated the presence of nonallelic epistatic interactions. A six-parameter model revealed that dominance (h) was more effective than the additive (d) gene action due to higher magnitude of resistance. Among the epistatic effects, 'additive × additive' (i) action was more important as compared with the 'additive × dominance' (j) component. Complementary epistasis was present in three crosses (WL 6975/PBW 343, WL 6975/HD 2687, and WL 6975/HD 2009), whereas duplicate epistasis also was observed in three other crosses (W 485/PBW 343, W 485/HD 2687, and W 485/HD 2009). The implications of various gene actions in breeding for resistance against Karnal bunt in wheat is discussed.

The production of wheat is adversely affected by a number of factors including various biotic stresses. Karnal bunt of wheat (KB) has gained greater note in recent years because of its widespread prevalence in the main wheat-growing region of northern India causing significant qualitative and quantitative losses. Because the disease is soil, air, and seed borne, only limited success in control can be achieved through fungicides. Breeding of resistant cultivars is an effective method to combat this disease. We undertook a systematic study to explore the genetic basis of resistance to KB, which is a prerequisite for breeding KB-resistant cultivars of wheat.

Genetic resources with resistance or a low level of resistance to KB have been identified. Resistance can be transferred from these genotypes to high-yielding wheat cultivars through a breeding program. Much information on the nature and relative magnitude of the genetic components of variation (additive and dominance) has been generated by diallel analysis, which does not provide knowledge on nonallelic gene actions operating in the inheritance. A nonallelic interaction could inflate the measure of additive and dominance components. Therefore, identifying and estimating the components of epistasis, along with the additive and dominance components, is important so that fixed components can be exploited using suitable breeding techniques. The present study was carried out to assess the nature and magnitude of gene action on disease resistance.

Materials and methods. Two KB-resistant stocks (W485 and WL 6975) and three well-adapted and promising but KB-susceptible cultivars (PBW 343, HD 2687, and HD 2009) were sown in an RBD design with two replications at the Experimental Farm of DWR, Karnal. Crosses were made among promising wheat cultivars and the resistant genetic stocks in a diallel fashion. After harvest, a portion of the F_1 seed and the parental lines were sown for backcrossing BC_1 ($F_1 \times P_1$) and BC_2 ($F_1 \times P_2$) progenies at the Wheat Summer Nursery (WSN), Dalang Maidan, Lahaul Spiti (H.P.) during 2006. Twenty-nine populations consisting of six F_2, six F_1, six BC_1, six BC_2, and the parents were sown in a randomized block design with two replications during the 2006–07 crop season. Each plot consisted of five 2-m rows spaced 30 cm apart and maintaining a 5-cm plant-to-plant distance for the parents, F_1s, BC_1, and BC_2, and 10 2-m rows of spaced 30 cm apart maintaining a 5-cm plant-to-plant distance for the F_2s. In each replication, 10 plants of each parent, BC_1, and BC_2; five plants from each F_1; and 25 plants from each F_2 were randomly selected and tagged. All selected plants were artificially inoculated with an aqueous suspension of allantoid sporidia of *T. indica* (50,000 spores/mL) into the boot (growth stage 49) using a hypodermic syringe, followed by misting by a perfo-spray system (Warham 1984). At maturity, separate spikes of each plant in different generations were harvested. Threshed seeds were examined for disease incidence by manual sorting and counting percent infection.

Seeds were rated for resistance based on the type of sorus produced. Sorus size was grouped broadly into four grades and a numerical rating of 0.25, 0.5, 0.75, and 1.0 was assigned to each grade (Aujla et al., 1989). The percentage of grain showing KB infection with the numerical rating and the partial coefficient of infection (CI) value was obtained. The data were subjected to a scaling test (Mather 1949) and generation mean analysis (Hayman 1958).

Results and discussion. The cultivars W 485 and WL 6975 showed resistant to Karnal bunt, whereas PBW 343, HD 2687, and HD 2009 were susceptible. The F_1 mean infection was significantly lower than the midparent value, indicating the predominance of resistance over susceptibility in all the six crosses (Table 2). In the F_2, mean infection was significantly less than that of the respective P_2 in all crosses. Infection scores in the BC_1 were less than those of the P_2 and F_2, which indicated the transfer of dominant resistance genes from the P_1 (resistant parent), whereas in the BC_2, it was higher than in F_1 and BC_1, indicating a corresponding dilution of the resistance genes by crossing with a susceptible parent (P_2).

Table 2. Mean performance of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) for percent coefficient of infection for resistance to Karnal bunt.

Cross	Mean					
	P_1	P_2	F_1	F_2	BC_1	BC_2
W 485 / PBW 343	0.16 ± 0.11	28.19 ± 2.08	4.16 ± 0.89	13.27 ± 1.63	0.15 ± 0.07	9.28 ± 1.67
W 485 / HD 2687	0.16 ± 0.11	37.06 ± 3.82	0.70 ± 0.38	26.69 ± 2.54	1.78 ± 0.31	8.07 ± 1.29
W 485 / HD 2009	0.16 ± 0.11	42.26 ± 2.19	1.23 ± 0.82	19.04 ± 2.90	0.35 ± 0.15	15.43 ± 1.56
WL 6975 / PBW 343	0.74 ± 0.29	28.19 ± 2.08	14.96 ± 1.68	17.53 ± 2.34	17.74 ± 2.45	36.87 ± 4.09
WL 6975 / HD 2687	0.74 ± 0.29	37.06 ± 3.82	2.06 ± 0.84	14.10 ± 1.67	0.22 ± 0.12	16.57 ± 1.79
WL 6975 / HD 2009	0.74 ± 0.29	42.26 ± 2.19	5.91 ± 1.14	14.23 ± 1.86	2.30 ± 0.27	16.92 ± 1.39

A generation mean analysis was made separately for each cross to determine additive, dominance, and epistatic gene effects. Of the four scaling tests (A, B, C, and D) at least one, two, three, and four scales were found significant in all crosses, indicating the presence of nonallelic, epistatic interactions (Table 3). The A, B, C, and D individual scaling tests indicated the presence of an epistatic interaction for resistance to KB in all the crosses; at least one scaling test was significant. Therefore, the six-parameter model was applied. Estimates of standard notations of the six parameter model for resistance to KB are presented in Table 4 (p. 79). All types of epistatic interactions, additive (d), dominance (h), additive × additive (i), additive × dominance (j), and dominance × dominance (l), were significant in four crosses (WL 6975/HD 2009, W 485/PBW 343, W 485/HD 2687, and W 485/HD 2009), whereas additive (d), dominance (h), additive × additive (i), and dominance × dominance (l) types of epistasis were found significant in two crosses (WL 6975/PBW 343 and WL 6975/HD 2687).

Table 3. A, B, C, and D scaling tests in the different cross combinations of wheat for Karnal bunt resistance. * and ** indicate significance at the 5 and 1 percent levels, respectively.

Crosses	Scaling test			
	A	B	C	D
W 485/PBW 343	-4.03** ± 0.91	-13.80** ± 4.03	16.43* ± 7.07	17.13** ± 3.66
W 485/HD 2687	2.70** ± 0.74	-21.62** ± 4.62	68.17** ± 10.89	43.54** ± 5.25
W 485/HD 2009	-0.69 ± 0.88	-12.63** ± 3.89	31.29** ± 11.91	22.30** ± 6.00
WL 6975/PBW 343	19.78** ± 5.19	30.59** ± 8.61	11.27 ± 10.18	-19.55** ± 6.69
WL 6975/HD 2687	-2.37* ± 0.92	-5.98 ± 5.30	14.48* ± 7.89	11.41** ± 3.80
WL 6975/HD 2009	-2.06 ± 1.29	-14.33** ± 3.72	2.10 ± 8.09	9.24* ± 3.98

Chand et al. (1989) reported both additive and dominance gene effects of a diallel set involving the parents WL 711 and HD 2009 (KB susceptible) and WL 2217, UP 1008, WL 1562, Sonalika, VL 421, HB 208, TZPP, and WG 2038

Table 4. Components of generation means using a six-parameter model for Karnal bunt resistance in six cross combinations. m, mean; d, additive effect; h, dominance effect; i, additive × additive; j, additive × dominance, and l, dominance × dominance type of gene interactions. * and ** indicate significance at the 5 and 1 percent levels, respectively.

Crosses	Parameters					
	m	d	h	i	j	l
WL 6975/PBW 343	17.53** ± 2.34	-19.14** ± 4.77	39.60** ± 13.52	39.10** ± 13.38	-5.41 ± 4.88	89.46** ± 21.62
WL 6975/HD 2687	14.10** ± 1.67	-16.36** ± 1.80	39.66** ± 07.88	-22.82** ± 07.60	1.81 ± 2.63	31.16** ± 10.67
WL 6975/HD 2009	14.23** ± 1.86	-14.63** ± 1.42	34.07** ± 08.12	-18.48* ± 07.97	6.14** ± 1.80	34.87** ± 09.88
W 485/PBW 343	13.27** ± 1.63	-9.13** ± 1.67	-44.27** ± 07.45	-34.26** ± 07.32	4.89* ± 1.97	52.08** ± 09.73
W 485/HD 2687	26.69 ± 2.54	-6.3** ± 1.33	-104.99** ± 10.69	-87.09** ± 10.59	12.16** ± 5.33	106.01** ± 12.11
W 485/HD 2009	19.04** ± 2.90	-15.08** ± 1.56	-64.59** ± 12.08	-44.61** ± 12.00	5.97** ± 1.91	57.92** ± 13.45

(KB resistant). The predominant role of additive gene effects was shown in the inheritance of KB resistance by Nanda et al. (1995) and Sharma et al. (2005). Singh et al. (1995) reported three, independently segregating loci with partial dominance. Other genetic studies on KB resistance in wheat have indicated that one to nine major genes control the resistance to KB in various wheat germ plasm. The genes have been identified as influencing reaction to the pathogen (Morgunov et al. 1994; Fuentes-Davila et al. 1995; Singh et al. 1995a, b, 1999. Villareal et al. (1995) and Singh et al. (1994) also reported the analysis of six basic generations of intervarietal crosses between three resistant (HD 29, W 485, and HP 1531) and two susceptible (WL 711 and HD 2329) parents amplifying the involvement of one to two major genes together with some minor genes/modifiers imparting resistance. In the widely studied cross 'HD 29/WL 711', resistance has been shown to be controlled by a single recessive gene (Bag et al. 1999). In another study, additive gene action was observed to be more important in the genetic control of KB % infection, whereas dominant gene action was pronounced for coefficient of infection (Sharma et al. 2001).

A comparison between dominance (h) and 'dominance × dominance' (l) for negative and positive signs of gene effects revealed the preponderance of duplicate type of epistasis for resistance to KB in three cross combinations, W 485/PBW 343, W 485/HD 2687, and W 485/HD 2009. Duplicate-type epistasis will be a hindrance for the improvement of the population where dominance-type gene effects also exist and, thus, heterosis can not be exploited. Gill and Aujla (1987) reported that resistance was dominant over susceptibility and subject to duplicate epistasis.

The preponderance of complimentary type of epistasis for resistance to KB was observed in three cross combinations, WL 6975/PBW 343, WL 6975/HD 2687, and WL 6975/HD 2009, evidence for the occurrence of dominance (h) and 'dominance × dominance' (l) for negative or positive genes effects in contrast to complimentary gene effects where both positive and negative signs appear. Complementary-type epistasis, which is more favorable genotype improvement, was found in this study. The complementary type of epistasis also has been reported by Villareal et al. (1995).

The high frequency of epistasis observed in the present study proves the importance of nonallelic interactions for genetic control of resistance to KB in wheat. Our results show that dominance (h) effects and 'dominance × dominance' (l) epistatic effects were comparatively more important for the inheritance of KB resistance in all cross combinations, supporting the active role of nonallelic gene interactions for genetic improvement of KB resistance in wheat. Therefore, breeding methods such as reciprocal and recurrent selection by intermating desirable F_2 segregates followed by selection will help in breeding KB-resistant cultivars.

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Evaluation of wheat genotypes under different soil, tillage and production conditions through participatory varietal selection approach in India.

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Summary. Field experiments assessed the genetic potential of improved and promising wheat genotypes under different soil types, tillage options (zero and surface seeding), and production conditions (timely and late sowing) for their suitability to eastern and far-eastern parts of India. A benchmark survey identified the issues and problems of the region and four to five major problems were identified. Based on the survey results, a set of 12–15 promising, bread wheat genotypes, including released cultivars, was selected. Experiments were conducted under different production conditions (late and timely sowings), tillage options (zero and surface seeding), and problematic soils (saline and alkaline soils). We concluded that in undulating areas where soil moisture is very high, cultivars HUW 468, HW 2045, and NW 1014 performed better and gave higher yields when sown through surface seeding. Similarly, under late-sown conditions, DBW 14, NW 1014, HW 2045, HD 2643, and DL788-2 performed better than others. Zero-tillage technology was found more useful than other tillage options, because it helped to advance wheat sowing by 10–15 days in otherwise late-sown areas, and cultivars such as PBW 343, DBW 14, and HW 2045 were found suitable, because they outyielded others. At each site, one or more of the experimental genotypes showed high or good grain yield, acceptable maturity, plant height, and disease resistance compared to the check cultivars. These improved cultivars already are released in the region and many have been used in breeding programs as parents. Identification of wheat genotypes with high grain yield in individual sites underlines their value for increasing grain yield and agronomic performance. An impact assessment identified the preferred traits/cultivars of the farmers and revealed that yield is still the first choice of farmers, followed by maturity duration, plant height, plant stand, early vigor, and grain appearance. The results of this study will help breeders to produce cultivars that would be quickly accepted among farmers.

Bread wheat is a major staple food in the Indo-Gangetic Plains (IGP) of south Asia. India is one of the largest wheat producers in the world with about 27 x 10^6 ha under cultivation and production hovering around 70 x 10^6 tons (Anonymous 2001, 2005a). The demand for wheat is expected to be approximately 109 x 10^6 tons to feed a 1.3 billion population by the year 2020 to provide 180 g of wheat per person per day in India. The IGP comprise the northwestern and eastern parts of the major wheat-growing area of the country. The North Eastern Plains Zone (NEPZ) is an eastern region of India that includes the eastern UP, Bihar, Jharkhand, West Bengal, Assam, and Orissa provinces and accounts for almost 9 x 10^6 ha out of the total 27.0 x 10^6 ha area under wheat. Although the yield potential of wheat in NEPZ is about 4.5 t/ha, farmers realize a yield of just 2.2 t/ha. The constraints to potential and actual yield (technology gap, socio-economic factors, and climate) and the effects of a rice–wheat cropping system on wheat production have been discussed (Singh 1998; Jag Shoran 2003). Wheat generally is grown during the winter (mid-November to mid-April), but late receeding

of rains coupled with a delayed harvest of the preceding wet-season crops, such as basmati rice, groundnut, toria, pigeon pea, cotton, potato, and sugarcane, force wheat to be sown late, even into mid-January (Aslam et al. 1989). Wheat planting is often delayed due to the dominant rice–wheat cropping (Hobbs and Giri 1997).

Another important factor to consider is the temperature regime wherein a sizeable area in this region of India gets hot winds that coincide with grain filling (spike initiation to anthesis) and ripening (anthesis to maturity) in late-sown wheat, thus adversely affecting the grain growth and quality during the months of March and April (Anonymous 2001; Nagarajan 2002). Low productivity is observed under high temperatures, due to a reduction in the number of effective tillers/plant or per unit land area, number of grains/spike, and 1,000-kernel weight. Identifying high-yielding wheat genotypes for the IGP is a challenging task, because wheat cultivation practices and microclimates in the region are diverse (Sharma and Duveiller 2004). Keeping all the above in view, we initiated a multipronged strategy to deal with the problems directly or indirectly affecting wheat yields and to give an impetus to a lagging wheat-improvement program in this region through a project planned and executed by the Directorate of Wheat Research, Karnal.

Materials and methods. The wheat area in the eastern and far eastern parts of the country is ridden with number of diverse production factors related to soil types, temperature fluctuations, and moisture regimes that limit production potential of available wheat cultivars. The farmers grow only a few of the improved wheat cultivars available for cultivation in this region. Considering these problems, the northeastern region was chosen for participatory cultivar selection involving the farmer's participation. The experimental sites selected were near Pusa, Ranchi, Bilaspur, and Varanasi. To facilitate trial management and data recording at different sites, a field book, containing details of layout, blank data recording sheets, and other necessary instructions for trial management and data recording was provided to each collaborator. Different sets of improved but promising cultivars (12–15) along with checks were selected for specific production conditions such as saline-alkaline soils, timely and late-sown conditions, high-moisture areas along with different tillage options such as zero and surface (Table 5).

Table 5. List of the improved wheat cultivars and checks tested at four sites using farmers' preferred attributes.

Center	Cultivars and checks used	Preferred attributes
IARI–Pusa	Test cultivars: HD 2733, PBW 343, HP 1731, HP 1761, HP 1744, HD 2643, HW 2045, PBW 443, PBW 373, HUW 468, K 9107, NW 1012, NW 1014, HI 1418, HI 1454, HI 149 Checks: UP 262, HUW 234, C 306, Sonalika	Grain yield, maturity duration, plant height
IGKV–Bilaspur	Test cultivars: GW 190, DL 788-2, GW 273, HW 2004, GW 173, LOK 1, MP 5013, GW 322, DL 803-3, HI 1500, HI 1490, HD 2781, HI 1498, RAJ 1555, GW 1172 Checks: Sujata, C 306, WH 147, Sonalika	Plant stand, early vigor
BAU–Ranchi	Test cultivars: HP 1731, HP 1633, HD 2733, HD 2643, HUW 468, LOK 1, NW 1012, NW 1014, K 9107, DL 788-2, DL 803-2, PBW 343, PBW 373, HW 2045, PBW 443, HP 1761, UP 2338 Checks: UP 262, RR 21, Kanchan, Kundan, C 306, HUW 234, Sonalika	Grain appearance, spike size
BHU–Varanasi	Test cultivars: HUW 468, PBW 343, HD 2643, RAJ 3765, HUW 533, KRL 1-4, KRL 19 Checks: HUW 234, UP 262, Sonalika	Disease resistance, foliage color

The field trials were planted in completely randomized block design with two replicates. Individual plots were seeded using the standard seed rate of 120 kg/ha. Each genotype was grown in an individual plot having 50 30-m rows spaced 0.25 m apart. In most cases, the trials were planted within the recommended sowing period under each production condition. Recommended doses of fertilizers, irrigation schedule, and other management practices were applied at each site.

Data were recorded for the predecided attributes under each production condition. At maturity, plant height was measured for each plot from ground level to the tip of the spikes. Days-to-maturity was recorded when peduncles changed color. After maturity, plots were individually harvested and threshed. Grain yield was recorded on an indi-

vidual plot basis at each site. Thousand-kernel weight was recorded from grains randomly taken from each plot. Each 'year × site' combination was considered a unique and random environment, whereas genotypic effect was analyzed as fixed. The highest yielding genotype was compared with the checks to assess their genetic superiority. Along with grain yield, other agronomic characters were considered to determine superiority and adoption potential of the highest yielding experimental lines. Each experiment was conducted at a minimum of five locations for 3 years. The farmers and scientists were invited for a joint evaluation of the experiments. Only the farmers determined the traits of preference for each production condition. The location data were analyzed, and the results are presented below.

Results and discussion. The production condition experiments conducted for 3 years were analyzed for the cultivars that suited each production condition and tillage option along with the preferred traits. A significant effect was observed for location on grain yield, 1,000-kernel weight, days-to-heading and maturity, and plant height each year (ANOVA not shown). The genotypes differed significantly ($P < 0.05$) for most of the traits each year. The 'genotype × site' interaction was significant ($P < 0.05$) for all traits, suggesting that the relative genotypic values for these traits changed significantly over sites. A wide range of values among genotypes for individual traits indicated wide variation. Variation among sites for each production condition in all years suggested significantly distinct environments (data not shown). The least significant difference was estimated and used for comparing the performance of genotypes under saline soils. Performance, with respect to grain yield, greatly varied across sites and production conditions, suggesting diversity among the sites. The most suitable genotypes for each production condition and for the different sites were identified based on performance primarily judged by grain yield, mean 1,000-kernel weight, maturity, plant height, and resistance.

Table 6. Performance of promising wheat genotypes under saline soil conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India.

Genotype		HUWL 2081	NWL(S) 13	KRL 19	LSD
Salinity	pH	8.3	8.5	8.3	—
	Ece	0.32	0.28	0.33	—
Maturity duration		123	124	125	2.11
1,000-kernel weight (g)		41.4	38.1	40.4	2.93
Yield (Q/ha)		39.5	38.8	37.3	1.40

Evaluation of genotypes for salinity tolerance. Of the 15 genotypes, including advanced lines that were evaluated at five locations, and based on the mean yield performance and attributing traits for salinity/alkalinity resistance, only two genotypes, HUWL 2081 and NWL(S) 13, recorded significantly higher grain yields than the best check cultivar KRL 19. The rest of the genotypes, including the checks KRL 1-4 and KH 65, were found comparable to the best check cultivar KRL 19 (Table 6).

Evaluation of genotypes under zero tillage. We observed that wheat sown after November has a decrease in grain yield by 30 kg/ha/day; the decrease after December is 50 kg/ha/day. To advance wheat sowing and minimize losses, using zero-tillage technology was emphasized (Singh 1994; Singh et al. 2004). Zero-tillage technology involves wheat seeding in untilled rice fields with the help of a specially designed fertilizer and a seed drill with an inverted T-type furrow opener. In addition to savings on tillage costs for timely and late-sown conditions, this technology has the potential for higher productivity where wheat sowing is delayed due to the late maturity of forecrops such as sugarcane, potato, toria, rice, cotton, or pigeon pea**.** Based on the results from three crop seasons, comparative performance of promising wheat genotypes under zero-tillage technology are presented (Table 7). From 3 years of experiments, the yield levels of late-sown cultivars under zero tillage were comparable to a timely sown wheat crop. However, cultivar differences for yield under zero tillage were conspicuous (Table 7).

Table 7. Performance of promising wheat genotypes under zero-tillage conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India (IR-TS, irrigated timely sown; IR-LS, irrigated late sown; ± the standard error.

Genotype	PBW 343	HUW 468	HW 2045	HP 1744	DBW 14	NW 1014
Production condition	IR-TS	IR-TS	IR-TS	IR-LS	IR-LS	IR-LS
Duration (days)	130 ± 3.5	120 ± 2.9	115 ± 4.1	113 ± 4.6	106 ± 4.0	115 ± 3.8
Plant height (cm)	95 ± 2.3	90 ± 1.9	100 ± 2.4	100 ± 2.8	79 ± 1.4	100 ± 3.7
1,000-kernel weight (g)	40 ± 1.5	43 ± 0.8	39 ± 1.0	39 ± 1.1	40 ± 2.1	37 ± 1.7
Yield (Q/ha)	50 ± 2.4	40 ± 2.7	45 ± 1.9	43 ± 1.7	46 ± 4.1	45 ± 3.9
Protein (%)	11.5 ± 0.4	10.5 ± 0.7	12.5 ± 1.2	12.5 ± 1.0	12 ± 0.6	11.5 ± 1.0

Surface seeding needs no tillage. Surface seeding is the broadcasting of dry or soaked wheat seeds a few days before or after harvest of paddy crop under wet/saturated soil conditions (Singh 2004). This technology was used in lowland rice fields for taking wheat crop after the harvest of paddy crop. Three genotypes, HUW 468, HW 2045, and NW 1014, gave significantly higher grain yield in comparison to other genotypes. We concluded that in the undulating areas of eastern India where soil moisture restricts the wheat sowing, the above three cultivars could be grown under surface seeding to harness the maximum profit by increasing the cropping intensity (Table 8).

Table 8. Performance of promising wheat genotypes under surface seeding at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India (IR-TS, irrigated timely sown; IR-LS, irrigated late sown; ± the standard error.

Genotype	HUW 468	HW 2045	NW 1014
Production condition	IR-TS	IR-TS	IR-LS
Duration (days)	120 ± 1.4	115 ± 1.2	115 ± 1.3
Plant height (cm)	90 ± 2.0	100 ± 1.9	100 ± 1.7
1,000-kernel weight (g)	43 ± 0.8	39 ± 0.9	37 ± 0.7
Yield (Q/ha)	40 ± 3.2	45 ± 3.4	45 ± 2.9

Table 9. Performance of wheat cultivars under late sown conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India.

Genotype	Yield (Q/ha)	Plant height (cm)	Disease score		Grain size
			Leaf blight	Brown rust	
DBW 14	45.75	85.0	24	0	Bold
NW 1014	43.97	105.0	35	0	Medium
HW 2045	37.82	98.0	35	0	Medium
RAJ 3765	37.32	89.0	46	0	Medium
HD 2643	36.97	95.0	34	0	Medium
DL 788-2	35.00	85.0	46	0	Bold
HUW 234	23.97	87.0	35	60S	Small
CD (P= 0.05)	4.16	5.3	—	—	—

Suitability of cultivars to late-sown conditions. A set of 15 promising wheat genotypes was taken for evaluation under late-sown conditions in eastern India where the recently released genotype DBW-14 outyielded others. This unique genotype, in addition to high yield, shorter duration, and better disease tolerance, also possessed a good degree of terminal heat tolerance and produced bold grains. Some of the other better-performing genotypes included NW 1014, HW 2045, HD 2643, DL 788-2, and RAJ 3765 (Table 9).

A number of promising genotypes were identified from the different trials conducted in three production conditions (timely, late, and rainfed) and used for on-farm seed production to increase the horizontal spread of modern, high-yielding wheat genotypes (Table 10). Cultivation of any of the farmer-preferred wheat genotypes based on need

Table 10. Performance of promising wheat genotypes under different production conditions at experimental sites near Pusa, Ranchi, Bilaspur, and Varanasi, India.

Genotype	Duration (days)	Plant height (cm)	1,000-kernel weight (g)	Yield (Q/ha)	Protein (%)
Irrigated, timely sown					
PBW 343	130	95	40	50	11.5
HD2733	125	85	42	50	11.0
K 9107	125	105	45	45	12.0
NW 1012	115	90	38	45	10.5
HUW 468	120	90	43	40	10.5
CD (P= 0.05)	3.7	5.2	2.1	4.3	1.2
Irrigated, late sown					
HW 2045	115	100	39	45	12.5
RAJ 3765	110	90	40	40	10.5
HD 2643	110	85	41	40	13.0
HP 1744	113	100	39	43	12.5
DBW 14	106	79	40	46	12.0
NW 1014	115	100	37	45	11.5
CD (P= 0.05)	2.8	7.4	1.9	3.0	1.4
Rainfed					
K 8027	115	98	43	30	10.0
K 8962	100	115	50	30	11.5
HDR 77	105	75	36	25	11.5
CD (P= 0.05)	4.5	7.4	3.3	2.9	1.0

and production conditions will improve yield and reduce the cost of cultivation if matching production technology is followed.

Wheat cultivars meeting the ranking of traits preferred by the farmers' choice. Wheat cultivars possessing high grain yield along with high 1,000-kernel weight, early maturity, medium to tall plant height, and acceptable resistance levels are of paramount importance to the farmers in the regions. This study is the first comprehensive effort to employ collaborative efforts to identify improved wheat genotypes for different production conditions. Using information generated through an impact-assessment survey, we observed that the farmers still rank grain yield as the first choice followed by maturity duration and plant height when deciding which cultivars to grow for different production conditions. The participatory, cultivar-selection approach might help in increasing the extent of genetic diversity by using number of genotypes fulfilling the farmers' choice of traits (Witcombe et al. 2001). The rank of the farmers' preferred traits and choice of cultivars available are summarized in Table 11.

Table 11. Ranking of farmers' preferred traits and their available choices.

Trait	Rank	Available choices
Grain yield	I	HD 2733, DBW 14, NW 1014,HW 2045, HUW 468, HD 2643
Maturity duration	II	NW 1014, DBW 14, DL 788-2
Plant height	III	DBW 14,HUW 468, HD 2733
Plant stand	IV	DBW 14,HUW 468, NW 1014
Early vigor	V	DBW 14,HD 2643, NW 1012
Grain appearance	VI	DBW 14, K 9107, HW 2045
Ear head size	VII	K 9107, HW 2045, DBW 14
Disease resistance	VIII	HUW 468, HW 2045, DBW 14
Foliage color	IX	DBW 14,NW 1014, HUW 468

We found that grain yield continued to be the number one choice of the farmers when selecting a cultivar, followed by maturity duration, plant height, plant stand, early vigor, grain appearance, and spike size. In the northeast plains of India, however, maturity duration obviously is an important trait to fit into the shorter wheat-growing season and avoid grain shrivelling from the adverse effects of late heat. The resource-poor farmers in theses remote areas, who still grow old genotypes (Ortiz-Ferrara et al. 2006), would benefit the most by adopting these high-yielding cultivars. The tolerance mechanism of a genotype to biotic and abiotic stresses will help in improve the yield ability even under stressed environments (Ortiz et al. 2008), which may be the reason that early vigor and grain appearance are traits considered by farmers when selecting a cultivar. These efforts are being linked with participatory approach of germ plasm dissemination in the IGP especially benefiting small and marginal farmers (Ortiz-Ferrara 2001; Witcombe et al. 2001; Ortiz-Ferrara et al. 2007). The superior performance of identified genotypes over the checks indicates that farmers across the regions could benefit by adopting the high-yielding wheat genotypes for specific production conditions. In particular, resource-poor farmers in the remote areas who still grow Sonalika (Ortiz-Ferrara et al. 2006) would benefit the most by adopting these high-yielding, experimental lines.

We concluded that suitable wheat cultivars are available to fulfil the farmers' preferred traits. These results demonstrate the important role that PVS experiments play in identifying the production conditions of specific wheat genotypes to increase wheat yields in regions where the livelihood of farmers are integrally associated with wheat production. The adoption of different tillage technologies for growing wheat under diversified soils and production conditions also can enhance wheat yields significantly in eastern India. A future wheat-improvement program should combine as many traits of farmers' preference as possible in a cultivar to be developed for commercial cultivation.

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Characterization of wheat accessions for various metric and morphological traits.

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Summary. Advanced material of 430 wheat genotypes developed through the All India Coordinated Wheat Improvement Project (AICWIP) were characterized for 10 metric and 25 morphological traits as per DUS norms. These genotypes were grouped into different classes with respect to various traits and promising genotypes for each metric trait that was identified. Character association between these metric traits showed a high association between days-to-heading and maturity, spikelets/spike, and seeds/spike; protein content; and heading and maturity period. Desirable correlations also were observed between the traits, which can be harnessed in germ plasm improvement activities.

India is the second largest wheat-producing country at the global level. Wheat yield in the past few decades has increased, mainly due to improved germ plasm. The All India Coordinated Wheat Improvement Programme has the primary mandate to develop cultivars for different agroclimatic zones and production conditions for which wheat genotypes are put in a 3-tier, multilocational testing system consisting of the National Initial Varietal Trial (NIVT), the Advanced Varietal Trial-I (AVT-I), and the Advanced Varietal Trial-II (AVT-II). These genotypes are supposed to be high yielding, resistant to biotic stresses, and tolerant to abiotic stresses. Presently, wheat cultivars are available that suit different climatic conditions and can be fitted into different cropping sequences. Although all cultivars tested in final trial year are not identified for release, these materials are promising for many aspects and can be further utilized in breeding programs as donor lines. A trial was conducted to characterize such elite genotypes and some released cultivars for various metric and morphological traits following DUS norms.

Materials and methods. The experimental material consisted 430 wheat genotypes pooled from AVT-II trials including some released cultivars. The experimental material represented *T. aestivum* subsp. *aestivum,* and *T. turgidum* subsps. *durum* and *dicoccum*, and triticale strains. These genotypes were planted at the DWR farm for two consecutive seasons under timely sown conditions in an augmented block design along with three checks Sonalika, Kalyansona, and PDW 215 (Surum). The plot size was a double row 2.5-m long. The recommended practices were followed in order to raise a healthy crop. Data were recorded on metric and morphological DUS characters using 10 randomly selected plants/spikes

for as per the standard norms (Kundu and Nagarajan 1998) (Table 12). The data were analyzed to work out range and mean for metric traits and frequency of genotypes in different classes of all the traits was also calculated.

Results and discussion. The 430 genotypes included in the study consisted of 364 *T. aestivum* subsp. *aestivum,* 60 *T. turgidum* subsp. *durum,* two *T. turgidum* subsp. *dicoccum,* and four Triticale cultivars. The analysis showed a wide range and more variability for all the metric traits (Table 13). The frequency of genotypes in different classes was calculated for all traits under study (Fig. 7; Table 14, p. 87). The identification of promising genotypes for each of the metric characters suggested that there is hope for further improvement of wheat cultivars. Promising genotypes for various metric traits are shown in Table 15 (p. 88). Early maturing genotypes are considered desirable to fit in various crop sequences. Spike length, number of spikelets, and seeds/spike are the trait that directly or indirectly contribute to the yield. Similarly, high

Table 12. Metric and morphological DUS characters recorded on 450 wheat genotypes pooled from the Advanced Varietal Trial-II, Karnal, India.

Metric traits
Days-to-50% heading, days-to-maturity, plant height (cm), spike length (cm), number of spikelets/spike, number of seeds/spike, flag leaf length (cm), flag leaf breadth (cm), 1,000-kernel weight (g), and protein content (%)
Morphological traits
Plant growth habit, coleoptile color, auricle color, auricle pubescence, flag leaf angle, waxiness, foliage color, angle of spike, spike color, spike shape, spike density, awn length, awn color, outer glume shoulder shape, outer glume pubescence, glume beak length, glume beak curvature, grain color, grain shape, grain texture, grain size, brush hair length, brush hair profile, germ width, and grain crease

Table 13. Range, mean, coefficient of variability, and standard error for metric traits recorded on 450 wheat genotypes pooled from the Advanced Varietal Trial-II, Karnal, India.

Character	Minimum	Maximum	Range	Mean	Coefficient of variability	Standard Error
Days-to-heading	71.0	125.0	54.0	93.0	6.85	0.31
Days-to-maturity	121.0	175.0	54.0	133.0	6.04	0.39
Plant height (cm)	61.0	151.0	90.0	95.0	10.61	0.49
Spike length (cm)	6.0	16.8	10.8	10.4	16.09	0.08
Number of spikelets / spike	14.0	28.0	14.0	19.0	10.43	0.10
Number of seeds / spike	30.0	96.0	66.0	55.0	17.28	0.46
Flag leaf length (cm)	16.7	42.0	25.3	28.1	14.20	0.19
Flag leaf breadth (cm)	1.1	2.8	1.7	1.9	15.05	0.02

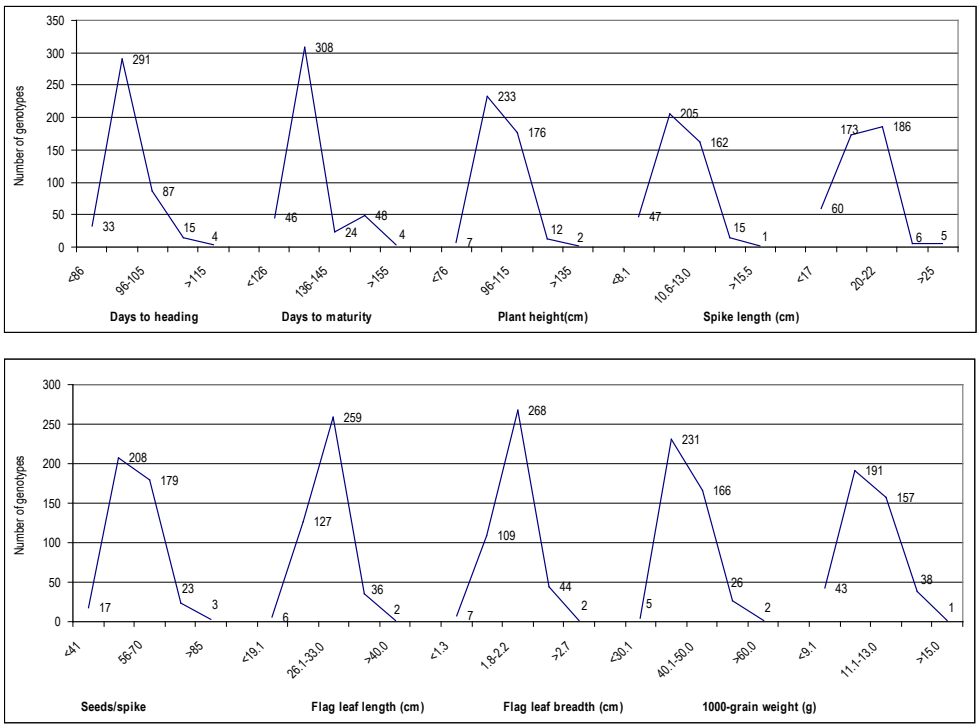

Fig. 7. Frequency distribution for the ten metric traits of days-to-heading, days-to-maturity, plant height (cm), spike length (cm), seeds/spike, flag leaf length (cm), flag leaf width (cm), and 1,000-kernel weight (g) for the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India.

Table 14. Frequency distribution for various morphological characters of the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India.

Character	Frequency of genotypes in different classes
Plant growth habit	Erect – 233, Semi-erect – 191, Semi-spreading – 6
Coleoptile color	Green – 402, Pink – 6
Auricle color	Dark purple – 81, Purple – 83, Colorless – 266
Auricle pubescence	Dense –58, Moderate – 202, Sparse – 98, Absent – 70
Flag leaf angle	Erect – 220, Semi-erect – 199, Semi-curved – 9, Recurved – 2
Waxiness	Waxy – 126, Partially waxy – 304, Nonwaxy – 1
Foliage color	Dark green – 53, Green – 335, Light green – 42
Angle of spike	Erect – 181, Semi-erect – 198, Semi-drooping – 41, Drooping – 10
Spike color	White – 361, Brown – 69
Spike shape	Tapering – 331, Parallel – 99
Spike density	Lax – 85, Intermediate – 221, Dense – 79, Very dense – 45
Awn Length	Long (> 10cm) – 76, Medium (6.6–10 cm) – 277, Short (< 6.5 cm) – 77
Awn color	White – 319, Brown – 68, Black – 43
Outer glume shoulder shape	Sloping – 79, Round – 133, Square – 150, Elevated – 68
Outer glume pubescence	Densely pubescent – 19, Pubescent – 32, Nonpubescent – 379
Glume beak length	Long (> 5 mm) – 178, Medium (2–5 mm) – 196, Short (< 2 mm) – 56
Glume beak curvature	Strong – 8, Medium – 209, Weak – 212
Grain color	White – 25, Amber – 396, Red – 8
Grain Shape	Ovate – 145, Oblong – 238, Elliptical – 45
Grain texture	Hard – 153, Semi-hard – 24, Soft – 36
Grain size	Bold – 97, Medium – 290, Small – 43
Brush hair length	Long – 102, Medium – 212, Short – 116
Brush hair profile	Pointed – 133, Medium – 148, Blunt – 149
Germ width	Wide–62, Medium–311, Narrow–57
Grain crease	Shallow–72, Medium–180, Deep–178

thousand-grain weight shows grain boldness that is one of the major yield components. Among the bold seeded genotypes, most are durum but few aestivum genotypes, such as RW 482, HW 3029, K 9266, HS 396, K 9706, K 9263, HD 2733, and K 9545, also have been identified to possess bold grains. Flag leaf is considered as most efficient leaf for photosynthesis and for this reason, large flag leaf is desirable for selecting the genotypes that can have efficient carbon assimilation system. Protein content is an important quality parameter and the genotypes having more protein content coupled with bold grains may be promising for improving nutritional quality.

Correlations between the metric traits were computed and the results revealed a high and positive correlation between days-to-heading and maturity, spikelets/spike, seeds/spike, protein content, heading, and maturity period (Table 16, p. 88). Genotypes with delayed heading and maturity had comparatively more protein content. Protein content also was positively associated with spike length and seeds/spike. Plant height showed positive association with maturity period and spike length. Number of spikelets/spike and seeds/spike had good association with heading and maturity period as well as spike length. Flag leaf length and breadth were found positively associated with each other. We concluded that there is a wide range of variation for almost all the metric traits in the experimental material, and promising genotypes for various metric traits can be further utilized in germ plasm improvement programs. The correlations between various traits can be utilized for selection of better genotypes for various purposes.

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Table 15. Promising wheat genotypes for various metric traits of the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India (D, *T. turgidum* subsp. *durum*; Di, *T. turgidum* subsp. *dicoccum*; and T, triticale.

Character	Criteria	Genotypes
Days-to-heading	< 85	BW 267, AKW 381, BW 1055, UP 2447, HD 2680, PBW 276, HD 1925, HD 2122, HUW 227, HW 135, K 9262, K 9323, K 9324, K 9334, K 9533, PBN 332, PBW 332, RAJ 3385, WH 423, BW 1050, DL 975-1, DL 3776, K 9545, VL 687
Days-to-maturity	< 123	AKW 1071, BW 1055, HP 1659, HPW 54, HUW 326, HUW 327, HUW 435, HW 135, HW 517, K 9305, K 9334, K 9351, PBW 332, VW 189
Plant height (cm)	< 76.0	HD 1941, HD 2160, HD 2412, HW 1085, K 9451, Lal Bahadur, UP 2418
Spike length (cm)	> 13.0	K 8708, HD 2747, HPT 6 (T), HW 2045, GW 147, HI 1277, HS 361, HS 369, K 9545, VL 802, VL 804, HD 2122, HD 2705, UP 2425, HS 396, K 9743
Number of spikelets/spike	> 22	HPT 6 (T), TL 2780 (T), TL 2877 (T), HS 355, HS 361, K 9706, VL 801, WH 534, PDW 276 (D), TL 2908 (T), DDK 1013 (Di)
Number of seeds/spike	> 80	K 9451, VL 801, DWR 241, GW 147, K 9743, VL 802, HS 396, HUW 516, HW 2062-1
Flag leaf length (cm)	> 37.0	J 411, HP 1529, HD 2504, J 407, UP 2447, VL 707, HD 2747, K 8965, K 8946
Flag leaf breadth (cm)	> 2.4	HUW 55, RW 482, BW 267, GW 147, HB 501, HPW 89, HPW 143, HS 322, HS 361, HUW 311, HUW 510, HW 1085, K 9212, UP 2375
1,000-kernel weight (g)	>52.0	PDW 274 (D), MACS 2846 (D), TL 2908 (T), RW 482, AKW 38-5(D), DW 1001 (D), PDW 251 (D), HW 3029, HI 8498 (D), DWR 1013 (D), K 9266, HS 396, PDW 247 (D), K 9706, K 9263, HD 2733, NIDW 9 (D), NIDW 15 (D), PDW 248 (D), K 9545, MACS 3125 (D)
Protein content (%)	>13.0 & TGW>40g	K 8504 (D), WH 882 (D), K 8904, K 8705, DWR 1013 (D), P 10950, HD 2643, PBW 276, NI 8841, J 478, MACS 2846 (D), NIAW 129, K9743, JU 126 (D), K 8706, PBW 271, NG 14-4-1-10, JU 69 (D)

Table 16. Correlation coefficients between the various metric traits of the 450 wheat genotypes pooled from the Advanced Varietal Trial–II, Karnal, India.

Character	Days to maturity	Plant height	Spike length	Number of spikelets/spike	Number of seeds/ spike	Flag leaf length	Flag leaf breadth	1,000-kernel weight	Protein content
Days-to-heading	0.779	0.118	0.065	0.263	0.219	-0.066	-0.208	0.013	0.351
Days-to-maturity		0.236	0.160	0.261	0.265	0.108	-0.281	0.173	0.504
Plant height			0.303	0.228	0.057	0.195	0.013	-0.032	0.107
Spike length				0.313	0.224	0.268	0.055	-0.152	0.279
Spikelets/spike					0.549	-0.043	0.065	-0.039	0.145
Seeds/spike						0.027	0.093	-0.067	0.225
Flag leaf length							0.218	0.091	0.116
Flag leaf breadth								0.158	-0.254
1,000-kernel weight									0.060

Genotypic effects of spring wheat on yield and nitrogen uptake, utilization efficiency, and harvest index.

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Summary. Ten spring wheat genotypes (four Indian and six Mexican) were evaluated after 180 and 300 Kg N/ha applications at CIMMYT (Centro Internacional de Mejoramiento de Maiz y Trigo), near Ciudad Obregon, Sonora, Mexico, during 1997–98 and 1998–99 for their yield potential, N concentration in grain and straw, and their relationships. From a pooled analysis, the effect of N rates on biomass, yield, and yield-attributing characters was not significant, whereas

genotypic effects on the abovementioned characters as well as on grain N concentration, uptake, nitrogen harvest index (HI), and utilization efficiency were significant. From the combined analysis across years, grain yield ranged from 7.81 t/ha (Pavon 76) to 9.13 t/ha (Baviacora 92) and HI from 39.5 % (Pastor) to 45.1 % (Baviacora 92). The range of grain N concentration was from 1.99 % (Baviacora 92) to 2.23 % (Rayon 89), uptake from 147.6 kg/ha (Pastor) to 169.5 kg/ha (UP 2338), and nitrogen utilization efficiency from 29.8 kg grain/kg N uptake (Pavon 76) to 35.6 kg grain/kg N uptake (Baviacora 92). Grain yield correlated (r) positively with HI (0.66), NHI (0.62), and grain N uptake (0.77), and negatively with N concentration in grain (-0.68) and straw (-0.64). The correlation between HI and NHI was highly positive (0.89), suggesting that enhancing these two indices could lead to higher grain yield and protein content. Therefore, these two indices should be given more emphasis for enhancing yield potential of spring wheat genotypes.

Introduction. The advent of semidwarf wheat increased yield potential during the mid-1960s. The high yielding, semidwarf, photo insensitive, wheat cultivars released after the 'Green Revolution' were selected to respond to high N input (Earl and Ausubel 1983). Genetic selection was for high harvest index (HI) under medium to high N rates, whereas, HI and NHI (nitrogen harvest index) in wheat might respond differently to N fertilizer depending on the amount and timing of the application. Efficiency in dry matter partitioning or HI is defined as the ratio of grain yield to total biomass at maturity (Donald 1962). Efficiency in N partitioning or N harvest index is defined as the ratio of N uptake by grain to total N uptake at maturity (Austin and Jones 1975).

Generally, an inverse relationship between grain yield and grain N concentration has been reported in bread wheat (Cox et al. 1985; Stoddard and Marshall 1990). However, the degree of this relationship varies with soil fertility, water availability, and other environmental factors. Maximizing grain yield and N concentration in grain with optimum N use also is essential. Nitrogen dose depends upon the yield level of the crop and the apparent nitrogen recovery. Hobbs et al. (1997) envisage that a wheat crop yielding 7.0 t/ha might require 330, 254, and 206 kg N/ha provided it shows 50, 65, and 80 % apparent N recovery, respectively. They assumed that a wheat crop without N can yield only up to 2 t/ha. Nitrogen use efficiency can be defined as the product of uptake efficiency (total N uptake/applied N through fertilizer) and utilization efficiency (yield/total N uptake). At low N rates, uptake efficiency is dominant compared to utilization efficiency, whereas utilization efficiency is relatively more dominant than uptake efficiency at high N rates (Ortiz Monasterio et al. 1997). In the past, more emphasis was given to higher grain yield irrespective of the N concentration in the grain. Therefore, our objective was to evaluate important Indian and Mexican spring wheat genotypes released during the last quarter of the 20th century for yield potential, N concentration in grain and straw, and their relationships.

Materials and methods. The experiment was at CIMMYT near Ciudad Obregon, Sonora, Mexico (27.33'N, 109.09'W, and 38-m above sea level). The soil type was a coarse sandy clay, mixed montmorillonitic typic calciorthid, low in NO_3^- N (29.5 ppm) and NH_4^+ N (6.1 ppm), medium in available P (7.7 ppm) and organic matter (0.89 %), high in K (557 ppm), and alkaline (pH = 8.0) in nature. The minimum temperature in November, December, January, and March was about 1°C lower in 1998–99 than in 1997–98.

The study consists of two N levels (180 and 300 kg/ha) in main plots and 10 historical spring wheat genotypes (six from Mexico; Baviacora 92, Seri 82, Pastor, Pavon 76, Rayon 89, and Bacanora 88 and four from India; PBW 343, UP 2338, WH 542, and HD 2329) in subplots, which were grown in a split-plot design with three replications. The crop was sown during the last week of November by plot drill into dry soil followed by irrigation to give about 300 viable seeds/m^2 in rows, 20 cm apart. At sowing time, 100 kg N/ha was applied as urea and 46 kg/ha phosphorous as Single Super Phosphate. Potash was not applied due to inherent high content of potassium (557 ppm) in the soil (0–15 cm depth). A top dressing of 200 kg N/ha through urea was made at stage DC 31 (Zadoks et al. 1974) followed by irrigation. Herbicides, such as Topik (Clodinafop-propargyl) at 250 ml/ha and Brominal (Bromixinil at 1.5 l/ha) + Harmony (Thiofensulfuron @ 25 g /ha) were used with a Knap Sack sprayer at the two-leaf weed stage for control of grassy and nongrassy weeds, respectively.

A net plot of 3.6 m^2, excluding border rows and ends, was harvested manually 7–10 days of after physiological maturity. All yield and yield-attributing characters were obtained using methods as described by Bell and Fischer (1994). At physiological maturity, a subsample of 50 tillers/plot was taken and dried for 48 hours at 70°C. Thereafter, these were threshed and 'straw + chaff' samples were collected. Grains collected from these tillers were weighed and added in yield of the plot. Afterwards, these grain and 'straw + chaff' samples were dried and ground separately. Nitrogen estimation of grain and straw was performed by the Kjeldahl method (Humphries 1956). The data of the experiment were analyzed on pooled basis by using MSTATC. The mean of the two years data were used for correlation study of important parameters.

Results and discussion. From an across years analysis, the effect of N rates of on biomass, yield, and other component characters was equal (data not given), whereas cultivar differences were significant (Table 17). Baviacora 92 was significantly taller (103 cm) and HD 2329 significantly shorter (84.4 cm) than other cultivars. Generally, the genotypes studied took 132 to 136 days between emergence to maturity, except HD 2329, which was about one week earlier. The Mexican cultivar Baviacora 92 produced the maximum biomass (17.82 t/ha), grain yield (9.13 t/ha), and 1,000-kernel weight (48.2 g) despite being lowest in spikes/m^2 (370). Seri 82 recorded the highest HI (45.9 %) and grain/spike (46.7), whereas Pastor had the lowest HI (39.5 %) and HD 2329 the lowest grain/spike (31). Cultivar differences in grain yield were in agreement with those of others (Stapper and Fischer 1990 b). At the same place, in a set of historical cultivars, Sayre et al. (1997) reported that average yield increased linearly from 66.8 q/ha (Pitic 62) to 84.8 q/ha (Bacanora 88). Generally, cultivars possessing higher spikes/m^2 showed lower 1,000-kernel weight and vice versa.

Table 17. Genotypic differences in plant height, biomass, yield and its attributing characters in pooled analysis across years.

Parameter	Plant height (cm)	Biomass (kg/ha)	Yield (kg/ha)	HI (%)	1,000-kernel weight (g)	Spikes/m^2	Grain/ spike
PBW 343	94.4	16,117	8,281	45.2	47.0	408	38.2
UP 2338	90.0	17,554	8,837	44.3	45.1	407	42.4
Baviacora 92	103.3	17,815	9,134	45.1	48.2	370	45.4
Seri 82	91.9	16,683	8,708	45.9	42.0	392	46.7
Pastor	100.9	17,687	7,924	39.5	44.8	460	34.3
WH 542	86.7	17,093	8,572	44.1	35.4	481	44.4
HD 2329	84.4	15,549	7,971	45.1	44.7	510	31.0
Pavon 76	99.2	17,191	7,808	40.0	38.7	541	33.2
Rayon 89	96.9	17,746	8,082	40.2	36.2	522	37.9
Bacanora 88	86.8	17,766	8,815	43.8	36.4	490	43.8
LSD (P=0.05)	1.7	727	302	1.5	1.2	31	2.7

The effect of N rates on nitrogen concentration and uptake in the grain and NHI was not significant, whereas straw N concentration, uptake, and NUTE were significantly higher at 300 kg N/ha compared to the 180 kg N/ha application rate (data not given). From the means of two years data (Table 18), the range of grain N concentration, uptake, and total uptake was from 1.99 % (Baviacora 92) to 2.23 % (Rayon 89), from 147.6 kg/ha (Pastor) to 169.5 kg/ha (UP 2338), and from 223 kg/ha (Pastor) to 241 kg/ha (Pavon 76), respectively. The range of straw N concentration was from 0.58 % (Bacanora 88) to 0.79 % (Pavon 76) and uptake from 53.6 kg/ha (PBW 343) to 80.4 kg/ha (Pavon 76). The maximum NUTE value was 35.6 kg grain/kg N uptake in Baviacora 92 and a minimum 29.8 kg grain/kg N uptake in Pavon 76. The highest

Table 18. Cultivar differences in N concentration in grain and straw, uptake, NUTE and NHI in pooled analysis across years.

Parameters	N Concentration (%)		N Uptake (kg/ha)			NUTE (kg grain/ kg N uptake)	NHI (%)
	Grain	Straw	Grain	Straw	Total		
PBW 343	2.19	0.60	159.6	53.6	213	34.3	74.9
UP 2338	2.18	0.66	169.5	64.3	233	33.3	72.5
Baviacora 92	1.99	0.66	160.3	65.1	225	35.6	71.1
Seri 82	2.14	0.64	163.9	57.3	221	34.7	74.2
Pastor	2.12	0.71	147.6	76.8	224	31.2	65.9
WH 542	2.07	0.63	157.8	59.5	217	35.2	72.6
HD 2329	2.20	0.71	154.3	60.4	215	32.7	71.9
Pavon 76	2.19	0.79	152.5	80.4	233	29.8	65.5
Rayon 89	2.23	0.66	158.3	70.6	229	31.0	69.3
Bacanora 88	2.08	0.58	161.9	57.9	220	35.3	73.5
LSD (P=0.05)	0.04	0.05	6.94	6.93	9.8	1.24	2.6

NHI was in PBW 343 (74.9 %) and lowest in Pavon 76 (65.5 %). Similar findings also have been reported by various workers (Halloran and Lee 1979; Dhugga and Waines 1989).

Grain yield correlated positively with HI (0.66), NHI (0.62), grain N uptake (0.77), and negatively with N concentration in grain (-0.68), straw (-0.64), and straw N uptake (-0.54). The correlation between HI and NHI was highly positive (0.89), whereas between HI and straw N uptake, it was highly negative (-0.89). Sinclair (1998) showed that NHI is directly dependent on HI and, therefore, a positive association between HI and NHI is generally expected. A positive correlation between HI and NHI has been reported in durum wheat (Desai and Bhatia 1978) and in bread wheat (Loffler and Busch 1982). Nitrogen harvest index also showed a positive association with N uptake by grain (0.72) and negative trend with straw N concentration (-0.83) and straw N uptake (-0.98), as is generally expected. To gain more information on the relationship between HI and NHI, mean NHI over two N rates and years was regressed on mean HI. The slope (b = 0.67) of the regression line, 1% increase in HI was accompanied by 0.67 % increase in NHI, suggests that improvement in NHI has lagged behind HI in wheat-breeding programs. Recently, Ehdaie and Waines (2001) also observed that a 1% increase in HI was accompanied by 0.84% increase in NHI, corroborating our findings. Biomass at maturity did not correlate well with any of the important parameters. Therefore, grain yield and protein could be maximized with selection of cultivars with high HI and NHI.

Conclusion. This study of important Indian and Mexican spring wheat cultivars at high N levels (180 and 300 kg/ha) resulted in significant differences in yield, N concentration, uptake, NUTE, and NHI. The positive correlation of grain yield with HI (0.66), NHI (0.62), and grain N uptake (0.77), and negative correlations with grain (-0.68) and straw (-0.64) N concentration exhibited the possibility of further increases in yield under high-input conditions. HI and NHI correlated positively (0.89), which suggests that enhancing these two indices could lead to higher grain yield.

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Effect of delayed nitrogen application on yield and quality of wheat.

S.C. Tripathi.

Abstract. A field experiment was conducted at Karnal to enhance grain yield, nitrogen use efficiency, and protein content by initially stressing the crop for nitrogen and rescheduling at later stages when the demand is generally high. Omitting basal nitrogen and applying it whe the plants are two-thirds at the first node plus one-third in flag leaf/flowering or three-fourths at first node plus one-fourth at anthesis gives an additional grain yield (about 2 q/ha) due to higher 1,000-kernel weight and grains/spike, compared to recommended applications when the plants at one-half basal plus one-half at crown-root initiation (CRI) or one-third basal plus two-thirds at first node. The number of spikes/m^2 was higher with the recommended N application than when it is delayed application. Furthermore, skipping basal N and applying it at later stages resulted in significantly higher N content and uptake in the grain. These treatments also recorded higher NUE (6–10 %), protein content, total N uptake (7–15 kg/ha), and nitrogen harvest index (NHI) than under recommended N application practices. However, full N applied at the first-node stage had the lowest NUE (58.0 %). This study emphasizes that initial N stress followed by a split application of N at crucial stages enhances the protein content by utilizing more N uptake, higher NUE (68-72 %), and NHI.

Nitrogen use efficiency in wheat decreases with an increase in nitrogen rate and ranges from 30–77 % (Kumar et al. 1995; Sarkar et al. 1994). Generally, nitrogenous fertilization of a wheat crop is recommended in two, equal applications, at the basal, crown-root initiation stage and when the plant leaves are one-third basal and two-thirds at the first node, i.e., stage DC 31 (Zadoks et al. 1974). However, timing the exogenous N application should be based on the demand of the crop and N capacity of the soil. The wheat crop germinates approximately 6–8 days after sowing under timely sown conditions and the crown roots, responsible for nutrient extraction, start developing at 21 days after sowing. The nutrients stored in the endosperm of the seed and the inherent N present in the soil are sufficient for crop emergence and to meet N demand up to the development of the crown-root system. Therefore, a majority of the applied basal N remains unutilized by the crop during early stages and might be lost leading to lower nitrogen recovery. Under initial condition of N stress, roots will penetrate deeper for nutrients resulting in plants tolerant to lodging.

During formation of the first node (stage DC 31), the crop requires maximum N because of the simultaneous processes of stem elongation/development and forming the number of spikelets/spike. Therefore, this time is when the crop should be given maximum N, so that full potential can be achieved. Generally, an inverse relationship exists between grain yield and grain N concentration in bread wheat (Cox et al. 1985; Stoddard and Marshall 1990). Thus, maximizing yield and grain N concentration to harness maximum N recovery and protein content is needed. We evaluated initial N stress and different timings of subsequent nitrogen applications, including the existing recommendations as a control, with the objective of enhancing yield, NUE, NHI, and protein content in wheat.

Materials and methods. A field experiment was conducted at the Directorate of Wheat Research, Karnal (Latitude 29°43' N, longitude 76°58' E; altitude 245 m) during the winter seasons of 1999–2000 and 2000–01. The average annual precipitation at Karnal is >600 mm and is erratic. The trial included eight N application timings (T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis) replicated three times in a randomized block design. The soil of experimental plot was a sandy loam with low organic carbon (0.359 %) and available nitrogen (139.0 kg/ha) and medium in available phosphorous (17.6 kg/ha) and potassium (151.0 kg/ha). Phosphorous and potash were applied at 60 and 40 kg/ha, respectively, through single super phosphate and muriate of potash, and 150 kg N/ha was applied through urea. During both years, sorghum was raised as a forecrop to exhaust soil fertility and the wheat PBW 343 was sown during the second week of November. Irrigation was applied at all critical stages of the crop. Weeds were controlled by an application of Clodinafop (60 g ai/ha) in 400 L of water at 2–3 leaf stage of the weed. Biomass, harvest index (HI), and yield and its attributing characters were recorded/calculated as per standard procedures. Estimation of nitrogen in the grain and straw was by the Kjeldahl method (Humphries 1956). Nitrogen harvest index, calculated as the ratio of N uptake by grain to total N uptake at maturity (Austin and Jones 1975), was used to estimate the efficiency of N partitioning. Yearly and pooled data for all the parameters were analyzed using MSTATC.

Results and discussion. From the pooled analysis, maximum grain yield (66.09 q/ha) was recorded when N was applied whe plants were at two at stage T_6, which was about 1–2 q/ha more than all other treatments. In general, providing an initial N stress resulted in higher grain yield (T_5–T_8 treatments) compared to other treatments, mainly due to higher

Table 19. Effect of timing of N application on yield attributes and yield of wheat in experiments at Karnal, India. Treatments were T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis.

Treatment	Grain yield (q/ha)			Straw yield (q/ha)			Spikes/m²			Grain/spike			1,000-kernel weight (g)		
	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled
T_1	25.91	19.80	22.86	54.9	31.1	43.0	228	243	236	25.4	18.4	21.9	45.95	42.45	44.19
T_2	64.74	61.74	63.24	121.9	86.5	104.2	462	411	436	29.1	33.0	31.1	48.22	46.25	47.23
T_3	65.46	62.99	64.23	114.0	82.5	98.3	454	430	442	30.9	32.5	31.7	46.83	45.41	46.12
T_4	64.96	60.48	62.72	108.3	69.9	89.1	448	378	413	31.3	36.4	33.9	46.47	44.49	45.48
T_5	67.02	63.90	65.46	112.4	83.4	97.9	443	373	408	32.5	36.7	34.6	46.76	47.59	47.17
T_6	66.96	65.21	66.09	114.3	72.3	93.3	451	363	407	31.4	37.0	34.2	47.44	48.73	48.08
T_7	66.49	61.92	64.21	117.3	78.3	97.8	461	339	400	29.3	37.4	33.4	48.35	49.11	48.73
T_8	67.34	64.15	65.74	119.3	68.9	94.1	482	314	398	29.4	40.4	34.9	47.78	50.75	49.26

Table 20. The effect of N scheduling on N content and uptake in grain and straw in field experiments at Karnal, India. Treatments were T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis.

Treatment	N Concentration (%)						N uptake (kg/ha)						Total N uptake (kg/ha)		
	Grain			Straw			Grain			Straw					
	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled
T_1	1.256	1.253	1.254	0.307	0.290	0.298	32.6	26.0	29.3	16.8	9.1	12.9	49.4	35.2	42.3
T_2	1.628	1.586	1.607	0.345	0.347	0.346	105.3	97.9	101.6	42.0	30.0	36.0	147.4	127.9	137.6
T_3	1.641	1.503	1.572	0.348	0.350	0.349	107.4	94.7	101.1	39.7	28.9	34.3	147.1	123.7	135.4
T_4	1.593	1.519	1.556	0.357	0.372	0.364	103.5	91.7	97.6	38.6	26.0	32.3	142.0	117.7	129.9
T_5	1.730	1.641	1.685	0.343	0.348	0.346	115.9	104.9	110.4	38.6	29.2	33.9	154.5	134.0	144.3
T_6	1.794	1.711	1.753	0.342	0.348	0.345	120.1	111.6	115.9	39.0	25.3	32.2	159.2	136.9	148.0
T_7	1.761	1.729	1.745	0.347	0.355	0.351	117.0	107.1	112.1	40.6	27.9	34.3	157.6	134.9	146.3
T_8	1.823	1.775	1.799	0.340	0.345	0.342	122.8	113.9	118.4	40.6	23.8	32.2	163.4	137.6	150.5
CD (P = 0.05)	0.095	0.126	0.077	0.01	0.01	0.007	8.5	11.7	7.0	3.3	6.4	3.5	8.2	13.3	7.6

1,000-kernel weight and number of grain/spike (Table 19, p. 93). Even a 75% N application at the first node (DC 31) and 25% at flag leaf or flowering stage significantly increased 1,000-kernel weight compared to N applications at the recommended time. These observations were similar to Sharma and Tiwari (2004), who reported higher wheat yields at different N levels (60, 120, and 180 kg/ha) by skipping a basal, N dressing and splitting the application in contrast to traditional practices. Similar N stress treatments followed by split applications yielded lower spike/m^2 compared to treatments T_2 or T_3. Grain and straw yield, number of spike/m^2, and 1,000-kernel weight in 1999–2000 were higher than 2000–01 because of more favorable climatic conditions. The number of grains/spike were higher in 2000–01 compared to 1999–2000.

Exposing the crop to initial N stress and followed by augmentaion with two split doses resulted in significantly higher grain N concentration and uptake compared to other treatments (Table 20, p. 93). On the other hand, straw N concentration and uptake were equal among treatments with initial N stress and recommended practices. Significantly higher straw N concentration (0.364%) were found when whole N was applied at first node stage in the pooled analysis. Total N uptake in treatments with delayed N (T_6 or T_7) was higher than in the recommended N application. Initial N stress followed by a split application of N enhanced the ability of plants to absorb more N. The pooled analysis (Table 21) showed a significantly higher NUE (68–72%) with delayed N treatments (T_5 to T_8) compared to the recommended N practice (58–63 %). The lowest NUE was recorded when full N was applied at the first-node stage. A higher NHI is more significant than higher NUE in reflecting higher yields. In this study, delayed N application (T_5 to T_8) recorded high NHI (76.6 to 78.9 %) compared to T_2 and T_3 (73.9–74.8%). In a study of ten, high-yielding spring wheat genotypes (Indian and Mexican) at CIMMYT, Mexico, Tripathi et al. (2004) reported that high yield could be achieved with higher HI (r = 0.66) and NHI (r = 0.62). Furthermore, omitting basal N application and splitting the N doses (T_5 to T_8 treatments) gave significantly higher protein content (10.5–11.3%) compared to the recommended practice (9.8–10.0%). Therefore, delayed N application enhances wheat yield, total N uptake, NUE, NHI, and protein content.

Table 21. Effects of N scheduling on protein content, NUE, and nitrogen harvest index (NHI) in field experiments at Karnal, India. Treatments were T_1, control; T_2, one-half of the plants basal + one-half at stage CRI; T_3, one-third basal + two-thirds at first node; T_4, at first node; T_5, two-thirds at first node + one-third at flag leaf; T_6, two-thirds at first node + one-third at anthesis; T_7, three-fourths at first node + one-fourth at flag leaf; and T_8, three-fourths at first node + one-fourth at anthesis.

Treatment	Protein content (%)			NUE (%)			NHI		
	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled	1999–2000	2000–01	Pooled
T_1	7.85	7.83	7.84	—	—	—	0.655	0.724	0.690
T_2	10.17	9.91	10.04	65.33	61.80	63.53	0.714	0.765	0.739
T_3	10.26	9.39	9.83	65.13	59.00	62.06	0.730	0.766	0.748
T_4	9.96	9.49	9.72	61.73	55.00	58.04	0.728	0.777	0.752
T_5	10.81	10.26	10.53	70.06	65.86	68.04	0.750	0.782	0.766
T_6	11.21	10.69	10.95	73.20	67.80	70.46	0.754	0.816	0.785
T_7	11.01	10.81	10.91	72.13	66.46	69.73	0.742	0.795	0.768
T_8	11.39	11.09	11.25	76.00	68.26	72.13	0.751	0.828	0.789
CD (P=0.05)	0.59	0.79	0.48	4.7	5.4	3.5	0.029	0.045	0.026

In this two-year study, we observed that providing an initial N stress followed by split applications of N at later stages (T_2 and T_3 recorded higher yield compared to T_5 to T_8). Protein content, NUE, and NHI also improved significantly compared to conventional practices. In wheat, delayed N application enhances nitrogen use efficiency and NHI with a simultaneous increase in grain quality.

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Induced, high-yielding mutants in wheat.

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Mutation techniques are a novel approach for enhancing the level of genetically conditioned variability of a species within a short time. Selection can isolate superior genotypes (mutants) for various traits. Because wheat is a self-pollinated crop, mutagenesis is an alternative approach for generating variability. Investigations on the effects of chemical mutagens in inducing variability have received much attention because of their utmost importance in plant breeding. Among chemical mutagens, ethyl methane sulphonate (EMS) and sodium azide (SA) were used for inducing mutations in cereals (Panse and Sukhatme 1967; Awan et al. 1980). An experiment was aimed at isolating and characterizing the mutants for yield traits using EMS and SA in wheat.

For the mutagen treatment, 1,000 healthy seeds of four high yielding wheat genotypes, HP1633, HP1731, K9006, and K9107, were presoaked in distilled water for 1 hour and, thereafter, treated in separate sets containing freshly prepared 0.01, 0.02, 0.03, and 0.04M EMS and 0.5, 1.0, 1.5, and 2.0 mM SA in phosphate buffer. The pH was 7.0 for EMS and 3.0 for SA. The seeds were completely submerged in the solutions (500 mL) for 4 hours and then washed thoroughly in running water for two hours before sowing to remove the residual chemicals. One thousand untreated dry seeds of all the four genotypes were soaked separately in distilled water for 4 hours and served as a control for comparison with mutagen-treated seeds.

A total of 36 treatment combinations, including four controls, were sown immediately after treatment with EMS and SA at the Agriculture Research Farm, Banaras Hindu University, Varanasi. The plot size was 20 5-m rows of with an inter- and intrarow spacing of 25 cm (EMS) and 10 cm (SA). From each treatment, all the plants that represented the M_1 generation were harvested separately for raising the M_2 generation. Seeds from individual M_1 plants were space planted in single, 5-m row. Untreated seeds (control) also were sown after each tenth row for comparison. Individual plants were observed for various yield traits, and nine plants showing wide differences were selected and harvested separately for raising the M_3 generation. These mutants showing variability for yield traits were observed at various doses of EMS and SA. The mutants were confirmed as true breeding, because all the mutant seeds gave rise to morphologically similar plants in the M_3 that were quite distinct from the control.

All the nine mutants were harvested and planted in randomized block design with 3 replications in double row plots of 5-m length. Ten plants from each mutant progeny row were taken at random and characterized for plant height (cm), number of tillers/plant, openness of flower glumes (degree), ear length (cm), number of grains/spike, 100-seed weight (g), yield/plant (g), grain shining, ear position, and lodging. The data were subjected to ANOVA according to Georgiev (1982).

The ANOVA for yield traits, using mutant and control populations, indicated that all the treatments differed significantly for plant height, number of tillers/plant, openness of floret, spike length, number of grains/spike, 100-seed weight, and yield/plant (Table 22, p. 96). Both EMS and SA were effective in inducing variability in wheat genotypes at both low and high concentrations that depended on the sensitivity of the genotype to the chemical and their concentra-

Table 22. Analysis of variance for various traits in wheat mutants (** Significant at the 1% level).

Source	df	Plant height (cm)	Number of tillers/plant	Openness of flower (degree)	Spike length (cm)	Number of grains/ spike	100-kernel weight (g)	Yield/ plant (g)
Replication	2	0.56	0.02	0.002	0.001	0.01	0.001	0.03
Treatment	12	453.62**	11.79**	1.27**	9.63**	22.12**	0.95**	16.85**
Error	24	0.64	0.03	0.004	0.006	0.03	0.001	0.06
Total	28							

Table 23. Performance of mutants and their control for various traits in wheat (characters in *italics* are the alterations/mutations compared to control; ** significant at the 1% level).

Mutant	Treatment	Yield/ plant (g)	Plant height (cm)	Number of tillers/ plant	Open-ness of flower (degree)	Spike length (cm)	Number of grains/ spike	100-kernel weight (g)	Grain	Spike position	Lodging
HP1633											
Control	—	15.43	96.89	9.56	3.17	11.38	45.68	3.56	Normal	Semi drooping	Susceptible
1	0.5 mM SA	18.45**	97.23	9.39	5.47**	11.56**	51.68**	4.63**	Normal	Semi drooping	Susceptible
HP1731											
Control	—	18.46	90.01	10.22	2.83	12.10	53.19	3.57	Normal	Semi erect	Susceptible
2	0.01 M EMS	20.42**	91.56	9.87	3.13**	12.32**	54.35**	3.74**	*Shining*	Semi erect	Susceptible
3	2.0 mM SA	16.62	75.27 **	10.25	3.03**	12.10	53.47	3.01	Normal	Semi erect	Susceptible
K9006											
Control	—	19.24	108.26	9.28	3.37	13.78	55.32	4.03	Normal	Semi erect	Susceptible
4	0.01 M EMS	22.18**	104.26**	9.81**	3.17	15.27**	55.40	4.63**	*Shining*	Semi erect	Susceptible
5	0.02 M EMS	20.99**	105.07**	15.40**	3.53**	15.11**	55.65*	3.95	*Shining*	Semi erect	*Resistant*
6	1.5 mM SA	19.77*	105.45**	9.54	3.63**	16.37**	55.47	3.75	Normal	*Erect*	Susceptible
K9107											
Control	—	21.71	108.74	9.37	3.10	12.86	52.42	4.69	Normal	Erect	Resistant
7	0.03 M EMS	23.81**	107.64	9.54	3.27**	12.43	53.62**	4.93**	*Shining*	Erect	Resistant
8	1.0 mM SA	18.33	76.60**	9.63	3.47**	11.13	52.91**	3.62	Normal	Erect	Resistant
9	1.5 mM SA	22.01	79.78**	14.33**	3.37**	10.46	55.98**	2.83	Normal	Erect	Resistant
S.E. ±		0.20	0.65	0.14	0.05	0.06	0.14	0.03			

tion. Mutant 1 was derived from the parent HP1633, whereas mutants 2 and 3 were isolated from HP1731. Three mutants were isolated from each of the remaining parents, K9006 (mutants 4, 5, and 6) and K9107 (mutants 7, 8, and 9). Out of these nine mutants, six showed a significant yield advantage over the respective parent cultivar on a per plant basis (Table 23) and also were promising for yield-component characteristics. In addition to these six high-yielding mutants, three dwarf mutants were isolated from HP 1731 and K 9107. Among these, mutant 9 was dwarf mutant with high tillering and more grain/spike. All mutants except mutant 4 had a high degree of openness of florets compared to the parents, which is expected to promote out-crossing and could be utilized effectively in a hybrid development program.

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Augmenting the Indian wheat improvement program through national nurseries.

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Summary. The Directorate of Wheat Research (DWR) coördinates five national nurseries each year in which genotypes are evaluated in multilocation testing and promising genotypes showing superiority over respective checks for three or more years are identified/confirmed as donors for specific traits. These genetic stocks are important in Indian wheat-improvement programs.

Introduction. India has a very rich biodiversity in wheat. The Green Revolution in India is the result of the introduction of exotic wheat genotypes from the USDA and CIMMYT. CIMMYT, as an international center for wheat improvement, has played an important role in enriching our wheat biodiversity through various international nurseries and trials, which were utilized extensively by various wheat-improvement programs in India. Similarly, the DWR is recognized as a major wheat program in India and has played a significant role in developing and distributing wheat germ plasm in the form of national nurseries to various coördinating centers. At the national level, the DWR coördinates five nurseries every year through which genotypes are evaluated in multilocation testing. These nurseries are the Yield Component Screening Nursery (YCSN), the Salinity/Alkalinity Tolerance Screening Nursery (SAN), the Short Duration cum Late Heat Tolerance Screening Nursery (SDN), the Drought and Heat Tolerance Screening Nursery (DHTSN), and the Quality Component Screening Nursery (QCSN). These national nurseries are for multilocation evaluation and identification of donors along with their utilization at various centers. In this study, the effectiveness of the different national nurseries and their role in wheat-improvement programs is explored.

Methods. The nurseries constituted by the DWR each year consist of genotypes developed from various wheat programs at the Directorate as well as at the various centers. During their evaluation, genotypes contribute in different nurseries as their objectives are evaluated primarily at the Directorate and promising/suitable genotypes are promoted to the multilocation evaluation. The genotypes that perform better for three or more years are confirmed as genetic stocks for a particular character. Information regarding confirmation of the genotypes as genetic stocks has been collected since 1985, and their utilization is based on three criteria, tested/identified/released in coördinated trials as a cultivar, registered as a genetic stock, and used as a parent of an entry.

Results and discussion. A large number of genotypes (269) have been confirmed as genetic stocks during last 20 years.

Yield Component Screening Nursery – AKW 810, AKW 2862-2, DBPY 2000-3, DBPY 2000-4, DBPY 2000-5, DL 218-6, DL 153-2, K 9212, K 9941, Lok Bold, M 81-195-5, PBN 1479, Raj 3461, RD 45, RD 108, RD 185, RD 211, RD 213, RD 214, RD 524, RD 557, Sel.III-50, UP 2425, UP 2467, UP 2468, UP 2490, WR 180, WR 196, WR 765, WR 775, WR 887, WW 2084, YCN 28, and YCN 33 for 1,000-kernel weight; CMH-74, AKW 1948, AKW 2248, AKW 2344, AKW 2591, AKW 2660, AKW 2956, AKAW 2264, AKAW 2665, CMH 76A-962, GW 9906, JNGW 4, JNGW 11, KYZ 9712, LBP 98-301, LBP 98-304, MP 3054, MP 3075, NI 8729, PBN 1786, Raj 3486, UP 2327, VW 9113, VW 9641, WR 107, WR 201, WR 484, WR 782, WR 783, WR 798, WR 885, WR 999, YC-BW-13, YCN 39, and YCN 41 for grain/spike; HI 601, ISD 8, K 9006, LBP 98-307, NI 9768, PBN 4456, RWS 3331, RWS 3332, UNC 39-13, UNC 47-2, WW 2180, WW 2218 and YCN 35 for tillers/meter; AKAW 2344, JNGW 9, SW 2005, VW 9676, WR 829, and WR 849 for grain and tiller number; K 9922 and Lok 2 for 1,000-kernel weight and tiller number, and AKW 1071 for 1,000-kernel weight and grain and tiller number.

Quality Component Screening Nursery – CPAN 1946, CPAN 2016, CPAN 2019, GW 9912, HD 2674, HD 2793, HP 1765, ISD 215, K 9006, K 9107, K 9507, K 9906, KC 974, KYZ 9652, KYZ 9718, KYZK2K 13, MBL 2, MBL 5, NP 761, PR 2, PR 3, PR 5, PR 8, PR 9, PR 12, PR 19, PR 21, PR 22, PR 23, PR 42, PR 48, QBS 102, QBS 103, RD 363, RD 524, Sel. III 50, UP 301, VL 490, WR 5, and WR 758.

Short Duration cum Late Heat Tolerance Screening Nursery – GW 9715, GW 9904, WR 544, NCS 209 AKW 770, 85D-245, GW 2000-6, AKW 50, AKW 204, DL 7-6, J 83-39, M 80-239, P 2045, RD 191, and WH 423-6 for early heading and maturity; DBW 11, GW 2000-4, HD 2327, HD 4594, UP 2425 and WR 251 for 1000-Grain weight; CBW 12, PBN 4588, RWP 9912, RS 386, UP 2496, and WJ 89 for grain/spike; 85D-47, 85D-50, AKW 2862-1, DL 218-6, HD 2469, HD 2472, KC 975, P 10987, P 10988, WR 225, WR 703, and WR 704 for short duration and 1,000-kernel weight; AKW 619, GW 9711, GW 9712, HD 2402, HW 2045, HD 2316, HD 2367, HD 2449, HD 2516, NCS 157, UP 2260, UP 2281, UP 2282, and VH 36 for short duration and grain yield; and 85D-204, AKW 90-1, AKW 381, and Lok 1 for short duration, 1,000-kernel weight and grain yield.

Salinity/Alkalinity Tolerance Screening Nursery – AKW 65-1, BAU 2267, BW 1022, BW 1052, DL 770-2, HD 2385, HP 1529, Job 603, Job 666, Job 673, K 9006, K 9351, K 9353, K 9507, Kharchia 65, KNS 7, KNS 11, KNS 57, KNS 59, KNS 75, KRL 1-4, KRL 2-22, KRL 3-4, KRL 4-1, KRL 4-4, KRL 4-6, KRL 4-8, KRL 4-10, KRL 13, KRL 28, KRL 32, KRL 35, KRL 36, KS 133, Lok 1, M 3096, M 3097, M 3098, MPJ 12, NI 5439, NW 1001, NW 1032, NW 1053, NW 1065, NW 1067, NW 1082, NW (S) 93-3, NW (S) 93-9, NW (S) 93-11, NW (S) 93-21, Raj 3077, Raj 3730, Raj 3732, RK 59, RK 67, RK 76, SNH 9, Sonalika, WH 157, and WR 814.

Drought and Heat Tolerance Screening Nursery – 21 (S) Ad, A-9-30-1, AKW 65-1, AKW 470-7, CM 59, GWL 331, HD 2815, Hindi 62, Hyb 65, Job 828, K 8027, Kharchia 65, MP 3054, Narmada 4, NI 5439, NI 8223, Pissi local, RS 352, RS 488, RS 491, RS 519, RS 626, RS 629, RS 634, Sujata, WR 502, WR 741, and WT 245

Among the nurseries, most germ plasm lines confirmed as sources for different traits were from the YCSN, followed by those from the SAN and SDN. The YCSN and SDN evaluate genotypes for yield-component traits and a number of genotypes were confirmed as a source either singly or in combination. Out of 91 genotypes confirmed through the YCSN, 34 were confirmed for 1,000-kernel weight, 35 for grain/spike, and 14 for high tiller number. AKW 1071 was confirmed as a source for all three characters under the YCSN, whereas K 9922 and Lok 2 were confirmed for high grain weight and tiller number. Similarly, promising genotypes having short duration and yield components were confirmed as donors after 3–4 years of evaluation. Of the 57 genotypes confirmed from the SDN, four genotypes, 85D-204, AKW 90-1, AKW 381, and Lok 1, were high-yielding genotypes with short duration and bold seeds.

Three groups, based on utilization, included genotypes tested/identified/released in a coördinated system as a cultivar, used as a parent in breeding programs, or registered as genetic stocks with the National Board of Plant Genetic Resources (NBPGR). In the study, utilizing germ plasm lines as parents was considered only for those entries that were included in the All India Coordinated Trials. Out of 269 genotypes confirmed through the various national nurseries, only 59 (approximately 21.93%) genotypes passed these three criteria (Table 24). A maximum 35.09% of the genotypes

Table 24. Utilization pattern of genetic stocks confirmed from the various national nurseries. Genotypes used as parents are in *italics*, and genotypes tested/identified/released as cultivars are underlined. An asterisk (*) indicates that the line was registered with National Board of Plant Genetic Resources as a genetic stock. Nurseries include the Yield Component Screening Nursery (YCSN), the Salinity/Alkalinity Tolerance Screening Nursery (SAN), the Short Duration cum Late Heat Tolerance Screening Nursery (SDN), the Drought and Heat Tolerance Screening Nursery (DHTSN), and the Quality Component Screening Nursery (QCSN).

Nursery	Genotypes identified	Utilization (%)	Genetic stocks
YCSN	91	16.48	*DL 218-6*, *DL 153-2, JNGW 4, JNGW 11*, *K 9006*, *K 9212*, K 9941, *NI 8729*, *SW 2005*, UP 2425, *WR 107*, *WR 484*, *WW 2218, YC-BW-13, YCN 39*
SDN	57	35.09	*AKW 381,* AKW 619, *AKW* 770, AKW 2862-1*, CBW 12, DBW 11, *DL 218-6*, *HD 2327, HD 2367*, *HD 2402*, *HD 2449*, *HD 2469*, *HD 4594*, *HW 2045*, *Lok 1, UP 2282, UP 2425, WR 225,* WR 251, *WR 544*
SAN	60	25.00	*DL 770-2*, *HD 2385*, *K 9006*, *K 9351*, *K 9507*, *Kharchia 65*, *KRL 1-4*, *KRL 3-4**, *Lok 1*, *NI 5439*, *Raj 3077*, *Sonalika*, *WH 157*
DHTSN	28	32.14	*A-9-30-1*, HD 2815, *Hindi 62**, *Hyb 65*, *K 8027*, Kharchia 65, Narmada 4, NI 5439, Sujata
QCSN	40	20.00	ISD 215*, *K 9006*, *K 9107*, *K 9507*, K 9906, MBL 2*, MBL 5*, *UP 301*
Total	269	21.93	

utilized were from the SDN followed by the DHTSN (32.14%) and SAN (25%) (Fig. 5, p. 99). The utilization trend of germ plasm lines revealed that out of 269 genotypes confirmed as genetic stocks, 15% were used as parents and about 12% were evaluated as an entry in a coördinated trial. When the performance of genotypes from an individual nursery was studied, we found that highest percent of entries evaluated as cultivars was from the DHTSN (28.57%) and SDN (19.30%). More genotypes from the SAN (21.67%) and SDN (15.79%) were used as donor parents in breeding programs (Fig. 5, p. 99). Three genotypes, ISD 215, MBL 2, and MBL 5, were confirmed from the QCSN and registered as genetic stocks with the NBPGR. In addition, three genotypes registered as genetic stocks with the NBPGR, AKW 2862-1, KRL 3-4, and Hindi 62, from the SDN, SAN, and DHTSN, respectively, were confirmed as donors for different traits.

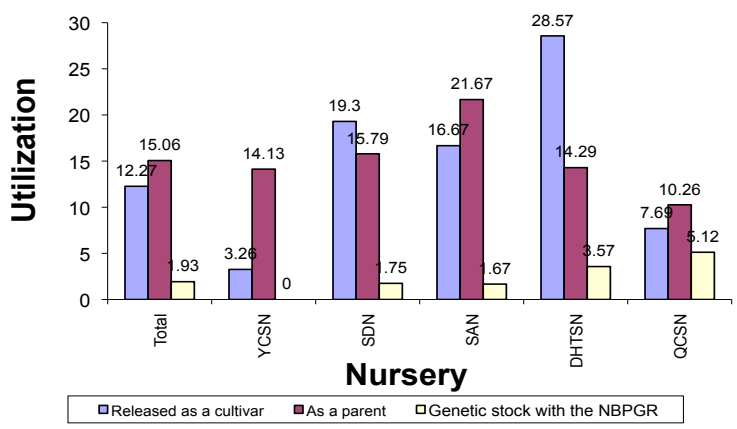

Fig. 5. Utilization of genotypes from the various multilocation nurseries in India, including the Yield Component Screening Nursery (YCSN), the Salinity/Alkalinity Tolerance Screening Nursery (SAN), the Short Duration cum Late Heat Tolerance Screening Nursery (SDN), the Drought and Heat Tolerance Screening Nursery (DHTSN), and the Quality Component Screening Nursery (QCSN).

The study also revealed that a few genotypes were confirmed as donors through different nurseries. Among these, K 9006 was identified as good source for tillers from the YCSN, for high protein and bold grain through the QCSN, and for tolerance to salinity/alkalinity through the SAN. Other genotypes that were identified as donors from different nurseries were DL 218-6 from the YCSN (1,000-kernel weight) and SDN; Sel.III-50 from the YCSN (1,000-kernel weight) and QCSN; MP 3054 from the YCSN (grain/spike) and DHTSN; Lok 1 from the SDN and SAN; and K 9507 from the SAN and QCSN.

Inferences can be drawn from this information regarding role of these national nurseries in Indian wheat-improvement programs. From the time of the Green Revolution, Indian wheat-improvement programs have benefited very much from exotic materials and, as a result, most of the cultivars released have had their origin either as a direct selection from this exotic material or from 'indigenous × exotic' combinations (Fig. 6). At the same time, the indigenous wheat-improvement programs also existed through direct selection; 'indigenous × indigenous', and 'indigenous × exotic crosses' (Singh et al. 2006). These indigenous materials include landraces of economic importance, especially as donors for quality and heat stress and indigenously developed breeding lines. Although the overall utilization of the identified genotypes from these national nurseries was less (21.85%), their role in germ plasm improvement and enhancement is encouraging. The genotypes identified from the DHTSN and SDN were utilized as genotype tested/identified/released under the AICWIP, whereas a maximum percent of genotypes used as donors were from the SAN and SDN. Genotypes identified from various nurseries or registered with the NBPGR are made available to various centers for their efficient utilization through the NGSN. The future prospects for these nurseries is very hopeful. Although the pace of utilizing these materials is slow, their effective and efficient use is encouraging and will enhance further genetic variability in wheat-improvement programs.

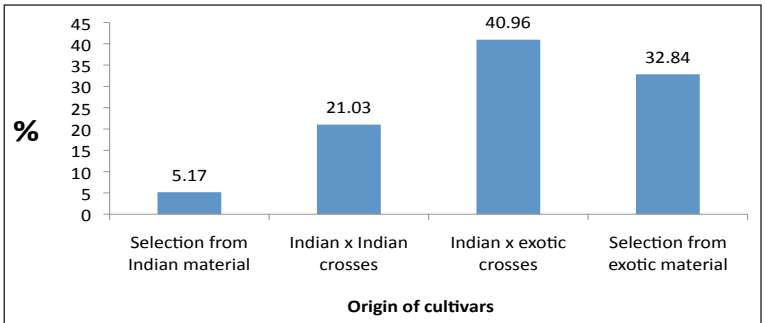

Fig. 6. Origin of released cultivars under the under All India Coordinated Trials.

Acknowledgments. The authors are thankful to all the coöperators involved in organizing and conducting of the national nurseries.

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ITEMS FROM ITALY

CONSIGLIO PER LA RICERCA E LA SPERIMENTAZIONE IN AGRICOLTURA, Unità di ricerca per la valorizzazione qualitativa dei cereali (CRA–QCE), Via Cassia, 176, 00191 Rome, Italy.

Indexed data for comparing the reaction to cereal soilborne mosaic virus of durum wheat cultivars assayed in different seasons.

V. Vallega and C. Rubies-Autonell, A.M. Pisi, and C. Ratti (University of Bologna, Dipartimento di Scienze e Tecnologie Agroambientali).

Cereal soilborne mosaic virus (CSBMV) is widespread in Italy, where it often causes yield reductions of ~50–70% on susceptible wheats. A total of 89 durum wheat cultivars were assayed in seven seasons (1995–96, 1996–97, 2000–01, 2001–02, 2002–03, 2003–04, and 2004–05) in a field near Bologna with natural inoculum sources of CSBMV. Each trial was comprised of 30–33 cultivars, grown in 10-m^2, solid-seeded plots and distributed according to a randomized block design with three replicates. Nineteen cultivars were tested for 4–7 seasons and 58 cultivars for 1–2 seasons. Symptom severity was scored on 2–4 dates in each season using a 0–4 scale. DAS-ELISA was performed on extracts from a bulk of the youngest or second youngest fully expanded leaf of 10 or 15 plants/plot collected on one (1996 and 2001) or two dates. Grain yield and other agronomic traits also were recorded. To minimize the confounding effects of disease pressure, differences between seasons, the symptom score, and ELISA data collected for each cultivar on different dates were averaged and subsequently indexed as a percent of the highest mean observed among all cultivars assayed in that season; grain yield data also were indexed.

The 89 cultivars demonstrated a wide and continuous range of reactions to CSBMV (Table 1, p. 100-101), both in terms of symptom severity (index range = 4.5–100.0%), ELISA value (index range = 3.4–100.0%), and grain yield (index range = 35.5–100.0%; data not shown). Various cultivars consistently presented mild symptoms and low ELISA values in various seasons, yet none proved completely resistant. It should be noted that, although symptom score and ELISA value indexes were closely correlated (r = 0.850***), they produced different and sometimes contrasting resistance cultivar rankings, particularly in the case of cultivars tested for only one or two seasons. A wide and continuous

Table 1. Symptom score and ELISA value indexes (%), and rankings for 89 durum wheat cultivars assayed for resistance to cereal soil-borne mosaic virus near Bologna, Italy, from 1995–96 to 2004–05.

Cultivar	No. of years tested	Symptom score		ELISA value		Cultivar	No. of years tested	Symptom score		ELISA value	
		Index	Rank	Index	Rank			Index	Rank	Index	Rank
Louxor	1	6.7	3	6.1	4	Norba	1	18.8	21	50.6	54
Neodur	7	12.1	12	3.4	1	Torrebianca	5	38.7	52	34.9	41
Ares (Ionio)	4	9.5	7	6.9	6	Vendetta	1	35.6	46	38.3	43
Campodoro	1	4.5	1	13.0	13	Tresor	2	35.4	45	38.9	44
Meridiano	5	11.4	11	6.4	5	Virgilio	2	50.8	58	26.6	33
Dylan	3	9.0	4	10.0	9	Quadrato	4	37.0	47	40.9	47
Nefer	1	4.6	2	15.2	17	Verdi	3	29.7	36	49.0	52
Giusto	1	17.4	17	10.5	11	Appio	2	37.9	50	42.8	48
Colorado	5	18.2	20	10.8	12	Exeldur	2	33.9	41	53.4	56
Valerio	1	24.7	29	4.7	3	Italo	2	37.6	49	52.3	55
Ceedur	1	10.1	8	19.4	24	Plinio	1	37.5	48	61.2	61
Pietrafitta	2	11.2	10	19.1	22	Colosseo	4	42.3	56	60.4	60
Provenzal	5	26.2	31	4.4	2	Sorrento	1	69.4	66	38.9	45
Solex	6	12.5	14	19.3	23	Ixos	3	40.2	54	68.2	63
Baio	1	10.1	9	25.2	31	Creso	6	55.3	60	58.0	58
Levante	2	28.6	35	7.3	7	Portobello	1	58.4	61	55.3	57

Table 1. Symptom score and ELISA value indexes (%), and rankings for 89 durum wheat cultivars assayed for resistance to cereal soil-borne mosaic virus near Bologna, Italy, from 1995–96 to 2004–05.

Cultivar	No. of years tested	Symptom score		ELISA value		Cultivar	No. of years tested	Symptom score		ELISA value	
		Index	Rank	Index	Rank			Index	Rank	Index	Rank
Tiziana	3	23.0	25	13.1	14	Giove	1	67.2	64	64.3	62
Lloyd	3	17.4	18	20.4	25	Ofanto	2	55.1	59	79.5	66
Parsifal	2	17.9	19	23.5	28	Claudio	5	78.8	73	75.7	65
Cosmodur	2	20.8	23	21.9	26	Portorico	5	67.3	65	89.9	76
Duilio	7	24.2	27	19.1	21	Prometeo	2	98.2	87	59.4	59
Avispa	3	30.5	37	13.2	15	Anco Marzio	1	86.5	78	72.4	64
Fiore	2	39.3	53	7.5	8	Giemme	2	64.3	63	95.5	85
Flavio	2	23.3	26	24.4	29	Ciccio	2	61.0	62	99.0	86
Svevo	1	33.5	40	15.6	18	Marco	2	78.4	72	83.3	69
Gianni	5	24.6	28	24.7	30	Balsamo	2	75.3	70	90.4	77
San Carlo	5	26.8	32	22.7	27	Derrick	2	79.7	74	87.1	71
Rusticano	1	33.3	39	17.5	20	Platani	2	75.0	69	93.2	79
Grecale	2	40.6	55	10.3	10	Vettore	2	86.1	77	82.5	67
Peleo	1	9.4	6	43.0	49	Simeto	7	74.4	68	94.5	80
Vitron	2	12.3	13	40.8	46	Sorriso	1	76.5	71	94.6	81
Canyon	1	38.0	51	15.2	16	Vinci	1	71.2	67	100.0	89
Brindur	1	9.4	5	44.7	51	Orobel	5	82.2	75	89.4	74
Portofino	2	21.9	24	32.3	38	Vesuvio	3	88.7	80	87.2	72
Iride	6	26.0	30	29.3	35	Cannizzo	3	87.8	79	88.3	73
Valsalso	1	20.5	22	34.8	40	Grazia	5	93.0	84	86.0	70
Preco	1	12.5	15	43.6	50	Bronte	1	83.0	76	99.4	87
Vitomax	3	27.3	33	29.2	34	Carioca	1	100.0	88	82.5	68
Normanno	2	27.4	34	29.3	36	Cirillo	3	93.9	85	89.5	75

range of reactions to CSBMV in terms of symptom severity and ELISA value, as well as a higher similarity between symptom and ELISA index rankings, was observed for the 19 cultivars assayed four or more seasons (Table 2). The grain yield index also became more closely related to the other two indexes when analysis' were restricted to the 19 cultivars assayed four or more seasons. These 19 rather closely related cultivars, representing only 22% of those examined, showed no less than six distinct levels of resistance to CSBMV, suggesting that they differed for at least three major CSBMV resistance genes.

Table 2. Symptom score, ELISA value, and grain yield indexes (%) and rankings for 19 durum wheat cultivars assayed for CSBMV resistance in four or more seasons (Bologna, 1995–96 – 2004–05).

Cultivar	No. of years tested	Symptom score		ELISA value		Grain yield	
		Index	Rank	Index	Rank	Index	Rank
Neodur	7	12.1	3	3.4	1	85.3	4
Ares (Ionio)	4	9.5	1	6.9	4	86.7	2
Meridiano	5	11.4	2	6.4	3	86.1	3
Colorado	5	18.2	5	10.8	5	83.0	5
Provenzal	5	26.2	9	4.4	2	89.8	1
Solex	6	12.5	4	19.3	7	78.6	10
Duilio	7	24.2	6	19.1	6	80.1	7
Gianni	5	24.6	7	24.7	9	78.8	9
San Carlo	5	26.8	10	22.7	8	80.7	6
Iride	6	26.0	8	29.3	10	79.3	8
Torrebianca	5	38.7	12	34.9	11	76.1	11
Quadrato	4	37.0	11	40.9	12	74.7	12
Colosseo	4	42.3	13	60.4	14	65.5	15
Creso	6	55.3	14	58.0	13	70.7	13
Claudio	5	78.8	17	75.7	15	35.5	19
Portorico	5	67.3	15	89.9	18	55.6	16
Simeto	7	74.4	16	94.5	19	52.8	17
Orobel	5	82.2	18	89.4	17	66.5	14
Grazia	5	93.0	**19**	86.0	**16**	48.2	**18**

Predicting agronomic performance of durum wheat cultivars on the basis of CSBMV concentration and symptom severity evaluations made on different dates.

C. Rubies-Autonell, C. Ratti (University of Bologna, Dipartimento di Scienze e Tecnologie Agroambientali), and V. Vallega.

Different sets of cultivars of durum wheat were tested over seven seasons in a field near Bologna, Italy, with natural inoculum sources of CSBMV. Each trial was comprised of 30–33 cultivars. Symptom severity, DAS-ELISA absorbance, and various agronomic characters were investigated. In each season, symptom severity was scored on 2–4 dates using a 0–4 scale, whereas DAS-ELISA was performed on extracts from a bulk of the youngest or second youngest fully expanded leaf of 10 or 15 plants/plot collected on one (1995–96 and 2000–01) or two dates. The cultivars were grown in 10-m^2, solid-seeded plots distributed according to a randomized block design with three replicates. The effects of CSBMV on the agronomic performance of cultivars manifesting diverse symptom severity were estimated by regression analysis. The data collected were used to estimate the damage caused by CSBMV and to identify the most informative dates for rating symptom severity and assessing virus concentration.

Symptom scores above 3.0 were associated with mean grain yield and mean plant height reductions of 48% and 25%, respectively, as well as with notable decreases in kernel weight and test weight (Table 3). Even mild symptoms caused appreciable negative effects on grain yield (-9%) and plant height (-5%). Mean ELISA absorbance (Table 4) was significantly (P = 0.05) correlated with mean symptom severity, grain yield, and plant height in all seven seasons, with kernel weight and test weight in four seasons, and with heading date in two seasons. Mean symptom severity also was more closely correlated with grain yield and plant height than with the other three agro-

Table 3. Mean actual performance and estimated effects of cereal soilborne mosaic virus (CSBMV) for durum wheat cultivars with different symptom severity grown in a field with CSBMV near Bologna, Italy, over seven seasons.

Symptom score (0–4)	Actual grain yield	Reduction (%)	Actual plant height	Reduction (%)	Actual kernel weight	Actual test weight	Actual heading date
0.0–1.0	4.66	8.7	81.4	4.6	42.4	78.4	40
1.0–2.0	3.97	22.2	78.2	8.4	41.6	77.6	41
2.0–3.0	2.97	41.8	70.4	17.5	38.5	76.7	41
3.0–4.0	2.64	48.2	64.1	24.9	36.1	77.1	43

Table 4. Correlations between ELISA absorbance values on different dates and agronomic characters and mean symptom score for 89 durum wheat cultivars grown in a field with cereal soilborne mosaic virus near Bologna, Italy, in trials comprised of 30–33 cultivars.

Year	No. of cultivars	Date	Grain yield		Plant height		Kernel weight		Test weight		Heading date		Mean symptom Score	
1996	33	26 March	-0.710	**	-0.721	**	-0.516	**	-0.383	*	0.523	**	0.855	**
1997	33	4 April	-0.736	**	-0.436	**	-0.351	*	-0.409	*	0.170	ns		
		7 May	-0.720	**	-0.462	**	-0.428	*	-0.583	**	0.282	ns		
Mean ELISA			-0.752	**	-0.468	**	-0.412	*	-0.533	**	0.246	ns	0.826	**
2001	30	21 March	-0.570	**	-0.404	*	-0.079	ns	-0.371	*	—		0.808	**
2002	30	13 March	-0.709	**	-0.790	**	-0.231	ns	-0.472	**	0.099	ns		
		3 April	-0.467	**	-0.511	**	-0,074	ns	-0.152	n.s.	0.173	ns		
Mean ELISA			-0.703	**	-0.781	**	-0.206	ns	-0.422	*	0.130	ns	0.862	**
2003	31	13 March	-0.853	**	-0.667	**	-0.547	**	-0.635	**	0.332	ns		
		2 April	-0.897	**	-0.773	**	-0.401	*	-0.536	**	0.391	*		
Mean ELISA			-0.920	**	-0.758	**	-0.494	**	-0.612	**	0.413	*	0.942	**
2004	31	30 March	-0.816	**	-0.746	**	-0.431	*	-0.313	n.s.	0.244	ns		
		22 April	-0.861	**	-0.784	**	-0.524	**	-0,310	n.s.	0.267	ns		
Mean ELISA			-0.874	**	-0.797	**	-0.497	**	-0.325	n.s.	0.266	ns	0.928	**
2005	32	6 April	-0.501	**	-0.744	**	-0.179	ns	0.240	n.s.	0.119	ns		
		20 April	-0.507	**	-0.669	**	-0.204	ns	0.139	n.s.	0.087	ns		
Mean ELISA			-0.519	**	-0.732	**	-0.197	ns	0.200	n.s.	0.108	ns	0.819	**

nomic traits (Table 5). In four out of five seasons, ELISA correlations with grain yield and plant height were practically identical for the two sampling dates considered; only in 2002 was the earlier date (13 March) distinctly more informative; correlations with kernel weight and test weight also were similar on different dates. The correlation of symptom score with grain yield and plant height were essentially identical for the various sampling dates considered, except for the first scoring date in 2005 (18 March), which proved markedly less informative than the three subsequent dates. Correlations with kernel weight, test weight, and heading date also proved similar on different dates. The results indicated that multiple symptom and ELISA observations allow more meaningful CSBMV-damage estimates only with respect to the more loosely associated agronomic traits (kernel weight, test weight, and heading date), whereas a single scoring and sampling date suffices to produce reliable grain yield and plant height reduction estimates. However, symptom score and ELISA value rankings among cultivars change, sometimes substantially, during the season, thus rendering multiple observations mandatory for adequately classifying the response of single cultivars to CSBMV.

Table 5. Correlations between CSBMV-symptom severity on different dates and agronomic characters and mean ELISA absorbance for 89 durum wheat cultivars grown in a field with CSBMV near Bologna, Italy, in trials comprised of 30–33 cultivars.

Year	No. of cultivars	Date	Grain yield		Plant height		Kernel weight		Test weight		Heading date		Mean ELISA	
1996	33	26 March	-0.760	**	-0.776	**	-0.647	**	-0.458	**	0.609	**		
		17 May	-0.757	**	-0.786	**	-0.601	**	-0.382	*	0.735	**		
Mean symp.			-0.773	**	-0.800	**	-0.638	**	-0.425	*	0.693	**	0.855	**
1997	33	26 March	-0.657	**	-0.558	**	-0.364	*	-0.288	ns	0.515	**		
		4 April	-0.761	**	-0.484	**	-0.180	ns	-0.298	ns	0.352	*		
		16 April	-0.825	**	-0.494	**	-0.439	**	-0.461	**	0.348	*		
		24 April	-0.777	**	-0.541	**	-0.365	*	-0.444	**	0.363	*		
Mean symp.			-0.812	**	-0.556	**	-0.368	*	-0.408	*	0.418	*	0.826	**
2001	30	19 February	-0.635	**	-0.655	**	-0.224	ns	-0.344	ns	-			
		5 March	-0.604	**	-0.675	**	-0.306	ns	-0.342	ns	-			
		21 March	-0.615	**	-0.595	**	-0.261	ns	-0.279	ns	-			
Mean symp.			-0.630	**	-0.653	**	-0.273	ns	-0.325	ns	-		**0.808**	**
2002	30	28 February	-0.514	**	-0.711	**	-0.087	ns	-0.223	ns	0.110	ns		
		13 March	-0.606	**	-0.771	**	-0.077	ns	-0.225	ns	0.247	ns		
		3 April	-0.653	**	-0.784	**	-0.132	ns	-0.286	ns	0.319	ns		
		22 April	-0.698	**	-0.789	**	-0.137	ns	-0.442	*	0.189	ns		
Mean symp.			-0.651	**	-0.803	**	-0.114	ns	-0.307	ns	0.233	ns	0.862	**
2003	31	13 March	-0.914	**	-0.835	**	-0.549	**	-0.515	**	0.332	ns		
		2 April	-0.859	**	-0.767	**	-0.563	**	-0.499	**	0.469	**		
		16 April	-0.912	**	-0.850	**	-0.545	**	-0.531	**	0.367	*		
Mean symp.			-0.913	**	-0.834	**	-0.564	**	-0.526	**	0.396	*	0.942	**
2004	31	18March	-0.790	**	-0.730	**	-0.456	**	-0.327	ns	0.335	ns		
		30 March	-0.823	**	-0.754	**	-0.589	**	-0.317	ns	0.318	ns		
		15 April	-0.891	**	-0.766	**	-0.521	**	-0.363	*	0.319	ns		
		22 April	-0.775	**	-0.665	**	-0.481	**	-0.286	ns	0.283	ns		
Mean symp.			-0.859	**	-0.765	**	-0.537	**	-0.340	ns	0.330	ns	0.928	**
2005	32	18 March	-0.395	*	-0.569	**	-0.155	ns	0.213	ns	0.036	ns		
		1 April	-0.552	**	-0.712	**	-0.417	*	0.246	ns	0.105	ns		
		6 April	-0.635	**	-0.796	**	-0.435	*	0.257	ns	0.105	ns		
		18 April	-0.687	**	-0.777	**	-0.391	*	0.282	ns	0.151	ns		
Mean symp.			-0.633	**	-0.782	**	-0.400	*	0.272	ns	0.116	ns	0.819	**

Inheritance of resistance to CSBMV in lines derived from a cross between durum wheat cultivars Neodur and Cirillo.

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Most of the durum wheat cultivars marketed in Italy are quite susceptible to CSBMV and none was found completely resistant. The same observation was made for a large number of durum wheat cultivars from other countries. A high proportion of the few, highly CSBMV-resistant cultivars identified are derived from Edmore wheat and, therefore, a reasonable assumption is that Edmore and its CSBMV-resistant derivatives carry a major CSBMV-resistance gene or gene-block. To test this hypothesis, 160 F_8 RILs obtained by single-seed-descent from a cross between cultivars Neodur (a resistant derivative of Edmore) and Cirillo (highly susceptible) were grown during 2007–08 in a field with natural inoculum sources of CSBMV near Bologna. The lines and parental cultivars were grown in 2.4-m^2, solid-seeded plots distributed according to a randomized block design with three replicates and evaluated for symptom severity (on 11 March, 27 March, and 15 April) and ELISA absorbance (on 11 March and 15 April). Symptom severity was scored on a 0–4 scale. DAS-ELISA was determined on extracts from a bulk of the youngest fully expanded leaf of 15 plants/plot. Grain yield, test weight, kernel weight, and plant height also were recorded.

Symptom scores and ELISA values were significantly correlated, and both parameters showed significant negative associations with each of the four agronomic traits examined, particularly with grain yield and plant height. Symptom-severity score frequency distributions showed a markedly greater proportion of resistant lines (about 96 vs. 64) on all three observation dates and eight major peaks (Fig. 1, p. 105). Grain yield, plant height, and ELISA-absorbance means for the lines contributing to each of the eight major symptom frequency-peaks were highly differentiated and closely matched the values expected for the corresponding symptom score peaks. The ELISA value distributions also revealed a greater proportion of resistant lines (about 89 vs. 71) and seven distinct, major peaks. Most of the major frequency peaks obtained for each of the two resistance parameters were bi-modal. Segregation distortions analogous to that causing a preponderance of CSBMV-resistant types have often been reported for RILs and may be attributed to various factors; particularly to genetic interactions and, in the case of materials obtained by SSD, which cumulate the effects of multiple generations, to selective advantages of the corresponding genes or gene-blocks. The number of genes (2.8, 3.4, and 3.1 for 11 March, 27 March, and 15 April, respectively) estimated by the formula of Wright approximately corresponds to that envisaged by the major peaks in the frequency distributions. Nonwithstanding segregation distortion, we concluded that the cultivar Neodur contributed at least three, possibly linked, major genes that account for the 7–8 major frequency peaks and their seemingly bi-modal form. The study gave evidence of the presence of a sizeable temporal change in the relative degree of resistance of the lines in terms of both symptom severity and ELISA absorbance causing substantial changes in resistance ranking order among lines. This temporal change may be attributed to the diverse duration of the efficacy of the resistance genes identified or to genes controlling morphological or phenological plant traits affecting the onstart and/or progress of CSBMV infection. We have observed previously and reported resistance rankings changes between cultivars during the course of a same season; the present experiment offered the opportunity to validate the phenomenon in a common genetic background. Presently, the 'Neodur/Cirillo' population is being profiled to identify the QTL associated with its specific CSBMV-resistance genes and to elucidate the nature of the genes causing a temporal change in resistance and of that originating the inheritance pattern distortion.

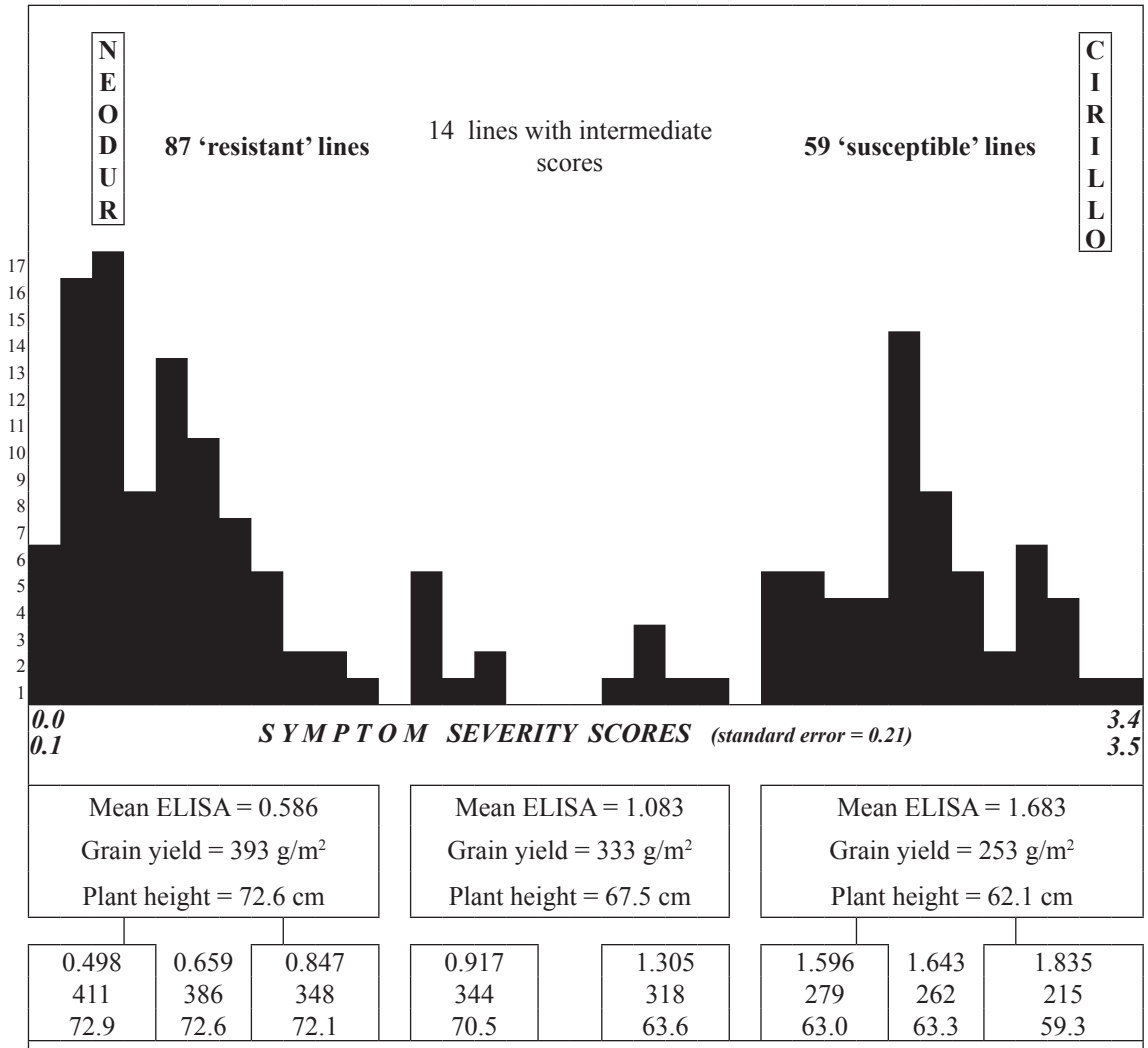

Fig. 1. Number of lines derived from the durum wheat cross 'Neodur/Cirillo' with different CSBMV symptom severity scores (0–4 scale; means of 27 March and 15 April, 2008) and mean ELISA value, grain yield (g/m^2), and plant height (cm) of the lines corresponding to the eight major frequency peaks.

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Inheritance of resistance to cereal soilborne mosaic virus in a durum wheat population of lines derived from the cross ' Meridiano / Claudio': results of a two-year study.

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Only a few of the nearly 200 durum wheat cultivars assayed in Italy for resistance to cereal soilborne mosaic virus (CSBMV) have shown to express very mild symptoms as well as a low virus concentration under severe disease pressure, and none of them has proven completely resistant to either CSBMV symptom expression or infection. Indeed, most of the cultivars tested so far exhibit a consistent array of intermediate reactions, suggesting that their reaction to CSBMV is governed by numerous genes.

A population consisting of 184 RILs obtained via single-seed descent by Produttori Sementi Bologna S.p.A., Italy, from a cross between the durum wheat cultivars Meridiano (resistant) and Claudio (moderately susceptible) was assayed during 2006–07 and 2007–08 in a field with natural inoculum sources of CSBMV at Cadriano (Bologna). In each season, the RILs, parents, and the cultivar Grazia (a susceptible control inserted at regular intervals) were evaluated for resistance on the basis of symptomatology on four dates and ELISA absorbance on two dates. The plants were grown in 2.4-m^2, solid-seeded plots distributed according to a randomized block design with two replicates. Symptoms were scored on a 0–4 scale. Virus concentration was estimated by DAS-ELISA, on leaf samples. Grain yield, kernel weight, and test weight also were measured. The data from the first season were reported (Ann Wheat Newlsett 54:76), those obtained in the 2007–08 trial are summarized in Table 1 and

Table 1. Symptom severity score frequency (%) distribution at four sampling dates in 2008 for 184 lines from a 'Meridiano/Claudio' population assayed during 2007–08 in a field with natural inoculum sources of CSBMV at Cadriano (Bologna), Italy.

Symptom severity interval	Frequency (%)			
	3 March	11 March	25 March	10 April
0.00–0.10	44.6	13.0	32.1	13.6
0.11–0.20	2.7	4.9	7.1	9.2
0.21–0.30	7.6	4.9	4.9	6.5
0.31–0.40	3.3	4.3	3.3	7.1
0.41–0.50	4.9	2.7	2.2	7.1
0.51–0.60	0.0	0.5	0.0	0.5
0.61–0.70	2.7	1.6	1.1	2.2
0.71–0.80	3.3	3.3	1.1	3.3
0.81–0.90	2.7	3.3	0.5	1.1
0.91–1.00	3.3	3.8	0.0	0.5
1.01–1.10	0.0	0.0	0.5	0.0
1.11–1.20	2.2	1.6	1.1	0.5
1.21–1.30	3.8	2.7	0.5	0.5
1.31–1.40	2.7	0.5	0.5	1.1
1.41–1.50	3.3	1.6	0.0	0.0
1.51–1.60	0.0	0.0	0.0	0.0
1.61–1.70	4.9	0.5	1.1	1.1
1.71–1.80	2.7	1.6	0.5	1.6
1.81–1.90	1.1	1.1	1.1	1.1
1.91–2.00	0.5	1.6	2.2	1.1
2.01–2.10	0.0	0.0	0.0	0.0
2.11–2.20	1.1	1.1	2.2	0.5
2.21–2.30	1.6	2.2	1.6	1.1
2.31–2.40	0.0	3.3	4.9	3.8
2.41–2.50	0.5	2.7	4.3	2.7
2.51–2.60	0.0	0.0	0.0	0.0
2.61–2.70	0.0	4.9	2.7	5.4
2.71–2.80	0.0	4.3	7.1	4.9
2.81–2.90	0.5	2.2	6.0	7.6
2.91–3.00	0.0	8.2	3.3	9.2
3.01–3.10	0.0	0.0	0.0	0.0
3.11–3.20	0.0	4.3	5.4	4.3
3.21–3.30	0.0	4.9	1.6	2.2
3.31–3.40	0.0	4.3	0.5	0.0
3.41–3.50	0.0	2.7	0.0	0.0
3.51–3.60	0.0	0.0	0.0	0.0
3.61–3.70	0.0	0.0	0.0	0.0
3.71–3.80	0.0	1.1	0.0	0.0
3.81–3.90	0.0	0.0	0.0	0.0
3.91–4.00	0.0	0.0	0.0	0.0

Table 2. Disease pressure was severe in both seasons, as testified by the mean symptom scores (3.8 in 2007 and 3.6 in 2008) recorded for Grazia at the time of maximum symptom expression.

Analysis of symptom score and ELISA absorbance frequency distributions indicated a complex inheritance of CSBMV-resistance, involving no less than four major genes, various modifiers, and a different timeline of the expression of resistance. Transgressive segregation, moreover, indicated that both the resistant (Meridiano) and the moderately susceptible parents (Claudio) contributed favorable alleles. Despite the favorable genes contributed by the latter cultivar, however, RILs completely resistant to CSBMV were not recovered. Indeed, leaf samples from all the RILs assayed were found ELISA-positive on at least one of the four collection dates, and all except two RILs gave ELISA-positive results on at least two dates. Moreover, the only RIL that remained symptom-free throughout the two seasons (i.e., on eight scoring dates) proved ELISA-positive on two out of collection dates. Eighteen of the 184 RILs assayed had overall mean symptom scores lower than the resistant parent; 15 of these RILs also showed lower overall mean ELISA absorbances; 9 produced higher grain yields; 10 showed higher test weights; and 11 showed higher kernel weights. Two RILs performed better than cultivar Meridiano in regard to all of the five parameters considered. Further trials are being set up to establish whether any of the above 18 RILs are indeed more resistant to CSBMV than cultivar Meridiano.

The RILs also were profiled with molecular markers (158 SSRs), and an association map spanning 2,050 cM was obtained. Preliminary results indicate that at least four QTL accounted for most of the phenotypic variation observed. A major QTL was associated to *Xwmc243* (distal telomeric region of chromosome arm 2BS),with the favorable allele contributed by Meridiano. The additional favorable QTL all located in the distal regions of the short and long arms of chromosome group 5 (particularly in chromosome 5A), were contributed by both parents. The QTL identified in the distal regions of 5AL (*Xwmc524*) and 5BL (*Xbarc243*) could represent the homoeologous copies of the major QTL identified in bread wheat (*Sbm1*).

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Table 2. Symptom severity score frequency (%) distribution at four sampling dates in 2008 for 184 lines from a 'Meridiano/Claudio' population assayed during 2007–08 in a field with natural inoculum sources of CSBMV at Cadriano (Bologna), Italy.

Symptom severity interval	Frequency (%)	
	11 March	10 April
0.000–0.050	12.5	21.2
0.051–0.100	2.7	3.3
0.101–0.150	3.3	0.5
0.151–0.200	1.6	1.1
0.201–0.250	1.6	0.5
0.251–0.300	0.5	0.0
0.301–0.350	0.0	0.5
0.351–0.400	1.6	0.0
0.401–0.450	2.2	1.1
0.451–0.500	1.6	0.0
0.501–0.550	2.7	0.5
0.551–0.600	2.2	0.5
0.601–0.650	1.1	0.0
0.651–0.700	1.6	1.1
0.701–0.750	1.1	1.1
0.751–0.800	2.7	0.5
0.801–0.850	1.6	0.5
0.851–0.900	2.2	2.2
0.901–0.950	3.3	2.7
0.951–1.000	1.1	4.9
1.001–1.050	2.7	4.9
1.051–1.100	2.7	0.5
1.101–1.150	1.1	1.1
1.151–1.200	1.1	0.0
1.201–1.250	0.5	1.6
1.251–1.300	1.1	1.1
1.301–1.350	1.6	0.0
1.351–1.400	2.2	0.5
1.401–1.450	1.1	1.1
1.451–1.500	0.5	3.8
1.501–1.550	1.6	0.5
1.551–1.600	3.3	1.1
1.601–1.650	2.2	1.6
1.651–1.700	1.1	0.5
1.701–1.750	0.0	2.2
1.751–1.800	2.7	0.5
1.801–1.850	2.7	0.5
1.851–1.900	1.6	1.1
1.901–1.950	7.1	3.3
1.951–2.000	4.9	6.5
2.001–2.050	8.7	17.9
2.051–2.100	1.6	7.1
2,101–2,150	0.5	0.0

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ITEMS FROM JAPAN

NATIONAL INSTITUTE OF CROP SCIENCE (NICS) – NATIONAL AGRICULTURE AND FOOD RESEARCH ORGANIZATION (NARO)
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A possible transmission route for common wheat to Japan by the distribution of high-molecular-weight glutenin subunit Glu-D1f; two transmission routes to Japan, a direct route via China and one via the Korean peninsula.

Hiro Nakamura.

High-molecular-weight (HMW) glutenin subunits make up a group of seed endosperm proteins of common wheat. This group has been extensively explored during the past 25 years, and its members have an important effect on the quality of bread and/or noodles made from wheat. HMW glutenin alleles, such as *Glu-D1*, are of particular significance for Japanese bread and/or udon products (Nakamura and Fujimaki 2002). The *Glu-D1f* allele has a major influence on Japanese common wheat. It is thus important to understand the genetic diversity of this allele in noodle-culture zones such as Asia compared with bread-culture zones such as Europe, Canada, and the USA (Nakamura 2001, Nakamura and Fujimaki 2001). Common wheat (2n=42, AABBDD) is thought to have originated about 7,000 years ago in the Middle

and Near East and was subsequently transported to Europe, Africa, southern Asia, and China. The cultivation of wheat can be traced back to 3,000 years ago in China (Zhang 1983), where it was a major crop at the time (Sun et al. 2000). Some common wheat cultivars were transported along the so-called Silk Road through China to the Far East, the Korean Peninsula, and finally Japan. Little is known, however, about the precise route of transmission of common wheat to Japan. Previous studies have concentrated on the variation in the HMW-glutenin *Glu-D1* allele, and the factors that have affected its distribution in different parts of the world (Nakamura 1999, 2000a, b, and c, 2001; Nakamura et al. 1999; Nakamura and Fujimaki 2001, 2002). Recently, a specific route of transmission for common wheat to eastern China and Japan was suggested (Nakamura 2002). Variation in the frequency of the *Glu-D1f* allele in different wheat varieties suggested a possible transmission route for common wheat to the Far East and Japan (Nakamura 2002). Distribution of the *Glu-D1* alleles throughout Asia, including the Korean Peninsula, was examined to estimate the route by which common wheat reached the most geographically remote regions of its production in the Far East, Japan.

The present study showed that carriers of the *Glu-D1f* allele were distributed across a limited region of Asia, comprising southern and northern Japan, Xinjiang in northwest China, Nanjing, and Zhejiang in southeastern China, Beijing in northeast China, the Korean Peninsula, and Afghanistan (Nakamura 2008). However, the allele was relatively rare in wheat cultivars from north Japan, the Korean Peninsula, China, and Afghanistan. The frequencies of *Glu-A1, Glu-B1,* and *Glu-D1* alleles in common wheat varieties are known to differ between Japan and other countries (Nakamura et al. 1999, Nakamura 1999). The HMW glutenin 2.2 subunit controlled by the *Glu-D1f* allele was frequently found among Japanese improved cultivars, as well as in Japanese landraces. However, only a few of the Korean, Chinese, and Afghani wheat cultivars possessed this allele. *Glu-D1f* was reported to be rare in previous studies of the worldwide distribution of *Glu-1* alleles (Nakamura and Fujimaki 2002). Moreover, this allele was found to be more common in wheat seed storage proteins from Japan than in those from bread-culture zones (Nakamura 2000a, b, c, 2001). The present study showed that the *Glu-D1f* allele was more common in Japan than elsewhere in Asia, including the Korean Peninsula. The frequency of this allele was shown to be in excess of 35% among improved Japanese cultivars and 25.3% among Japanese landraces, whereas it was found in only 1.4% of Chinese cultivars, 6.9% of Korean cultivars, and 9.5% of Afghani cultivars, respectively. This allele was identified in five Chinese cultivars (two in Xinjiang, one in Jiangsu, one in Zhejiang, and one in Beijing), in five cultivars from the Korean Peninsula, and in two Afghani cultivars. These results suggest that there are no other wheat cultivars possessing the *Glu-D1f* allele in any other region of Asia. In this study, the Far East implies only the Korean peninsula and Japan, not including eastern China (Nakamura 2008). The Far East, Japan is remote from most other wheat growing areas. In the course of its long journey and its adaptation to diverse local environments, Japanese common wheat appears to have depleted its genetic diversity. The frequency of the *Glu-D1f* allele differed between the Japanese and other Asian common wheat cultivars, including those from the Korean peninsula. Therefore, it is possible that all Japanese wheat cultivars have a common heritage. This hypothesis explains the similarities in *Glu-1* patterns among Japanese wheat cultivars. The distribution of an adaptively neutral character revealed by this study suggests two specific routes of transmission for common wheat to the Far East: either to eastern China and Japan, or to eastern China, the Korean Peninsula, and Japan. In the first scenario, wheat was introduced from Afghanistan, transported to Xinjiang in northwest China, to Shaanxi, Nanjing, and Zhejiang in southeast China, and then to southern Japan along the Silk Road. In the second scenario, wheat was introduced from Afghanistan, transported to Xinjiang in northwest China, to Shaanxi and Beijing in northeast China, to the Korean Peninsula, and then to southern Japan. During the course of its transmission and its adaptation to diverse local environments, Japanese common wheat has developed a unique set of glutenin alleles including the worldwide rare *Glu-D1f* allele, which is correlated with the quality of Japanese Udon products. Two possible transmission routes for common wheat through the Far East were detected in this study, a Chinese Route that was previously reported (Nakamura 2002b), and a new one via the Korean peninsula (Nakamura 2008).

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ITEMS FROM MEXICO

CIMMYT—INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER
Lisboa 27, Apartado Postal 6-641, 06600 México, D.F., México.

Wheat chemistry and quality improvement.

Roberto J. Peña.

Quality characterization/screening for wheat quality improvement. At CIMMYT, wheat experimental lines are tested for quality attributes and classified according to its potential end-use. Breeders and agronomists receive quality data, a classification of the lines according to their potential end use, and recommendations of the best sources of quality. This action helps breeders to identify lines to be used as quality sources in new crosses and allows screening and selection of quality-desirable lines throughout the breeding process. The wheat quality classification we use was developed based on observed and documented relationships between specific quality traits and end-use quality (bread, cookies, noodles, pasta, etc); actual observation of wheat-based food processing in different countries; and consultations with NARS.

Crop improvement, quality testing/screening. Approximately 18,700 entries were tested for wheat quality characterization using a few rapid small-scale tests to full-quality analysis. The tested materials included late-segregating lines (tested in Obregon), advanced lines (from both the spring and winter wheat programs), elite lines for candidates to international nurseries, and lines from national programs and special projects in breeding and agronomy (tested in El Batan).

Breeders received recommendations on the best quality sources (for diverse uses) to include in new crosses. We also suggested which lines to advance or include in international nurseries or to consider for cultivar registration (in the case of National programs).

In addition, SDS–PAGE to determine *Glu-1*/*Glu-3* glutenin composition and T1B·1R translocation status was applied to 8,000 bread and 4,175 durum wheat samples. The samples analyzed for glutenin composition were part of the wheat-improvement programs and special projects, including theses work of graduate students.

Sources of grain quality. Identifying the best sources of quality for new crosses has been an effective strategy to combine grain yield and quality. The proportion of lines having acceptable to excellent quality in the CBRF (2007–08) and CBBWIR (2007–08) populations were 40.2% and 27.1% , respectively. The top 10 best sources of gluten extensibility

Table 1. Best sources of quality of the crossing block populations sown in Obregon, Mexico in 2007–08 (Glutenin strength rated as strong (S) or medium strong (MS)).

Cross	Pedigee	Gluten strength	HMW-glutenins			LMW-glutenins		
			Glu-A1	*Glu-B1*	*Glu-D1*	*Glu-A3*	*Glu-B3*	*Glu-D3*
CBBWIR 2007–08								
Juchi F2000	TC920338-S-9C-04R-1C-0R-1C-0R	S	2*	7+9	5+10	e	c	a
CHEN/*Ae. tauschii* //2*Weaver/3/ Oasis/5*BORL95	CMSS99M00619S-040M-030Y-030M-15Y-1M-0Y	S	1	7*+8	5+10	b	d	b
Waxwing*2/Varis	CGSS04Y00020T-099M-099Y-099ZTM-099Y-099M-3WGY-0B	MS	2*	7+9	5+10	c	h	b
Kingbird	CMSS99M00216S-040M-030Y-030M-16Y-2M-0Y	S	2*	17+18	5+10	b	h	b
Kiritati//Attila*2/Pastor	CGSS02Y00142S-099M-099Y-099M-35Y-0B	S	1	17+18	5+10	c	i	b
Kiritati// PBW65/2*SERI.1B	CGSS02Y00139S-099M-099Y-099M-14Y-0B	S	1	17+18	5+10	c	i	b
3570		MS	1	7+8	5+10	c	g	a
Waxwing*2/Brambling	CGSS01B00053T-099Y-099M-099M-099Y-099M-22Y-0B	MS	2*	7*	5+10	c	b	b
Waxwing*2/Tukuru	CGSS01B00058T-099Y-099M-099M-099Y-099M-12Y-0B	MS	2*	7*	5+10	c	b	b
Whear/Sokoll	CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B	MS	1	13+16	2+12	c	b	c
CBRF 2007–08								
INIA Churrinche		S	2*	7+8	5+10	a	b	a
Attila*2/PBW65//Berkut	CMSA01M00074S-040P0M-030ZTM-040SY-040M-35Y-0M-0SY	S to MS	2*	17+18	2+12	c	g	b
Whear/Vivitsi/3/80.1/3* Batavia//2*WBLL1	CGSS03B00079T-099Y-099M-099Y-099M-13WGY-0B	MS	2*	7+9	5+10	d	h	b
ND643//2*Attila*2/ Pastor	CGSS02B00113T-099B-099Y-099M-099Y-099M-7WGY-0B	MS	2*	17+18	5+10	e	h	c
ND643/2*WBLL1	CGSS02B00105T-099B-099Y-099M-099Y-099M-1WGY-0B	MS	2*	7+9	5+10	c	h	b

(a mayor challenge in wheat quality improvement) from each crossing block population are shown in Table 1 (p. 111). Several of these lines showed HMW-glutenin subunits 1 or 2*, 18+18 or 7+8, and 5+10, and a predominance of *Glu-B3* LMW-glutenin subunits h, b, and g, which have shown to be the most beneficial for gluten extensibility.

To continue with the emphasis on quality improvement, two quality CB trials (CBBWIRIQ and CBRFIQ) including the best sources of gluten strength and extensibility were prepared (58 lines for Ravi Singh and 92 lines for Yann Manes) to facilitate breeders the use of the best sources of quality in new crosses during the Y. 08-09 crop cycle.

Quality methodologies. In order to satisfy the quality testing/screening needs of both the spring and winter wheat programs comprised within the GWP of CIMMYT and those of collaborating partners, it is necessary to use reliable analytical methods that offer high throughputs. During 2008, accelerated protocols were developed to increase the number of lines analyzed for dough rheological properties by at least 100%.

Alveograph. Thanks to the acquisition of the modern Alveo-Consitograph in 2006, we standardized and modified the methodology used with the small-scale (60-g flour) old alveographs in such away that the number of samples tested per day increased from 20–25 to 45–50 in 2008.

Bread-making test. Modifications in the bread-making protocol and the more efficient use of equipment and staff allowed us to increase from 30 to 50 the number of lines tested for bread-making properties in 2008. This action allowed us to offer bread-making quality data again, after 3 years of not being able to perform this test due to the loss of one staff member.

Mixolab. An accelerated method for the use of the Chopin–Mixolab as tool to evaluate/screen for gluten and for starch properties was developed. The new accelerated Chopin-Mixolab protocol allows determining dough (gluten) mixing properties as well as starch pasting properties using one, single, small flour sample. The accelerated protocol also was found to have a highly significant correlation with Falling Number, a test determining grain sprouting. Therefore, the Mixolab protocol has a plus when screening wheat lines sown under high-rainfall conditions. The accelerated Mixolab protocol has been submitted as a section of the Mixolab Handbook, which will be distributed internationally (Peña and Posadas-Romano, Submitted in 2008).

DON analysis. The low-cost (50–60% lower) analytical test, based on a commercial fluorimetric kit protocol (Fluoroquant) for determining DON concentration developed in 2007, was validated using wheat lines cultivated in Uruguay, Paraguay, and Batan. An HPLC analysis of DON extracts obtained with the commercial test kit and low-cost extraction protocols were very similar ($R^2 > 0.96$ was obtained in all comparisons). Gabriel Posadas from the Wheat Chemistry and Quality Laboratory will travel to Uruguay in 2009 to implement the low-cost protocol in the laboratory of INIA-La Estanzuela by in early 2009. With this we complete our responsibility in the Fusarium–toxin analysis subproject of the INIA-Spain-Procisur-CIMMYT project.

Advances in the development of NIRS calibrations. In 2008, NIRS was used in both Obregon (breeding programs; Conservation Agriculture; Agronomy-Harvest Plus) and El Batan for hardness, moisture, grain protein, and straw-N.

Durum wheat breeding.

Karim Ammar.

Summary. The competitiveness and global relevance of the germ plasm produced in the last two years have been clearly and successfully enhanced. We have been able to develop and identify lines combining high yield potential, good performance under water-limited conditions, and good-to-excellent functional quality attributes. The situation with regards to low yellow color in CIMMYT's germ plasm has been turned around, with 75–80% of the lines evaluated in the last two years showing acceptable-to-excellent color. More importantly, our use of as many sources of resistance to leaf rust as possible, since the appearance of the BBG/BN race in 2001, has provided us with sufficient genetic variability to be able to withstand unaffected the loss of one source of resistance (*Lr27+Lr31*) with the appearance of a new race BBG/BP in 2008. This loss did not affect our capacity to distribute highly improved germ plasm in sufficient numbers. Marker-assisted selection has enabled us to start pyramiding leaf rust resistance genes not present in durum wheat (*Lr19* and *Lr47*) and accumulating them on top of other effective genes present in durum wheat, including *Lr14a* for which reliable flanking markers are now available. Marker use also has allowed us to transfer stem rust resistance genes into durum backgrounds and will help us address more effectively, in the medium term, the stem rust vulnerability of our germ plasm in Ethiopia. Finally, our interaction with the Tunisian NARS has enhanced our capacity to effectively ad-

dress the susceptibility of our germ plasm to *Septoria tritici*.

Stem rust screening in Kenya and Ethiopia. For the second year (2008), we have sent an extensive collection of advanced lines (candidates for next international nurseries), crossing parents, and special genetics stocks to be screened in the off-season for their reaction to stem rust at the EARI Debre-Zeit station in Ethiopia. This year, the epidemic development of the disease was hampered by drought and established late, resulting in the data being unreliably positive, with a very high proportion of lines with low infection reactions (Table 2). In comparison, the 2007 off-season was characterized by an intense epidemic and resulted in an extremely low frequency of lines showing low infection reactions (~2.2%). In addition, we are considering the reaction from our secondary screening at Njoro in Kenya were a subset of the promising lines from the 2007 Debre-Zeit screening were evaluated in 2008. Although all of the lines with low reactions at Debre Zeit in 2007 were resistant in Njoro, many of those resistant in Njoro did not hold their resistance in Debre-Zeit, which is consistent with the belief that the main stem rust race in Kenya is $Ug99_{vir\ Sr24+}$, whereas in Ethiopia, there must be additional races specifically virulent on durum wheat (avirulent on bread wheat) that overcome most of the resistance effective in Kenya, confirming the absolute need to work in Ethiopia, not Kenya, for durum wheat. Based on all the results and information at hand, we were able to identify lines that may show some promise in terms of widely effective resistance to stem rust, in both Ethiopia and Kenya (Table 2).

***Septoria tritici* screening in Tunisia.** A relatively lower incidence of *S. tritici* was seen at the Tunisian hot spot of Béja (INRAT) in 2008. Nevertheless, the epidemic was intense enough to differentiate highly susceptible lines from real promising lines. The frequency of promising lines evaluated in 2008 (below 5 in the 1-digit scale used) was very similar to that screened in 2007 under a more intense epidemic and again was extremely low (less than 4%). The last two years of screening, including

Table 2. Some promising lines for resistance to stem rust in Ethiopia and Kenya. BBG/BP refers to the most recent race that appeared in Mexico in 2008 against which these lines were tested in El Batan during the summer cycle. R = resistant, S = susceptible, SR = slow rusting, T = trace, M = moderate, MS = moderately susceptible, MR = moderately resistant.

Cid	Sid	Cross	Selection history	Leaf rust BBG/BP	Debre Zeit, Ethiopia 2007	Debre Zeit, Ethiopia 2008	Njoro, Kenya 2008
477707	47	CMH83.2578/4/D88059/WARD/YAV79/3/ACO89/5/2*SOOTY_9/ RASCON_37/6/1A.1D 5+10-6/3*MOJO/3/AJAIA_12/F3LOCAL (SEL. ETHIO.135.85)//PLATA_13	CDSS02B00720S-0Y-0M-8Y-1M-04Y-0B	R	T	10S	10S
421913	70	CBC 509 CHILE/SOMAT_3.1/3/RASCON_37/TARRO_2//RASCON_37	CDSS00B00444T-0TOPY-0B-13Y-0M-0Y-1M-0Y	R	5MS	10MR	5R/MR
148658	71	HUALITA	CDWS91M377-9M-030Y-030M-1Y-0M-0BRL-1Y-0B	R	5MR/MS	15M/MS	1R
456178	39	KUCUK_2/PATA_2/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	CDSS02Y00306S-0Y-0M-26Y-0Y	R	20R/MR	15MS	1R
477769	10	RCOL/POHO_1/3/DIPPER_2/BUSHEN_3//SNITAN	CDSS02B00782T-0TOPB-0Y-0M-1Y-3M-04Y-0B	S	5MR/MS	10MR	1R
173245	37	SVANE_1/AKAKI_4	CDSS94Y00096S-5M-0Y-0B-1Y-0B-0BLR-1Y-0B	SR	0	10M	1R
137790	143	THKNEE_9/MOJO_2	CDSS93B00037S-25M-0Y-0B-0Y-5B-1Y-0B-0BLR-2Y-0B	SR	10MS	10MR	1R
173731	44	CPAN.6018/2*RAJ1555//2*PORRON_4	CDSS94Y00582M-E-3M-0Y-0B-2Y-0B-0BLR-2Y-0B	SR	15R/MR	15MS	1R

2008, were, however, useful to identify lines that consistently show some promise as sources of resistance within our germ plasm. Thirteen such lines (Table 3) have been and continue to be used extensively in crosses with the best resistance sources from the Tunisian program.

Table 3. Promising lines for reaction to *Septoria tritici* based on data from Béja, Tunisia (INRAT). Reactions of the most resistant lines are in grey.

CID	SID	Cross	Selection history	2007	2008
148658	71	HUALITA	CDWS91M377-9M-030Y-030M-1Y-0M-0BLR-1Y-0B	—	2
403149	249	BCR/GUEROU_1/3/MINIMUS_6/PLATA_16//IMMER	CDSS99B00319S-0M-0Y-121Y-0M-0Y-0B	2	3
283822	56	USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79//8/POD_9	CDSS96Y00484S-3Y-0M-0Y-1B-0Y-0B-0B-0BLR-2Y-0B	2	3
261495	18	SOMAT_4/SILVER_1	CDSS95B00182S-2Y-0M-0Y-2B-0Y-0B-0B	4	3
417954	142	SOMAT_3.1//WODUCK/CHAM_3/5/AJAIA_16//HORA/JRO/3/GAN/4/ZAR	CDSS00Y01093T-0TOPB-2Y-0BLR-3Y-0B-0Y-0B	4	3
403142	269	AINZEN_1/6/CHM82A.1062/3/GGOVZ394//SBA81/PLC/4/AAZ_1/CREX/5/HUI//CIT71/CII	CDSS99B00312S-0M-0Y-51Y-0M-0Y-1B-0Y	4	3
327961	41	AJAIA_3/SILVER_16//AJAIA_13/YAZI	CDSS97Y00618S-1Y-0M-0Y-0B-0B-2Y-0BLR-1Y-0B	4	4
328423	51	PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CHEN/ALTAR 84/3/HUI/POC//BUB/RUFO/4/FNFOOT	CDSS97Y01080T-0TOPM-3Y-0M-0Y-0B-0B-2Y-0BLR-4Y-0B	5	4
328178	58	LD357E/2*TC60//JO69/3/FGO/4/GTA/5/SRN_1/6/TOTUS/7/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/8/SOM-BRA_20/9/STOT//ALTAR 84/ALD	CDSS97Y00835S-0TOPM-4Y-0M-0Y-0B-0B-3Y-0BLR-4Y-0B	5	4
283798	47	SORA/2*PLATA_12//SRN_3/NIGRIS_4	CDSS96Y00460S-4Y-0M-0Y-1B-0Y-0B-0B-0BLR-2Y-0B	5	4
328510	30	RASCON_37/2*TARRO_2/4/ROK/FGO//STIL/3/BISU_1/5/MALMUK_1/SERRATOR_1	CDSS97Y01167T-0TOPM-2Y-0M-0Y-0B-0B-1Y-0BLR-4Y-0B	5	5
404000	32	CBC 509 CHILE/4/SKEST//HUI/TUB/3/SIL-VER/5/GREEN_14/YAV_10/AUK	CDSS99B01170T-0TOPY-0M-0Y-4Y-0M-0Y-2M-0Y	5	5
261494	50	SOMAT_4/INTER_8	CDSS95B00181S-0M-1Y-0B-1Y-0B-0Y-0B-0BLR-2Y-0B	5	5

3rd International Stem Rust Resistance Screening Nursery (3rdSRRSN).

Ravi P. Singh, Julio Huerta-Espino, Sridhar Bhavani, Sybil Herrera-Foessel, Davinder Singh, and Pawan K. Singh.

The presence of effective race-specific and adult-plant resistance was characterized by testing selected advanced breeding lines in the seedling stage with Ug99 and Ug99 + *Sr24* races at the USDA–ARS Cereal Disease Laboratory, St. Paul, MN, USA. Seedling tests with leaf rust races also were conducted in greenhouses in Mexico to determine the presence of those alien stem rust-resistance genes that are linked to leaf rust-resistance genes in the same translocation. Molecular markers also were applied for genes such as *Sr24*, *Sr25*, and *Sr26* to confirm their presence. These studies form the basis of resistance genes given in Table 4. One-hundred five entries (plus checks) were included in the 3rdSRRSN based on 2006–07 and 2007 screening results from Njoro, Kenya.

Table 4. Stem rust resistance (based on 2006–07 and 2007 screening results at Njoro, Kenya) of entries included in the 30th Elite Selection Wheat Yield Trial (30thESWYT), the 42nd International Bread Wheat Screening Nursery (42ndIBWSN), and the 3rd Stem Rust Resistance Screening Nursery (3rdSRRSN).

Nursery	30thESWYT		42ndIBWSN		3rdSRRSN	
Category	**# entries**	**% entries**	**# entries**	**% entries**	**# entries**	**% entries**
Adult-plant resistance						
R (10–15% severity)	1	2.2	4	2.5	0	0.0
R–MR (15–20% severity)	11	24.4	13	8.0	18	17.1
MR (30% severity)	15	33.3	27	16.7	38	36.2
MR–MS (40% severity)	7	15.6	36	22.2	0	0.0
MS (50–60% severity)	2	4.4	38	23.5	0	0.0
S (100% severity)	0	0.0	21	13.0	0	0.0
Race-specific resistance						
Sr25	6	13.3	4	2.5	11	10.5
Sr24 + Sr36	0	0.0	0	0.0	4	3.8
Sr33	1	2.2	1	0.6	0	0.0
SrTmp	1	2.2	3	1.9	4	3.8
SrSynt	0	0.0	0	0.0	4	3.8
SrSha7	0	0.0	0	0.0	4	3.8
SrND643	0	0.0	1	0.6	11	10.5
SrHUW234	1	2.2	3	1.9	2	1.9
Sr unknown	0	0.0	2	1.2	9	8.6
Unclassified	0	0.0	9	5.6	0	0.0

USAID–Ug99 Resistant Varieties Seed Multiplication Project.

Fifteen, Ug99 wheat lines were multiplied at El Batan, Mexico, during the 2008 crop season in a 3.3-ha plot. Ten normal and three early maturing lines were selected for the seed project based on their performance in the 3rd Elite Bread Wheat Yield Trial (3rd EBWYT) in various countries (Table 5, p. 116). The early maturing line Francolin#1, although not included in the 3rd EBWYT, performed very well in the northeastern Gangetic Plains in on-farm trials and was, therefore, selected form multiplication and shipment to Bangladesh, Nepal, and India.

A total of 13 tons of seed was produced and processed and packaged. Seed quantities shipped to various countries are summarized in Table 5 (p. 116). Egypt has already made significant progress in multiplying five Ug99-resistant

Table 5. Ug99-resistant wheat lines included in the USAID–Seed Project and seed quantities shipped (shipment to India pending Import Permit).

CIMMYT name	Cross	Maturity	Country and seed quantity (kg)							
			Bangladesh	Nepal	Pakistan	Turkey	Afghanistan	Egypt	Ethiopia	India
DANPHE #1	KIRITATI//2*PBW65/2*SERI.1B	Normal		100					100	
KINDE #1	PBW343*2/KUKUNA//KIRITATI	Normal								100
PICAFLOR #1	KIRITATI//SERI/RAYON	Early	100	100			50		100	100
PAURAQUE #1	WAXWING*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	Early	100	100						100
GRACKLE #1	WAXWING*2/KUKUNA	Normal						25		
BECARD #1	WBLL1*2/KIRITATI	Normal		100						
MUNAL #1	WAXWING*2/KIRITATI	Normal		100	300	100	50		100	
FRANCOLIN #1	WAXWING*2/VIVITSI	Early	100	100						100

entries selected from 2nd EBWYT, hence smaller quantities of new lines were sent. The remaining seed is stored to cater any future needs.

Evaluation of stem rust resistance in wheat materials from different countries during 2008 in Kenya.

A main-season, stem rust screening nursery (June–October) was planned and finalized jointly by KARI, CIMMYT–Kenya, and international collaborators. More than 18,000 lines of spring wheat, 2,600 lines of winter wheat, and 700 lines of barley from 20 countries were planted and screened (Table 6). The plots were established well apart from some of the late-sown material, which did not perform well, probably for a range of reasons, particularly the late arrival of seed and poor seed quality. Artificial rust epidemics were created using inoculum collected from previous-year screening nurseries. Rust infection was excellent and disease pressure was quite heavy. The infection type on the controls/differentials showed virulence for genes *Sr31* and *Sr24* in the screening nursery indicating the likely presence of Ug99 and its variant Ug99 + *Sr24* in the screening site. *Sr36* was partially effective, probably because of the low frequency of Sr36 virulence in the pathogen population. Lines with notable resistance included *Sr25* derivatives, several tall Giza (Egypt) lines, derivatives of the Chinese wheat Sha7, Canadian materials (Thatcher background plus *Lr34*), some ICARDA and CIMMYT lines, and several Egyptian and CIMMYT durum wheats. A varied response of materials with *Sr2* also was evident.

Table 6. Number of wheat lines screened and resistant lines selected from different countries at KARI Njoro (Kenya) during the main season 2008.

Country	No. of lines screened		Resistant lines selected
	Spring	Winter	
Australia	1,862	9	18
Argentina	112	—	12
Canada	1,400	2	21
CIMMYT	3,049	657	151
Egypt	228	—	12
ICARDA	5,908	111	16
India	318	—	4
Iran	371	179	3
Israel	10	—	—
Kazakhstan	259	—	13
Kenya	1,305	—	40
Nepal	125	—	1
Pakistan	135	—	—
South Africa	140	—	11
Sudan	70	—	—
Turkey	130	270	7
Uruguay	290	—	13
USDA	2,433	1,450	-
Total	18,145	2,678	322

Communications/logistics were established with relevant scientists/originators for scoring their material. More than 20 scientists from different countries visited their germ plasm materials and assistance was provided for data taking and selections. The low frequency of resistant materials remained a common feature among wheat materials from many countries with more than 80% of the screened germ plasm susceptible. The data has been documented and sent to the collaborators. From the resistant material, an elite set of 322 lines was selected to further characterize and determine the inheritance of resistance or for use as a source of resistance in crossing programs.

Cloning of Lr34/Yr18 and the development of diagnostic marker.

The highlight of 2008 has been the cloning of the pleiotropic leaf rust/yellow rust/powdery mildew resistance gene *Lr34/Yr18/Pm38* and acceptance of a paper in *Science*. The success of the cloning involved a strong collaboration between CIMMYT, CSIRO, and the University of Zurich, where CIMMYT's main role was generating deletion mutants and phenotyping mapping populations. *Lr34/Yr18/Pm38* turned out to be a new kind of resistance gene.

The abstract of *Science* paper is as follows: "Durable disease resistance in crops has great relevance for agriculture and breeding, but is not understood well at the molecular level. Durable resistance is often partial and controlled by several genes. *Lr34* is an important genetic component of resistance to three of the most devastating fungal pathogens in wheat: leaf rust, stripe rust, and powdery mildew. *Lr34*-based resistance has been durable for more than 50 years, is deployed globally, and specifically acts in the adult-plant stage. Here, we show that *Lr34* encodes an ATP-binding cassette transporter of the pleiotropic drug resistance subfamily. Wheat alleles of *Lr34* conferring resistance or susceptibility differ by three sequence polymorphisms which are conserved in all three breeding lineages with *Lr34* in the global wheat gene pool. The *Lr34* gene stimulates senescence-like processes in the flag leaf tips and edges."

The cloning success also has resulted in the development of a diagnostic molecular marker by CSIRO, which is under validation.

Development and characterization of an RIL mapping population for a single, slow-rusting resistance gene on chromosome 7BL.

An F_5 RIL mapping population of about 400 lines was developed from two sister lines and phenotyped at Cd. Obregon, Mexico, for fine mapping of a new, slow-rusting (adult-plant) leaf rust-resistance gene located in chromosome 7BL. The leaf rust severity response of the resistant parent (two sister-lines) was 15MS, whereas the susceptible parent showed 100S. Segregation confirmed involvement of a single, slow-rusting resistance gene. The population is planted for the second year evaluation during 2008–09 to confirm the phenotypic responses. Molecular mapping studies confirmed the location of this gene to 7BL (Fig. 1). The chromosomal region where the gene is located corresponds to a gene-rich area where a cluster of defense-response genes and the seedling-resistance gene locus *Lr14a* are located.

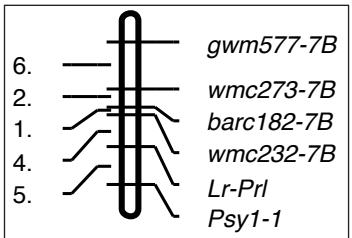

Fig. 1. Linkage map with the slow-rusting resistance gene (*Lr-Prl*) and its association with four microsatellite markers, and the CAPS marker *Psy1-1* associated with yellow pigment, based on a population of the first sister-line (198 F_5 lines).

Development of durum wheat germ plasm with slow-rusting resistance to leaf rust.

A total of 1,843 advanced lines of durum wheat, obtained from 28 three-way and four-way crosses of slow-rusting durum wheats carrying 2–3 minor additive genes, were grown during 2007, and 106 lines with enhanced resistance and desirable agronomic and grain characteristics were chosen for leaf rust and grain yield in nonreplicated trials. An additional 62 lines with race-specific resistance also were selected. Slow-rusting lines with high levels of resistance and acceptable yield performance comparable to that of Jupare C2001 were identified. Leaf rust severities of the lines were considerably higher at El Batan compared to 2007–08. The best identified durum wheat lines are being used at present for continued breeding to develop lines with high, stable levels of durable resistance to leaf rust.

Association mapping of leaf, yellow and stem rust resistance in an historical Elite Selection Wheat Yield Trial (ESWYT) set.

A total of 170 entries from five historical ESWYT trials (ESWYT 1, 6, 10, 20, and 24) were evaluated for leaf, yellow, and stem rust resistance in El Batan and Toluca, Mexico, in 2007, and in Kenya in the off and main season in 2008 under high disease pressure to races MBJ/SP and MCJ/SP (for leaf rust), PBW343 (for yellow rust), and Ug99 + *Sr24* (for stem rust). This same ESWYT set had been used previously to identify regions associated with leaf, yellow, and stem rust; powdery mildew; and grain yield based on historical data that had been collected between 1979 and 2004. The final rust-severity ratings taken for the three rusts and the area under the disease progress curve for leaf rust and the coefficient of infection for stem rust together with already available genotypic data and chromosome maps were used for an association analysis. Chromosomal regions were identified with markers associated to leaf, yellow, and stem rust resistance genes that are effective to the predominant races of relevance today and the number of significant markers in each region (Table 7). The same trial was sown in 2008–09 for a second year of leaf rust data and will be sown in Toluca, Mexico, during 2009. A gene-postulation test for leaf rust resistance was carried out in 2008 in the greenhouse to confirm the regions identified through association genetic analysis and investigate the power of this tool to identify regions with known genes that are present in each line. Seedlings of the same 170 entries were inoculated with 13 different races of *P. triticina* and infection-type response were compared to the differential sets of isogenic lines with known leaf rust-resistance genes. The leaf rust-resistance genes identified through gene postulation were *Lr1*, *Lr3*, *Lr10*, *Lr14a*, *Lr13*, *Lr16*, *Lr17*, *Lr19*, *Lr24*, and *Lr27* + *Lr31*. Additional unknown seedling resistance genes were present in some of the lines. The infection-type response from each of the 13 races were transformed to quantitative data and association analysis made from the response from each race; the analysis is still in process. From the known seedling genes identified in the greenhouse test, only *Lr19* and *Lr24* are effective to the predominant races used in the field trial. Regions whit slow-rusting resistance genes, such as *Lr34*, were confirmed from the association analysis based on field data. Further analysis will help identify regions with unknown slow-rusting resistance genes.

Table 7. Chromosomal regions possessing DArT markers associated with resistance to current races of leaf (LR) and yellow (YR) rust in Mexico and stem rust race Ug99 (SR) in Kenya. The number of markers associated in each chromosome arm given in parenthesis.

Chromosome	Short arm	Long arm	Unknown arm
1A	LR(1), YR(1), SR(2)	LR(3), YR(1), SR(1)	YR(1), SR(1)
1B	LR(15), YR(2)	YR(2), SR(1)	LR(3), SR(1)
1D		YR(6), SR(2)	SR(1)
2A	YR(2)	SR(1)	SR(2)
2B	SR(3)	LR(4), SR(4)	LR(1), SR(1)
2D	LR(1)		YR(1)
3A		LR(1), SR(2)	
3B	LR(1), YR(8), SR(4)	LR(2), YR(4), SR(4)	LR(1), SR(1)
3D			
4A		LR(2), YR(5), SR(1)	YR(3), SR(1)
4B	LR(3), SR(1)	LR(1), YR(1), SR(2)	YR(2), SR(2)
4D	LR(1)		
5A	YR(1)	LR(1)	YR(1), SR(1)
5B	LR(1), YR(2), SR(1)	LR(1), YR(2), SR(3)	LR(1)
5D			
6A	SR(1)	LR(7), SR(4)	
6B	LR(1), YR(5), SR(3)	SR(1)	YR(1), SR(1)
7A	LR(2), YR(1), SR(3)	LR(3), SR(1)	SR(1)
7B	SR(2)	LR(2), YR(4), SR(3)	YR(1)
7D	LR(2), YR(2), SR(2)		LR(1), YR(1), SR(7)

Stem rust resistance: Development of mapping populations.

Development of 15 mapping populations was completed during 2008 (Table 8). These populations were planted as single replicates at Njoro, Kenya, during the 2008–09 season for first-year, stem rust phenotyping and in screenhouse at El Batan, Mexico, for seed multiplication. Three or four populations will be selected based on the phenotyping results for second-year phenotyping in replicated trials and molecular characterization.

Table 8. A summary of the populations developed for mapping uncharacterized sources of adult-plant resistance to stem rust and planted for phenotyping at Njoro, Kenya, during 2008–09.

PBW343 / parents with adult-plant resistance	Generation	No. of RILs
JUCHI	F_6	225
KIRITATI	F_6	225
PAVON76	F_6	225
DUCULA/2*PRINIA	F_6	225
PGO/SERI//BAV92	F_6	225
Kenya Nyangumi	F_6	225
Kenya Kudu	F_6	225
Kenya Swara	F_6	225
Kenya Fahari	F_6	225
KINGBIRD	F_5	200
CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/WEAVER/5/ 2*KAUZ /6/FRET2	F_5	150
PFAU/WEAVER*2//KIRITATI	F_5	150
PGO//CROC_1/*Ae. tauschii* (224)/3/2*BORL95/4/CIRCUS	F_5	150
BABAX/3/OASIS/SKAUZ//4*BCN/4/PASTOR	F_5	150
HE1/3*CNO79//2*SERI/3/ATTILA/4/WH 542	F_5	150
HPO/TAN//VEE/3/2*PGO/4/MILAN/5/SSERI1	F_5	150

Mapping of stem rust resistance: Identification of genomic regions governing seedling resistance to Ug99.

Five populations, where a resistant parent possibly carried previously an uncharacterized race-specific resistance gene to Ug99 race of stem rust pathogen, were used in molecular mapping (Table 9). Segregating F_3 and F_4 populations were characterized for seedling stem rust response in the greenhouse of the USDA–ARS, St. Paul, MN, USA, by Dr. Yue Jin. The populations also were characterized in the field at Njoro, Kenya, during 2007–08 and 2008.

Table 9. Wheat lines with uncharacterized race-specific resistance genes to stem rust race Ug99 of included in molecular mapping of resistance (IT = infection type).

Resistance source	IT	Susceptible parent	IT
MILAN/SHA7/3/THB/CEP7780//SHA4/LIRA/4/SHA4/CHIL (F_3 population)	2	PBW343	33+
NINGMAI 9415.16//SHA4/CHIL/3/NINGMAI 50 (F_3 population)	2–	PBW343	33+
CHEN/*Ae. tauschii*//2*EAVER/3/OASIS/5*BORL95 (F_3 population)	2–	PBW343	33+
CHEN/*Ae. tauschii* (TAUS)//BCN/3/CMH81.38/2*KAUZ (F_4 population)	3–	PBW343	33+
NING9415/3/URES/BOW//OPATA/4/NINGMAI 7 (F_4 population)	2–	PBW343	33+

A bulk-segregant analysis was used to identify marker-trait associations. Bulks were constituted by pooling DNA of 10 individual families each from nonsegregating resistant and nonsegregating susceptible classes. We used 213 microsatellite primers uniformly spread over the A, B, and D genomes. Markers that exhibited polymorphism among the resistant and susceptible bulks and parents were genotyped on the unscrambled HR and HS families and preliminary mapping analysis was performed. Recombination fractions were calculated with the MAP MANAGER Version QTXb20 using the Kosambi mapping function.

Greenhouse evaluation for resistance to tan spot and Stagonospora nodorum blotch.

Two sets of material from the Irrigated Bread Wheat Program included i) an irrigated, bread wheat set of 105 lines (the same lines also were included in the second-year *Fusarium* testing) and ii) an historical ESWYT set of 170 entries used for association mapping. Three experiments were conducted in the greenhouse for each disease. Each experiment was conducted as a randomized block design with two replicates. Each replicate consisted of the complete set of genotypes planted in trays. The experimental unit consisted of four plants/entry and 48 entries were planted in each tray.

The *Pyrenophora tritici-repentis* race 1 isolate Ptr-1 was used to induce tan spot. Race 1 is highly virulent and the most prevalent race worldwide. The *Phaeosphaeria nodorum* isolate SN-4 was used to induce Stagonospora nodorum blotch. Two-week-old seedlings were inoculated and rated eight days later for disease reaction based on a 1–5 scale. A mean rating of less than 2 was considered resistant, and those higher than 2 were considered to be susceptible.

Irrigated bread wheat set. For tan spot 35 entries were resistant while 70 were susceptible and in case of Stagonospora nodorum blotch 18 entries were resistant and the remaining 87 entries were susceptible. Many entries were resistant to one disease and susceptible to the other or vice-versa, however, nine entries were resistant to both the diseases (Table 10, p. 116).

Historical Elite Selection Wheat Yield Trial (ESWYT) set. This set was comprised of 170 wheat lines derived from five CIMMYT elite spring wheat yield trials (ESWYT 1 (1979), ESWYT 6 (1984), ESWYT 10 (1988), ESWYT 20 (1999), and ESWYT 20 (2004)). Eighty-nine genotypes were resistant and 81 were susceptible to tan spot; 33 entries were resistant and the remaining 137 entries were susceptible to *Stagonospora nodorum* blotch. Many entries were resistant to one disease and susceptible to the other or vice-versa, however, 26 entries were resistant to both the leaf spotting diseases (Table 10, p. 121).

Association mapping of tan spot resistance.

The molecular data generated earlier on the historical ESWYT set of 170 wheat lines and tan spot resistance data presented above were used for association mapping analysis. Results reveal that genomic regions on short arm of chromosomes 1A, 1B, and 6B and long arm of chromosomes 4A, 6A, 2B, 3B, 5B, and 7B may play important role in conferring resistance to tan spot induced by *P. tritici-repentis* race 1. Some of the above genomic regions contributing to tan spot resistance have been previously identified; however, novel genomic regions were identified in this study. Findings of this study reveal that CIMMYT wheat germ plasm is likely to contain novel sources of resistance to tan spot.

General wheat pathology.

Etienne Duveiller, M. Mezzalama, J. Murakami, N. Lozano, F. Lopez, J. Segura, A. Djurle, N. Schlang, P. Singh, M. Preciado, and M-E. Leymus.

Fusarium head blight research. Fusarium head blight or scab is one of the most destructive fungal diseases affecting wheat. The disease reduces kernel weight, yield, and flour extraction rates particularly in warm and humid wheat-growing areas. Fusarium species causing FHB produce mycotoxins that contaminate the grain and have been shown to be harmful to human and animal health. The mycotoxins of primary concern are the trichothecenes the most common of which in scabby grain is deoxynivalenol (DON) produced by *F. graminearum* and *F. culmorum*.

Table 10. Disease reaction of genotypes resistant to tan spot (TS) and *Stagonospora nodorum* blotch (SNB) in seedling evaluation under greenhouse conditions. Plants were rated on a 1–5 scale, and the data presented is mean of three experiments each with two replicates.

CID #	SID #	Cross	TS	SNB
Irrigated bread wheat set				
480918	25	PBW343*2/KUKUNA/3/PASTOR//CHIL/PRL	1.58	1.75
465822	91	CHEN/AE.SQ//2*OPATA/3/TILHI/4/ATTILA/2*PASTOR	1.67	1.60
482087	21	CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/WEAVER/5/2*KAUZ/6/ PRL/2*PASTOR/7/FISCAL	1.64	1.88
459285	75	THELIN/3/BABAX/LR42//BABAX/4/BABAX/LR42//BABAX	1.78	1.61
448391	74	BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	1.58	1.88
448436	114	PFAU/WEAVER*2//TRANSFER#12,P88.272.2	1.63	1.72
373440	145	80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	1.25	1.63
90292	248	NG8675/CBRD	1.58	1.75
90248	173	SHA3/CBRD	1.53	1.46
Historical Elite Selection Wheat Yield Trial set				
7760	9	DOVE	1.92	1.99
7668	42	SUNBIRD	1.58	1.72
7668	6	SUNBIRD	1.76	1.49
7691	18	GENARO T 81	1.28	1.58
8256	8	TTR/BOW	1.69	1.76
8918	10	SAP/MON	1.74	1.97
7691	319	VEERY	1.28	1.67
9704	5	SASIA	1.67	1.72
8176	7	SIBIA	1.56	1.78
7507	8	FASAN	1.38	1.63
53292	49	CARACARA	1.38	1.92
7691	50	SERI M 82	1.40	1.74
8195	5	RAYON F 89	1.56	1.71
7896	254	BACANORA T 88	1.38	1.99
43379	332	TOROCAHUI S2004	1.75	1.63
67414	39	IRENA/KAUZ	1.33	1.83
122467	76	OASIS/5*BORL95	1.85	1.83
65950	13	KAUZ*2/YACO//KAUZ	1.92	1.76
160593	23	SUPER SERI #2	1.86	1.83
160593	43	SERI*5//AGA/6*YR	1.58	1.86
98843	59	BUC/PRL//WEAVER	1.94	1.96
114906	319	CHEN/*Ae. tauschii* (TAUS)//BCN/3/KAUZ	1.42	1.92
118879	206	CROC_1/*Ae. tauschii* (205)//KAUZ/3/ATTILA	1.24	1.58
118879	209	CROC_1/*Ae. tauschii* (205)//KAUZ/3/ATTILA	1.35	1.58
120854	182	CHOIX/STAR/3/HE1/3*CNO79//2*SERI	1.56	1.55
134029	124	SW89.5181/KAUZ	1.63	1.95
		6B-662	1.92	2.38
		6B-365	3.40	3.37
		Glenlea	3.71	3.42
		Saloumini	1.54	1.58

CIMMYT started a breeding program for FHB resistance in the early 1980s with the routine screening of conventional and distantly related Triticeae germ plasm. In 1989, CIMMYT and China initiated a shuttle-breeding and germ plasm exchange program focusing on the integration of FHB resistance from Chinese wheats into high-yielding CIMMYT germ plasm. As a result, many Chinese derivatives have been included in the CIMMYT international nurseries that are distributed around the world.

Field screening. Until 2005, CIMMYT conducted field screening activities at the experiment station of Toluca, Mexico (2,640 masl), where the humid environmental conditions during the summer are particularly favorable to the development of the disease but, nevertheless, unverifiable and not possible to control. Since 2006, we modified our FHB screening system for greater accuracy and precision by shifting our operations to El Batan, Mexico, implementing an automated, programmable misting system, and using precision CO_2 sprayers for liquid inoculum application. The system allows the systematic and detailed screening of up to 9,000 plots (1–1.5-m double row) per year in the fields. The materials tested each year include advanced materials from the irrigated and rainfed CIMMYT wheat breeding programs, synthetic derivatives and wide crosses, elite triticale materials, multiple mapping populations, and introductions of new FHB-resistant materials. In 2008, in addition to the screening program, three trials were included under this screening system:

- a trial to confirm and assess the mycotoxin content of 36 advanced lines that have been evaluated in two previous years and tested for type-II resistance in the greenhouse in 2008,
- a trial to evaluate the effect of exposure to the misting system on DON content in two resistant and two susceptible lines depending on the harvest time (i.e., immediately after ripening vs. harvesting the entire screening field, which only can be done after late entries have been scored), and
- an experiment to assess the correlation between DON content and incidence/severity of FHB and its spatial distribution in the field.

Greenhouse screening. Mexican *F. graminearum* strains and other *Fusarium* species isolated from farmers fields and causing head blight were characterized. Suitable isolates to use in field screening, evaluating aggressiveness, and for chemotype and species verification were determined. Type-II resistance in wheat lines that have shown low FHB index and low mycotoxin content in the field were conducted.

DON evaluation. Quantification of DON in the most promising lines used the RIDASCREEN® FAST DON ELISA (R-Biopham AG, Germany). We also evaluated alternative methods for DON quantification including (qPCR).

Molecular pathology and marker-assisted selection. This work involved identifying Mexican *Fusarium* species and chemotype determination, evaluating alternative methods for DON quantification including (qPCR), and using MAS (3BS markers) in selected crosses made by the breeders.

International seed exchange network. Distributed the eleventh Scab Resistance Screening Nursery (11th SRSN) in 2008 and coördinated the Fusarium International Preliminary Spring Wheat Nursery (FIPSWN) and the Fusarium International Elite Spring Wheat Nursery (FIESWN) proposed by the 'Global Fusarium Initiative'.

Monitoring of long-term agronomy trials. This program is collaborating with CIMMYT's wheat agronomy group to investigate the long-term effects of conservation agriculture practices and rotation on FHB incidence, severity, and DON accumulation. Two years of data are already available.

Distribution of the 11th Scab Resistance Screening Nursery (SRSN). The SRSN was started at CIMMYT in 1985. These nurseries have consisted of the best FHB-resistant material identified through CIMMYT's FHB-screening trials and have been distributed to interested programs around the world upon request. In 2008, 54 sets of the 11th SRSN were distributed worldwide under the Standard Material Transfer Agreement adopted by the Governing Body of the International Treaty on Plant Genetic Resources for Food and Agriculture. This nursery includes the 47 best-performing, CIMMYT bread wheat lines and can be requested by anyone interested in improving wheat for resistance to FHB. Characteristics of the lines, including FHB index, DON content, and Fusarium damaged kernels (FDK) are reported in Table 11 (p. 123).

Spot blotch screening in Agua Fria, Puebla, Mexico. Spot blotch, caused by *Cochliobolus sativus*, emerged as a major threat to wheat production in the warmer, nontraditional wheat-growing areas in the late 1980s. This foliar disease causes significant yield losses annually (15–20% on average in South Asia) endangering the livelihoods of millions of small farmers. Effective measures in the field are needed to mitigate the impact of spot blotch on food security in af-

Table 11. List of bread wheat lines included in the 11th Scab Resistance Screening Nursery distributed by CIMMYT during 2008 with data on field performance in the previous year.

Entry	Cross	FHB Index	DON (ppm)	FDK %
6401	NG8675/CBRD//SHA5/WEAVER	7.2	0.8	12.5
6402	80456/YANGMAI 5//SHA5/WEAVER	5.1	1.4	17.5
6403	EMB16/CBRD//CBRD	14.4	—	.—
6404	MAYOOR//TK SN1081/*Ae. tauschii* (222)/4/CS/LE.RA//CS/3/PVN/5/PRINIA	9.4	2.0	8.0
6405	GONDO/CBRD	5.1	0.8	25.0
6406	YANGMAI 5*2/4/MOR/VEE#5//DUCULA/3/DUCULA	13.1	4.8	65.0
6407	SUM3/3/CS/LE.RA//CS/4/YANGMAI 158	12.0	1.5	30.0
6408	BAU/MILAN//CBRD	9.1	1.1	40.0
6409	SHA3/SERI//G.C.W 1/SERI/3/SHA3/SERI//YANG87-142	10.3	1.1	50.0
6410	80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	6.8	1.1	19.0
6411	80456/YANGMAI 5/3/PF70354/BOW//DUCULA/4/DULUS	7.0	2.1	25.0
6412	WUH1/VEE#5//CBRD	10.2	0.6	20.0
6413	SHA4/CHIL/4/CAR422/ANA//TRAP#1/3/STAR	10.3	2.3	50.0
6414	EMB16/CBRD//CBRD	4.6	0.5	4.0
6415	GAMENYA	91.9	8.0	—
6416	TNMU/6/CEP80111/CEP81165/5/MRNG/4/YKT406/3/AG/ASN//ATR	14.8	0.8	3.3
6417	FALCIN/*Ae. tauschii* (312)/3/THB/CEP7780//SHA4/LIRA	44.7	—	—
6418	SHANGHAI	13.9	1.2	11.3
6419	FRTR/MTA	5.5	1.2	1.0
6420	HEILO	11.7	2.5	33.3
6421	SUMAI #3	3.9	0.3	8.0
6422	SUMAI #3,AUT	2.8	—	—
6423	NG8675/CBRD//MILAN/3/NG8675/CBRD	9.1	0.4	5.3
6424	NING MAI 9558	10.4	3.9	20.0
6425	TINAMOU	10.4	1.5	7.3
6426	TRAP#1/BOW//TAIGU DERIVATIVE	9.8	0.7	7.0
6427	SHA3/CBRD	6.3	1.1	2.0
6428	SUM3/3/CS/LE.RA//CS/4/YANGMAI 158	8.9	0.5	8.0
6429	TRAP#1/BOW//TAIGU DERIVATIVE	9.8	0.7	8.0
6430	EMB27/KLORI	9.6	0.5	1.7
6431	GONDO/TNMU	10.0	3.1	14.7
6432	IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)	10.4	1.0	3.3
6433	IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (190)	14.0	1.6	12.0
6434	BR23/EMB27	5.8	0.5	4.0
6435	YANGMAI 5	6.9	2.1	15.3
6436	ATTILA/TNMU//TNMU	3.5	1.0	10.0
6437	SHA5/WEAVER//GONDO	2.1	0.5	45.0
6438	RUSS/7/OPATA/6/68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	3.9	0.9	20.0
6439	SHA5/WEAVER//80456/YANGMAI 5	4.2	0.6	6.0
6440	RUSS/7/OPATA/6/68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	5.1	0.7	40.0
6441	VERDE/7/OPATA/6/68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (878)	5.1	2.5	4.0
6442	CROC_1/*Ae. tauschii* (205)//KAUZ/3/PRL/SARA//TSI/VEE#5	6.5	0.7	8.0
6443	SRN/*Ae. tauschii* (358)//MILAN/SHA7	5.3	1.5	30.0
6444	GONDO	5.3	0.5	70.0
6445	PBW343/WBLL1//PANDION	4.0	1.3	4.0
6446	SKAUZ/BAV92//CHUM18/7*BCN	4.8	3.4	35.0
6447	CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92	5.1	5.5	20.0

fected areas. A review of three decades of work on spot blotch in wheat has been prepared and accepted for publication in *Journal of Phytopathology* (in press). The review summarizes the global knowledge on genetic improvement and crop-management strategies to minimize yield losses based on latest field research. Recent studies have shown that spot blotch severity is highly influenced by stress factors affecting crop physiology, which in turn affects host tolerance and resistance to the pathogen. Soil nutrient and water stress aggravate spot blotch-induced grain yield losses. Heat stress, which is gradually increasing in Asia, causes higher levels of disease damage. Genetic improvement is the cornerstone of a sustainable control of spot blotch in all affected regions. Resistance is essentially based on Chinese and South American sources and interspecific crosses with broadly adapted semidwarf germ plasm. A list of genotypes consistently reported in the last 10 years to have at least partial resistance to spot blotch, along with their inheritance of resistance, has been compiled to help breeding programs. Because the fungus is aggressive under conditions of high relative humidity and heat, which in turn influences plant susceptibility, a synthesis of the different tools for scoring disease severity is given. Because resistance is incomplete, the ultimate goal is the accumulation of minor genes for resistance in adapted, high-yielding genotypes. The use of resistant cultivars, timely seeding, adequate fertilization, crop rotation, and the judicious use of fungicides can be part of an integrated pest-management strategy for controlling yield losses due to spot blotch.

If the base of genetic resistance has to be expanded including through the use of new interspecific crosses or synthetic derivatives, field screening against spot blotch in Mexico should not be overlooked. This was confirmed again in Agua Fria, Mexico, in March 2008 at a CIMMYT maize station at the limit of Puebla and Veracruz where several hundreds advanced lines from the GREU program were tested. Typical spot blotch symptoms could be observed and scoring was conducted easily in second half of February. The Global Wheat Program resumed activities in Agua Fria in December, 2008, for future activities supporting the CSISA project in South Asia. The wheat pathology laboratory produced about 150-kg sorghum grain based inoculum that has been incubated for approximately six weeks at room temperature after been inoculated with three local *C. sativus* strains.

Screening for tan spot resistance in El Batan and Oaxaca, Mexico. Tan spot is considered to be the most important foliar wheat disease associated with zero tillage, because the fungus can over-winter on stubble. Screening for resistance in the field is cumbersome and difficult; the production of inoculum in sufficient quantity is complicated and slow because conidia are important for the disease development but are only induced under specific light requirements. Tan spot development is relatively slow in El Batan and symptoms are difficult to assess, because plants are submitted to earlier attacks by other foliar pathogens such as rusts. In Mexico, at least two races (1 and 2, based on host specific toxins) are known to exist. In 2008, systematic field screening in pathology plots continued at El Batan using race 1, the most commonly found race globally. A range of approximately 120 wheat entries known to show differences in resistance were field-tested from June to late September.

The inoculum-production protocol was revised and the rate of conidia production in the laboratory was improved. We confirmed the difficulty of establishing tan spot epidemics at El Batan. With the arrival of Dr. P. Singh, more effort has been done on seedling screening in the greenhouse. With support from SIDA/Sweden, we also have increased efforts towards setting up a high-throughput system for screening under hydroponics. This system still needs some adjustment but should help us select resistant materials based on seedling evaluations such as those done in Queensland, Australia. In collaboration with INIFAP, screening for resistance under natural epidemics continued for a second year in Yanhuitlan (Oaxaca) a location where CIMMYT used to screen efficiently for tan spot resistance until 1997. The performance of promising entries in El Batan and Oaxaca in 2008 is given in Table 12 (p. 125).

Leaf samples affected by tan spot were positively identified in the Oaxaca area, Tlaxcala, Guanajuato, and the State of Mexico in 2008 expanding our isolates collection and allowing us to refine our study of the race structure in the country. These strains will be characterized in early 2009 under a project sponsored by the Swedish Government. The objective is to make screening for tan spot resistance in wheat more effective in CIMMYT's global wheat-breeding program.

Table 12. Field results (double-digit score) of some of the most promising genotypes under tan spot epidemics at El Batan and Oaxaca (Mixteca), Mexico, in 2008.

			Oaxaca 2008				El Batan 2008			
			Rep 1		Rep 2		Rep 1		Rep 2	
CID	SID	Cross name	D1	D2	D1	D2	D1	D2	D1	D2
7572	0	MILAN Resistant Check	0	0	2	1	4	2	3	2
463293	51	AC8528/FRET2	1	1	0	0	4	2	4	2
20026	580	MILAN/SHA7	0	0	0	0	4	2	5	2
73478	615	SHA3/SERI//G.C.W 1/SERI	0	0	0	0	4	2	5	2
213007	798	ALD/COC//URES/3/MILAN/SHA7	0	0	0	0	5	2	4	2
13594	182	MILAN/AMSEL	1	1	0	0	4	2	6	2
213008	761	ALD/COC//URES/3/FCN	2	1	1	1	4	2	5	2
213007	788	ALD/COC//URES/3/MILAN/SHA7	1	1	0	0	5	2	5	2
213024	781	MILAN/SHA7/3/ALD/COC//URES	0	0	1	1	3	2	5	3
5230	0	TOROPI	3	2	2	1	4	2	4	2
303317	131	EMB16/CBRD	0	0	1	1	6	2	6	2
66483	1	M3	0	0	0	0	5	2	5	3
213024	783	MILAN/SHA7/3/ALD/COC//URES	0	0	0	0	5	2	5	3
213008	760	ALD/COC//URES/3/FCN	1	1	1	1	7	2	5	2
373305	625	EMB16/CBRD//CBRD	2	1	4	2	4	2	5	2
287012	0	INIA BOYERO	3	2	2	1	6	2	4	2
21597	4193	CATBIRD	0	0	1	1	5	3	7	2
21035	0	SABUF	0	0	0	0	5	3	5	3
481810	110	PFAU/MILAN/4/VEE/TRAP#1//ANGRA/3/PASTOR	0	0	0	0	6	3	6	2
213023	761	GUAM92/FCN	1	1	0	0	3	2	8	3
435388	110	MILAN/10/ZIY98*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA	1	1	1	1	4	2	7	3
8050	89	ITAPUA 40-OBLIGADO	2	1	2	2	3	2	7	3
424190	1	KLEIN DON ENRIQUE	1	1	4	2	5	2	5	3
213006	809	ALD/COC//URES/3/GUAM92	1	1	2	2	5	3	7	2
440369	186	MAYOOR//TK SN1081/*Ae. tauschii* (222)/3/CBRD	1	1	1	1	6	2	7	3
7919	1625	TINAMOU	3	1	3	2	6	2	7	2
435183	89	FOW/JA903//PASTOR	1	1	2	1	8	2	8	2
450351	72	ZIY98*2/PBW65//BERKUT	1	1	0	0	5	3	7	3
67414	56	IRENA/KAUZ	1	1	0	0	6	2	8	3
425914	83	SLVS//ZIY98*2/M10 (MUTATED C-306)	1	1	0	0	7	3	5	3
469796	1	INIA CHURRINCHE	2	1	4	2	7	2	7	2
7027	5	CIANO T79 Susceptible Check	6	2	6	2	8	4	8	4

CIMMYT bread wheat for semiarid Mexico.

Yann Manès.

Performance of material coming from physiological crossing. Of the 205 candidates to the 27th Semi-arid Wheat Screening Nursery (SAWSN) evaluated in northwest Mexico, 48 (23%) came from crosses made by the physiology group combining complementary, drought-adaptive physiological traits (PT). When this group was compared with those based on conventional crossing, they showed similar yields in irrigated environments but outperformed significantly the conventional group in the drought trials each year for three consecutive years (Table 13). Based on these results, PT lines constitute 25% of the genotypes of the 27th SAWSN and 32% of the 17th SAWYT, which will be evaluated by many national wheat programs in developing countries.

Table 13. Evaluation of crosses made by combining complementary, drouth-adaptive physiologica traits (PT) and conventional crosses for three consecutive years (2006–08) in the 27th Semi-arid Wheat Screening Nursery (SAWSN) evaluated in northwest Mexico.

Candidates to 27th SAWSN	Number of lines	Full irrigation Obregon 2008 Group ave % Tacupeto	Drought Obregon 2008 Group ave % Vorobey	Drought Obregon 2007 Group ave % Vorobey	Drought Obregon 2006 Group ave % Tacupeto
Conventional crosses	157	95.1	90.4	95.5	103.1
PT crosses	48	94	92.8	97.9	107.7
LSD 5%		Not significant	2.4	2.4	4.6

The physiological data generated by Matthew Reynolds' group in drought trials on these 48 lines and their parents, planted in the same evaluation trials, has confirmed that some lines have cumulated most of the good physiological attributes of their parents, which was seen in elite x elite crosses and in crosses involving Mexican landraces.

This data is very encouraging for the use of physiological information on designing crosses. The CIMMYT rainfed-wheat breeding program now applies systematically this approach. The Physiology Wheat Group evaluates in detail part of the rainfed crossing block, mainly new elite lines sent to semiarid international nurseries, and returns to us the most outstanding lines, indicating for each the main physiological attributes. We then use crosses combining the physiological information with yield, disease resistance, and end-user quality. Of crucial importance to maximize the chances of success is the way breeding populations are managed during the selection. The traits for stress involved in the model that underlies the physiological crossing are likely to be controlled quantitatively by many genes. Large breeding populations are necessary to maintain enough variability during the mass-selection phase and reach the yield-testing stage with enough lines to have a good probability of identifing the few that will have accumulated many, positive yield alleles. This new strategy of wheat breeding involves fewer crosses written from more parental information and larger populations generated. Without talking of converting an entire wheat -breeding program, one could envision allocating a significant part of this resource to a few crosses and, for the rest of the program, keep selecting from a large number of crosses that always will remain necessary to explore the germ plasm.

Evolution of a semiarid, bread wheat breeding scheme. The last year of three years of yield testing, PYT, YT, and candidates was 2007–08. PYT and YT have been selected similarly with one yield plot under full irrigation and replicated yield trials under drought and selected lines as candidates to the 28th SAWSN. Next year and onward, we will have two years of yield testing, 1 = PYT, second = candidate. This will save one year in the breeding scheme.

We also are working at reducing the timeframe of the early generation phase. Formerly at CIMMYT, selected bulks were running until the F_6, then $F_{6:7}$ head-rows were derived, and selected to Advanced Lines (ALs) or PYT from Obregon and Toluca. One if the first changes made in 2007 was to debulk all F_5s and F_6s from Toluca to give $F_{5:6}$ and $F_{6:7}$ head-rows in Obregon. In 2007, we also debulked the best looking F_4 crosses. We had in total 18,618 F_5, F_6, and F_7 head-rows in Obregon from which we selected 3,716 ALs (selection rate 20%) from which we selected 2,147 PYTs. This process allows all lines promoted to PYT to be selected for good agronomic type and leaf and stem rust resistance in Obregon and for good agronomic type, and leaf and stripe rust and *S. tritici* resistance in Toluca and El Batan. Given

that most $F_{4:5}$ rows selected in Obregon in 2008 showed good uniformity, we pursued the process, and this year debulked all F_4s and F_5s to head-rows in Obregon.

Table 14 shows the evolution of the breeding scheme. We have saved one and a half years in the breeding scheme, reducing the whole cycle from 7 to 5.5 years. This process reduces the bulk phase. The advantages of the selected bulk scheme are clear in term of simplicity and cost-saving, however it also brings some risks:

1. drifting towards tallness because of loss of height reference when selecting plants within the bulks (unless planting specific checks) and
2. drifting towards lateness, when strong selection for disease resistance is made, unless special attention is given to grain filling and earliness (which we try to do).

Table 14. Evolution of the new CIMMYT, Mexico, breeding scheme (Ob = Obregon, To = Toluca, and Ba = El Batan nursery sites; YT = yield trial, AL - advanced line).

Year	Station	Old scheme	New scheme	Station	Old scheme	New scheme
1	Obregon	Crossing	Crossing	Toluca	Crossing	Crossing
1	Toluca	F_1	F_1	Obregon	F_1	F_1
2	Obregon	F_2	F_2	Toluca	F_2	F_2
2	Toluca	F_3	F_3	Obregon	F_3	F_3
3	Obregon	F_4	F_4	Toluca	F_4	F_4
3	Toluca	F_5	F_5	Obregon	F_5	Head-rows
4	Obregon	F_6	Head-rows	Toluca/El Batan	F_6	ALs head-rows
4	Toluca/El Batan	ALs	ALs head-rows	Obregon	Head-rows	PYT
5	Obregon	PYT	PYT	Toluca/El Batan	ALs	
5	Toluca/El Batan			Obregon	PYT	YTC
6	Obregon	YT	YTC	Toluca/El Batan		
6	Toluca/El Batan			Obregon	YT	
7	Obregon	YTC		Toluca/Ba		
7	Toluca			Obregon	YTC	

The breeder cannot select all the plants himself in the bulks. He needs, however, to check all crosses before individual plant selection starts and decide to either discard crosses when no good plants can be found or make sure many plants are selected in the good crosses, to maintain good genetic variability, especially for quantitative traits such as yield and quality, and give enough options to the breeder for head-row selection. If this work is not done, the risk is that all crosses will be treated in the same way, giving too much importance to bad or mediocre crosses and not enough emphasis on the best ones.

Another innovation of the scheme is a pedigree step at the AL phase. From the head-rows selected in Obregon, we derive a family of four head-rows planted in El Batan. Bulks from head-rows are sown and selected in Toluca. The head-rows of the best families selected in Toluca are selected in El Batan, giving one more generation to select for uniformity and exploiting additional genetic variation in the good-looking families. With this two-step process of head-row selection, we may pursue the reduction of the selected bulk phase, debulking also from the F_3 next year the best looking F_3 populations or back-crosses (equivalent to F_4), further reducing the breeding cycle by six months.

ME6 (high-latitude) crossing and breeding strategy. Until 2007, crossing for the ME6 was split equally between crossing for North Kazakhstan and western Siberia (KASIB) and crossing for the other ME6 regions, e.g., China's Heilonjiang province and Canada. The wheat-growing area in Heilonjiang is quite a small, less than a 10^6 ha, in comparison to the KASIB area, about twenty millions. Canadian wheat breeders have very stringent market quality requirements, therefore the CIMMYT ME6 breeding material would have very little chance of development in Canada. For these two reasons, we have stopped ME6 crossing for other regions than KASIB and doubled the breeding effort for KASIB. We now make about 100 back or top-crosses per cycle, about 200 crosses per year for North Kazakhstan and Siberia. The High Latitude Wheat Screening Nursery will be discontinued.

Like the ME4, a large part of the ME6 crosses is dedicated to resistance to Ug99. However, as opposed to ME4, ME6 Ug99 breeding focuses more on the use of major genes because of the risk of Ug99 spreading in KASIB seems lower than in South Asia, so major genes could bring an acceptable solution at the moment, and because most KASIB cultivars are highly susceptible to stem rust, and breeding with APR would be very difficult in Kenya with photoperiod-sensitive, ME6 material.

KASIB yield data analysis presented at the KASIB meeting held in Pavlodar in August ,2008, showed that there is little 'G x E' in the region, making it possible to find high-yielding lines/cultivars with broad adaptation. These lines will have priority use for crossing. The correlation analysis showed that some sites predict better global performance than others, in particular Omsk in Siberia and Karabalyk in North Kazakhstan. Until 2008, material selected in Mexico was sent only to Shortandy. From 2009, it will be sent to Omsk and to Karabalyk as well. Shuttle materials will be selected from the data and observations collected at these two sites, and then sent to all breeders of the KASIB network.

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Reaction of durum wheats to black point in southern Sonora, Mexico.

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Introduction. More than 100 species of fungi, including *Alternaria*, *Fusarium*, and *Helminthosporium* spp., can be isolated from newly harvested wheat grain. These fungi are most important in humid field environments, where they infect seed when relative humidity exceeds 90% and seed moisture content exceeds 20%. Rainfall during seed maturation favors black point (BP), as well as humid weather prevailing for a few days prior to harvest (Prescott et al. 1986). Expanding green kernels are most susceptible. Premature seed senescence also promotes BP because many of the fungi are saprophytic (Wiese 1987). *Alternaria alternata* and *Bipolaris sorokiniana* are generally considered the primary causal agents of the disease (Mathur and Cunfer 1993). Infected ears may look normal, but there may be elliptical, brown to dark brown lesions on the inner side of the glumes. The disease is more pronounced as brown to dark brown or blackish, localized discolored areas, usually around the embryo end of seeds (Adlakha and Joshi 1974; Hanson and Christensen 1953; Rana and Gupta 1982; cited by Mathur and Cunfer 1993). The discoloration also may occur near the brush, in the crease or any part of the seed and may be light or dark or with a distinct margin. Severe infection causes discoloration and shriveling of the whole seed (Adlakha and Joshi 1974). In southern Sonora, Mexico, black point is an endemic disease of durum and bread wheat, although incidence is variable from year to year. Wheat-breeding programs select for disease resistance during seed evaluation after harvest, however, there is not a formal project on BP in Sonora. The objectives of this work were to evaluate the reaction of durum wheat elite advanced lines, pre- and candidate lines for commercial release, and commercial cultivars to BP after harvest in year 2008.

Materials and methods. The materials evaluated consisted of various nurseries. The evaluation was by visual inspection taking in to consideration the relative amount of affected grains in the sample, but without considering the area or the percentage of affected area. The rating scale was as follows: 0 = healthy grains, 1 = low incidence of black point, 2 = moderate, and 3 = high incidence. The following nurseries were evaluated: a) Advanced Yield Trial consisting of 171 entries planted on 15 November, 2007, in block 810, in a clay soil with pH 7.5; 100 g per entry were analyzed; b) pre-candidate lines for commercial release consisting of 62 entries, planted on 27 December, 2007, in block 910, in a heavy sandy clay loam soil, pH 7.5; grains from five spikes were evaluated; c1) commercial cultivars, four groups with five replications (four spikes each) of Altar C84 and Júpare C2001 planted on 22 November, 2007, in block 710, in a clay soil with pH 7.8; c2) commercial cultivars Altar C84, Nacori C97, Rafi C97, Atil C2000, Júpare C2001, Samayoa C2004, and Banamichi C2004, planted on 15 November, 2007, in block 810, 100 g were evaluated; c3) commercial cultivars Júpare

C2001, Samayoa C2004, Banamichi C2004, and Platinum planted on 8 and 21 November and 10 December, 2007, in block 710, under overhead irrigation, grains from ten spikes per date were evaluated; d) 17 candidates for commercial release with origin in wheat season 2006–07 and another group from 2007–08 planted on 8 and 21 November and 10 December, 2007, in block 710, under overhead irrigation, grains from ten spikes per date were evaluated; e) a group of 25 elite advanced lines with origin in wheat season 2006–07, planted on 8 and 21 November and 10 December, 2007, in block 710, under overhead irrigation, grains from ten spikes per date were evaluated; and f) 72 progenies derived from single spikes of 23 genotypes, planted on 27 December, 2007, in block 910, the product of three spikes was evaluated (total number of spikes = 4,968).

Results and discussion. *Advanced Yield Trial*. One hundred and two lines did not show any infected grain, 63 had level 1, and six were level 2. Ten lines out of the 102 which did not show infected grains are shown in Table 1.

Table 1. Ten lines from the Advanced Yield Trial that did not show black point-infected grains in the field at one planting date during the crop season autumn–winter 2007–08, in the Yaqui Valley, Sonora, Mexico.

Line	Pedigree and selection history
1	AINZEN_1//PLATA_6/GREEN_17 CDSS99B00315S-0M-0Y-66Y-0M-0Y-2M-0Y
2	ALTAR 84/BINTEPE 85/3/ALTAR 84/STINT//SILVER_45/4/LHNKE/ RASCON//CONA-D CDSS99B01265T-0TOPY-0M-0Y-12Y-0M-0Y-1M-0Y
3	SOMAT_3/PHAX_1//TILO_1/LOTUS_4/3/SOOTY_9/RASCON_37 CDSS01B00473S-17M-0M-0Y-0Y
4	SOOTY_9/RASCON_37//CAMAYO CGSS02Y00004S-2F1-6Y-0B-1Y-0B
5	MINIMUS/COMB DUCK_2//CHAM_3/3/FICHE_6/4/MOJO/AIRON/5/ SOMAT_3.1 CDSS02Y00233S-0Y-0M-9Y-0Y
6	LABUD/NIGRIS_3//GAN/3/AJAIA_13/YAZI/4/SORA/2*PLATA_12// SOMAT_3 CDSS02Y00358S-0Y-0M-21Y-0Y
7	CF4-JS 21//RASCON_39/TILO_1 CDSS02Y00439S-0Y-0M-3Y-0Y
8	CBC 509 CHILE/5/2*AJAIA_16//HORA/JRO/3/GAN/4/ZAR CDSS02Y01222T-0TOPB-0Y-0M-5Y-0Y
9	SOOTY_9/RASCON_37//CAMAYO CGSS02Y00004S-2F1-6Y-0B-1Y-0B
10	SOOTY_9/RASCON_37//GUAYACAN INIA CGSS02Y00011S-2F1-5Y-0B-2Y-0B-2Y-0B

Precandidate lines for commercial release. Twenty-five lines did not show any infected grain, 31 had level 1, and six with level 2. The ten lines out of the 25 that did not show infected grains are shown in Table 2 (p. 130).

Commercial cultivars. In the c1 nursery, no infected grains with black point were detected in any of the replications of the four groups of commercial cultivars Altar C84 and Júpare C2001. In the c2 nursery, commercial cultivars showed differences in disease incidence; Altar C84 and Júpare C2001 did not show any infected grains, whereas Samayoa C2004 showed the highest disease incidence (Table 3, p. 130). In nursery c3, commercial cultivars showed differences in disease incidence; Júpare C2001 and Platinum showed a disease range of 0–3, Samayoa C2004 from 1–3, and Banamichi C2004 from 0–1 (Table 4, p. 130). The results from the last two groups of commercial cultivars clearly show that Samayoa C2004 had the highest black point incidence with and without the overhead irrigation, whereas Júpare C2001 and Platinum reached the highest incidence in some of the evaluations under overhead irrigation.

Candidates for commercial release. Lines originating in 2006–07 that did not show infected grain in all planting dates were SOOTY_9/RASCON_37//STORLOM (CGSS02Y00006S-2F1-21Y-0B-10Y-0B) and SOOTY_9/RASCON_37// LLARETA INIA (CGSS02Y00010S-2F1-15Y-0B-5Y-0B), whereas line 1A.1D5+10-6/3*MOJO//RCOL/4/ARMENT// SRN_3/NIGRIS_4/3/CANELO_9.1 (CDSS02Y00408S-0Y-0M-6Y-0Y) showed the highest disease incidence. Lines originating in 2007–08 that did not show infected grains in all planting dates were ARTICO/AJAIA_3//HUALITA/3/ FULVOUS_1/ MFOWL_13/4/RASCON_39/TILO_1 (CDSS02Y01178T-0TOPB-0Y-0M-4Y-0Y) and LHNKE/HCN//

Table 2. Ten precandidate lines for commercial release that did not show black point-infected grains in the field at one planting date during the crop season autumn–winter 2007–08, in the Yaqui Valley, Sonora, Mexico.

Line	Pedigree and selection history
1	RCOL/POHO_1/3/DIPPER_2/BUSHEN_3//SNITAN CDSS02B00782T-0TOPB-0Y-0M-1Y-3M-04Y-0B
2	PLATA_6/GREEN_17//RCOL/3/SNITAN/SOMAT_3//FULVOUS_1/MFOWL_13 CDSS02B00199S-0M-9Y-06Y-2M-1Y
3	PLATA_6/GREEN_17//SNITAN/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1 CDSS02B00200S-0M-18Y-06Y-4M-1Y
4	SOOTY_9/RASCON_37//TILO_1/LOTUS_4/3/SOMAT_3/PHAX_1// TILO_1/LOTUS_4 CDSS02B00385S-0M-20Y-06Y-1M-1Y
5	CMH74A.630/SX//TSI/3/GUANAY/4/2*D86135/ACO89//PORRON_4/5/SOOTY_9/RASCON_37/3/ SOOTY_9/TARRO_1//AJAIA_2 CDSS02B00713S-0M-16Y-06Y-1M-1Y
6	STORLOM/3/RASCON_37/TARRO_2//RASCON_37/4/D00003A CDWS02FM00018S-0M-2Y-06Y-3M-1Y
7	STOT//ALTAR 84/ALD/3/AUK/GUIL//GREEN/4/GODRIN/GUTROS//DUKEM/3/THKNEE_11 CDSS04Y00283S-30Y-0M-06Y-3M-1Y
8	NUS/SULA//5*NUS/4/SULA/RBCE_2/3/HUI//CIT71/CII*2/5/ARMENT//SRN_3/NIGRIS_4/3/CANE-LO_9.1 CDSS04Y00888T-0TOPB-26Y-0M-06Y-2M-1Y
9	KOFA/8/GEDIZ/FGO//GTA/3/SRN_1/4/TOTUS/5/ENTE/MEXI_2//UI/3/YAV_1/GEDIZ/6/SOMBRA_20/7/ STOT//ALTAR 84/ALD CDSS04SH00003S-26Y-5M-6Y-4M-1Y
10	MOHAWK/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13/8/ THKNEE_11/9/CHEN/ALTAR/3/HUI/POC//BUB/RUFO/4/FNFOOT CDSS04SH00022S-22Y-2M-1Y-2M-1Y

Table 3. Black point incidence in commercial durum wheat cultivars planted on 15 November, 2007 in block 810 during the crop season autumn–winter 2007–08, in the Yaqui valley, Sonora, Mexico.

Cultivar	Disease incidence (range)
Altar C84	0
Nacori C97	1
Rafi C97	0–1
Atil C2000	0–1
Júpare C2001	0
Samayoa C2004	0–2
Banamichi C2004	0–1

Table 4. Black point incidence in commercial durum wheat cultivars planted on 8 and 21 November and 10 December, 2007, in block 710 under mist irrigation during the crop season autumn–winter 2007–08, in the Yaqui valley, Sonora, Mexico.

Cultivar	Disease incidence (range)
Júpare C2001	0–3
Samayoa C2004	1–3
Banamichi C2004	0–1
Platinum	0–3
Banamichi C2004	0–1

PATA_2/3/ CAMAYO/5/ CREX//BOY/YAV_1/3/ PLATA_6/4/PORRON_11 (CDSS02Y01197T-0TOPB-0Y-0M-7Y-0Y). Lines with the highest disease incidence were MUSK_1// ACO89/FNFOOT_2/4/ MUSK_4/3/ PLATA_3// CREX/ALLA/5/OLUS*2/ ILBOR//PATKA_7/YAZI_1 (CDSS02Y00786T-0TOPB-0Y-0M-2Y-0Y), 1A.1D 5+10-6/3*MOJO//RCOL/4/ ARMENT//SRN_3/NI-GRIS_4/3/CANELO_9.1 (CDSS02Y00408S-0Y-0M-4Y-0Y), TADIZ/3/ SOMAT_3/ PHAX_1//TILO_1/LOTUS_4 (CDSS02B00456S-0Y-0M-7Y-1M-04Y-0B), and CNDO/PRIMADUR//HAI-OU_17/3/ SNITAN/4/STOT//ALTAR 84/ALD/5/CNDO/ PRIMADUR// HAI-OU_17/3/SNITAN (CDSS02Y01208T-0TOPB-0Y-0M-22Y-0Y).

Elite advanced lines. Lines that did not show infected grains in all planting dates were ADAMAR_15//ALBIA_1/AL-TAR84/3/SNITAN/9/USDA595/3/ D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9 (CDSS02Y00214S-0Y-0M-5Y-0Y), GREEN_2/HIMAN_12//SHIP_1/7/ECO/ CMH76A.722//YAV/3/ALTAR84/4/ AJAIA_2/5/KJOVE_1/6/MALMUK_1/ SERRATOR_1 (CDSS02Y00287S-0Y-0M-10Y-0Y), MUSK_1//ACO89/ FNFOOT_2/4/ MUSK_4/3/PLATA_3//CREX/ALLA/5/OLUS*2/ILBOR//PATKA_7/YAZI_1 (CDSS02Y00786T-0TOPB-0Y-0M-2Y-0Y), AINZEN_1/3/SN TURK MI83-84 503/LOTUS_4//MUSK_4/6/CMH82A.1062/3/GGOVZ394//

SBA81/PLC/4/AAZ_1/ CREX/5/HUI//CIT71/CII (CDSS00B00307T-0TOPY-0B-33Y-0M-0Y-1B-0Y), and ZHONGZUO/2*GREEN_3//SORA/2*PLATA_12/10/PLATA_10/6/MQUE/4/ USDA573//QFN/AA_7/3/ALBA-D/5/ AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CHEN/ ALTAR 84/3/HUI/POC//BUB/RUFO/4/FNFOOT (CDSS02Y00213S-0Y-0M-30Y-0Y).

Lines with highest level of disease incidence were RASCON_22/RASCON_21// MOJO_2/3/GUANAY/4/ RCOL/5/SORA/2*PLATA_12//SOMAT_3 (CDSS01B00292S-0Y-0M-11Y-0Y), PLATA_6/GREEN_17//RCOL/3/ RYPS27_3/SKARV_3 (CDSS02Y00371S-0Y-0M-1Y-0Y), BRAK_2/AJAIA_2// SOLGA_8/3/CANELO_8// SORA/2*PLATA_12/4/YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN (CDSS02Y00763T-0TOPB-0Y-0M-4Y-0Y), and RCOL/GUANAY *2//SOMAT_3/ GREEN_22 (CDSS02Y01193T-0TOPB-0Y-0M-19Y-0Y).

Progenies derived from single spikes. Genotypes that did not show infected grains with black point in any of the progenies were SOMAT_4/INTER_8//BCRCH_1/3/ SOOTY_9/RASCON_37 (CDSS02Y01276T-0TOPB-0Y-0M-17Y-0Y), and TGBB/ CANDEF//LALA/GUIL/3/BONVAL/4/TILO_1/LOTUS_4/5/TILO_1/LOTUS_4 (CDSS02B01344T-0TOPB-0Y-0M-2Y-2M-04Y-0B). Five genotypes showed a disease incidence of level 2 in one of their progenies, and none showed level 3.

With the exception of the commercial cultivar Samayoa C2004, none of the lines reached the highest disease incidence (level 3) when grown without the overhead irrigation, and despite of the various planting dates influenced by different weather conditions (Figs. 1 and 2). During the last two weeks of January, the average temperature range was 10.4–18.6°C and 56.2–89.6% relative humidity. In February, the average temperature range was 11.9–20.3°C and 54.0–76.3% relative humidity. In March, the average temperature range was 11.7–18.9°C and 47.5–70.4% relative humidity. During the first two weeks of April, the average temperature range was 17.7–21.8°C and 49.5–69.2% relative humidity. The wheat crop season was quite dry; only 6.2 mm on rain were recorded on 24 January and 1 mm on 17 March.

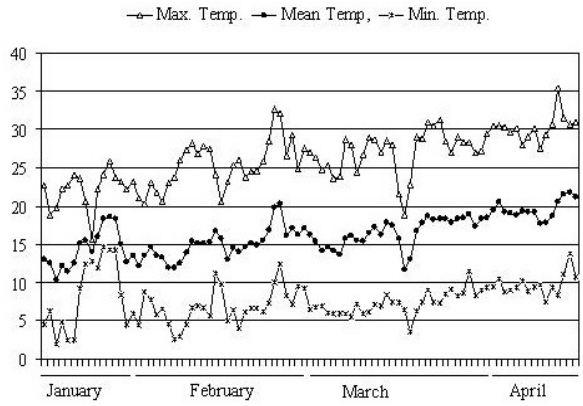

Fig. 1. Daily maximum, minimum, and mean temperature (°C) during 16 January–15 April, 2008, in blocks 710–910 in the Yaqui Valley, Sonora, Mexico.

Commercial cultivars Júpare C2001 and Platinum, some candidates for commercial release, and some elite advance lines showed the highest disease incidence (level 3) when subjected to the overhead irrigation during anthesis–first stage of kernel formation (Zadoks et al. 1974; stages 60 to 69–71). Further testing of some lines and cultivars would be necessary to corroborate their reaction so that they can serve as sources of resistance to black point. Because overhead irrigation is used to evaluate wheats for Karnal bunt resistance in the field (Fuentes-Davila and Rajaram 1994; Fuentes-Dávila and Trethowan 2007), the system also could be used to evaluate wheat germ plasm for resistance to black point.

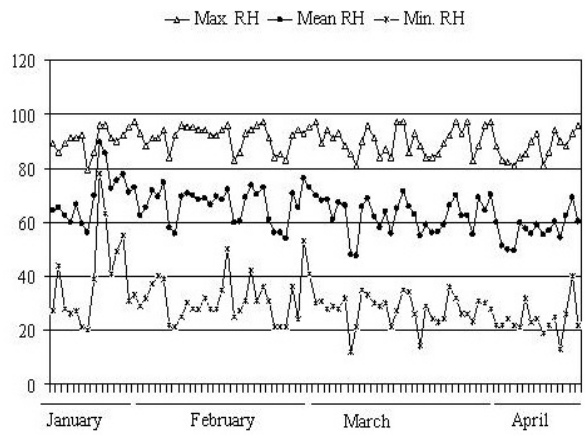

Fig. 2. Daily maximum, minimum, and mean humidity (%) during 16 January–15 April, 2008, in blocks 710–910 in the Yaqui Valley, Sonora, Mexico.

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Effect of yellow berry on wheat seed emergence at three sowing depths.

Teresa de Jesús Ruiz-Vega, Juan Manuel Cortés-Jiménez, and Guillermo Fuentes-Dávila.

Summary. The effect of yellow berry and sowing depth on seed germination were studied in the durum wheat cultivar Banamichi C2004. Seedling emergence decreased significantly as the sowing depth increased. Yellow berry affects neither seed germination nor its interaction with sowing depth.

Introduction. In southern Sonora, Mexico, wheat occupies up to 220,000 ha. Considering that a common practice is to use 120 kg of seed/ha, the demand for the region is in the order of 26,400 ton. For wheat export, regulations establish a limit of 10% of grain affected by yellow berry, a characteristic that has a negative correlation with protein content in the grain. According to Ottman and Doerge (1994), nitrogen is the factor with the highest impact on grain protein content, so application of nitrogen during heading is recommended in order to avoid yellow berry (Miezan et al. 1977; Linquist et al. 1992). Currently, the price of nitrogen has increased more than 100%. Reduced production costs in fields used for seed multiplication and not destined for export could be realized if the application of 50 nitrogen units recommended to avoid yellow berry is eliminated. An economic impact of approximately $321,428 USD could be generated considering a cost of $1.43 USD per unit of nitrogen of urea and an area of 4,500 ha used for seed production in the region. However, determining the effect of yellow berry upon wheat seed germination and seedling initial vigor, the objectives of this study, is nececcary.

Materials and methods. Seed of the durum wheat cultivar Banamichi C2004 was used in this study, which was conducted under laboratory conditions. One seed lot had 100% yellow berry incidence and the other only healthy seed. Seeds were sown in plastic pots (1.3-kg capacity, 20 seeds/pot) with clay soil, pH 8.2, at 1-, 2-, 3-, and 4-cm depths. The soil was previously sieved (2.0 mm) and water applied until reaching soil capacity, which was determined by the saturation value. Water conductivity was 0.45 dS/m. A factorial experimental design with six replications was used. Counts of seedling emergence were made daily. The pots also were weighed every 3 days in order to supply the water lost by evaporation.

Results and discussion. Highly significant differences were found between the sowing depth treatments. Yellow berry did not affect seedling emergence, and no interaction between these two factors was detected (Table 5). Greater sowing depth correlated with less seedling emergence with differences up to 20% (Fig. 3). In a parallel experiment, we observed that the percentage of germinated seed that was able to emerge was 76.45% and the total seed germinated was 76.97%, indicating that less emergence at greater depth is not due to germination failure but rather due to a lack of vigor to emerge. On average, a difference of 0.83% was observed in favor of seed with yellow berry when

Table 5. Percent seedling emergence of the durum wheat cultivar Banamichi C2004 as a function of sowing depth and yellow berry (Tuckey, p = 0.01, 16.86).

Depth (cm)	Yellow berry		
	Without	With	Average
1	82.50	83.33	82.92 a
2	85.00	85.83	85.42 a
3	75.00	72.50	73.75 ac
4	67.50	62.50	65.00 bc
Average	77.50 a	76.04 a	

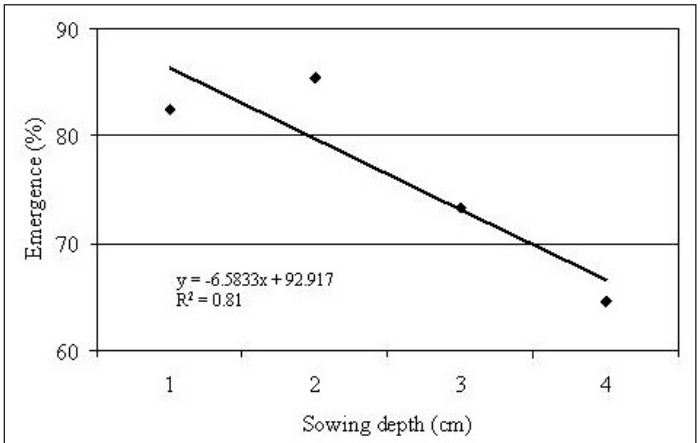

Fig. 3. The relationship between percent seedling emergencs and sowing depth of the durum wheat cultivar Banamichi C2004 *in vitro*.

germination was evaluated, even when seedlings had not emerged (data not shown). Similarly, 1.46% more seed with yellow berry emerged when considering only those that emerged independently of those that germinated. The observed less emergence at 1-cm depth than at 2 was attributed to more unfavorable humidity conditions, because the seed is closer to the surface and the soil cracked, however, there was no statistical difference. Seed affected with yellow berry had 96.67 and 90% germination when incubated in Petri plates and plastic Gerber-type bottles, respectively (Ruiz-Vega et al. 2009), without interaction with the soil. Seed germination reached 76.97% when seed was sown in plastic pots with soil, even at low sowing depths.

Conclusions. Yellow berry does not affect the process of germination and emergence of wheat seed, sowing depth does not affect seed germination but does reduce emergence of seedlings, and no interaction between yellow berry and sowing depth occurs.

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Effect of containers on wheat seed germination affected with yellow berry.

Teresa de Jesús Ruiz-Vega, Juan Manuel Cortés-Jiménez, and Guillermo Fuentes-Dávila.

Summary. The effect of two types of containers and three levels of yellow berry incidence on germination was evaluated using seed of the wheat cultivar Banamichi C2004. The highest percent germination was obtained with the Gerber-type bottle. Yellow berry did not affect germination, and there was no interaction between both factors.

Introduction. The occurrence of yellow berry is a common problem in wheat grown in southern Sonora, Mexico. Grain affected with yellow berry is characterized by low nitrogen content, which might be corrected by application of this element during heading of the wheat plant (Miezan et al. 1977). Wheat farmers are interested in the effect of yellow berry on seed germination; therefore, determining the interaction between these factors, and at the same time, evaluating laboratory techniques that are cheap, simple, fast, and that could be implemented by wheat producers is necessary. Seed germination by laboratory analysis is defined as the emergence and development of the esential structures that indicate for each class of seed analyzed its hability to become a normal plant under favorable conditions (Samaniego 2008). The importance of this process for the seed is vital, because no germination produces no plants and no harvest. Our objective was to evaluate the effect of two types of containers and three levels of yellow berry incidence upon seed germination and the initial hypocotyl growth in durum wheat seed.

Materials and methods. Two experiments were performed to assess seed germination of the durum wheat cultivar Banamichi C2004 using healthy seed and seed lots with 50 and 100% yellow berry incidence. The first experiment used 8.5-cm Petri plates and plastic Gerber-type bottles (6.5 cm in diameter). Ten seeds per treatment were placed on porous filter paper of the same diameter as the container. Four mL of distilled water were added to the container at planting; thereafter, 2 mL were added every 24 h for three days. Containers were kept open. A factorial experimental design with three replications was used. For the second experiment, only Gerber-type plastic bottles were used, adding a total of 8 mL of distilled water over a period of 11 days, and the bottles were kept closed.

Table 6. Percent seed germination of commercial durum wheat cultivar Banamichi C2004, in seed lots with different incidence of yellow berry incubated in two different type of containers.

Yellow berry incidence (%)	Petri plate	Plastic Gerber-type bottle	Average
0	66.67	100.00	83.33 a
50	63.33	96.66	80.03 a
100	96.67	90.00	93.33 a
Average	75.55 a	95.55 b	

Results and discussion. The occurrence of yellow berry did not affect wheat seed germination statistically (Table 6, p. 133). Significant differences were observed in germination in the two containers used, which agrees with the report of Román (2000); there was no interaction between both factors. Average seed germination in the bottle was 20% higher than that in the Petri plate, with the exception of the 100% yellow berry treatment, where seed germination was 6.67% higher in the Petri plate than in the bottle. Results from the first experiment indicated that there was a tendency to lower percent seed germination in bottles as yellow berry increased, however, this could not be corroborated in the second experiment. Figure 4 shows seed germination in both types of containers. In the second experiment, after 11 days of incubation in plastic bottles, more than 50% of the seeds with yellow berry and those without yellow berry, reached more than 8.3 cm in height (Table 7). We noticed that seed lot with 50% incidence of yellow berry had 70% of seeds that reached more than 8.3 cm in height; 13.3% more than healthy seed.

Fig. 4. Seed germination test of the durum wheat cultivar Banamichi C2004 in Petri plates and plastic, Gerber-type bottles.

Table 7. Percent seed germination of commercial durum wheat cultivar Banamichi C2004, in seed lots with different incidence of yellow berry incubated in plastic Gerber-type bottles.

Yellow berry (%)	≥ 8.3 cm	3 cm	1 cm	< 1 cm	Total (%)
0	56.66	26.66	10.00	6.66	100.00
50	70.00	23.33	6.66	0.00	100.00
100	53.33	30.00	13.33	3.33	100.00

Conclusions. Significant differences were observed between the containers evaluated; Gerber-type bottles with closed caps are better. The presence of yellow berry on wheat seed does not affect seed germination.

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Evaluation of Larrea tridentata dichloromethanic extract for control of karnal bunt in the field.

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Introduction. Karnal bunt or partial bunt of wheat was reported in Mexico in 1972 by Durán. This disease has become an important problem for wheat growers and certified seed producers in northwestern Mexico due to export restrictions (Fuentes-Dávila et al. 1996). In mature grains, the disease appears as sori enclosing a black powdery teliospore mass. Infection of wheat florets by wind-borne sporidia occurs after heading. The disease has a minor effect on yield, but may affect wheat quality if the level of infected grain is greater than 3%. Several fungicides for seed and foliar treatment have been shown to be useful in management of the disease (Krishna and Singh 1982; Singh and Singh 1985; Smilanick et al. 1987; Warham et al. 1989; Salazar-Huerta et al. 1997; Figueroa-López and Álvarez-Zamorano 2000; Fuentes-Dávila et al. 2005; Fuentes-Dávila 2007); however, they are not 100% effective and in some cases not economically profitable. Plants produce a wide variety of natural compounds that possess antifungal activity (Hoffmann et al. 1983). The use of natural bioactive substances for control of fungi has gained attention due to problems associated with chemical agents; these include resistance of pathogens to chemicals, toxicity to users, detection of residues in export commodities for human consumption, contamination of the environment, and adverse effects on beneficial organisms (Guerrero-Rodríguez et al. 2007; Suárez-Jiménez et al. 2007). Vallejo-Cohen et al. (1999) reported that *in vitro* tests of eight plant extracts caused 85 to 97% mycelial growth inhibition of *T. indica* and one showed 100% control. Rivera-Castañeda et al. (2001) reported that dichloromethane (DCM) extracts from *Chenopodium ambrosiodes* and *Encelia farinosa* reduced the radial

mycelial growth of *T. indica*, but total inhibition occurred with 500 mg/mL of the DCM extract from *Larrea tridentata in vitro*. Therefore, our objective was to evaluate the ability of such extract from *L. tridentata* on control of Karnal bunt in the field.

Materials and methods. Leaves and stems from *L. tridentata* were collected from native populations in the Sonoran desert and sun-dried for several weeks. Both leaves and stems (500 g) were extracted with DCM (1,000 mL) using a Soxhlet apparatus. The plant extract was then evaporated under reduced pressure in a rotary evaporator at 40°C and 700 mmHg. The DCM extract was dissolved in 100 mL acetone or 100 mL distilled water at a concentration of 1 g/L and used for the field tests with commercial bread wheat cultivar Bacanora T88, susceptible to Karnal bunt, which was sown on 16 November, 2005, on 20 beds with two 20-m rows. Inoculum was prepared using one-year-old teliospores that were disinfected with sodium hypochlorite 0.5% while centrifuging at 3,000 rpm for 2 min (Fuentes-Dávila and Rajaram 1994). After two rinses with sterile distilled water, they were plated on 1.5% water-agar and incubated at room temperature (20–22°C). Upon germination, pieces of agar with the growing fungus were transferred to potato-dextrose-agar (PDA) for multiplication. To obtain allantoid sporidia, pieces of PDA with the fungus were inverted onto the lids of sterile glass Petri plates containing a small amount of water. Sporidia were collected daily, counted with a haemacytometer, and adjusted to a concentration of 10,000 sporidia/mL for inoculations. Treatments used in this experiment were the following: 1) inoculation of the extract into the boot (Zadoks 48-49) (1 mL) and inoculum injection (1 mL) the following day, 2) inoculation with the fungus (1 mL) and extract injection (1 mL) the following day, 3) inoculation with the fungus (1 mL) and application of extract spray, 4) inoculation with the fungus (0.5 mL) and injection of extract (0.5 mL), and 5) injection of extract (0.5 mL) and inoculation with the fungus (0.5 mL). Harvest was carried out manually and the evaluation and counting of healthy and infected kernels was by visual inspection. The experiment was repeated twice. The first round of inoculations were made on 27 February, 2006, and the second on 1 March, 2006. Forty heads were used for each treatment and date.

Results. Spikes inoculated with the extract showed conspicuous damage with yellowing and wrinkle plant tissue. Treatment 1, which consisted in injection of 1 mL of the extract and of inoculum the following day, caused the greatest number of unemerged spikes (Table 8, p. 136). Treatment 2 (injection of inoculum and the extract the following day) caused the greatest number of spikes halfway emerged without grain. These two treatments had three (1) and four (2) emerged spikes with grains and only one spike in each treatment had infected grains (42.62 and 39.22% infection, respectively). In addition to damaging plant tissue, the extract did not affect the fungus because Karnal bunt infection was high.

Treatments four and five, which were similar to one and two but with 0.5 mL less inoculum and 0.5 mL less extract, were more benign on inoculated plants. With these treatments, spikes formed without emerging, spikes emerged with and without grains, and spikes halfway emerged without grains. For spikes emerged with grains, treatment four in February had ten with a range of infection 0.00–62.50%, but the 18 spikes from March did not have any infected grain. Treatment five in February had 19 with a range of infection 0.00–50.00%, whereas on 22 March the range was 0.00–32.61%. As in treatments one and two, the extract did not affect the fungus.

Treatment 3,, which consisted in spraying the extract on the inoculated heads, caused the highest infection levels. All spikes emerged normally, and the infection range was 0.00–96.46 for February and 0.00–78.23 for March. The percentage of infection reached in some inoculated heads indicated that the extract at the concentration used in this study was stimulatory for the fungus, because the mean of the three highest infection levels in the susceptible check bread wheat cultivar WL-711 used in other experiments during the 2005–06 season was 78.63% and under overhead mist irrigation. Because the *L. tridentata* DCM extract at 500 ppm was fungitoxic to *T. indica in vitro*, showing a complete inhibition of teliospore germination after 21 days, trying different concentrations for field testing is worthwhile.

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Table 8. Results of application of dichloromethane extract from *Larrea tridentata* for control of *Tilletia indica* in artificially field-inoculated, bread wheat cultivar Bacanora T88.

Spike formed, without grains	Spike formed, emerged with grains	Spike formed, halfway emerged without grains
Treatment 1 [27 February, 2006]		
34	2 spike 1 healthy grains = 35 infected grains = 26 % infection = 42.62 spike 2 healthy grains = 35 infected grains = 0 % infection = 0.00	4
Treatment 1 [1 March, 2006]		
20	1 spike 1 healthy grains = 67 infected grains = 0 % infection = 0.00	19
Treatment 2 [27 February, 2006]		
5	3 spike 1 healthy grains = 52 infected grains = 0 % infection = 0.00 spike 2 healthy grains = 54 infected grains = 0 % infection = 0.00 spike 3 healthy grains = 7 infected grains = 0 % infection = 0.00	32
Treatment 2 [1 March, 2006]		
2	1 spike 1 healthy grains = 31 infected grains = 20 % infection = 39.22	27
Treatment 3 [27 February, 2006]		
	40 Range of infection 0.00–96.46	
Treatment 3 [1 March, 2006]		
	40 Range of infection 0.00–78.23	
Treatment 4 [27 February, 2006]		
19	10 Range of infection 0–62.50 Emerged without grains – 11	
Treatment 4 [1 March, 2006]		
	18 Range of infection 0.00 Emerged without grains – 12	10
Treatment 5, February 27, 2006		
5	19 Range of infection 0 Emerged without grains 9	7
Treatment 5 [1 March, 2006]		
7	22 Range of infection 0.00–32.61 Emerged without grains – 4	7

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Evaluation of elite triticale advanced lines for resistance to Karnal bunt under artificial field inoculation in the Yaqui valley, Sonora, Mexico, during the crop season 2007–08.

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Introduction. Karnal bunt occurs naturally on bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). Affected kernels usually are partially infected and completely infected ones are rare (Mitra 1935; Bedi et al. 1949; Chona et al. 1961). Since the early 1980s, Meeta et al. (1980) and Fuentes-Davila et al. (1992) have reported about the resistance and inmunity shown by triticale cultivars and experimental advanced lines under artificial inoculations; however, maintaining the monitoring new lines for their reaction to *T. indica* is important, especially for those lines intended for commercial use. Our objective was to evaluate 20 elite, triticale advanced lines for resistance to Karnal bunt.

Materials and methods. Twenty elite, triticale advanced lines were evaluated for Karnal bunt resistance during the crop season 2007–08 in block 710 in a clay soil with a pH 7.8. Planting dates were 8 and 21 November and 6 December, 2007 using approximately 10 g of seed for a bed with two 1-m rows. A mist-irrigation system was used 3–5 times/day (15 min each time) to provide a humid environment in the experimental area. Inoculation was by injection during the boot stage applying 1 mL of an allantoid sporidial suspension (10,000/mL) to ten heads/genotype. Harvest was carried out manually, and the evaluation and counting of healthy and infected grains was by visual inspection. Tested genotypes included several advanced lines generated by the collaborative project between The International Maize and Wheat Improvement Center (CIMMYT) and The National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP) (Table 9, p. 138).

Table 9. Elite triticale advanced lines artificially inoculated with Karnal bunt (*Tilletia indica*) in three planting dates during the crop season 2007–08 in the Yaqui valley, Sonora, Mexico.

Line	Pedigree and selection history
1	POLLMER_2.1.1 CTY88.547-22RES-1M-0Y-2M-1Y-0M-1B-0Y
2	DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9/4/SONNI_3 CTSS99Y00115S-1Y-0M-0Y-8B-1Y-0B
3	BAT*2/BCN//CAAL/3/ERIZO_7/BAGAL_2//FARAS_1 CTSS99Y00246S-1Y-0M-0Y-5B-1Y-0B
4	LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/MANATI_1/7/ARDI_1/TOPO 1419//ERIZO_9/3/2*KETTU_1 CTSS01Y00040S-1M-3Y-3Y-4M-0Y
5	PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/ SUSI_2/5/AR/SNP6//TARASCA 87_2/C,S10/3/POR-SAS_4-1/4/CHACAL_3-2 CTSS01Y00150S-4Y-010M-1Y-10M-0Y
6	AR/SNP6//TARASCA 87_3/C,S10/3/URON_5/TATU_1/4/BULL_10/ MANATI_1/3/ELK 54/BUF_2//NIMIR_3/5/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9 CTSS02B00002T-25Y-4M-4Y-1M-1Y-0M
7	CHEN/CENT.ELVON/7/LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/ BULL_10/MANATI_1/8/PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/SUSI_2 CTSS02B00073T-10Y-3M-3Y-2M-1Y-0M
8	CMH73A.497/3*MEXI75//CENT.BRAZIL/5/ERIZO_12/2*NIMIR_3/3/Z9/ZEBRA 31//ASAD/4/FOCA_2-1/6/PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/SUSI_2 CTSS02B00083T-2Y-4M-4Y-4M-1Y-0M
9	HUI/TUB//CENT.TURKEY/3/CAAL/7/LIRON_2/5/DIS B5/3/SPHD/PVN// YOGUI_6/4/KER_3/6/BULL_10/MANATI_1 CTSS02B00107T-19Y-1M-3Y-4M-1Y-0M
10	1715/CENT.DOUKALA/7/LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/ 4/KER_3/6/BULL_10/MANATI_1/8/FAHAD_8-2*2//PTR/PND-T/3/GAUR_3/ ANOAS_2//BANT_1/4/HARE_7265/YOGUI_1//BULL_2 CTSS02B00134T-20Y-5M-1Y-4M-2Y-0M
11	BW32-1/CENT.SARDEV/7/LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/ BULL_10/MANATI_1/8/MERINO/JLO//REH/3/HARE_267/4/ARDI_4/5/PTR/CSTO//BGLT/3/RHINO_4-1/4/HARE_7265/YOGUI_3/6/BULL_10/MANATI_1 CTSS02B00149T-28Y-1M-1Y-4M-1Y-0M
12	PAVON/CENT.SARDEV/6/CMH77A.1024/2*YOGUI_1//CIVET#2/3/JLO 97/CIVET/4/MANATI_1/5/ERIZO_11/YOGUI_3/7/PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/SUSI_2 CTSS02B00167T-8Y-6M-1Y-1M-2Y-0M
13	SN64/EER/3/ERIZO_15/FAHAD_3//POLLMER_2.1/5/PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/SUSI_2 CTSS02B00172T-21Y-1M-1Y-4M-1Y-0M
14	STAR/CENT.CHINA/5/ARDI_1/TOPO 1419//ERIZO_9/3/LIRON_1-1/4/FAHAD_4/FARAS_1/6/YOGUI_3/ERIZO_11//ONA_2/POSS_1-2 CTSS02B00178T-23Y-5M-3Y-1M-2Y-0M
15	TURACO/CENT.SARDEV/7/LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/ 4/KER_3/6/BULL_10/MANATI_1/8/LIRON_2/5/DIS B5/3/SPHD/PVN// YOGUI_6/4/KER_3/6/BULL_10/MANATI_1 CTSS02B00186T-8Y-3M-3Y-4M-1Y-0M
16	CMH82.1082/ZEBRA 31/7/LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/ KER_3/6/BULL_10/MANATI_1/8/LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/ KER_3/6/BULL_10/MANATI_1 CTSS02B00268T-53Y-5M-1Y-1M-2Y-0M
17	CAAL/3/T1494_WG//ERIZO_10/2*BULL_1-1 CTSS02B00380S-11Y-1M-4Y-2M-2Y-0M
18	LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/MANATI_1/7/ DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9 CTSS02B00413S-22Y-2M-3Y-2M-1Y-0M
19	TICKIT/4/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9 CTSS03SH00006S-1Y-3M-2Y-4M-2Y-0M
20	HX87-244/HX87-255/5/PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/SUSI_2 CTSS03SH00028S-23Y-4M-3Y-2M-2Y-0M

Results. Although the overhead mist irrigation is important for obtaining infection by artificial inoculation, especially when seasons are dry and warm (Apodaca-Millán 1998), weather conditions play an important role in the outcome of the inoculation. During the last two weeks of January, 2008, the average temperature range was 10.4–18.6°C and 56.2–89.6% relative humidity (AGROSON 2009). In February, the average temperature range was 11.9–20.3°C and 54–76.3% relative humidity. In March, the average temperature range was 11.7–18.9°C and 47.5–70.4% relative humidity. During the first two weeks of April, the average temperature range was 17.7–21.8°C and 49.5–69.2% relative humidity. The wheat crop season was quite dry; the only rain was 6.2 mm on 24 January and 1 mm on 17 March. The range of infection for the first planting date was 0.00–1.69% with a mean of 0.25; 13 lines did not have any infected grain (Fig. 5). The range of infection for the second planting date was 0.00–7.95%, with a mean of 0.66; 15 lines did not have any infected grain. For the third planting date, the range of infection was 0.00–2.89 with a mean of 0.34; 16 lines did not show any infected grain. The difference between the mean percent infection of the first, second, and third planting dates and the mean of the three highest levels of infection of the suceptible check KBSUS 1 (95%) was 94.75, 94.34, and 94.66%, respectively. The frequency of lines in the different infection categories are shown in Fig. 6. In the overall results, nine lines did not show infected grain, eight fell within the 0.1–2.5 infection category, two were in the 2.6–5.0 category, and one was in the 5.1–10 infection category (Table 10). Lines with less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). Salazar et al. (1990) reported that pubescence in glumes of some wheats conferred a mechanical barrier to penetration by the fungus, which also may operate in triticale. Rye may be a source of morphological resistance for triticale to this disease (Warhan 1988). These results indicate that although the high level of resistance to Karnal bunt in triticale has been maintained in the new, elite germ plasm coming out of the CIMMYT program, collaborative efforts between INIFAP and CIMMYT must continue in order to detect lines that

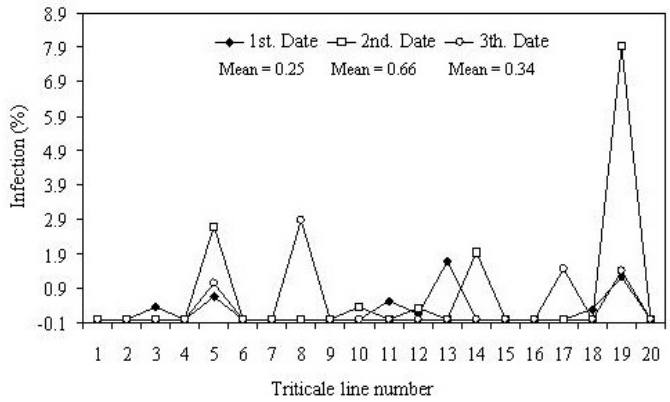

Fig. 5. Percentage of infection with Karnal bunt (*Tilletia indica*) of 20 elite triticale (*XTriticosecale*) advanced lines artificially inoculated in the field during the 2007–08 crop season on three dates in the Yaqui Valley, Sonora, Mexico.

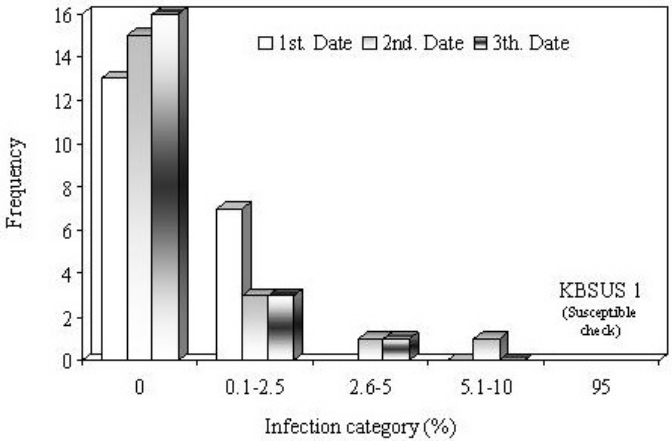

Fig. 6. Results of artificial field inoculation on three dates with Karnal bunt (*Tilletia indica*) of 20 elite triticale (*XTriticosecale*) advanced lines in the Yaqui Valley, Sonora, Mexico, during the 2007–08 crop season. The level of infection of KBSUS 1 is the mean of the three highest infection scores.

Table 10. Elite triticale advanced lines artificially inoculated with Karnal bunt (*Tilletia indica*) in three planting dates during the crop season 2007–08 in the Yaqui valley, Sonora, Mexico, which showed infection levels greater than 2.5%.

Line	Pedigree and selection history
	Infection level 2.6–5.0%
5	PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/ SUSI_2/5/AR/SNP6//TARASCA 87_2/C,S10/3/ PORSAS_4-1/4/CHACAL_3-2 CTSS01Y00150S-4Y-010M-1Y-10M-0Y
8	CMH73A.497/3*MEXI75//CENT.BRAZIL/5/ERIZO_12/2*NIMIR_3/3/Z9/ZEBRA 31//ASAD/4/FOCA_2-1/6/ PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/TOPO 1419//ERIZO_9/3/SUSI_2 CTSS02B00083T-2Y-4M-4Y-4M-1Y-0M
	Infection level 5.1–10.0%
19	TICKIT/4/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9 CTSS03SH00006S-1Y-3M-2Y-4M-2Y-0M

might be susceptible to Karnal bunt in order to ensure adequate levels of resistance in materials released for commercial cultivation in Mexico and elsewhere.

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Agronomic characteristics of four commercial bread wheat cultivars and six advanced lines in trials carried out in the Yaqui valley, Sonora, Mexico.

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Introduction. In northwest Mexico, wheat is the crop that occupies most of the cultivated area. In southern Sonora alone, it covers more than 300,000 ha. Durum wheat is cultivated in 74% of the area, whereas 80,247 ha are used for bread wheat. The average yield in the 2007–08 crop season was 6.18 ton/ha with a total production of 1.8 x 10^6 ton. Bread wheat production in the region since the late 1900s has been reduced drastically, because it is not competitive nationally and the production costs. These two factors are strongly affected by the national production system, which involves methods of irrigation, pest and disease control, fertilization, and high cost of fuel, among other factors. The collaborative wheat program between the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP) and the International Maize and Wheat Improvement Center (CIMMYT) has generated cultivars and elite lines of bread wheat with good yield potential and other outstanding characteristics that make this species a competitive crop in northwest Mexico. Our objective was to compare four commercial bread wheat cultivars and six elite advanced lines in yields trials in different planting dates.

Establishment of the trial. The study was carried out at the Experimental Station in the Yaqui valley, which belongs to the Northwest Regional Research Center of INIFAP, during the autumn–winter crop seasons of 2006–07 and 2007–08. The nursery consisted of 10 bread wheat genotypes, including four commercial cultivars released by INIFAP and six elite advanced lines from the wheat-breeding programs of CIMMYT. Planting dates were 15 and 30 November, 17 December, and 2 January, using 100 kg of seed/ha in beds 4 x 0.80 m with two rows. The experimental design was a factorial with completely randomized blocks and three replications. Fertilization consisted of 300 kg of urea/ha before sowing and 100 kg of urea/ha and 130 kg/ha of monoamonic phosphate during the first irrigation. Thirty-five days after sowing, the herbicide Situi xl was applied at the rate of 25 g of commercial product/ha. The trial was provided with a total of four furrow irrigations.

Results. The analysis of variance showed significant differences in yield of genotypes at the different planting dates. The cultivar Navojoa M-2007 showed the highest average yield during both crop seasons. All genotypes had a height smaller than 105 cm with the exception of cultivar Tacupeto F-2001, which is preferred by the wheat growers in northwest Mexico. Grain yield, plant height, and days to physiological maturity are presented in Table 11.

Table 11. Agronomic characteristics of the four commercial bread wheat cultivars and six advanced lines in trials carried out in the Yaqui Valley, Sonora, Mexico, during the crop seasons 2006–07 and 2007–08.

Cultivar or line [and selection history]	Grain yield (kg/ha)	Days-to-physiological maturity	Plant height (cm)
Tacupeto F-2001	6,585 b	116	105
Kronstad F-2004	6,325 c	116	103
Roelfs F-2007	6,490 bc	114	104
Navojoa M-2007	7,027 a	115	104
Toba97/Pastor [CMSS97M05756S-040M-020Y-030M-015Y-3M-1Y-3M-0Y]	6,265 bcd	116	103
Chen/*Ae. tauschii*//2*Opata/3/Babax/4/Jaru [CMSS99Y03521T-040M-040Y-040M-040SY-040M-5Y-010M]	5,950 e	118	104
Sunco/2*Pastor [CMSS99Y05530T-10M-040Y-040M-040SY-040M-14Y-010M]	6,446 bcd	114	99
Pfau/Weaver//Kiritati [CGSS01Y00155S-099Y-099M-099M-50Y-0B]	6,263 bcd	114	99
D67.2/P66.270//*Ae. tauschii* (320)/3/CUNNINGHAM [CMSS99M02230S-040M-040SY-6M-3Y-0M-10Y]	6,233 bcd	115	104
Wbll1*2/Brambling [CGSS01B00062T-099Y-099M-099M-099Y-099M-60Y-0B]	6,279 bcd	108	102
LSD (0.05) = 220			

The lines and cultivars evaluated in this trial stand out for their yield stability under constrasting crop conditions, which could be observed at all four planting dates, where the most recently released cultivar Navojoa M-2007 showed an interesting response under restricted irrigation, maintaining its yield superiority. The production of better bread wheat cultivars will bring about greater interest in their cultivation by farmers in southern Sonora. Therefore, in addition to yield trials, other studies on industrial quality and resistance to diseases have been conducted. Navojoa M-2007 and other outstanding lines showed resistance to yellow rust, a disease that has become more relevant in this part of Mexico during the last three years. Disease resistance to the most important diseases is an important aspect that will help to promote a mosaic of cultivars in southern Sonora.

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Reaction of elite bread wheat lines and cultivars to Karnal bunt artificially inoculated during the 2007–08 crop season in the Yaqui Valley, Sonora, Mexico.

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Introduction. The most susceptible plant species to Karnal bunt is *T. aestivum*. Under artificial inoculation, some lines may show more than 50% infeted grain (Fuentes-Dávila et al. 1992; 1993). The causal agent of this disease is the fungus *Tilletia indica* (Mitra 1931; syn. *Neovossia indica*). Although *T. indica* may affect durum wheat (*T. turgidum* subsp. *durum*) and triticale (X*Triticosecale*; Agarwal et al. 1977), the level of infected grain generally is very low. Control of this pathogen is difficult because teliospores are resistant to physical and chemical factors (Krishna and Singh 1982; Zhang et al. 1984; Smilanick et al. 1988). Chemical control can be accomplished by applying fungicides during flowering (Fuentes-Dávila et al. 2005); however, this measure is not feasible when quarantines do not allow tolerance levels for seed production. Resistant wheat cultivars are the best mean to control this disease. The objective of this work was to evaluate 18 elite advanced bread wheat lines and two commercial cultivars for resistance to Karnal bunt.

Materials and methods. Eighteen elite, advanced bread wheats and the cultivars Tacupeto F2001 and Kronstad F2004 were evaluated for Karnal bunt resistance during the autumn-winter in 2007–08 crop season in block 710 in a clay soil (pH 7.8), in the Yaqui Valley, Sonora, Mexico (Table 12). Planting dates were 8 and 21 November and 10 December,

Table 12. Elite bread wheat lines and commercial cultivars artificially inoculated with karnal bunt (*Tilletia indica*) in the field in three planting dates, during the crop season fall-winter 2007-2008, in the Yaqui valley, Sonora, Mexico.

Entry	Pedigree	Selection history
1	TACUPETO F2001	CGSS95B00016F-099Y-099B-099Y-099B-15Y-0B
2	KRONSTAD F2004	CMSS92Y01425T-16Y-010M-010Y-010Y-1M-0Y-50EY-0Y
3	KAMB1*2/KUKUNA	CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B
4	ATTILA/PASTOR	CMSS97Y04045S-040Y-050M-040SY-030M-14SY-010M-0Y
5	TOBA97/PASTOR	CMSS97M05756S-040M-020Y-030M-015Y-3M-1Y-3M-0Y
6	CHEN/AE.SQ//2*OPATA/3/BABAX/4/JARU	CMSS99Y03521T-040M-040Y-040M-040SY-040M-5Y-010M
7	SUNCO/2*PASTOR	CMSS99Y05530T-10M-040Y-040M-040SY-040M-14Y-010M
8	PFAU/WEAVER//KIRITATI	CGSS01Y00155S-099Y-099M-099M-50Y-0B
9	D67.2/P66.270//*Ae. tauschii* (320)/3/CUNNINGHAM	CMSS99M02230S-040M-040SY-6M-3Y-0M-10Y
10	WBLL1*2/BRAMBLING	CGSS01B00062T-099Y-099M-099M-099Y-099M-60Y-0B
11	WBLL1*2/BRAMBLING	CGSS01B00062T-099Y-099M-099M-099Y-099M-12Y-0B
12	WBLL1*2/BRAMBLING	CGSS01B00062T-099Y-099M-099M-099Y-099M-73Y-0B
13	KAMB1*2/KIRITATI	CGSS01B00070T-099Y-099M-099M-099Y-099M-23Y-0B
14	KIRITATI/WBLL1	CGSS02Y00138S-099M-099Y-099M-12Y-0B
15	THELIN/2*WBLL1	CGSS02Y00079T-099B-099B-099Y-099M-6Y-0B
16	KAMB1*2/BRAMBLING	CGSS01B00069T-099Y-099M-099M-099Y-099M-20Y-0B
17	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2	CMSA00Y00582S-0P0Y-040M-040SY-030M-1ZLM-0ZTY
18	PASTOR/WBLL1	CMSA00Y00587S-0P0Y-040M-040SY-030M-26ZLM-0ZTY
19	T.DICOCCON PI225332/*Ae. tauschii* (895)//WBLL1/3/2*WBLL1	CMSA01M00336T-040Y-14M-010Y-6ZLM
20	BETTY/3/CHEN/*Ae. tauschii*//2*OPATA	CMSW00WM00150S-040M-040Y-030M-030ZLM-3ZTY-0M

2007, using a 1-m bed with two rows. Inoculations were carried out by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) (Fig. 7) during the boot stage (Fig. 8) in ten heads from each line and cultivar. An overhead, mist-irrigation system was used to provide high relative humidity in the experimental area. Harvest was done manually, and the counting of healthy and infected grains was done visually to determine the percentage of infection. Evaluated lines originated from the collaborative project between the International Maize and Wheat Improvement Center (CIMMYT) and the National Institute for Forestry, Agriculture and Livestock Research in Mexico (INIFAP).

Fig. 7. Allantoid secondary sporidia of *Tilletia indica*.

Fig. 8. Artificial inoculation by boot injection.

Results and discussion. The range of infection for the first planting date was 0.00–22.42%, with a mean of 6.70; three lines did not have any infected grains (Fig. 9). The range of infection for the second planting date was 1.71–20.16%, with a mean of 8.48. For the third planting date, the range of infection was 0.62–11.35 with a mean of 5.31. Figure 10 shows the frequency of lines in the different infection categories in the three dates. The suceptible check KBSUS 1 had 95% infection. In the overall results, five lines fell within the 2.6–5.0 infection category, three in the 5.1–10.0 category, and twelve in the 10.1–30 infection category (Fig. 11, p. 144). Lines with less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994).

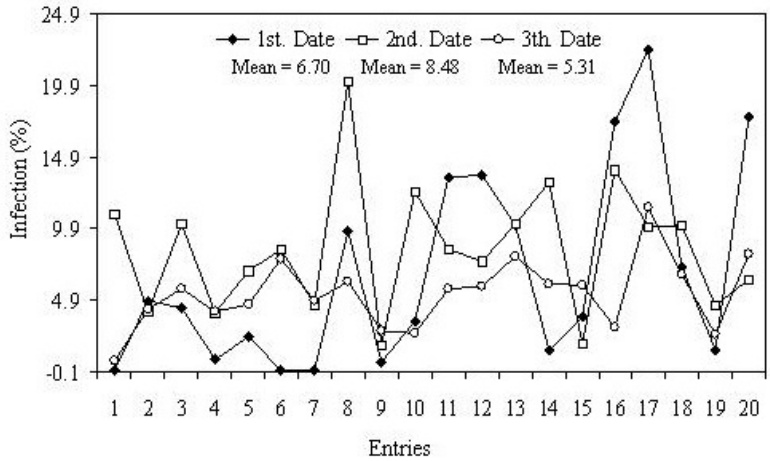

Fig. 9. Percent infection with Karnal bunt (*Tilletia indica*) of 18 elite, advanced bread wheat lines and two cultivars artificially inoculated in the field on three dates with in the Yaqui Valley, Sonora, Mexico, during the 2007–08 crop season.

Sixty percent of the entries were moderatly susceptible to susceptible, including cultivar Tacupeto F2001 and the line KAMB1*2/KUKUNA. Tacupeto did not show greater infection levels than 10.89% probably due to escape, because it did not have infected grains at the first planting date and 0.62% infection at the third date. This cultivar is one of the two leading bread wheats in southern Sonora because of preference by the milling industry. Susceptibility to Karnal bunt and to stripe rust, however, makes it necessary to apply fungicides; therefore, it is important to look for other cultivars that have been released by INIFAP. Kronstad F2004 and four lines (ATTILA/PASTOR, SUNCO/2*PASTOR, D67.2/P66.270// *Ae. tauschii* (320)/3/CUNNINGHAM, and T.DICOCCON PI225332/*Ae. tauschii* (895)// WBLL1/3/2*WBLL1) showed infection levels between 2.6 to 5.0%, so they are considered resistant and good prospects for commercial release.

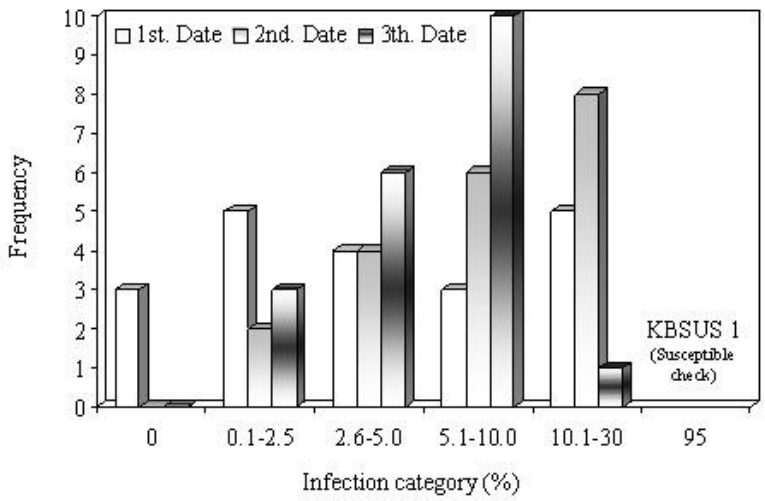

Fig. 10. Results of artificial field inoculation with Karnal bunt (*Tilletia indica*) on three dates of 18 elite, advanced bread wheat lines and two cultivars in the Yaqui Valley, Sonora, Mexico, during the 2007–08 crop season. The level of infection of KBSUS 1 is the mean of the three highest infection scores

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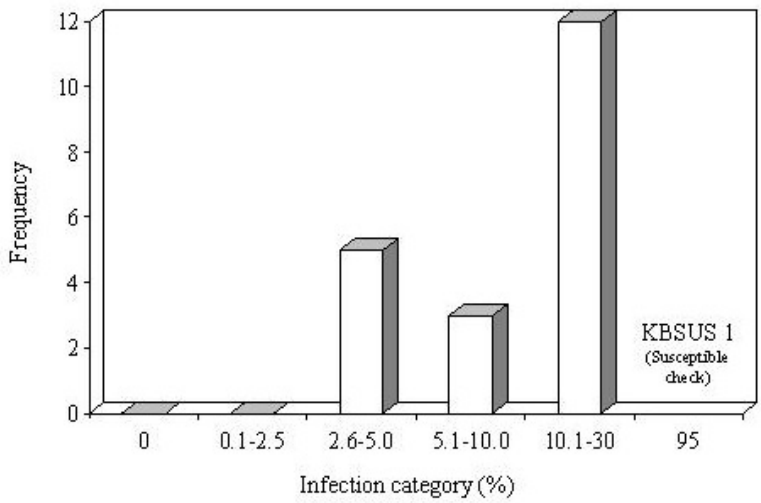

Fig. 11. Overall rating of 18 elite advanced bread wheat lines and two cultivars artificially inoculated in the fiels on three dates with Karnal bunt (Tilletia indica) in the Yaqui Valley, Sonora, Mexico, during the 2007–08 crop season. The level of infection of KBSUS 1 is the mean of the three highest infections scores

Use of climatology for temperature risk analysis for cultivation of wheat and other agricultural crops in Southern Sonora, Mexico.

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Introduction. The concept of climatic change has become relevant recently and can defined as the deviation of the average expected meteorological time for a given location and during a specific period of time of the year (IPCC 2001). Although there have always been changes and cycles of climatic stability as part of the natural rearrangements on the earth, the climatic system of the planet has changed in an important fashion during the last few years, which with no doubt has been caused by industrial activities, forestry, agriculture, and livestock. Gases that cause the greenhouse effect play an important role in the natural warming, an estimated significant temperature increment (0.6 ± 0.2ºC), of the earth during the twentieth century (IPCC 2001). In Mexico, livestock and agriculture are the sectors with greater contribution (50%) of methane emissions, therefore, this sector is taking into consideration the climatic change as a component of development, eliminating risky practices for the environment within the corresponding production system (INE and SEMARNAP 1999).

Every year, variations in yield recorded in agricultural production systems are induced by diseases, pests, weeds, technological management (irrigation or sowing method), soil type, fertilization, cultivar, an others not less important such as climate, which has great influence on agricultural activities. The state of Sonora is located in a region of the

country where anomalies in climatic behavior have been detected in previous years, mainly in rainfall and temperature (Jáuregui 2004). The availability and transfer of climatic analyses is important for the study of environmental phenomena, which are in continuous evolution on the planet, therefore, it is reasonable to widen and strategically systematize the climatic information of the national network. This information will be important for adjusting or establishing new management strategies for forestry, agriculture, and livestock production systems in the near future.

Progress in adaptation to new climatic conditions or to a posible climatic change in the most important agricultural regions of Mexico, will be a function of the technology available, institutional agreements, financing, and education of the population (Chapela 2004). The Yaqui and Mayo Walleys, located in southern Sonora, are an important agricultural region, therefore, studying the climate to understand its impact in this sector, which will allow us to develop an efficient production system, is necessary.

Climate and the agricultural activities; critical temperatures for plants: thermal threshold (TT). In the agricultural sector, temperature influences the development of some crops and affects their yield (Vargas et al. 2001). Besides water, temperature is the bioclimatic element that promotes or limits the increase of the vegetative plant biomass. The optimum temperature limits for plant growth is a topic that regained importance in the 1970s. Because there are temperature limits or thermic thresholds (Fig. 12) in each specific crop, temperature could be optimum, or in an extreme case, as vital as the maximum and minimum temperature, where both thermic conditions could lead the plant to a resting or latent stage, including death depending if they are winter crops or the summer exceeds their TT (Table 13). Similarly, when temperature exceeds the bearable TT in some crops, damage could be gradual in relation to exposure time as the lethal limits approach. However, deterioration magnifies as the thermic oscillation (TO) becomes greater during the day or night (Gastiazoro 2003; Muñoz 2003). Most plant species have a maximum pollen viability between 18 and 20ºC (Escaich et al. 1997). Castilla (1992) reported that temperatures below 10–12°C for several days affect the productivity of vegetable crops; similarly, summer crops are affected when temperatures are greater than 30°C. The plant requires thermal continuity for optimal development, that is, heat accumulation (thermal hours) or cold (cold hours) in the case of summer crops (cotton, vegetables) or winter crops (wheat, oat, maize) respectively, which determine germination, growth, flowering, reproduction, and fruit development.

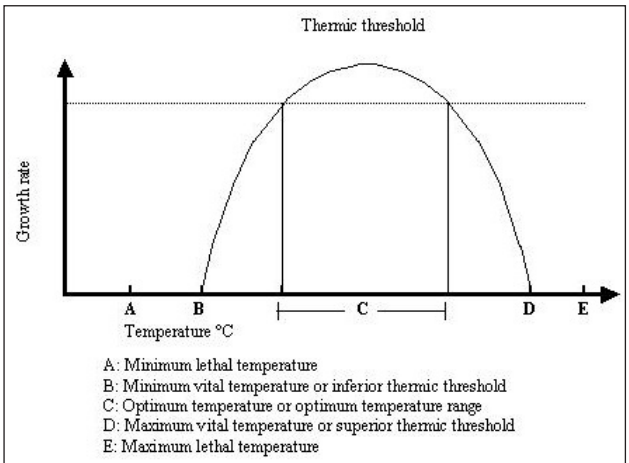


Fig. 12. Graphic representation of the location of the plant thermal limits.

Table 13. Optimum thermal (°C) requirements for different crops in southern Sonora, Mexico.

Crop	Biological minimum	Optimum day	Optimum night	Optimum RH (%)	Source
Wheat	2–6	15–20	16–18	60–70	Del Pozo et al. 1987
Tomato	10–12	21–24	15–20	50–60	Benacchio 1982
Pepper	10–12	20–28	16–20	50–70	Muñoz 2003
Cucumber	12–14	17–22	18–21	70–90	Castilla 1992
Melon	12–14	24–30	18–21	70–90	Nisen 1990
Watermelon	10–13	24–30	20–25	85–90	De la Torre 1999
Cauliflower	3–5	17–20	12–15	65–70	Nisen et al. 1990
Asparagus	6–8	20–25	18–25	60	Yuste 1997

Furthering our knowledge about climate has allowed for many applications in agriculture, where a relationship between climate and yield has been found. A good example is the yield predictive model in crops based on climatic analysis and field data. These models might help to make decisions on agrifoodstuff activity and commercialization

stronger in the short to medium term. However, the use of climate data as substitute for other field data might provide a reliable forecast for wheat yield (Banayan et al. 2003), as well as for maturity of cotton (Ryan et al. 2005). At the same time, climate influences population dynamics of pests such as white fly (*Trialeurodes vaporariorum*), because temperature affects duration of the immature stages and the flying capacity of adults (Liu et al. 1994), causing fast development of pests at 10–30ºC. Sánchez et al. (2002) found that an accumulation of 35ºC/day is necessary for the appearance of immature stages of the pest and indicated that starting from this threshold, the white fly population tripled for each grade of increase.

Materials and methods. The climatic data analyzed corresponded to the period January 2002 to December 2006 collected from 35 weather stations located in southern Sonora, which comprises the irrigation districts of the Yaqui and Mayo Valleys. Eight stations belong to the National Water Commission (CNA, 2007). Data from 19 of the other 27 stations is updated constantly and available on the internet: (http://clima.inifap.gob.mx, http://www.agroson.org.mx; In Spanish).

Based on data from several researchers (Table 13, p. 145), we analyzed the thermal thresholds (TT). The number of days with maximum and minimum daily temperature (MXT and MIT) were taken into consideration in order to determine the frequency of days with temperature equal or below 12ºC (Fx12) and a temperature equal or greater than 30ºC (Fx30). Thermal oscillation (TO) during the day and night was analyzed from each month of the year. The difference between the average MXT and the maximum MXT recorded in a given month was used to determine the superior TO (STO). Similarly, the inferior thermal oscillation (ITO) was calculated by the difference between the average MIT and the minimum value of MIT recorded in a given month (Table 14). The digital outline of Fx12 and Fx30 of each weather station were captured and interpolated in an ArcView platform in order to analyze its annual shift (Figs. 13 and 14, p. 147). The same maps were used to locate areas thermically homogeneous since they show the average temperature during the winter and summer (Fig. 15, p. 147).

Table 14. Thermal oscilation in the agricultural area of Southern Sonora (MXT, maximum daily temperature; MIT, minimum daily temperature; MXTO, maximum thermal oscillation; MITO, minimum thermal oscillation). Daily average temperature (ºC) from 2002 to 2006.

	Yaqui Valley				Mayo Valley			
Month	MXT mean	MXTO (°C)	MITO mean	MITO (°C)	MXT mean	MXTO (°C)	MITO mean	MITO (°C)
January	25	+6	7	–5	24	+5	8	–5
February	26	+6	8	–5	25	+5	8	–5
March	28	+7	8	–4	27	+6	8	–4
April	31	+6	11	–4	30	+5	11	–5
May	35	+5	14	–5	34	+4	14	–5
June	37	+4	21	–6	36	+4	20	–6
July	37	+5	24	–4	37	+6	25	–3
August	38	+5	25	–3	37	+3	25	–3
September	37	+7	24	–5	36	+6	24	–4
October	34	+7	18	–6	34	+6	18	–6
November	30	+7	12	–6	30	+7	12	–6
December	26	+6	7	–5	25	+6	7	–6

Results and discussion. The maximum average temperature indicates that the agricultural area of the Yaqui valley is 1ºC warmer from December to September with respect to the agricultural area of the Mayo valley (Table 14). On the other hand, the minimum temperature is similar with the exception of the month of January, where there is a differential of 1ºC less in the Yaqui Valley. The maximum temperature registered during the day within an urban area is 1–3ºC greater with respect to an agricultural valley and minimum temperatures are 2–3ºC greater. This temperature differential makes the urban area a true heat center with respect to the agricultural area. In relation to MXT (Table 14), we observed that in the Yaqui Valley, MXTO can reach 30ºC in the cold months (December to February), whereas the MITO may reach 2ºC in the Yaqui Valley and 3ºC in the Mayo Valley. Because Table 13 (p. 145) and Table 14 are related, you can observe that the TO that occurs in the agricultural area of the Yaqui Valley exceeds the minimum temperature limits and the biological maximum that these species require for optimum growth, especially for cucumber and melon. Muñoz (2003) mentioned that when the maximum day temperature greatly differs from the minimum night temperature imbalances in growth are

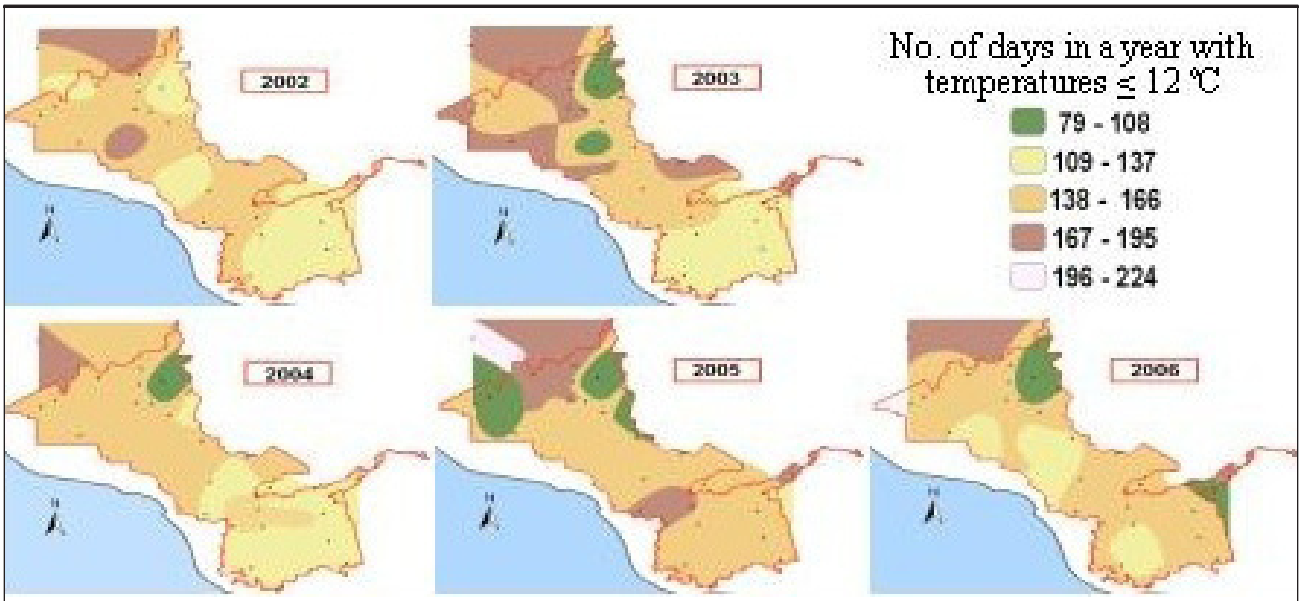
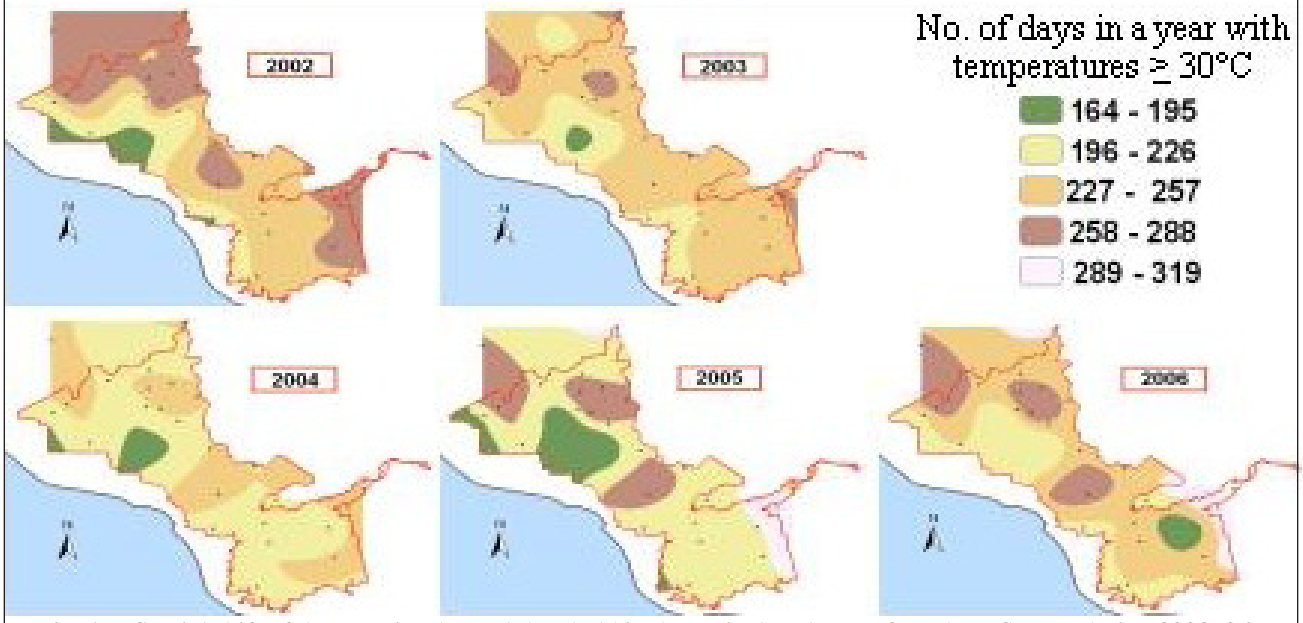


Fig. 13. Spatial shift of the inferior thermal threshold in the agricultural area of southern Sonora during 2002–06.



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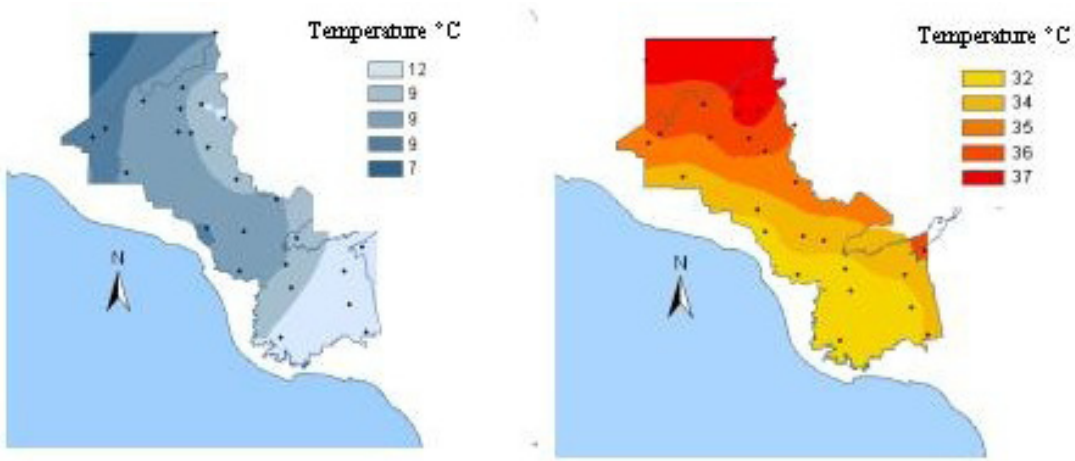

Fig. 15. Behavior of the minimum and maximum daily temperatures in southern Sonora based on the homogeneous characterization of temperature.

caused. A large part of the explanation regarding yield variation in the region is due to the fact that crops established during the autumn and winter get a heat stress produced by the high frequency of days with thermal oscillation that exceed the tolerable limits and cause cummulative damage.

The inferior thermic threshold (ITT) during December to March (Fig. 13, p. 147) was 21.6% (79 d) with respect to the year and 53.4% (195 d) in the Fx12 depending on the zone and year, showing a greater occurrence in year 2003 (three regions) and 2005 (two regions). These zones are the most at risk for frosts, with a tendency to show a Fx12 with a slightly less ocurrence (109–137) mainly in the northern part of the Yaqui Valley. The occurrence of a superior thermic threshold (STT) (Fig. 14, p. 147) in southern Sonora covered most of the agricultural area during 2002 in the Yaqui Valley even when an Fx30 occurred with greater frequency the same year in an area of the Mayo Valley.

Fx12 and Fx30 occur annually with shifts of different magnitude in the entire agricultural area, occurring more frequently in the northern parts. In contrast, these variables show a lesser tendency to occur both toward the southern zone. For the central part of the territory, both thresholds occur with a frequency of days between 109 to 166 for Fx12 and days 196 to 257 for Fx30. Years 2005 and 2006 registered an increment of Fx12 towards the southern part of the agricultural area and Fx30 towards the southwest. In both years, three areas with 258–288 days with Fx30 were observed. Finally, in the south of the agricultural area, which mainly comprises the Mayo Valley, indicates a moderate frequency of Fx30 for 2006 (Fig. 15, p. 147). The threshold temperature analyzed through spatial distribution and sketched by year (Figs. 14 and 15, p. 147) indicates that ITT and STT vary in distribution every year following the annual shift of precipitation influenced by the presence of climatologic phenomena and the dominant crop cover, showing some uncertainty in its distribution in each sowing cycle. The map sequence in Fig. 14 (p. 147) shows that the northern part of the agricultural area registers the highest frequencies of Fx12, which means that these are the areas where crops receive a frequency between 47–54% days of the year with greater stress from minimum temperatures. These show potential for a good accumulation of cold hours for autumn–winter seasons (wheat and maize), whereas those zones that tend to be warmer are risky because the superior thermal oscillation may limit good development of some cereals, mainly at the end of physiological maturity (from flowering to grain filling), which compromises yield in relation to climatic variation during the season.

For temperature homogenization or isothermal (Fig. 15, p. 147), the northwest zone shows characteristics of low temperature (7ºC) during the winter months, however, the central zone shows temperaturas of 9ºC to the southeast where the average IMT is 12ºC (Fig. 15, p. 147) and the average MXT might be from 34–37ºC. The northeast zone of the cuadricula of the valley appears to be the warmest, has the most thernal extremes, and shows the lowest IMT average. The analysis by season shows that its thermal properties are related with specific factors that annually make these zones cold, hot, moderate, or extreme. They are areas closer to the ocean, whereas both Buayseacobe and Tesia have the close presence of the typical shrub plant cover, climatologically characterizing this agricultural portion. This analysis does not takesrelative humidity into consideration. However, relative humidity is an important climatic variable in the equation used to estimate the temperature–humidity index (THI), which complements the humidity effect upon temperature severity. A new index recently is being developed that will include solar radiation and wind speed in addition to ambient temperature and relative humidity.

Conclusions. The annual and monthly temperature variation analyzed, points out to the northern and central regions in the agricultural area of the Yaqui valley, as the zone with the highest risk for production. The highest frequency of damaging thermic thresholds are registered in this area during the winter and summer months, although their effect occurs with different magnitude every year; it is noticeable only when damage by frost or heat occur in autumn and winter crops.

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ITEMS FROM PAKISTAN

NATIONAL AGRICULTURAL RESEARCH CENTER (NARC), ISLAMABAD
Wheat Wide Crosses, NARC, Islamabad, Pakistan.

The development of a wide-cross program in wheat in Pakistan.

A. Mujeeb-Kazi, Alvina G. Kazi, and Iqbal Ayub Khan.

The unequivocal status of wheat importance as a food cereal is paramount and the need to be on secure production grounds a national priority. A national coördination program exists that has alliances with all professionals involved in wheat improvement across the country with international linkages. However, the changing international scenarios

around wheat production in light of productivity constraints and new, sophisticated technologies necessitate that Pakistani researchers move with time and be proactive. This involves a swift research program re-structuring that generates outputs efficiently and execution of which demonstrates optimum use of top-class professional and economic factors.

National wheat yields are 2.6 t/ha and annual productivity around 21.6 x 10^6 tons as of mid-2008; a decrease from the 23.5 x 10^6 tons in mid-2007. An increase in productivity is necessary in the coming years to keep pace with population increases and food necessities. Global figures show that from the current 6.3 billion people around 8.2 billion will inhabit the planet by 2025, requiring a substantial annual increase in order to cope with this elevated population need. In Pakistan the short-term goals set for yield increases are to reach 2.9 t/ha, thus increasing the total yield to 26.41 x 10^6 t by mid-2010. This necessitates a consistent per annum growth and is an uphill task that requires some astute pro-active measures across several wheat research and developmental scenarios. These measures will encompass a wide range of factors that would integrate several disciplines within Pakistan and across our country boundaries. The strengthening emphasis will stringently focus upon time bound multifaceted integrated activities where the pre-requisite factors to determine such goals will impinge upon policy setting, partitioning of basic, strategic, applied research scenarios and timely facilitating budgetary allocations. The area under wheat cultivation has progressively increased and may have reached its maximum of 8.29 million hectares as of the 2004–05 crop cycle. Increasing planted area and not enhance yield levels per unit area is not a valid production strategy. Thus, the need to adapt to this situation and other production aspects requires a vision that recognizes change and addresses it through integrative technologies harnessing selective national and international expertise. Furthermore, the pressures of set cropping systems and international pathogenic variations pose a grave threat to our national production levels of wheat. A concerted effort is crucial to combat these looming constraints and give varietal outputs that will provide national security around durable resistance levels that can only be realized if we have the genetic strength in place via gene and varietal deployment coupled with changed outlook for wheat research.

Ideally, strengthening the wheat program should not relate to financial inputs alone, but should translate into 'scientific' strengthening structured across quality scientific scenarios that require a completely different operational mode in order to bring quantum productivity increases that Pakistan urgently needs.

Production is a realization contribution that is essentially controlled by environment, genetics of the crop, plus management. All parameters have to be in unison to provide maximum impact. Over the years we have seen shifts in stress factors that control biotic and abiotic stresses, seen an emergence of new management technologies, emphasis directed towards diverse cropping systems, prevailing dominance of mono-culture of a few varieties, seed supply and extension avenues being addressed or remaining elusive, and more emphatically attention being placed upon budgetary constraints. Thus, many facets are known to govern a crops performance with all being vital for delivering the end output measured by t/ha and the resulting annual national yield levels. Some clear priorities can be set and, if these are the major biotic or abiotic stresses that limit wheat production, then around these stress constraints will be embodied several supporting multiple objectives crucial for the crops performance where key abiotic or biotic stresses will also warrant research attention. If the genetic resource is scarce to provide the relevant genes then one has to rely on internationally acquired materials that fit the category of conventional and novel resources obtained from all contributors of the wheat families relatives.

Our reliance has accordingly been heavy on international nurseries and these to date have played a crucial role in Pakistan agriculture. The trend will continue to flourish but we are now seeing the dawn of new methodologies where hard to obtain resources can be assembled and harnessed. The future ahead for deriving maximum benefit from all types of genetic materials, utilize all applicable technologies that cover the three domains of basic, strategic and applied activities is well apparent to research professionals but not fully operational in Pakistani wheat research endeavors. On the applied front, major limitations that surround wheat productivity are combating stress constraints that encompass drought, heat, salinity, all three rusts, increase in aphid populations, observations for powdery mildew, barley yellow dwarf virus, Karnal bunt, and grain quality for starters. Other constraints are prevalent but to a lesser degree (eg., *Bipolaris sorokiniana* being one) and require attention for which a comfortable situation would be to rigorously monitor progress and development of all stresses even to the extent that we need to be cognizant of the situation beyond our own national boundaries. The danger of stem rust around Ug99 plus its variants from Kenya via Iran. Despite the constraint, priority production can only occur and be sustainable if multiple stress factors are well targeted around gene pyramiding strategies. These strategies have their roots within the explanation that follows.

Two other phases of crop improvement programs revolve around basic and strategic research. These are the

home grounds of quality scientific innovations and accordingly are complex to manage for applied goal pursuits. Over the last two decades however, the backbone structure has been well explained and a superior comfort zone for achieving success on a projected time scale has become visible. These two areas will tap on unique genes from hard to combine wheat relatives, place them in their best location within our top cultivars, and provide adequate genetic structure diversity associated with durable resistance potent to offer a sustainable production system.

Interlinked with the above three phases of research/production activities will be new efficiency enhancing technologies with their focus to be set by the priority goals of a wheat improvement program. To make such techniques viable it is imperative that capable groups in excellent structural surroundings and compatible minds are combined for collaborating and giving osmotically superior outputs around synergism. The current focus would elucidate the DNA polymorphism status of our wheat germ plasm so we can better use such germ plasm for our practical benefits and will be the basis of cementing genetic diversity in our wheat cultivars.

A mere understanding of diversity will not resolve the situation. There is a dire need to put this knowledge into applied domains in order to unravel the contributions of each wheat genome as well as its constituting chromosomes, thus allowing for finer data generation based upon which genes could be tagged and molecular mapping conducted. Hence, if the focus is rust resistance our strategy should be to develop such wheat varieties with multiple resistances aided by all top class tools of fungal diagnostics and screening sophistication with the ultimate correlation to be made through structured mapping populations that would unravel the genetic elements that contribute to this biotic stress trait. Supplementary to such biotechnological links would also be the doubled haploid technology that not only can assist the molecular mapping area but can also significantly reduce the time for variety stabilization by several generations.

In order to further the objectives of the program breeding initiatives will digress from the current prevalent approaches within the country to focus actively on accessing diversity that has either been scarcely used or not utilized at all. These sources are as follows:

1. use the mammoth diversity of the accessions of each of the three progenitor genomes of wheat;
2. exploit the AB-genome tetraploids suca as *T. turgidum* subsps. *dicoccum*, *dicoccoides*, and *carthlicum* and the ABD diversity of *T. aestivum* subsp. *spelta*;
3. exploit the following germ plasm for yield enhancement:
   a) the multiple-ovary trait that sets three seed/floret,
   b) synthetics with high 1,000-kernel weight, i.e., 60–65 g versus the normal 40–44 g,
   c) the large-spike character present in Buitre-type T7DS·7DL-7AG wheats called super wheats,
   d) the heterotic vigor of F_1 derivatives from quality wheat/wheat cross combinations that structure a hybrid wheat program using the F_1-based, doubled-haploid strategy,
   e) wheat/alien chromosome translocations other than the famous T1BL·1RS, and
   f) target genes for addressing stress constraints mediated by molecular markers for breeding efficiency;
4. in addition to 'adaptation' breeding, develop a volatile recombinant-breeding program that uses the elite, older cultivars not in present day use due to some stress susceptibility, land races, and novel genetic diversity by a limited backcrossing approach coupled by F_3-based doubled haploidy input.

A modified structure was initiated by the Federal Ministry of Agriculture under the leadership role given to a former CIMMYT wide cross expert who started activities in Pakistan from the end of 2004 from allocation in NWFP, Peshawar. The location changed to Islamabad in mid-2005 and since then the process of wheat research has taken up around the focus mentioned above. The basic theme of activities is to establish a infra-structure, generate a integrated research team and embark on a research program targeted to provide practical outputs. The *modus operandi* has been to maintain strong alliances with CIMMYT, Mexico, harness national linkages, have a multidisciplinary research team at base in Islamabad, extend further international alliances and generate lucrative funding through national and international sources.

After four regular and a few summer crop cycles the status of the wide cross and conventional outputs are highlighted in the *Newsletter* for the global community of colleagues to be informed of our building and initial wheat improvement efforts in Pakistan.

Evaluation of wheat germ plasm for resistance against Karnal bunt in Pakistan.

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Karnal bunt or partial bunt of wheat, caused by *T. indica*, is a disease of concern globally and is also a serious quarantine issue. Thus, cultivar release requirements include resistance to Karnal bunt as mandatory in Pakistan. Strict quarantine measures have been adopted in several countries that affect not only wheat grain trade but also germ plasm exchange.

Because the pathogen is seed, soil, and air borne, limited control is achieved through the application of fungicides (Singh et al. 1985). Crop rotation, seed certification, and different fungicide treatments can be used to manage the disease. However, these methods may not eliminate the disease. The preferred method of control is by developing resistant cultivars through screening against *T. indica*. Breeding for Karnal bunt-resistant cultivars requires a reliable screening method that facilitates the selection of segregating plants. Screening is by creating artificial epiphytotic conditions at boot leaf stage.

The combination of resistance from *Ae. tauschii* with field resistance of durum through synthetic hexaploids wheats can exploit the combined resistance of A, B, and D genomes for wheat improvement. This involves identifying synthetic wheats with resistance to Karnal bunt and then incorporating these synthetics in the breeding effort. Synthetics can be successfully crossed with commercial wheat cultivars (Mujeeb-Kazi and Rajaram 2002).

Germ plasm of 1,500 entries comprising of conventional wheat cultivars, synthetics, and their advanced derivates from crosses with bread wheats were screened for resistance against Karnal bunt. Screening protocols were similar to those reported by Mujeeb-Kazi et al. 2006. Thirty-three percent of the germ plasm was free of Karnal bunt. The limited conventional bread wheat lines included were predominantly susceptible. The advanced test lines derived from conventional wheat cultivars crossed with resistant synthetic hexaploids possessed a high frequency of derivatives that were Karnal bunt free. Disease ratings were from 0% to 65.0% and this screening is being repeated in the current cycle of 2008-2009. The lines after the 2008 May harvest were planted in Kaghan over the summer cycle and analyzed for powdery mildew resistance and this year yellow rust evaluations also are being conducted along with the KB screening. The cumulative screening will allow selection of entries with multiple biotic stress resistances coupled with superior phenological attributes required for varietal outputs. Only those entries that have scores of less than 3.0% infection across all spikes tested per entry will be advanced as potential varietal candidates.

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Virulence pattern of leaf rust in Pakistan.

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The occurrence of rust diseases in cultivated cereals has significantly influenced the development of human civilization (Rolf et al. 1992). Wheat rusts have historically been one of the major biotic stress production constraints in Asia and globally (Singh and Rajaram 1991). Leaf rust is a serious wheat production hazard (Mclntosh et al. 1995) and the most destructive and devastating disease due to its time of appearance, nature of attack, regular occurrence, and prolonged growing season that is prevalent for its development in the wheat growing areas of the world (Khan et al. 1997). Leaf rust incurs significant yield losses (Khan et al. 1987; Hussain et al. 1980).

In order to determine the presence and virulence of leaf rust distribution in Pakistan, a trap nursery comprising of 39 isogenic lines and 10 commercial bread cultivars with different *Lr* genes were planted and evaluated at four locations over two consecutive years. Morocco was the susceptible spreader ion and around the test plots. The four locations across two provinces were Karachi and Nawabshah (in SINDH), Bahawalpur, and Faisalabad (in PUNJAB). The study objective was to identify the naturally prevailing leaf rust virulences.

Entries with leaf rust resistance genes *Lr9, Lr19*, and *Lr28* were resistant at all locations. Leaf rust resistance genes *Lr1, Lr2a, Lr2b Lr2c, Lr3,Lr3ka, Lr3bg, Lr10,Lr11, Lr12, Lr14a, Lr14b, Lr16, Lr18, Lr20,Lr23, Lr24, Lr25, Lr26, Lr10, 27+31, Lr29, Lr30, Lr32, Lr33, Lrb*, and *Lr23+* indicated presence of virulence at most of the locations. The genes *Lr13, Lr22a, Lr34*, and *Lr35* possessed virulence at Karachi and Nawabshah. Partial virulence was observed on genes *Lr36* and *Lr37* at three locations. A majority of the commercial cultivars in Sindh showed susceptibility against leaf rust

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New stem rust virulence detected in Pakistan: a potential threat to adopted bread wheat breeding strategy against Ug99.

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Historically stem rust of wheat incurred serious yield losses in Indo-Pak region. The disease had been controlled successfully since introduction of semidwarf stem rust resistant wheats during the Green Revolution of 1960s and 70s. Resistance in the majority of the wheat cultivars currently sown in the region is mainly based on gene *Sr31* that is present in 80% of the developing countries leading wheat cultivars. The evolution of the *pgt* race Ug99 to be capable of overcoming resistance imparted by *Sr31* in Uganda during 1999 created an alarming situation throughout the world (Pretorius 2000). Pakistani wheat cultivars tested under Kenyan field conditions were highly susceptible to Ug99 (Anonymous 1995). The new race is expected to follow the path of *Yr9* virulence that began in eastern Africa and spread to this part of the world (Singh et al. 2004). Efforts to identify and incorporate genes resistant to Ug99 have been intensified to develop and distribute resistant germ plasm through centralized breeding programs.

The evolution of the *Sr31*-virulent stem rust race Ug99 created an alarming global situation, because stem rust resistance in the world's leading wheat cultivars is based on *Sr31*. Among genes found resistant to Ug99, *Sr13, Sr22, Sr24, Sr26, Sr29, Sr35*, and *Sr36* were thought to have some immediate value. Detection of Ug99 strains (variants) virulent to *Sr24, Sr32, Sr33, Sr35*, and *Sr36* already have negated the potential use of these important genes. In 2006, stem rust infection in the commercial wheat cultivar Sarsabz in our Sindh province created a concern. The symptoms of stem rust prevalence in Sindh reoccurred in 2007 and again in 2008. During this time period across the national terrain, stem rust followed a rapid migration path and was reported from Iran. Thus, concern emerged whether or not it also had entered Pakistan.

Pathogen samples collected in 2008 from Sindh were analyzed on a stem rust differential set and specifically checked on the T1BL·1RS translocated wheat cultivars with *Sr31*. Presence of Ug99 was nullified based upon the symptoms seen on the test set, and the *Sr31*-based stock that remained disease free under Pakistan test conditions. Our concern, however, is that the local race affects some of the genes that are reported to be of value for resistance to Ug99. Hence, our choice of genes to be deployed in our breeding programs for imparting stem rust resistance to both the local plus Ug99 race and its variants are narrowed.

Single-pustule isolates were analyzed from stem rust diseased samples collected from Sindh (farmers' fields) of Juddo and Mirpurkhas. Urediospores from pustules inocula were multiplied on the susceptible cultivar Morocco as described by Knott (1989). Single-pustule inocula were tested on ten-day-old seedlings of the tester host set consisting of 40 NILs, including three sets of the North American stem rust differentials (Roelfs and Martens 2007). Morocco and the commercial cultivar Sarsabz were included as checks (Table 1). After inoculation, the plant trays were transferred to a growth room set at conditions mentioned earlier. After 24 hrs incubation, seedling trays were transferred to the glasshouse set at 18-20°C. Stem rust data for seedling infection types, described by Stakman et al. (1962), was recorded on the 10th day after inoculation or when pustules on susceptible cultivar Morocco were sporulating. The Pgt race was designated following the international system of nomenclature (Roelfs and Martens 2007).

All the isolates were designated race *TRT-Sr/13, Sr25, Sr33, Sr*37 on the basis of seedling reaction (Stakman et al. 1962) on the three North American sets of differentials (Roelfs and Martens 2007). The seedling reaction of all NILs tested remained high, except for those with genes *Sr8a, Sr22, Sr24, Sr26+Sr9g, Sr27, Sr31*, and *Sr32* (Table 1). Lines with genes *Sr39, Sr40, Sr43, Sr44*, and *SrTmp* were not available and, thus, were not included in the test.

Seedlings with genes *Sr5, Sr6, Sr7a, Sr7b, Sr8b, Sr9a, Sr9b, Sr9d, Sr9e, Sr9f, Sr9g, Sr11, Sr12, Sr13, Sr14, Sr15, Sr16, Sr17, Sr18, Sr19, Sr20, Sr21, Sr23, Sr25, Sr28, Sr29, Sr30, Sr33, Sr34, Sr35, Sr36, Sr37*, and *Srwld* all had high infection types and were considered ineffective to the local race.

Table 1. Response of stem rust differentials to race *TRT-Sr13, Sr25, Sr33,* and *Sr37* in Pakistan.

Isogenic lines	*Sr* gene	High / low response to isolates			
		2007	2008		
		Juddo	Juddo	Matli	Badin
ISR5RA	*Sr5*	H	H	H	H
T. monococcum derivative	*Sr21*	H	H	H	H
Vernsten	*Sr9e*	H	H	H	H
ISR7BRA	*Sr7b*	H	H	H	H
ISR11RA	*Sr11*	H	H	H	H
W2691SR6	*Sr6*	H	H	H	H
ISR8ARA	*Sr8a*	L	L	L	L
CNS(TC2B)/LINE E	*Sr9g*	H	H	H	H
W2691SRTT1	*Sr36*	H	H	H	H
W2691SR9B	*Sr9b*	H	H	H	H
BTSR30WST	*Sr30*	H	H	H	H
LC/Kenya Hunter	*Sr17*	H	H	H	H
ISR9ARA	*Sr9a*	H	H	H	H
ISR9DRA	*Sr9d*	H	H	H	H
W2691SR10	*Sr10*	H	H	H	H
LINE G	*Sr7a*	H	H	H	H
Barleta Benvenuto	*Sr8b*	H	H	H	H
ISR5SB	*Sr9f*	H	H	H	H
CH.SP.(TC3B)	*Sr12*	H	H	H	H
W2691SR13	*Sr13*	H	H	H	H
Line Aseln	*Sr14*	H	H	H	H
W2691SR15NK	*Sr15*	H	H	H	H
ISR16RA	*Sr16*	H	H	H	H
LCSR19MG	*Sr19*	H	H	H	H
LCSR20MG	*Sr20*	H	H	H	H
SWSR22T.B.	*Sr22*	L	L	L	L
EXCHANGE	*Sr23*	H	H	H	H
BT SR24 A9	*Sr24*	L	L	L	L
LC SR25 ARS	*Sr25*	H	H	H	H
EAGLE	*Sr26+Sr9g*	L	L	L	L
Coorong triticale	*Sr27*	L	L	L	L
W2691SR28KT	*Sr28*	H	H	H	H
PUSA/EDCH	*Sr29*	H	H	H	H
LINE E/KVZ	*Sr31*	L	L	L	L
C77.19	*Sr32*	L	L	L	L
Tetra-Canthatch/*Ae. tauschii* RL5045)	*Sr33*	H	H	H	H
COMPARE	*Sr34*	H	H	H	H
W3763	*Sr35*	H	H	H	H
W2691 SRTT2	*Sr37*	H	H	H	H
BT/WLD	*SrWLD*	H	H	H	H
LCSR18PL	*Sr18*	H	H	H	H
SARSABZ (Check)	*Sr* 23	H	H	H	H
MOROCCO (Check)		H	H	H	H

The local races were virulent to *Sr5, Sr6, Sr7b, Sr9a, Sr9b, Sr9d, Sr9e, Sr9f, Sr9g, Sr10, Sr11, Sr12, Sr15, Sr16, Sr17, Sr18, Sr19, Sr20, S21, Sr23, Sr30, Sr34,* and *Srwld*, which was similar to that of Ug99. However, unlike Ug99, the local race is avirulent to *Sr8a* and *Sr31* and virulent to *Sr7a, Sr13, Sr14, Sr25, Sr28, Sr29, Sr33, Sr35, Sr36,* and *Sr37*. Stem rust resistance genes *Sr13, Sr14* from *T. turgidum*; *Sr28, Sr29* from *T. aestivum*; *Sr33* from *Ae. tauschii*, *Sr36, Sr37* from *T. turgidum* subsp. *timopheevii*, and *Sr35* from *T. monococum* were of special interest to breeders after the evolution of Ug99 (Singh et al., 2006). The capability of race TRT to infect these genes negates their usage and further limits the availability of stem rust resistance genes resistant to stem rust races TTKS and TRT.

Our strategy for addressing the imminent entering of Ug99 in Pakistan will be as follows.

a) Exploit the EBWYT trials that are distributed by CIMMYT, select the best performers, and deploy them in regions of concern. Accordingly, the three best performing lines have been acquired from CIMMYT based upon 2EBWYT yield performance data and these have been targeted for deployment to farmers' fields after rapid increase assistance from private growers.

b) Add the eight best performing lines across the Pakistani provinces where the 3EBWYT was tested and include another two lines that performed well in India. All 10 entries were increased in Kaghan in the summer of 2008 and are being further increased during the 2008–09 cycle after which they shall be deployed to progressive farmers in selected provinces focusing on lower Punjab and Sindh.

c) Utilize a volatile recombination breeding effort with the leading Pakistani high-yielding cultivars in crosses with the Elite II and 3EBWYT entries. In addition, the SRSN nursery obtained from CIMMYT has several desirable entries that possess derivatives from D-genome synthetic hexaploid wheats and tertiary gene pool genetic resources (e.g., *L. racemosus* and *Th. curvifolium*) that are also being exploited as donor sources in our recombination breeding efforts.

d) Focus on additional crosses utilizes the genes of interest that have value for Ug99 resistance and are avirulent to the local stem rust race. In addition, a major effort is in place to screen all available wheat genomic genetic stocks and their free-threshing advanced derivatives that are of superior agronomic types. The bulk of this diversity is D-genome based. The screening is done locally, and a limited set also is targeted for screening in Kenya.

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Screening of mapping population against powdery mildew under field and glass house conditions in Pakistan.

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Powdery mildew of wheat is becoming an important disease of wheat in Pakistan. The disease is mostly prevalent in cooler places where temperature ranges are between 15–22ºC with humidity up to 75% (Khan 2006). Due to the obligate parasitic and airborne nature of the organism it is very difficult to combat the disease. The best economical and the most effective mean to control the disease is to screen and identify genetic resistance. In Pakistan, data are scarce regarding this disease but its presence, however, has been observed to be on the rise and consequently artificial and natural screening in a hot spot will aid in identifying resistance thus promoting germ plasm security efforts.

Three DH-based combinations (Filin/Kariega comprising of 47 entries, Filin/Saar of 24 entries, and Kariega/Saar of 81 entries) were screened for seedling resistance under glass house conditions in Murree (artificial inoculation with a bulk collection from a rice-wheat field area in the Punjab province of Pakistan). The same materials also were screened for adult-plant resistance under field conditions in a natural hot spot at Kaghan. Both studies were conducted in the summer of 2008 during late May and mid-October.

Table 2. Disease reaction of the diverse germ plasm against powdery mildew seedling and adult-plant screening (S = susceptible, MS = moderately susceptible, MR = moderately resistant, and R = resistant).

Group	No. of Entries	Disease reaction							
		Field				Glass house			
		S	MS	MR	R	S	MS	MR	R
Filin / Kariega	47	2	6	4	35	17	24	3	3
Filin / Saar	24	0	0	0	24	3	19	2	0
Kariega / Saar	81	0	3	5	73	21	51	5	4

Under glass house conditions in the Murree research station of CDRP, a majority of the entries of all the three populations exhibited a susceptible to moderately susceptible reaction at the seedling stage. In contrast, under the adult-plant field screening majority of the same entries exhibited a resistant reaction (Table 2). Plant symptoms were recorded on the infection type scale starting from 0 to 9, where 0 is no visible fungal growth and 9 is abundant growth and sporulation (Hiura 1978). Double-digit scoring was utilized.

The above results are indicative of action of more than one gene in the respective entries where varied degrees of susceptibilities are observed at the seedling stage and resistance is present at the adult plant stage. These results are consistent with those of Khan (2006) who screened wheat plants of 'Poros-monos/M30' both at seedling and adult plant stage against powdery mildew. Such entries are desirable materials from which potential minor gene effects can be incorporated into breeding materials in order to achieve durable resistance.

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In-vitro screening of synthetic hexaploid wheat lines against Cochliobolus sativus in Pakistan.

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C*ochliobolus sativus* leaf blight is a world-wide, economically important foliar disease of wheat. Leaf blight or spot blotch mainly occurs in warm, humid wheat growing areas. In Pakistan, spot blotch has been observed in different agro-ecological wheat production zones especially where winter temperatures are warmer. Spot blotch was identified as a predominant pathogen of leaf spotting in the national wheat growing areas during 2003–06. Out of 87 isolates collected from different agro-ecological zones of wheat production, the most aggressive isolate P2-9 was used to screen the synthetic hexaploids wheat subsets Elite I and Elite II plus their durum female parents under in vitro conditions. None of the Elite I gave

Table 3. Screening of synthetic hexaploids (CIMMYT Elite II) against *Cochliobolus sativus* in 2005 and 2006 (scale: 0 = resistant, 1–2 = moderately resistant, 3–4 = moderately susceptible, and 5 = susceptible).

Entry #	Genotype	2005	2006
3	DVERD_2 / *Ae. tauschii* 214)	3	3
4	ARLIN_1 / *Ae. tauschii* (218)	2	2
9	STYUS / CELTA // PALS. /3/ SRM_5 /4/ *Ae. tauschii* (431)	3	3
10	LCK59.61 / *Ae. tauschii* (693)\	2	2
11	CETA / *Ae. tauschii* (1025)\	2	2
16	CPI / GEDIZ /3/ GOO / JO / CRA /4/ *Ae. tauschii* (1018)	2	2
18	CETA / *Ae. tauschii* (1038)	2	2
22	CETA / *Ae. tauschii* (368)	2	2
26	GAN / *Ae. tauschii* (206)	2	2
27	ARLIN_1 / *Ae. tauschii* (335)	2	2
28	GAN / *Ae. squar tauschii rosa* (335)	2	2

any indication of resistance. Nine Elite II entries (Table 3, p. 156) and three durum wheats were found to be moderately resistant across 2 years of *in vitro* studies. Additionally, 16 synthetic hexaploids of the Elite II subset and 12 durum wheats (Table 4) were moderately resistant and moderately susceptible, respectively, over the 2-year test. These entries classified as moderate may further be exploited in wheat-breeding programs to enhance allelic diversity across the three wheat genomes via the A and B genomes of durum wheats and the D genome of the synthetic entries. Where durum wheat shows desirable ratings and a synthetic is not identified in the same category, that entry also could be a candidate for breeding via the pentaploid route of recombination breeding.

Table 4. Screening of durum wheat parents against *Cochliobolus sativus* in 2005 and 2006 (scale: 0 = resistant, 1–2 = moderately resistant, 3–4 = moderately susceptible, and 5 = susceptible).

Entry #	Genotype	2005	2006
6	LARU	3	3
11	CPI / GEDIZ /3/ GOO // J0 / CRA	2	3
18	SNIPE / YAV79 / DACK / TEAL	3	3
19	TKSN1081	2	3
20	YAV-2 / TEZ	1	3
25	ARAOS	2	2
26	GAN	3	3
28	STY-US / CELTA // PALS /3/ SRN-5	2	2
29	AGAMI	3	3
30	YAV-3 / SCOT // J069 / CRA /3/ YAV79	3	2
43	FALCIN-1	2	2
46	KAPUDE-1	3	3

The in vitro screening methodology. The inoculum of single spore culture of the most aggressive isolate (P2-9) was multiplied on potato dextrose agar and was selected after aggressiveness analysis of 87 isolates, collected from different agro-ecological, wheat-production zones. Test tubes (20 cm x 3 cm) were filled a quarter from the bottom with cotton and distilled water (20 mL) was added in each tube. The prepared tubes were covered with aluminum foil, autoclaved, and were ready for experimental usage.

Screening. The test synthetic hexaploid wheat germ plasm with the durum parent cultivars is maintained as a working collection in the Wheat Wide Crossing program at NARC, Islamabad. This resource was produced in CIMMYT by their Wheat Wide Crosses program (Mujeeb-Kazi 2003). The materials were screened against the most aggressive isolate (P2-9) of *C. sativus*. The hexaploids wheat cultivar Wafaq was the check. Three seeds/tube were surface disinfected with a 1% Clorox solution for 1 min and placed on the moist cotton swab within each test tube. One 5-mm disc of the fungal isolate was placed adjacent to the seeds with the help of a cork borer. The tubes were placed in randomized manner in steel racks. After inoculation, tubes were recovered with aluminum foil and placed in the growth chamber at 25^0C for incubation. Data was recorded upon the appearance of spots on leaves on a 0–5 scale where 0 = no spotting symptoms, 1 = 1–5% spots, 2 = 6–20% spots, 3 = 21–40% spots, 4 = 41–60%, and 5 = more than 60% (IRRI 1996). The above scale is considered as 0 = resistant, 1–2 = moderately resistant, 3–4 = moderately susceptible and 5 = susceptible.

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Current scenario of yellow rust of wheat in Pakistan.

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Wheat in Pakistan is the main staple food and covers 8.2 x 10^6 ha. Of the many diseases that attack the wheat crop, rusts are by far the most important and have continued to ravage this crop since ancient times. The rust of wheat has historically been one of the major biotic production constraints both in Asia and rest of the world (Singh and Rajaram 1991). Yellow rust is one of the most important disease of the wheat in world (Roelfs et al. 1992). The annual yield losses due to wheat yellow rust have been estimated up to 8–75% (Elahinia 2000). Severe epidemics of the disease may result

in losses of up to 70% in commercial fields (McIntosh et al. 1995). Severe epidemics of the disease have reported in central and west Asia (Braun and Saari 1992; Torabi et al. 1995). Ahmad et al. (1991) reported an estimated US$ 8 x 10^6 revenue loss just in three districts of Baluchistan in Pakistan. Our objective was to identify the prevailing virulences of yellow rust in nature by planting yellow rust trap nurseries at different hot spots of the country. The principal and practical purpose for studying the rust population is to identify the effective genes.

The trap nursery specially designed for yellow rust comprised of 24 wheat isogenic lines and commercial cultivars were planted at four locations; Faisalabad, Peshawar, Nowshera, and Islamabad. This nursery was evaluated for 3 years. The locations represented different agro-ecological zones and hot spots where the conditions were mostly favorable for yellow rust development. Each entry was planted in single meter rows 30 cm apart. Two rows of rust susceptible spreaders (Morocco) were planted around the nursery. The observations were recorded on natural occurrence and first appearance of rust infection on susceptible check. The observation at all the locations on response of leaf rust was recorded according to the modified Cobb's Scale (Peterson et al. 1948).

Our results revealed that virulence factors for *Yr2, Yr6, Yr7, Yr9, Yr17, Yr27, Yr28*, Avocet *Yr-A*, Avocet+*YrA*, and Jupateco-S were present at all test locations. Similarly, *Yr1*, *Yr8, Yr18, Yr29*, and Jupateco-R had virulence at all the locations except Faisalabad. Yellow rust resistance genes *Yr24*, *Yr26*, and *YrCV* showed partial virulence. No virulence was observed on the yellow rust resistance genes *Yr5, Yr10, Yr15*, and *YrSP*. Tatara was the only cultivar that was found resistant during the study period. Tatara is widely grown in the northern area of the country and showed resistance most probably due to *Yr3* resistant gene against all the prevailing races of the yellow rust.

Yr6, Yr7, and *Yr9* are the most dominant genes that are postulated in our commercial cultivars, which suggests that the virulence for these genes are prevailing in the country as most of the wheat cultivars possessing these genes are continuously cultivated regularly in the most part of the country.

Following the initiation of use of genetic resources in wheat improvement, our integrated group has embarked on a strategy that will diversify the genetic composition of our varietal production efforts by utilizing conventional minor genes for durable resistance, focusing on targeted gene transfers that will promote gene and cultivar deployment aspects across the nations provinces creating internal barriers as an obstacle to rapid disease spread, incorporate intervention on use of molecular markers for adding to breeding efficiency, and capitalize on the vast novel genetic stocks that are available through our wide cross program that encompasses the genetic richness of each of the wheats three genomes and also taps on the allelic values of selected genomes from genera belonging to the secondary and tertiary gene pools.

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Evaluation of the Elite II synthetic hexaploid wheats to barley yellow dwarf virus and their molecular diversity.

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Wheat, one of the most important cereals in the world, has its production affected by various biotic and abiotic stresses. Of these stresses, barley yellow dwarf virus is an important and widespread viral disease. This disease can cause yield losses up to 75% in severe cases. Diverse genetic resistance sources provide a potent means that offer environmentally safe control measures. The resistant sources can be harnessed from about 325 perennial and annual species that are distributed within three gene pools of the tribe Triticeae. Currently, *Ae. tauschii,* which possesses diversity for BYDV is the prime source. This diploid, D-genome donor after crossing with elite durum wheat cultivars has generated a unique source of user-friendly germ plasm for wheat improvement. This process has produced over 1,000 synthetic hexaploid wheats, and an Elite II subset based upon multiple stress resistance/tolerance was established. In this study, the Elite II subset was screened against BYDV *in vitro* and *in vivo*, using DAC-ELISA (Table 5 and Table 6, p. 160). *In vitro* screening results showed that out of 33 genotypes, seven (3, 4, 5, 6, 14, 19, and 33) were resistant, and three (22, 28, and 31) tolerant. *In vivo* screening results showed that out of 33 genotypes, 19 (3, 4, 5, 9, 13, 14, 17, 18, 20, 22, 23, 25, 26, 27, 28, 29, 31, 32, and 33) were tolerant. From the cumulative *in vitro* and *in vivo* testing, 15 genotypes were stringently selected for assessing their diversity levels.

Table 5. Number of Elite II genotypes with barley yellow dwarf virus symptoms and positive to ELISA.

No.	Symptoms +ve	% plants showing symtoms	ELISA +ve	% Plants infected
1	—	—	—	—
2	4/5	80	0/5	0
3	0/5	0	4/5	80
4	0/5	0	4/5	80
5	0/5	0	0/5	0
6	5/5	100	5/5	100
7	3/5	60	4/5	80
8	4/5	80	5/5	100
9	0/5	0	5/5	100
10	4/5	80	5/5	100
11	2/5	40	5/5	100
12	3/5	60	5/5	100
13	0/5	0	5/5	100
14	0/5	0	5/5	100
15	1/5	20	5/5	100
16	3/5	60	5/5	100
17	0/5	0	5/5	100
18	0/5	0	5/5	100
19	2/5	40	5/5	100
20	0/5	0	4/5	80
21	2/5	40	5/5	100
22	0/5	0	5/5	100
23	2/5	40	5/5	100
24	—	—	—	—
25	0/5	0	5/5	100
26	0/5	0	5/5	100
27	0/5	0	5/5	100
28	0/5	0	5/5	100
29	0/5	0	4/5	80
30	2/5	40	5/5	100
31	0/5	0	5/5	100
32	0/5	0	5/5	100
33	0/5	0	5/5	100

Ten, decamer RAPD primers (OPG-1, OPG-2, OPG-3, OPG-4, OPG-5, OPA-3, OPA-4, OPA-5, OPA-8, and OPA-15) evaluated the diversity profile of the selected 15 SH entries. Out of these ten primers, five primers (OPG-2, OPG-3, OPG-5, OPA-4, and OPA-15) showed amplification with these genotypes, whereas another five did not amplify any genotype. Out of the positive five, OPG-2 amplified seven genotypes out of 15. All 15 genotypes were monomorphic for the 1,000-bp band. The primer OPA-4 amplified six genotypes out of 15. Genotypes 26, 28, and 29 were monomorphic for the 750-bp band. Genotype 22 was monomorphic for the band between 1,000 and 1,500 bp, whereas genotype 6 was polymorphic for the 750- and 1,500-bp bands. Genotype 18 was polymorphic for bands at 750 bp and between 1,000 and 1,500 bp. OPG-5 amplified four out of 15 genotypes, all of them monomorphic for the 750-bp band. OPA-15 amplified three out of 15 genotypes, whereas OPG-3 amplified only one genotype out of 15.

The most genetically similar lines were 1, 20, and 30. The value of similarity matrix ranged from 54–100% in which minimum similarity was manifested by genotypes 9 and 13; maximum similarity of 100% was shown between genotypes 1 and 20, 1 and 30, and 20 and 30. The dendrogram divided the genotypes into two major clusters without genotype 17, which remained independent of both clusters. Cluster A comprised of 11 (1, 20, 30, 6, 26, 28, 9, 29, 21, 22, and 7) and cluster B of three genotypes (13, 18, and 23).

We recommend that the allelic variation of the SH resistance germ plasm is a potent mean to enrich and improve bread wheat cultivars where BYDV is a production threat. Phenological data (Table 7, p. 160-161) provides an additional descriptor resource and sieve for targeting the best BYDV-tolerant synthetics for use in wheat breeding. An

Table 6. ELISA values and *in vitro* and *in vivo* scoring (0–9 scale; R = resistant, S = susceptible, and SLC = symptom-less carrier) for barley yellow dearf virus in Elite II lines.

No.	*In vitro*			*In vivo*		
	Symptoms	ELISA	Comment	Symptoms	ELISA	Comment
1	0.50/2	2.393/2	S	—	—	—
2	2.00/2	2.812/2	S	0.80/5	0.6848/5	S
3	0.00/1	0.568/1	R	0.00/5	0.794/5	SLC/T
4	0.50/2	0.608/2	R	0.00/5	0.8036/5	SLC/T
5	1.00/2	0.547/2	R	0.00/5	0.6608/5	SLC/T
6	0.00/2	0.576/2	R	1.60/5	1.0514/5	HS
7	0.50/2	2.417/2	S	0.80/5	1.0414/5	HS
8	3.00/3	2.521/3	S	1.80/5	1.0044/5	S
9	0.50/3	2.684/3	S	0.00/5	0.8204/5	SLC/T
10	0.66/3	2.527/3	S	0.80/5	1.0394/5	S
11	2.00/1	1.803/1	S	2.40/5	0.914/5	S
12	1.00/5	2.649/5	S	0.60/5	0.9992/5	HS
13	0.25/4	2.628/4	S	0.00/5	0.8686/5	SLC/T
14	0.00/2	0.919/2	R	0.00/5	0.9028/5	SLC/T
15	1.25/4	2.012/4	S	0.20/5	0.9226/5	HS
16	1.00/2	2.638/2	S	1.20/5	1.114/5	HS
17	0.33/3	2.515/3	S	0.00/5	0.9626/5	SLC/T
18	0.25/4	2.185/4	S	0.00/5	1.1218/5	SLC/T
19	1.00/4	0.572/4	R	0.80/5	0.8528/5	S
20	0.50/2	2.168/2	S	0.00/5	0.8900/5	SLC/T
21	0.50/2	2.112/2	S	0.60/5	0.8508/5	S
22	0.00/2	2.806/2	SLC/T	0.00/5	0.791/5	SLC/T
23	0.50/2	2.10/2	S	0.00/5	0.7802/5	SLC/T
24	1.00/1	1.802/1	S	—	—	—
25	1.00/2	1.497/2	S	0.00/5	0.8078/5	SLC/T
26	0.50/4	2.542/4	S	0.00/5	0.8698/5	SLC/T
27	1.00/2	1.60/2	S	0.00/5	0.8836/5	SLC/T
28	0.00/3	1.321/3	SLC/T	0.00/5	0.9688/5	SLC/T
29	0.50/2	2.289/2	S	0.00/5	0.8524/5	SLC/T
30	0.50/2	2.72/2	S	0.00/5	0.9372/5	S
31	0.00/3	2.177/3	SLC/T	0.00/5	0.9690/5	SLC/T
32	1.00/2	1.889/2	S	0.00/5	1.0198/5	SLC/T
33	0.00/1	0.811/1	R	0.00/5	0.8872/5	SLC/T

additional stringent round seasonal screening is mandatory prior to embarking on an applied program of genetic recombination and having elite germ plasm included that possesses *bdv1* and *bdv2* genes around germ plasm such as Anza, TC14, Kivu, and *Agrotricum*.

Table 7. Some phenological parameters of Elite II synthetic hexaploid entries (PIG = tiller pigmentation; PUB = Pubescence; FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (B = brown, LB = light brown, DB = dark brown, and W = whitish); PMA = days to physiological maturity; and TKW = 1,000-kernel weight (g))

Pedigree	PIG	PUB	FLOW	HT	AWN	PMA	TKW
SORA/*Ae. tauschii*(192)	—	—	—	—	—	—	—
CROC-1/*Ae. tauschii* (210)	+	—	117	115	B	152	30
DVERD2/*Ae. tauschii* (214)	—	—	128	120	LB	152	33
DVERD2/*Ae. tauschii* (218)	—	—	117	100	DB	145	33
TKSN1081/*Ae. tauschii* (222)	+	+	128	100	W	148	36
CAN/*Ae. tauschii* (236)	—	+	133	95	W	152	31
SORA/*Ae. tauschii* (323)	+	—	128	100	DB	145	33
D67.2/P66.270//*Ae. tauschii* (308)	+	—	117	60	LB	152	12
STY-US/CELTA//PALS/3/SRN5/4/*Ae. tauschii* (431)	+	—	126	90	LB	152	37
LCK59.61/*Ae. tauschii* (693)	+	—	117	115	LB	152	32
SKARV2/*Ae. tauschii* (304)	+	+	133	65	B	152	30
CETA/*Ae. tauschii* (1025)	+	+	112	95	LB	148	40
DOY-1/*Ae. tauschii* (1027)	+	—	133	100	LB	148	36

Table 7. Some phenological parameters of Elite II synthetic hexaploid entries (PIG = tiller pigmentation; PUB = Pubescence; FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (B = brown, LB = light brown, DB = dark brown, and W = whitish); PMA = days to physiological maturity; and TKW = 1,000-kernel weight (g))

Pedigree	PIG	PUB	FLOW	HT	AWN	PMA	TKW
CETA/*Ae. tauschii* (386)	+	+	133	90	LB	149	34
CETA/*Ae. tauschii* (392)	+	+	133	80	LB	149	27
CETA/*Ae. tauschii* (533)	—	—	112	85	LB	152	25
CPI/GEDIZ/3/GOO//JO/CRA/4/*Ae. tauschii* (1018)	+	—	133	110	B	152	46
CETA/*Ae. tauschii* (1031)	+	—	143	100	LB	145	44
CETA/*Ae. tauschii* (1038)	+	—	117	115	DB	145	35
CETA/*Ae. tauschii* (1046)	+	—	122	100	DB	145	38
CETA/*Ae. tauschii* (1053)	+	+	112	85	B	151	36
CROC-1/*Ae. tauschii* (212)	+	+	133	90	LB	148	36
CETA/*Ae. tauschii* (368)	+	+	117	95	LB	145	32
ARLIN-1/*Ae. tauschii* (430)	—	—	—	—	—	—	—
D67.2/P66.270//*Ae. tauschii* (497)	+	+	122	100	DB	145	32
D67.2/P66.270//*Ae. tauschii* (1015)	+	+	117	85	B	152	34
GAN/*Ae. tauschii* (206)	+	—	117	100	DB	139	33
ARLIN-1/*Ae. tauschii* (335)	+	—	126	100	DB	152	35
GAN/*Ae. tauschii* (335)	+	—	117	95	DB	145	33
68.111/RGB-U//WARD RESEL/3/STIL/4/*Ae. tauschii* (385)	+	—	133	100	DB	149	38
CETA/*Ae. tauschii i*(417)	+	+	133	105	B	152	34
68.111/RGB—U//WARD RESEL/3/STIL/4/*Ae. tauschii* (431)	+	—	117	100	DB	145	35
DOY1/*Ae. tauschii* (534)	+	—	133	100	LB	152	47

Molecular and phenological identification of diversity in some durum resources.

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Triticum turgidum is a unique tetraploid that has the potency to contribute allelic genetic diversity from its A and B genomes for both durum and bread wheat improvement and has been significantly used in the production of synthetic hexaploid wheats (*T. turgidum*/*Ae. tauschii*, 2n = 6x = 42; AABBDD). These synthetics have been a rich source of genetic diversity with a high potential for global wheat improvement that is associated with the D genome of *Ae. tauschii*. When SH wheats are used in breeding, the diversity of D-genome is exploited. However, the durum A and B genomes also play a significant role since they form a variation pool of allelic richness that in earlier decades was exploited via pentaploid breeding (*T. aestivum*/*T. turgidum*).

In the SH wheat production at CIMMYT, 51 durum wheat genotypes have been used and over 1,000 synthetics produced. The parameters analyzed in this study involving the 51 durums were related to phenological traits and molecular diversity as differentiated by RAPD and SSR primers.

According to phenological data, D-1, D-7, D-14, D-25, D-28, and D-48 performed very well in the field specially with reference to their yield-enhancing characters. Cluster analysis of RAPD primers revealed maximum genetic diversity in D-47 followed by D-12, D-26, and D-10, whereas SSR analysis showed D-24, D-25, D-33, and D-36 as the most genetically diverse lines.

Out of 22 RAPD primers used (OPA10, OPC7, OPE1, OPE2, OPE3, OPE4, OPE5, OPE6, OPE7, OPE8, OPE9, OPE13, OPH15, OPH16, OPL1, OPL8, OPL9, OPL10, OPL11, OPN19, OPN20, and OPS17), 12 primers showed clear and polymorphic amplification patterns in terms of band numbers. The total number of loci traced by these primers were 129, 75 of which were polymorphic according to population genetic analysis. The percentage of polymorphism among these genotypes was 58.13%, and the size of amplification ranged from 250 to 10,000 bp. The highest number of scorable bands was obtained with primer OPE1 and the lowest was with OPA10. Maximum genotypes (16) were amplified by primer OPE3 and minimum (1) by OPE4 and OPL1. RAPD primers OPE1 and OPE3 showed the highest polymorphism

and primer OPL8 the lowest. Genotype D-12 was amplified by maximum number of primers (7), whereas genotypes D-3 and D-13 were not amplified by any primer. Genotypes D-47 and D-12 showed maximum polymorphism. The efficiency of these primers to amplify the genotypes ranged from 16 genotypes by primer OPE13, 12 genotypes by OPE1 to eight genotypes by OPN19.

The value of the similarity coefficient of selected durum wheat lines ranged from 0.6133 (61.33%) to 0.100 (100%). Minimum similarity of 61.33% was shown by D-1 with D-26. The genotypes, which showed a value of maximum similarity of 100%, are D-22 with D-23 and D-34 with D-35 and D-44. The similarity of the remaining genotypes was between 83.89 to 100%. The dendrogram was divided into three main clusters. Cluster A included two genotypes D-1 and D-3 with a genetic distance of 0.1278 (12.78%). Cluster B was further divided into three subclusters. Subcluster B1 included a total of eight genotypes; D-2, D-6, D-11, D-22, D-23, D-24, D-13, and D-14. The genotypes D-22 and D-23 were genetically identical. D-2 showed a genetic distance of 0.2744 (27.44%). The genetic distance of the remaining genotypes of this subcluster ranged between 0 and 27%. Subcluster B2 included a total of 18 genotypes (D-29, D-48, D-34, D-35, D-44, D-37, D-43, D-45, D-38, D-41, D-49, D-50, D-51, D-32, D-36, D-42, D-25, and D-19) with a minimum genetic distance of 0 between D-34, D-35, and D-44. D-19 showed the maximum genetic distance of 0.3285 (32.85%). The genetic distance of the remaining genotypes ranged between 0 to 32.85%. Subcluster B3 included 13 genotypes (D-46, D-17, D-28, D-33, D-31, D-9, D-39, D-4, D-20, D-27, D-30, D-40, and D-47). The minimum genetic distance of 0.1128 (11.28%) was present between D-28 and D-38, and the maximum genetic distance of 0.4673 (46.73%) was exhibited by D-47. Cluster C included ten genotypes (D-5, D-7, D-8, D-15, D-16, D-18, D-10, D-12, D-21, and D-26. In this cluster, the minimum genetic distance of 0.0548 (5.48%) was present between D-5 and D-7 and the maximum genetic distance of 0.4257 (42.57%) was shown by D-12. The genetic distance of the rest of the genotypes in this cluster ranged between 5.48 to 42.57%.

A RAPD-based, cluster analysis of dendrogram depicted that subcluster B3 has the maximum diverse lines followed by cluster C. Genotype D-47 of subcluster B3 is the most diverse line among 51 selected durum wheat lines with genetic distance of 46.73%. D-12, D-21, D-26, and D-10 of cluster C also are considered as genetically diverse lines with genetic distances of 42.57, 40.0, 40.0, and 36.62% respectively. A total of 12 SSR primers (GWM47, GWM55.1, GWM120, GWM191, GWM333, GWM382, GWM388, GWM410, GWM493, GWM501, GWM526, and GWM674) were used to analyze the genetic diversity of 51 durum wheat genotypes. All 12 showed clear and polymorphic patterns. Population genetic analysis showed a total of 125 loci out of which 75 were polymorphic. The percentage of polymorphism is 60%. The size of amplification products ranged from 50 to 800 bp.

The highest number of scorable bands were obtained with primer GWM55.1 and the lowest number of bands were obtained with primer gwm410. The maximum number of genotypes (47) were amplified by primer gwm493 and the minimum (4) by GWM388. Primer gwm55.1 showed the highest polymorphism and primer gwm191 the lowest. Genotype D-30 was amplified by maximum number of primers (12), whereas genotype D-19 was amplified by only two primers. Genotype D-24 and D-25 showed maximum polymorphism. The value of similarity coefficient of selected durum wheat lines ranged from 0.5467 (54.67%) to 0.9867 (98.67%). Minimum similarity of 54.67% was shown by D-5 with D-33, whereas genotypes showing maximum similarity of 98.67% were D-19 with D-23.

The dendrogram of SSR-based, genetic diversity evaluation clearly indicated five main clusters A, B, C, D, and E. Cluster A included four genotypes D-1, D-9, D-10, and D-11. Among these genotypes, D-10 and D-11 were genetically less diverse showing a genetic distance of 0.1431 (14.31%) with the remaining genotypes, whereas genotypes D-1 and D-9 showed maximum genetic diversity of 0.1744 (17.44%). Cluster B included a total of 11 genotypes; D-7, D-19, D-23, D-27, D-37, D-51, D-28, D-36, D-45, D-39, and D-26. Among these genotypes, D-19 and D-23 showed the minimum genetic distance of 0.0134 (1.34%) with rest of the genotypes. D-26 showed the maximum genetic distance of 0.4673 (46.73%). The genetic distance of the remaining genotypes of this cluster remained between 0 to 46.73%. Cluster C included a total of 12 genotypes; D-12, D-20, D-49, D-50, D-18, D-35, D-29, D-47, D-48, D-43, D-44, and D-46. In this cluster, D-43 and D-44 were genetically similar with genetic distance of 0.098 (9.98%) with the rest of the genotypes. The maximum genetic distance of 0.4252 (42.52%) was shown between D-18 and D-35. The genetic distance of the remaining genotypes of this cluster fell in the range of 9.98% to 42.52%. Cluster D included total twelve genotypes; D-38, D-34, D-42, D-41, D-30, D-40, D-8, D-13, D-21, D-22, D-16, and D-17. A minimum genetic distance of 0.0270 (2.70%) was shown by D-16 and D-17, whereas D-38 showed maximum genetic distance of 0.4888 (48.88%). The genetic distance of remaining genotypes of this cluster stayed between 2.70 and 48.8%. Cluster E includes 12 genotypes; D-25, D-24, D-31, D-32, D-33, D-2, D-3, D-4, D-5, D-6, D-14, and D-15. Genotypes D-2 and D-3 showed a minimum genetic distance of 0.0408 (4.08%). The maximum genetic distance of 0.5333 (53.33%) was shown by D-24

followed by D-25 with genetic distance of 0.5108 (51.08%). The genetic distance of remaining genotypes of this cluster was between 4.08 and 53.33%.

An SSR-based cluster analysis of dendrogram depicted the same level of genetic diversity in cluster A and cluster C, whereas the minimum genetic diversity was shown by the genotypes of cluster B. Genotypes of cluster E showed the maximum genetic diversity in comparison to all the clusters of the dendrogram. Genotype D-24 of cluster E is the most diverse line among the 51 durum wheat lines with a maximum genetic distance of 53.33. D-25, D-33, and D-38 also are considered as genetically diverse lines.

The percentage of polymorphism among durum wheat lines in RAPD and SSR is 58.6 and 60, respectively, indicating the genetic diversity of durum wheat lines. RAPD primers showed an average of six polymorphic loci per primer amplified, whereas SSR primers showed an average of 6.25. The percentage of these polymorphic loci per primer is 8 and 8.33 % for RAPD and SSR primers, respectively.

RAPD and SSR analysis demonstrated that these durum genotypes can be recommended for targeted use of synthetic wheats with the selected durums and also can be good candidates for direct hybridization with national breadwheat cultivars forming the pentaploid breeding strategy to capture good genes from A and B genomes of these durum wheat lines. Rare has been the use of durums for breadwheat improvement, but the cultivar AS-2002 has a tetraploid parent in its pedigree. Although SHs in breeding bring in the durum genomic component, direct utilization also may be looked at that could encompass other tetraploids such as *T. turgidum* subsps. *dicoccum*, *dicoccoides*, and *carthlicum*. From the phenological descriptors of the 51 durum cultivars (Table 8, p. 163-164), selective usage of a few can be made, e.g., the

Table 8. Some phenological descriptors of the 51 durum cultivars used in D-genome-based synthetic hexaploid production. PUB = pubescence; FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (B = brown, DB = dark brown, LB = light brown, and W = whitish); PMA = days-to-physiological maturity; and TKW = 1,000-kernel weight (g).

No.	Pedigree	PUB	FLOW	HT	AWN	PMA	TKW	Nodes /spike	Grains /spike	Spike length (cm)
1	Croc-1	—	87	86	LB	101	45.0	8	45	9
2	Arlin-1	—	86	86	LB	105	18.5	10	16	9
3	Rok/Kml	—	81	105	LB	95	45.0	9	42	9
4	Altar84	—	89	78	LB	108	33.0	8	26	6
5	Dverd_2	—	87	76	LB	112	37.6	7	18	6
6	Laru	—	95	80	LB	110	34.4	8	35	8
7	68.111/RGB-U//Ward Resel/3/Stil	—	92	97	LB	108	51.4	9	46	10
8	68.111/RGB-U//Ward	—	95	103	LB	108	32.2	11	30	9
9	68.111/RGB-U//Ward/3/FGO/4/Rabi	—	88	103	LB	103	41.6	11	38	8
10	6973/Ward.7463//74110	—	90	99	LB	105	31.1	8	30	10
11	CPI/Gediz/3/Goo//Jo/Cra	—	85	102	LB	99	46.0	9	28	6
12	D67.2/P66.270	—	98	96	LB	110	37.0	11	41	10
13	Cerceta	—	88	102	LB	100	41.1	7	28	7
14	Sterna-DW	—	87	85	LB	106	46.5	8	31	7
15	Rabi//GS/Cra	—	99	86	LB	115	40.0	7	34	8
16	Sora	—	88	82	LB	102	38.4	10	31	9
17	Scaup	—	92	83	LB	112	32.0	9	42	11
18	Snipe/Yav79//Dack/Teal	—	87	76	LB	108	44.4	10	36	11
19	TK SN1081	—	82	72	LB	106	39.0	9	31	9
20	Yav_2/Tez	—	89	85	LB	114	38.4	10	47	10
21	Yarmuk	—	87	90	LB	102	35.1	9	34	9
22	Decoy 1	—	89	103	LB	115	34.8	10	48	9
23	Garza/Boy	—	100	68	LB	115	12.5	8	9	8
24	68.111/RGB-U//Ward	—	98	105	LB	108	27.1	19	18	9
25	Araos	—	89	75	LB	100	42.5	13	36	8
26	Gan	—	82	104	LB	98	35.5	11	41	9
27	Scoop_1	—	82	90	LB	95	41.2	9	45	8
28	Sty-Us/Celta//Pals/3/Srn_5	—	88	92	LB	93	44.2	10	28	8
29	Agami	—	87	93	LB	98	41.7	9	38	8
30	Yav_3/Scot//JO69/Cra/3/Yav79	—	92	88	LB	109	45.1	9	34	6
31	YAR	—	92	97	LB	109	45.1	9	32	7
32	68112/Ward	—	101	95	LB	118	39.9	8	33	8

Table 8. Some phenological descriptors of the 51 durum cultivars used in D-genome-based synthetic hexaploid production. PUB = pubescence; FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (B = brown, DB = dark brown, LB = light brown, and W = whitish); PMA = days-to-physiological maturity; and TKW = 1,000-kernel weight (g).

No.	Pedigree	PUB	FLOW	HT	AWN	PMA	TKW	Nodes /spike	Grains /spike	Spike length (cm)
33	FGO/USA2111	—	91	93	LB	105	37.5	8	30	5
34	ALG86/4/FGO/Pales//Mexi_1/3/ Ruff/FGO/5/ENTE	—	87	104	LB	98	39.9	10	40	5
35	BOTNO	—	102	97	LB	116	32.4	11	23	7
36	CIT71/CPI	—	103	90	LB	116	—	—	—	8
37	LCK59.61	—	100	96	LB	112	29.7	7	9	9
38	Trinakria	—	87	86	LB	99	37.1	7	15	8
39	Rascon_37	—	84	92	LB	95	32.3	9	44	7
40	Ajaia_9	—	100	78	LB	118	34.2	9	30	9
41	Cerceta	—	98	86	LB	108	43.4	8	17	10
42	Scot/Mexi_1	—	89	103	LB	104	37.7	10	43	8
43	Falcin_1	—	89	95	LB	105	37.6	8	37	7
44	Green-3	—	89	95	LB	104	47.3	7	37	7
45	Shag_22	—	89	87	LB	103	42.7	7	15	7
46	Kapude_1	—	100	85	LB	115	30.7	10	4	8
47	Arlequin	—	88	84	LB	100	39.9	10	62	7
48	Chen_7	—	87	88	LB	95	46.2	9	28	8
49	Aconchi 89	—	90	78	LB	106	36.5	10	48	7
50	Alcatraz_3	—	98	85	LB	120	30.9	8	48	9
51	Local Red	—	82	74	LB	95	25.0	8	13	8

1,000-kernel weight category permits targeting those durums that have a 1,000-kernel weight higher than 42g, which could be exploited for enhancing yield.

Screening of a synthetic hexaploid wheat subset to spot blotch.

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Wheat is the leading food grain of Pakistan and, being a staple cereal in the diet, occupies a central position in agriculture. In the southern province of Sind, where winter temperatures are warmer, leaf spot (spot blotch) has been noted and presence of *C. sativus* reported. The pathogen is considered aggressive and a cause of severe yield loss, even in the Punjab province.

A set of synthetic hexaploid wheats was grouped into different subsets. An enlarged set, comprised of 42 synthetic-based entries plus five Mayoor sister lines in conventional global use for wheat breeding and resistant to *C. sativus*, exhibited stress diversity upon screening under Pakistan conditions and also showed molecular diversity. The germ plasm was screened under in vitro and in vivo conditions. From the 47 lines screened, three were moderately resistant and 12 moderately susceptible under *in vitro* conditions.

Screening under field conditions revealed that 36 lines out of 47 showed moderate resistance, 10 lines showed moderate susceptibility, and one was resistant. From this germ plasm, 15 lines were selected (2, 4, 8, 19, 20, 23, 10, 16, 29, 31, 15, 18, 33, 32, 37) and subjected to molecular diagnostics to unravel their DNA polymorphism profile using RAPD primers. Out of the seven RAPD primers utilized, scorable bands were obtained with four RAPD primers (OPG-2, OPG-9, OPC-8, and OPG-13).

Based on the screening results, molecular diagnostics, and other phenotypic characterization (Tables 9, p. 165-166, and 10, p. 166), two promising moderately resistant lines (19 and 20) are recommended for incorporation of genetic diversity for spot blotch resistance by introducing its allelic resistance into Pakistani cultivars using a limited backcrossing method mediated by wheat/maize double-haploid production technique to accelerate the germ plasm output process.

Table 9. Phenotypic evaluation of 47 synthetic hexaploid wheat lines under study (Height = plant height at maturity; awn color; B = brown, LB = light brown, DB = dark brown, and W = white) and PMA = days-to-physiological maturity.

Line No.	Pedigree	Height (cm)	Awn color	PMA	Spike length (cm)	Grain weight (g)
1	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	100	DB	128	13	42
2	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* ((895)/3/MAIZ/4/ INQ91	97	DB	128	14	38
3	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	93	DB	128	13	38
4	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	101	LB	129	12	35
5	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	96	LB	129	12	36
6	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	93	LB	129	12	40
7	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	105	LB	129	15	42
8	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	97	LB	129	12	41
9	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ/4/ INQ91	99	LB	129	14	40
10	DOY1/*Ae. tauschii* (447)//CETA/*Ae. tauschii* (895)3/MAIZ/4/ INQ91	94	LB	129	13	50
11	BCN//CETA/*Ae. tauschii* (895)	100	LB	129	9	40
12	ALTAR84/*Ae. tauschii* (219)//2*SERI	98	LB	129	12	40
13	ALTAR84/*Ae. tauschii* (219)//OPATA	107	LB	129	12	40
14	SABUF/7/ALTAR84/*Ae. tauschii* (224)//YACO/6 /CROC-1/*Ae. tauschii* (205)/5/BRI2*3/4/…	97	LB	129	9	50
15	BCN/4/68.111/RGB-U//WARD/3/*Ae. tauschii* (325)	96	LB	129	10	49
16	SABUF/7/ALTAR84/*Ae. tauschii* (224)//YACO/6/CROC-1/*Ae. tauschii* (205)/5/BRI2*3/4	95	LB	129	10	41
17	SABUF/7/ALTAR84/*Ae. tauschii* (224)//YACO/6/CROC-1/*Ae. tauschii* (205)/5/BRI2*3/4	98	LB	129	13	40
18	ALTAR84/*Ae. tauschii* (191)//OPATA/3/ALTAR84/*Ae. tauschii* (224)//YACO	96	LB	129	12	50
19	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)/3/MAIZ	101	LB	129	12	46
20	DOY1/*Ae. tauschii* (447)//CETA/*Ae. tauschii* (895)/3/MAIZ	96	B	129	13	48
21	68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. tauschii* (629)	106	LB	136	13	48
22	FGO/USA2111//*Ae. tauschii* (658)	98	LB	136	12	46
23	68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae.tauschii* (878)	100	W	136	12	36
24	SCA/*Ae. tauschii* (518)	98	LB	136	12	38
25	GAN/*Ae. tauschii* (897)	95	LB	136	12	41
26	YAV-2/TEZ/*Ae. tauschii* (895)	106	LB	136	14	48
27	GREEN/*Ae. tauschii* (458)	88	LB	136	13	46
28	SCA/*Ae. tauschii* (409)	88	LB	136	13	45
29	CPI/GEDIZ/3/GOO//JO60/CRA/4/*Ae. tauschii* (409)	104	LB	136	13	39
30	ALTAR84/*Ae. tauschii* (502)	106	LB	136	12	40
31	GAN/*Ae. tauschii* (236)//DOY1/*Ae. tauschii* (447)	90	LB	128	12	54
32	GAN/*Ae. tauschii* (236)//CETA/*Ae. tauschii* (895)	90	LB	128	12	41
33	SCOOP1/*Ae. tauschii* (434)//CETA/*Ae. tauschii* (895)	89	LB	128	13	47
34	DOY1/*Ae. tauschii* (447)//CETA/*Ae. tauschii* (895)	90	DB	128	9	50

Table 9. Phenotypic evaluation of 47 synthetic hexaploid wheat lines under study (Height = plant height at maturity; awn color; B = brown, LB = light brown, DB = dark brown, and W = white) and PMA = days-to-physiological maturity.

Line No.	Pedigree	Height (cm)	Awn color	PMA	Spike length (cm)	Grain weight (g)
35	68.111/RGB-U/WARD/3/FGO/4/*Ae. tauschii* (629)/5/CETA/ *Ae. tauschii* (895)	86	LB	128	12	46
36	ALTAR84/*Ae. tauschii* (224)/2*YACO	88	LB	128	13	51
37	SABUF/ALTAR84/*Ae. tauschii* (224)/3/YACO/CRO-1/*Ae. tauschii* (205)	88	LB	128	13	51
38	BCN//SORA/*Ae. tauschii* (323)	95	DB	128	12	50
39	OPATA/3/SORA//*Ae. tauschii* (323)	91	DB	128	11	46
40	BCN/4/68.111/RGB-U//WARD/3/*Ae. tauschii* (325)	88	DB	128	12	44
41	BCN//DOY 1/*Ae. tauschii* (447)	108	DB	128	12	53
42	BCN/4/RABI//GS/CRA/3/*Ae. tauschii* (895)	101	DB	128	13	45
43	MAYOOR	97	LB	127	15	41
44	MAYOOR	97	LB	127	13	38

Table 10. Details of entires with moderate resistance and susceptibility to the spot blotck fungus *C. sativus* in *in vivo* and *in vitro* conditions.

In vivo			*In vitro*		
Scale	**Entry Detail**	**Reaction**	**Scale**	**Entry Detail**	**Reaction**
1–2	2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 31, 32, 33, 35, 37, 38, 41, 42, 43, 46, 47	MR	1–2	8, 23, 19	MR
3–4	1, 8, 14, 29, 30, 34, 36, 39, 44, 45	MS	3–4	2, 4, 10, 29, 15, 16, 18, 20, 31, 32, 33, 37	MS
0	40	R	0	—	—

Phenotypic evaluation and molecular characterization of selected wheat landraces of Pakistan.

Rabia Amir, Alvina G. Kazi, Aziz-ur-Rehman, Rumana Keyani, Attiq-ur-Rehman, Farrukh Bashir, and A. Mujeeb-Kazi.

Landrace cultivars undoubtedly represent an important source of genetic variation in wheat. Although modern cultivars are derived from traditional land races, significant, unexploited variation remains among and between landraces held in gene banks. Landraces have been used successfully to improve the stress adaptations in modern cultivars. This study determined the genetic diversity of selected landraces of Pakistan by RAPD and SSR primers. Some phenological traits including plant height, spike length, awn color, 1,000-kernel weight, grains/spike, nodes/spike, days-to-flowering, physiological maturity, and pubescence also were investigated (Table 11, p. 167).

Of the 12 RAPD primers used, six (OPG9, OPG11, OPG15, OPF18, OPO20, and OPS5) gave no amplification and the remaining six (OPA10, OPC8, OPG2, OPG6, OPG12, and OPG13) amplified the polymorphic pattern. The size of the amplification products ranged from 500 to 10,000 bp. The highest number of scorable bands was obtained with primers OPG-12 and OPG-6 and the lowest with primer OPA-10. The maximum number of genotypes (21) were amplified by primer OPG-2 and minimum (6) by OPG-13. Different primers showed variation in their ability to detect polymorphism. Primers OPA-10 and OPG-6 showed the highest polymorphism and primer OPC-8 the lowest. Wheat genotypes T12 and T18 were amplified by a maximum number of primers (5). Genotypes T15 and 8A were not amplified by any primer. Genotypes C-258 and T3 showed maximum polymorphism. The RAPD amplification data was used to obtain a similarity matrix and for dendrogram generation. The value of similarity coefficient ranged from 41 to 100%.

Table 11. Phenotypic evaluation of traits of 28 wheat landraces (FLOW = days-to-flowering; HT = plant height at maturity (cm); AWN = awn color (B = brown, LB = light brown, DB = dark brown, and W = whitish); PMA = days-to-physiological maturity; and TKW = 1,000-kernel weight).

Pedigree	PUB	FLOW	HT (cm)	AWN	PMA	TKW (g)	Nodes /spike	Grains /spike	Spike length (cm)
T1 (*T. durum* subsp. *durum*)	—	130	106.0	B	145	32.2	12	47	8.0
T2 (*T. durum* subsp. *durum*)	—	130	112.0	W	144	31.2	12	36	8.7
T3 (*T. durum* subsp. *durum*)	—	129	108.0	LB	142	30.3	12	25	10.2
T7 (*T. aestivum* subsp. *sphaerococcum*)	—	129	94.3	—	137	21.6	10	42	7.3
T8 (*T. aestivum* subsp. *aestivum*)	—	128	106.0	DB	137	30.5	8	34	8.2
T9 (*T. aestivum* subsp. *aestivum*)	—	127	104.3	DB	137	24.7	8	49	9.3
T12 (*T. aestivum* subsp. *aestivum*)	—	126	103.0	DB	145	25.2	7	79	9.6
T14 (*T. aestivum* subsp. *aestivum*)	—	123	99.0	LB	144	24.5	10	58	11.0
T15 (*T. aestivum* subsp. *aestivum*)	—	122	98.0	LB	145	26.6	10	34	11.0
T16 (*T. aestivum* subsp. *aestivum*)	—	128	104.0	LB	133	23.7	8	51	9.7
T17 (*T. aestivum* subsp. *aestivum*)	—	121	104.0	—	137	20.3	11	40	12.3
T18 (*T. aestivum* subsp. *aestivum*)	—	122	111.0	—	137	23.8	9	47	9.4
T20 (*T. aestivum* subsp. *aestivum*)	—	127	100.0	—	137	34.5	10	70	11.8
T24 (*T. aestivum* subsp. *aestivum*)	—	126	99.3	—	137	28.0	9	52	8.5
8A (Selection)	—	121	90.0	DB	144	29.4	11	31	8.8
D-9 (Barani)	—	122	105.0	LB	140	29.5	9	47	10.2
C-217 (C-516 / C-591)	—	125	106.0	B	140	36.6	8	48	8.7
C-228 (Hard Federation/9D)	—	119	111.3	B	144	31.2	9	45	9.8
C-245	—	120	108.0	LB	144	30.0	9	45	8.7
C-247	—	119	114.3	DB	144	30.5	10	55	8.0
C-248	—	126	104.0	B	144	27.8	11	40	9.8
C-250 (Hard Federation/9D)	—	128	102.0	LB	145	30.8	8	26	12.0
C-256	—	124	100.3	LB	133	21.7	8	43	9.3
C-258	—	125	85.0	—	133	37.2	7	29	8.8
C-269	—	124	94.0	—	137	32.6	10	51	10.0
C-271 (C-220 / IP165)	—	119	113.0	B	137	41.2	10	55	10.4
C-288	—	126	101.0	LB	137	33.1	10	46	7.5
C-518 (T9 / 8A)	—	119	103.0	B	140	28.0	8	43	7.7

Genotypes showing the least similarity were 2 with 11 (41%) and 6 with 21 (43%). Similarly, genotypes showing 100% similarity were 4 with 8, 16 with 17, and 26 with 27. The similarity of remaining genotypes was between 41 to 100%.

The dendrogram showed three clusters. Cluster A included two genotypes (T1 and C-247) with a maximum genetic distance of 0.1032 (10%). Cluster B had 21 genotypes (T2, T8, T15, 8A, D-9, C-217, C-228, C-288, C-518, C-271, C-245, C-248, T16, T24, T14, C-250, C-269, C-256, C-258, T17, and T20) with genetically similar genotypes being T8 and T15, C-217 and C-518, and C-288 and C-518. In this cluster, most genetically dissimilar genotypes were C-256 and C-258 with C-256, showing a genetic distance of 0.5996 (59%), and C-258, being the maximum genetically

diverse genotype of this cluster with genetic distance of 0.7129 (71%). The remaining genotypes of this cluster were in the range of 0.00 to 59%. Cluster C included five genotypes in which genotypes T7 and T9 showed the least genetic distance of 0.1252 (12%) and genotype T18 with maximum genetic distance of 0.8873 (88%). The remaining genotypes of this cluster had a genetic distance in the range of 12 to 75%. Thus, cluster analysis indicated genotypes C-258 and T-20 (71%) and genotypes T18 and T2 (88%) as being genetically the most distinct genotypes.

The SSR amplification data was used to obtain a similarity matrix and for generation of dendrogram using 15 SSR primers (GWM33, GWM106, GWM232, GWM337, GWM458, GWM642, GWM165, GWM194, GWM608, GWM609, GWM624, GWM11, GWM18, GWM550, and GWM582) of chromosomes 1D, 4D, and 1B. The value of similarity coefficient ranged from 40 to 95%. Genotypes with the least similarity were 4 with 27 and 9 with 27. The genotypes with 95% similarity are 17 with 18 and 18 with 19. The similarity of remaining genotypes ranged between 40 to 95%.

The dendrogram is divided into three main clusters; A, B, and C. Cluster A included three genotypes (T1, T2, and C-217). T1 and T2 being genetically identical showed a genetic distance of 0.0855 (8%) with the remaining genotypes, whereas C-217 had a genetic distance of 0.3267 (32%). Cluster B included 23 genotypes (T3, T8, C-228, C-245, C-247, C-269, C-271, T24, C-248, C-250, C-256, C-258, C-288, C-518, T9, T20, T18, T14, D-9, T7, T15, T16, and T17). This cluster showed minimum genetic distance between genotypes T3 and T8 (0.0855), C-228 and C-245 (0.0504), C-269 and C-271 (0.0678), C-258 and C-256 (0.1035), C-288 and C-518 (0.2191), T18 and T20 (0.0504), T14 and D-9 (0.1035), and T15 and T16 (0.0855). The maximum genetic distance of 0.4473 (44%) was shown by T7 in this cluster. The genetic distance of remaining genotypes of this cluster remained in the range of 5 to 70%. Cluster C included only two genotypes (T12 and C-258) with T12 showing a genetic distance of 0.8920 (89%) and C-258 of 0.645 (64%). Analysis of dendrogram revealed T12 and T7 (89%) and C-258 and T7 (64%) as most genetically distinct genotypes.

The six RAPD primers yielded on the average 17 bands/primer, whereas 15 SSR primers amplified on the average eight bands/primer. The average number of polymorphic bands/primer was higher in case of RAPDs (11.1) than SSRs (4.5). The percentage of polymorphism among wheat land races in RAPDs and SSRs was 66.6 and 68%, respectively, revealing that wheat land races are highly diverse and can be used for improvement of local Pakistani cultivars.

After morphological examination, genotypes T2, T3, T7, T18, C-217, and C-258 were found to be diverse. In case of the RAPDs, the amplification products of 28 landraces with six primers yielded a total of 102 scorable bands, 68 of which were polymorphic. Thus, the percentage of polymorphism among these genotypes was 66.6%. Primers OPA-10 and OPG-8 showed highest polymorphism. In the SSRs, the amplification product yielded a total of 112 scorable bands of which 83 were polymorphic. The percentage of polymorphism was 68%. Primers GWM337 and GWM194 showed highest polymorphism. The RAPD study indicated genotypes T3, T18, and C-258 as genetically most diverse, whereas the SSR study indicated genotypes T7, T12, and C-258 as most diverse. Thus, genotype C-258 is indicated as the most genetically diverse genotype.

Phenotypic evaluation and molecular characterization of selected wheat land races suggests that the allelic variation of this germ plasm can be used in improving new wheat cultivars for high yield, resistance to rusts, and desirable quality traits. The germ plasm is maintained as a working collection in Ayub Agricultural Research Institute, Faisalabad, and the gene bank storage in PGRI, National Agricultural Research Center, Islamabad.

In vitro screening of a double-haploid mapping population developed for spot blotch resistance with selective molecular characterization.

Hummera Nazir, Alvina G. Kazi, Shehzad Asad, Shamim Iftikhar, Usman Rahim, and A. Mujeeb-Kazi.

Wheat is the most important staple food crop of Pakistan that occupies more farmland than any other crop and is grown under irrigated and rain-fed conditions in Pakistan. Among fungal diseases, foliar pathogens other than rusts contribute significantly to low average yields of cereal crops. Spot blotch/leaf blight is the most severe constraint of wheat production in the countries of Southeast Asia where climates are warm and moist. Currently, this biotic constraint requires investigative research in our country.

The best method for controlling the disease is through use of resistant materials that can be used in breeding programs to obtain durable resistance to *C. sativus*. One such germ plasm form is from the primary gene pool that harnesses the D-genome accessional diversity of *Ae. tauschii* in the form of synthetic-hexaploid wheats. To gain more insight into genetic control, molecular mapping populations were developed previously at CIMMYT using the DH methodology. One population of 171 DH individuals is 'Mayoor//TKSN1081/*Ae. tauschii* (222)/3/Flycatcher'. This population was phenotyped by a stringent *in vitro* screening test. Selective commercial cultivars also were assessed for resistance or susceptibility. The screening results showed that out of the 171 DH entries, 12 lines (107, 112, 114, 116, 120, 122, 125, 128, 138, 144, 152, and 156) and three commercial cultivars (Chakwal-86, Kirin-95, and Bakhtawar-93) possessed moderate resistance to *C. sativus* (Table 12). These resistant lines were subjected to molecular evaluation for assessing their diversity levels. Five RAPD primers (OPG-2, OPG-5, OPG-8, OPG-10, and OPG-12) were evaluated for their diversity profiles, out of which OPG-12 amplified 12 out of 13 samples and two cultivars. The primer OPG-5 amplified nine double haploids out of 13 and one cultivar out of three. OPG-10 amplified a total of ten samples including eight double haploids and two cultivars. One hundred-one DNA fragments were amplified with four RAPD primers, with an average of 25 bands/primer. The number and size of the amplified fragments also varied with different primers. A maximum of 36 bands were amplified with primer OPG-12 and a minimum of seven fragments with primer OPG-8. The amplified products ranged from 500–2,500 bp. The genetic similarity between the population ranged between 0.4118 and 0.9412. The maximum coefficient (0.9412) was observed for pairs 1–2, 6–7, and 5–10, whereas the lowest coefficient (0.4118) was observed for pairs 5–7, 3–16, and 9–16. The remaining population had similarity coefficients between 0.4706 and 0.8824. Data from the RAPD primers indicated that DH entry 125 was the most genetically diverse and showed a maximum genetic distance with Kirin-95. Among the commercial cultivars, Chakwal-86 exhibited the maximum genetic distance with M.FCT-125. Hence, we recommend introducing its allelic resistance into commercial cultivars for sustainable production and making their moderate resistance more stable and durable. Phenology estimates provided an additional selective sieve for the preferential use of other moderately resistant lines in wheat breeding (Table 13).

Table 12. *In vitro* screening of commercial cultivars against *Cochliobolus sativus* (progressive 1–5 scoring scale where 1 = resistant and 5 = susceptible).

Cultivar	Leaf score	Response
Bakhtawar-93	2	MR
Inqilab-91	3	MS
Kirin-95	2	MR
Tandojam-83	5	S
SH-2002	5	S
Bhakkar-2002	4	MS
Fakhr-e-Sarhad	5	S
Marvi-2000	5	S
Tatara	5	S
Takbeer	5	S
AS-2002	4	MS
Iqbal-2000	5	S
Auqab-2000	5	S
Zarlashta	5	S
Wafaq-2001	5	S
Margalla-99	5	S
Chakwal-86	2	MR
Nowshera-96	3	MS
GA-2002	5	S
Manthar-3	4	MS

Table 13. Some phenological traits of 12 moderately resistant doubled-haploid entries in the mapping population (Mayoor//TKSN1081/*Ae. tauschii* (222)/3/Flycatcher) studied.

Line No.	Plant height (cm)	Awn color	Spike length (cm)	Grain weight (g)
107	97	light brown	11	32.3
112	104	light brown	10	43.4
114	100	light brown	12	38.0
116	109	light brown	12	38.8
120	104	light brown	10	33.0
122	93	light brown	10	37.6
125	98	light brown	12	47.8
128	103	light brown	9	43.1
138	107	light brown	12	35.8
144	107	light brown	10	32.0
152	118	light brown	10	39.2
156	113	light brown	12	34.7

Molecular fingerprinting of some advanced bread wheat-breeding lines resistant to stem rust (Ug99) and their utilization in wheat production.

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Stem rust of wheat is one of the three rusts that are a major production constraint for the cereal globally. Recently, an alarming situation has arisen due to Ug99 race in Kenya where susceptibility of Pakistani cultivars has been observed. Furthermore, the new race has reached Yemen and chances of it entering Pakistan are a few years away. Because our wheat germ plasm is vulnerable, internationally identified materials have been introduced for assessing adaptation, diversity, and release of suitable introduced germ plasm in stem rust affected areas. Our focus is on Sindh and lower Punjab, either directly or after being bred into the high yielding cultivars of these locations. We analyzed the 29 entries of the International Elite Bread Wheat Yield Trials (2EBWYT) for adaptation, phenology, and RAPD- and SSR-based molecular diversity.

Twenty-nine RAPD primers (OPC8, OPG11, OPG13, OPO20, OPG5, OPS6, OPF18, OPA10, OPA15, OPA2, OPA4, OPA11, OPU13, OPU14, OPU15, OPA1, OPA6, OPA9, OPO6, OPR6, OPR15, OPE1, OPE2, OPE3, OPE4, OPE5, OPE6, OPJ20, and OPN13) were used to detect genetic polymorphism at DNA level in the 29 2EBWYT lines. After screening the 29 primers, seven showed amplification. The efficiency of the primers to amplify the genotypes ranged from six genotypes by OPJ20 to five by OPU3 and two by OPN13. Population genetic analysis showed that the total number of loci is 140, out of which 36 are polymorphic with a percentage of 25.71. Scorable bands ranged from 500 to 2,000 bp. The maximum scorable bands (five) were shown in 2EBWYT-21 and the minimum number of bands (one) was in 2EBWYT-3, 2EBWYT-6, and 2EBWYT-13. The value of the similarity matrix ranged from 88.57% (minimum) between genotypes 2EBWYT-3 and 2EBWYT-20, 2EBWYT-20, and 2EBWYT-27. The maximum (100%) similarity between genotypes was observed between 2EBWYT-1 and 2EBWYT-4, -5, -10, -11, -16, -22, -23, -24, -26, -28, and -29; 2EBWYT-2 and 2EBWYT-8; 2EBWYT-4 and 2EBWYT-5, -10, -11, -16, -22, -23, -24, -26, -28, and -29; 2EBWYT-5 and 2EBWYT-10, -11, -16, -22, -23, -24, -26, -28, and -29; 2EBWYT-10 and 2EBWYT-11, -16, -22, -23, -24, -26, -28, and -29; 2EBWYT-11 and 2EBWYT-16, -22, -23, -24, -26, -28, and -29; 2EBWYT-16 and 2EBWYT-22, -23, -24, -26, -28, and -29; 2EBWYT-22 and 2EBWYT-23, -24, -26, -28, and -29; 2EBWYT-23 and 2EBWYT-24, -26, -28, and -29; 2EBWYT-24 and 2EBWYT-26, -28, and -29; 2EBWYT-26 and 2EBWYT-28 and -29; and 2EBWYT-28 and 2EBWYT-29.

The genetic distances among the 29 genotypes were used to construct a dendrogram by UPGMA analysis for determining grouping of 2EBWYT lines on the basis of similarities and differences. The dendrogram generated was divided into three clusters. Cluster A included a total of 12 genotypes (2EBWYT-1, -4, -5, -10, -11, -16, -22, -23, -24, -26, -27, and -29) all being genetically identical. Cluster B included nine genotypes (2EBWYT-14, -17, -2, -8, -9, -20, -12, -18, and -15) with a minimum genetic distance of 0 present between 2EBWYT-2 and -8, and 2EBWYT-15 showed the maximum genetic distance of 0.448. Cluster C included eight genotypes (2EBWYT-7, -20, -19, -25, -28, -21, -3, and -13) with a minimum genetic distance of 0.402 present between 2EBWYT-7 and 2EBWYT-20 and between 2EBWYT-25 and 2EBWYT-27. The maximum genetic distance of 0.587 was present in 2EBWYT-21 followed by 0.539 in 2EBWYT-18, and 0.492 in 2EBWYT-3 and 2EWBYT-13. A RAPD-based cluster analysis depicted that 2EBWYT-21 is genetically the most diverse line with maximum genetic distance of 0.587. Furthermore, 2EBWYT-3, -13, and -18 also were considered as diverse lines.

Twenty SSR primers (GWM33, GWM106, GWM232, GWM337, GWM458, GWM642, GWM165, GWM194, GWM608, GWM609, GWM624, GWM37, GWM44, GWM111, GWM121, GWM295, GWM350, GWM428, GWM437, and GWM635) specific to chromosomes 1D, 4D, and 7D, were used to screen the germ plasm and resulted in the identification of 12 primers showing the amplification. The efficiency of the SSR primers to amplify the genotypes ranged from six genotypes by primer GWM33 and two genotypes by primer GWM165 to six genotypes by primers GWM608, GWM44, and GWM635. Population genetic analysis showed that the total number of loci is 204 out of which 36 are polymorphic and their percentage is 17.65.

The value of the similarity matrix of the SSR primers ranged from 91.18% (minimum) between genotypes 2EBWYT-15 and 2EBWYT-9 and 2EBWYT-6 and 2EBWYT-21 and was 100% between genotypes 2EBWYT-22 and 2EBWYT-25. The dendrogram showed four clusters. Cluster A included ten genotypes (2EBWYT-1, -2, -3, -9, -10, -24, -26, -27, -7, and -8) with a minimum genetic distance of 0.087 present between 2EBWYT-24 and 2EBWYT-26 and maximum genetic distance of 0.448 present between 2EBWYT-9 and 2EBWYT-10. Cluster B included seven

Table 14. Phenological evaluation of 29 lines from the Second International Elite Bread Wheat Yield Trials sown at National Agricultural Research Center, Islamabad, Pakistan, in 2007–08 (Items for awn color; DB = dark brown, B = brown, LB = light brown, and W = whitish).

Entry No.	Pedigree	Pubescence	Days-to-flower	Height at maturity (cm)	Awn color	Days-to-physical marurity	1,000-kernel weight (g)	Nodes /spike	Grains /spike	Spike length (cm)
1	WBLL1*2/TUKURU	–	130	98	LB	135	20.9	12	46.0	13
2	FRET2/TUKURU//FRET2	+	130	96	LB	134	51.8	12	30.0	14
3	MILAN/S87230//BABAX	+	129	102	LB	132	29.8	12	53.0	13
4	ATTILA/3*BCN//BAV92/3/TILHI	+	129	98	LB	132	51.9	10	46.0	12
5	TILHI/PASTOR	–	128	95	LB	136	29.7	8	47.0	13
6	WAXWING*2/TUKURU	+	127	97	LB	132	34.8	8	60.0	19
7	FRET2*2/BRAMBLING	+	126	97	LB	132	38.1	7	54.6	13
8	WBLL1*2/BRAMBLING	+	123	96	LB	135	30.6	10	47.0	10
9	WBLL1*2/KIRITATI	–	122	99	LB	132	39.3	10	42.0	11
10	VORB/FISCAL	+	128	98	LB	132	49.2	8	34.0	13
11	CHIBIA//PRLII/CM65531/3/FISCAL	+	120	96	LB	132	48.2	11	48.0	14
12	BL2064//SW89-5124*2/FASAN/3/TILHI	+	121	96	LB	135	49.2	9	44.0	9
13	OASIS/SKAUZ//4*BCN/3/2*PASTOR	–	127	91	LB	132	34.4	10	40.0	9
14	KIRITATI/WBLL1	+	126	97	LB	133	44.9	9	61.0	11
15	PFAU/SERI.1B//AMAD/3/WAXWING	–	121	96	LB	132	29.1	11	56.0	10
16	WBLL1*2/BRAMBLING	–	122	100	LB	132	40.7	9	61.0	13
17	MUNIA/CHTO/3/PFAU/BOW//VEE#9/4/CHEN/….	+	125	94	LB	132	29.8	8	52.0	11
18	BABAX/LR24//BABAX*2/3/VIVITSI	–	119	97	LB	132	30.8	9	53.0	12
19	BABAX/LR24//BABAX*2/3/VIVITSI	–	120	97	LB	132	26.2	9	40.0	11
20	WAXWING*2/KIRITATI	–	119	98	LB	132	21.4	10	22.0	12
21	WBLL1*2/BRAMBLING	+	126	92	LB	132	28.6	11	47.0	13
22	PFAU/WEAVER*2//TUKURU	+	128	94	LB	132	31.4	8	36.0	10
23	KIRITATI//PRL/2*PASTOR	+	124	85	LB	132	37.6	8	30.0	10
24	WORRAKATTA/PASTOR	+	125	101	LB	136	39.1	7	58.0	12
25	TAM200/PASTOR//TOBA97	–	124	96	LB	132	26.4	10	48.0	10
26	HPO/TAN//VEE/3/2*PGO/4/MILAN/5/SSERI1	–	119	90	LB	133	35.1	10	38.0	11
27	PFAU/WEAVER*2//KIRITATI	+	126	95	LB	133	41.7	10	65.0	12
28	PFAU/WEAVER*2//KIRITATI	–	119	92	LB	133	51.2	8	41.0	11
29	SKAUZ/BAV92	+	126	103	LB	136	31.7	10	45.0	13

genotypes (2EBWYT-16, -23, -11, -20, -13, -28, and -29) with minimum genetic distance of 0.448 present between 2EBWYT-27 and 2EBWYT-29; 2EBWYT-13 showed the maximum genetic distance of 0.585 followed by 0.492 between 2EBWYT-11 and 2EBWYT-20. Cluster C included six genotypes (2EBWYT-8, -22, -25, -17, -18, and -19) with a minimum genetic distance of 0 between 2EBWYT-22 and 2EBWYT-25. The maximum genetic distance of 0.539 was manifested between genotypes 2EBWYT-18 and 2EBWYT-19. Cluster D included six genotypes (2EBWYT-12, -4, -5, -6, -14, and -15) with minimum genetic distance of 0.448 present between 2EBWYT-4 and 2EBWYT-5 and a maximum genetic distance of 0.693 for 2EBWYT-12, 0.639 between 2EBWYT-14 and 2EBWYT-15, and 0.587 in 2EBWYT-6.

An SSR-based cluster analysis of dendrogram depicted that 2EBWYT-12 is the most diverse line among the 29 2EBWYT lines with maximum genetic distance of 0.693. Furthermore, 2EBWYT-14 and 2EBWYT-15 also are considered as genetically diverse lines with genetic distance of 0.639.

Phenotypic data depicted that 2EBWYT-2, 2EBWYT-4, 2EBWYT-10, 2EBWYT-11, 2EBWYT-12, and 2EBWYT-28 are the best lines on the basis of yield enhancing characters (Table 14, p. 171). Cluster analysis of RAPD and SSR primers revealed that genotypes 2EBWYT-21 showed maximum diversity of 0.587 followed by 2EBWYT-18 and 2EBWYT-13 in case of RAPD primers, whereas SSR analysis depicted 2EBWYT-12, 2EBWYT-14, 2EBWYT-15, and 2EBWYT-6 as diverse genotypes. These results form the basis of direct line selection for wheat production security for stem rust and also provide the guideline for targeted breeding goals against the pathogen.

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ITEMS FROM THE RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE OF THE CENTRAL REGION OF NON-CHENOZEM ZONE
143026, Moscow region, Nemchinovka, Kalinina 1, Russian Federation.

Soft wheat hybrids showing no segregation for resistance to leaf rust.

V.G. Kyzlasov, I.F. Lapochkina, and N.R. Gainullin.

The soft winter wheat cultivar Nemchinovskaya 24 has demonstrated absolute resistance to leaf rust since the time of its releaset 20 years ago. In order to understand the genetic basis of the resistance, we crossed Nemchinovskaya 24 with tester lines of spring wheat with genes *Lr9*, *Lr24*, *Lr24 + Sr24*, *Lr27 + Lr31*, *Lr28*, *Lr29*, *Lr38*, and *LrTr*). The susceptible soft spring wheat Khakasskaya was used as a check.

The F_1 hybrids and their parental lines were not susceptible to leaf rust and that the resistance genes of their parental lines appeared to be dominant. The F_2 hybrid progeny of the cross 'Nemchinovskaya 24 / Khakasskaya' segregated according to a trihybrid pattern, 43 resistant plants : 21 susceptible plants (Table 1).

Table 1. Segregation patterns in the F_2 hybrids of crosses with Nemchinovskaya 24 (N24) and lines carrying *Lr* genes for resistance to leaf rust. Critical $\chi^2 = 3.84$.

Cross	Number of resistant plants	Number of susceptible plants	Ratio of resistant to susceptible plants		χ^2
			Observed	Expected	
N24 / Khakasskaya	120	64	42 : 22	43 : 21	0.324
N24 / *Lr9*	127	0	—	—	—
Lr24 / N24	80	6	13.3 : 1	15 : 1	0.078
N24 / *Lr24+Sr24*	157	0	—	—	—
Lr27+Lr31 / N24	122	7	17.4 : 1	15 : 1	0.149
Lr28 / N24	138	9	15.3 : 1	15 : 1	0.004
Lr29 / N24	61	4	15.3 : 1	15 : 1	0.001
N24 / *Lr38*	171	**0**	—	—	—
N24 / *LrTr*	181	**0**	—	—	—

We found the action of one main and two complementary inhibiting genes. F_2 hybrids between stocks with *Lr24, Lr27 + Lr31, Lr28,* and *Lr29* with Nemchinovskaya 24 segregated according to a dihybrid pattern (15 resistant: 1 susceptible). The F_2 progenies from lines with *Lr9*, *Lr24 + Sr24*, *Lr38*, and *LrTr* are interesting because no plants were susceptible to leaf rust. All the plants are

resistant. The experimental evidence indicates that the resistance genes of the parental forms are located on homologous chromosomes, but we have not identified them or determined their allelism. The question that remains unanswered is why the F_2 hybrid population of '*Lr24* / Nemchinovskaya 24' segregated for resistance to leaf rust, whereas the cross 'Nemchinovskaya 24 / *Lr24* + *Sr24*' produced no susceptible plants in the F_2.

Septoria sp. fungi affect all wheats to one extent or another. No fully disease-resistant wheat is known in the world collection. Plants with relative resistance are sensitive to the pathogen at later developmental stages. One example is the Bulgarian winter wheat PI476772 from the Moscow International Science and Technology Center's collection. The line also is resistant to leaf rust and highly resistant to mildew. Hybrid progenies from crossing this line with Nemchinovskaya 24 also are resistant to leaf rust (% infection in both F_1 and F_2 = 0), and *Septoria* develops late on them. According to preliminary data obtained by our laboratory, this Bulgarian wheat has the genotype *Lr10*, *Lr26*, and *Lr46*.

Nemchinovskaya 24 soft winter wheat is resistant to leaf rust. It will be necessary to identify the resistance genes. Using hybrid populations, which are not susceptible to leaf rust and not segregating for resistance, in soft wheat selection for resistance to leaf rust can be effective.

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The evaluation of spring bread wheat cultivars, NILs, and promising lines to leaf, stem, and stripe rusts in 2008.

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In 2008, during the vegetative period of spring bread wheat, leaf, stem, and stripe rusts epidemics were observed and evaluated. The severities of these diseases were different. Leaf rust was estimated as moderate. Atem and stripe rusts were observed as weak. Evaluation of a set NILs carrying *Lr* genes show that the severity of the leaf rust epidemic on susceptible cultivars was 50–55%. Highly resistant lines (IT = 0;1) had the genes *Lr9*, *Lr28*, and *Lr29* and gene combinations *Lr9+Lr19, Lr19+Lr24, Lr19+Lr25, and Lr19+Lr26*. Interestingly, genes *Lr28* and *Lr29* showed an IT = 0;1, but several years ago (2000) these genes had an IT = 3. Hence, within eight years sharp changes in the set of pathotypes has taken place, enablling *Lr28* and *Lr29* to be highly effective.

The evaluation of promising spring bread wheat lines to stem and stripe rusts was made in the southwest part of the Saratov region. An IT = 0 in the NILs and promising lines had the following combinations of *Sr* genes: *Sr24+Sr25* and *Sr25+Sr31*. The majority of spring bread wheat sowings in this zone include the cultivars L503, L505, Belyanka and Dobrynya. The cultivars L503, L505, and Dobrynya had ITs = 0; Belyanka had an IT of 3. Resistance to stripe rust in the L503, L50,5 and Dobrynya controlled by an unindentified *Yr* gene(s). This *Yr* gene(s) was transmited from the above-mentioned cultivars into the promising lines.

Agronomic performance of multilinear mixes on the basis of spring bread wheat cultivar Dobrynya.

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The perceived advantages of mixtures over their components in monoculture include larger yields, more stable performance, and improved and more durable resistance to diseases. In 2008, we investigated multilinear mixes on the basis of cultivar Dobrynya. These mixes include four components: Dobrynya, Dobrynya *Lr19+Lr9*, Dobrynya *Lr19+Lr24*, Dobrynya *Lr19+Lr25*, and all components in equal parts. We also used mixtures of the first (prepared in 2008) and second years (after cultivation in 2007). The control used all lines and Dobrynya. We looked at the agronomical traits heading date, plant height, resistance to lodging, 1,000-kernel weight, and grain productivity. For heading date, the

multilinear mixes did not differ from lines or cultivar. For plant height, the component liness did not significantly differ among themselves however, Dobrynya *Lr19+Lr24* was greater on average. Multilinear mixes did not significantly differ for platn height from the component average, but mixes of the first and the second year cultivation were higher than the components, averaging 5–6 cm. For lodging resistance, we observed that the first-year mix was more resistant than the component liness, but the second-year mix was not significantly lower. For 1,000-kernel weight, significance was not observed, but the first-year mix was higher than that of the second-year mix and lower than component average. For grain productivity, the first-year mix was not significantly different from component average, although an increase in productivity was 10%. The second-year mix was significantly higher than the component average at 26%. We are now analyzing pustule number for leaf rust on a susceptible component mixture, spike productivity, flour quality of components and mixes.

Influence on disease resistance of translocations from Thinopyrum intermedium; Th. elongatum; Secale cereale; T. turgidum subsps. durum, dicoccoides, and dicoccum; and T. timopheevii subsp. timopheevii in spring bread wheat lines.

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For four years (2005–08), spring bread wheat lines carrying translocations from *Th. intermedium; Th. elongatum; S. cereale*; *T. turgidum* subsps. *durum, dicoccum,* and *dicoccoides;* and *T. timopheevii* subsp. *timopheevii* were investigated for resistance to some diseases (Table 1). A combination of alien chromatin from several species in one genotype significantly improves disease resistance in these lines. The spring bread wheat line L2772, with chromatin from both *Th. intermedium* and *T. turgidum* subsp. *durum* has race-specific resistance to a loose smut and resistance to leaf rust, powdery mildew, and common bunt in comparison with the parental lines. Similar results have been obtained for line L2816 with *Th. elongatum* and *T. turgidum* subsp. *durum* chromatin. Line L2780, which combains chromatin from *Th. elongatum* and *T. timopheevii* subsp. *timopheevii* was nearly resistant to loose smut, leaf rust, and powdery mildew and

Table 1. The infection type (IT) of spring bread wheat lines to leaf rust, powdery mildew, loose smut, and common bunt.

Line	Pedigree	Leaf rust	Powdery mildew	Pathotypes				
				Loose smut			Common bunt	
				505	164	36	894	Tul 5
Donor species – *Thinopyrum elongatum*								
L3065	Saratovskaya 55/*Th. elongatum**3/ Saratovskaya 29	3	2	8.8	26.3	24.0	0.0	—
Donor species – *Triticum turgidum* subsp. *dicoccoides*								
L215	Saratovskaya 55*4/*T. turgidum* subsp. *dicoccoides*	0	0	28.8	21.5	65.0	20.0	17.0
Donor species – *Triticum turgidum* subsp. *dicoccum*								
L196	S58/*T. turgidum* subsp. *dicoccum**3// S58	1	2	70.0	66.8	51.1	5.7	5.2
Donor species – *Triticum timopheevii* subsp. *timopheevii*								
L2780	CI-12633/Л504	0	0	0.0	0.0	0.0	25.1	30.0
Donor species – *Triticum turgidum* subsp. *durum*								
L2816	Л528/Saratov. golden	0	0	6.3	4.7	16.7	5.4	13.8
Donor species – *Triticum turgidum* subsp. *dicoccum* + *Th. elongatum*								
L2358	L401/*T. turgidum* subsp. *dicoccum*/ L401/S55/L2033/S60/Prohorovka	0	0	0.0	0.0	0.0	7.3	9.0
Donor species – *Triticum turgidum* subsp. *durum* + *Secale cereale*								
L3630	L2040/Prohorovka	2	1	5.5	4.5	2.1	—	—
L805	L2040/Lut.13-80	0	2	4.8	8.5	1.3	—	—
Donor species – *Triticum turgidum* subsp. *durum* + *Th. intermedium*								
L2772	L164/L222	0	1	13.3	35.8	0.0	0.0	—

had a low level of a infection by common bunt. Resistance to a complex of diseases was shown line L2358, with *T. turgidum* subsp. *dicoccum* and *Th. elongatum* chromatin.

Of particular interest is L3065, which contains a chromatin from *Th. elongatum*. This line shows race-specific resistance to loose smut and pathotypes of common bunt but is susceptible to leaf rust and powdery mildew. Line L215, which was produced from crosses with *T. turgidum* subsp. *dicoccoides,* has resistance to leaf rust and powdery mildew, moderate resistance to common bunt, and race-specific resistance to loose smut. Small lesions from leaf rust and common bunt were shown line L196, which has chromatin from *T. turgidum* subsp. *dicoccum*, but is susceptible to the pathotypes of loose smut investigated here.

A combination in one genotype of alien genes with own genes from *T. aestivum* gives a positive effect. Thus, lines L3630 and L805, which include line L2040 in their pedigree (contains chromatin from *T. turgidum* subsp. *durum*), have shown a high level of resistance to the pathotypes of loose smut investigated, and they also have tolerance to leaf rust and powdery mildew.

These data show that combining several alien genes (chromatins) in one bread wheat genotype can produce lines with complex diseases resistance or lower the degree of damage.

Effects of an Lr26 translocation on grain productivity and grain protein content in spring bread wheat.

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The first fertile hybrids between wheat and rye were received in Saratov in 1918. However, the using the desirable genetic material from the rye genepool for improvement of spring wheat has been limited by undesirable linkages in the rye translocations, in particular with genes that decrease grain quality. At ARISER, based on the best Saratov-bred spring bread wheat cultivars, a set of NILs with the *Lr26* translocation were produced. The donors of the translocation with *Lr26* were Genaro 81 and an NIL of Thatcher. The Saratov population of leaf rust included virulent pathotypes to *Lr26* and *Lr19*. The combination of translocations with *Lr26* from *S. cereale* and *Lr19* from *Th. elongatum* is effective against the Saratov population of *P. triticina*. Under leaf rust epidemics in 2004 and 2005, this combination of translocations positively effected grain productivity (t/ha), grain protein content (%), and grain protein yield (t/ha). In the hard drought conditions of 2007, grain productivity and grain protein content of lines containing a combination of *Lr19* + *Lr26* did not significantly differ from the checks with only one translocation (*Lr19* or *Lr26*). The 6-year average of lines L706-02 and L785-02 (L503*5/Tc *Lr26*) compared with L503 were 0.20 and 0.41% for grain protein content and 12.9 and 6.1% for grain protein yield, respectively.

Effect of a translocation from Thinopyrum intermedium on preharvest-sprouting resistance in wheat lines.

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Preharvest-sprouting resistance is important for the production of grain from spring bread wheat in the Volga Region. The cultivars L503, L 505, Dobrynya (= L1089), and lines L 2032 and L 583) spring bread wheat have a translocation from *Th. elongatum* with *Lr19* and were resistant to preharvest sprouting (germination index from 0.12 to 0.32), but these cultivars and lines were susceptibile to the leaf rust population in Saratov.

The lines L400 and M6R, which have a translocation or whole chromosome from *Th. intermedium,* were resistant to the pathogen but highly susceptible to preharvest sprouting (germination index from 0.87 to 0.95). The F_7–F_{10} RIL populations with resistance to leaf rust and high grain yield and good quality flour is from a crosses between cultivars L503, L 505, Dobrynya, and lines L 2032 and L 583 (all red-grained) with two lines L400 and M6R (susceptible to preharvest spouting) were studied. A total of 41 lines and parents were grown in the field from 2003 to 2006. Each line was represented by a plot of seven 7-m rows with 0.15-m interrow spacing in a randomized complete-block design with four replications. Among the selected lines were 22 red-grained (germination index from 0.31 to 0.93) and 19 white-grained

(germination index from 0.74 to 0.95) lines. A total of 41 lines carried the translocation or the whole chromosome of *Th. intermedium* with preharvest sprouting resistance lower than the better parent.

Preharvest-sprouting resistance of the red-grained sibs and three NIL pairs were significant higher than that of the white-grained lines. L204 (red grained) and L205 (white grained) NILs were identical and equally susceptible to preharvest spouting. The germination index of lines 'BC$_1$F$_6$-8JI2032*2/M6R' was significantly higher than that of L2032. L400 is a 400S sib line that does not have the *Th. intermedium* translocation. The preharvest-sprouting resistance of 400S was significantly higher than that of L400 only in 2003.

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Using of cultivar mixtures of soft spring wheat for improving technological qualities of grain in the Russian Far East.

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Developing cultivars with high technological and baking qualities is the most complicated problem in soft spring wheat selection in the Russian Far East (Shindin and Cherpak 2005). To resolve that problem, we are interested in mixtures consisting of cultivars that are remarkable for their technological and baking qualities. Some scientists determined that cultivar mixtures, as complicated populations, are resistant to abiotic and biotic stresses and have more stable yields and grain quality than homologues cultivars under changeable weather conditions (Sekun 1951; Martynyuk 1964; Kuzmin 1966; Vedrov et.al 1998).

We used the cultivars Khabarovchanka, Zaryanka, and Lira 98, grown in the Far Eastern region, for our mixture. Lira 98 is most valuable for food grain quality among the three cultivars. Lira 98 is used to improve the technological and baking features of Khabarovchanka and Zaryanka, which are less valuable but highly productive and resistant to lodging and disease. A two-cultivar mixture (Khabarovchanka + Lira 98) was 50:50, and the three-cultivar mixture (Khabarovchanka + Lira 98 + Zaryanka) was 33:33:33%.

A comparative analysis of the cultivars and their mixtures showed that Lira 98 and two mixtures turned out to be the best ones by their technological and baking qualities (Table 1). According to the State Standards of the Russian Federation (GOST RF), grain from all the cultivars conforms to the standard of an appreciable sort of wheat. Also important is that the cultivar mixtures yield similar to the initial cultivars in the years of drought, and 10–15% higher in the years of humid weather.

Table 1. Technological qualities of soft spring wheat cultivars and their mixtures (average for years 2001–02).

Cultivars and mixtures	Grain vitreousness (%)	Dough elasticity (alveograph, mm)	Elasticity and stretching ratio (alveograph units)	Flour strength (alveograph units)	Gluten content (%)	Bread output from 100 g of flour (mL)	Baking quality (mark)
Khabarovchanka	56	115	1.9	311	32.4	871	3.6
Zaryanka	55	134	2.4	331	33.5	950	3.8
Lira 98	77	121	1.7	497	37.0	1,010	4.2
Khabarovchanka + Lira 98	66	110	1.2	469	32.4	1,040	4.2
Khabarovchanka + Lira 98 + Zaryanka	61	106	1.0	438	35.2	1,000	4.0

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Races of Puccinia graminis f. sp. tritici in the Russian Federation in 2007.

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The wheat stem rust pathogen, having an extremely high ability to evolve new, virulent phenotypes (such as Ug99), is one of the most important monitored pests that needs annual control in cereal-growing countries. Last year in the Russian Federation, the survival strategy of *P. graminis* f.sp. *tritici* was to emphasize barberry and wild grasses being limited on the wheat cultivars (Lekomtseva et. al. 2007).

In the summer of 2007, unfavorable conditions controlled the spread of stem rust in the European part of the Russian Federation (Central Region and Northern Caucasus) and Western Siberia. The average temperature was about 22ºC with 45% relative humidity in June–July. Local wheat cultivars were quite resistant to stem rust under these climactic conditions.

Barberry was heavily infected by *P. graminis* f.sp. *tritici* in all these regions during May and the first week of June. Furthermore, in early autumn, wild grasses (*Elytrigia*, *Phleum*, and *Festuca*) were severely damaged by wheat stem rust. The spores of *P. graminis* f.sp. *tritici* from barberry and wild grasses were collected and multiplied on the susceptible wheat cultivar Khakasskaya. Race identification of 32 monouredinial isolates of *P. graminis* f.sp. *tritici* was carried out using the standard technique of infection of 20 wheat lines, which were supplied by the USDA–ARS Cereal Disease Laboratory, St. Paul, Minnesota, USA, in 2005.

In Pgt nomenclature (Roelfs and Martens 1988), six races of *P. graminis* f.sp. *tritici* were revealed among the geographical samples (Table 1), and all phenotypes were combined in the single, highly virulent, Stackman's race 15. Race TKNTF (15) dominated in the different regions of the Russian Federation with a frequency of 75% in populations of the fungus.

The race composition of *P. graminis* f. sp. *tritici* on barberry in Northern Caucasus was significantly different from that in Central Russia and Western Siberia. Only two races were found in Central Russia with TKNTF (15) dominating. TKNTF also was prevalent in Western Siberia. No race was dominant of the five virulent phenotypes identified in the Northern Caucasus region, although one of these races was TKNTF (15). Intensive sexual process provides high variability of race composition on barberry in the mountains of Northern Caucasus. This determines

Table 1. Races of *Puccinia graminis* f.sp. *tritici* in some regions of the Russian Federation in 2007.

Race	Area	Plant host	Number of isolates
TKNTF	Central area	barberry	18
	Northern Caucasia	barberry	1
	Central area	couch grass	4
	Central area	fescue	1
TKSTF	Central area	barberry	1
TTSTF	Northern Caucasia	barberry	1
PKNTF	Northern Caucasia	barberry	1
TTNTF	Northern Caucasia	barberry	1
	Western Siberia	barberry	1
TKNRF	Central area	couch grass	2
	Central area	timothy grass	1
Total			32

this region as the most infective source of different virulent phenotypes of stem rust pathogen for cereal grasses. In Central Russia, race TKNTF dominated on coach grass (*Elytrigia*), timothy grass (*Phleum*), and fescue (*Festuca*) in addition to barberry. The virulent phenotype TTKS (Ug99) was not fixed in 2007 and was not found before (Lekomtseva et al. 2004, 2007). Some of the *Sr* genes of wheat, *Sr9b*, *Sr13*, *Sr24*, and *Sr31* were resistant to all stem rust isolates in 2007 (Table 2). Gene *Sr11* was susceptible during 2001–05 but is now resistant. All these genes are recommended for plant-breeding programs to use agains the wheat stem rust pathogen in the Russian Federation.

Table 2. Virulence of isolates of *Puccinia graminis* f.sp. *tritici* to Sr lines of wheat 2007 in the Russian Federation (%).

Gene	%	Gene	%	Gene	%	Gene	%
Sr5	100.0	*Sr9b*	9.3	*Sr11*	21.0	*Sr31*	0.0
Sr6	100.0	*Sr9c*	100.0	*Sr13*	00	*Sr36*	100.0
Sr7b	100.0	*Sr9d*	100.0	*Sr21*	97.0	*Sr38*	100.0
Sr8a	100.0	*Sr9e*	100.0	*Sr24*	0.0	*SrTmp*	100.0
Sr9a	100.0	*Sr10*	100.0	*Sr30*	100.0	*SrWld*	100.0

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Encapsulating winter wheat seed.

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Encapsulating seed creates a macronutrient environment for starting seed. The surface of seed adsorbs NPK and this is more effective than adding to in soil nearby. However, the negative effect of this method is an increase in the osmotic concentration of solution and the high sensitivity of seedlings.

Materials and methods. Seedlings of winter wheat were grown for 10 days at 21°C in plastic cups. Before germination, the seeds were encapsulated with four different solutions: 1 – H_2O, 2 – a 1% soluble, complex fertilizer (NPK), 3 – a 2.5% soluble, complex fertilizer (NPK), and 4 – a 5% soluble, complex fertilizer (NPK).

Results and discussion. The swelling dynamics of seed and the change in the seed humidity in first four days of growth depended upon the concentration of the treatment solution. High concentrations of solution diminished the speed of germination substantially (Fig. 1). The first negative effect observed on the encapsulated seeds was a decline in germination (Fig. 2, p. 180). Increasing the concentration of the treatment solution caused a decline in seed germination (black) and multiplied the number of seed that perished after primary germination (white) (Fig. 2, p. 180).

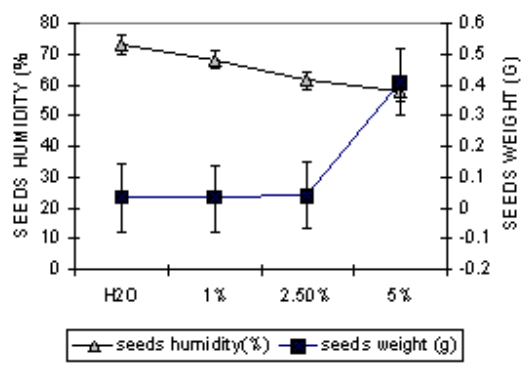

Fig. 1. Change in humidity and weight of seeds depending on concentration of an encapsulation solution (Control is H_2O only).

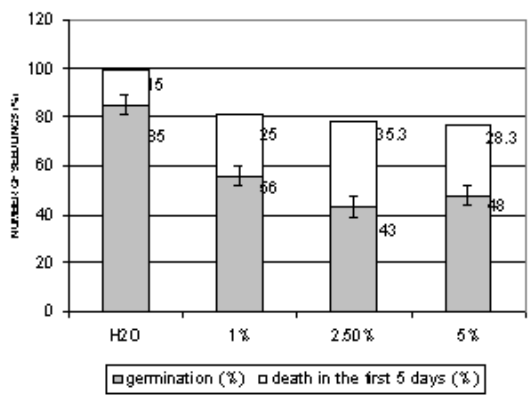

Fig. 2. Germination (%) and the number of dead seedlings after the first five days for different concentrations of encapsulation solutions (Control is H_2O only).

For the first seven days, a plant is nourished from the seed. For this reason, after four days H_2O-treated seedlings overtake encapsulated treated seeds by more then 20%. But at nine days after germination, encapsulated seeds begin to overtake the control plants in proportion to the treatment (Fig. 3).

Using seed encapsulation under soil stress conditions (at a high concentration of Al ions in the soil solution) reduces the negative effect of the high concentration of NPK in the treated seeds. At an increase in the soil solution of the aluminum ions in an encapsulation solution renders a protective effect, causing formation of Al complexes and an increase in seedling growth.

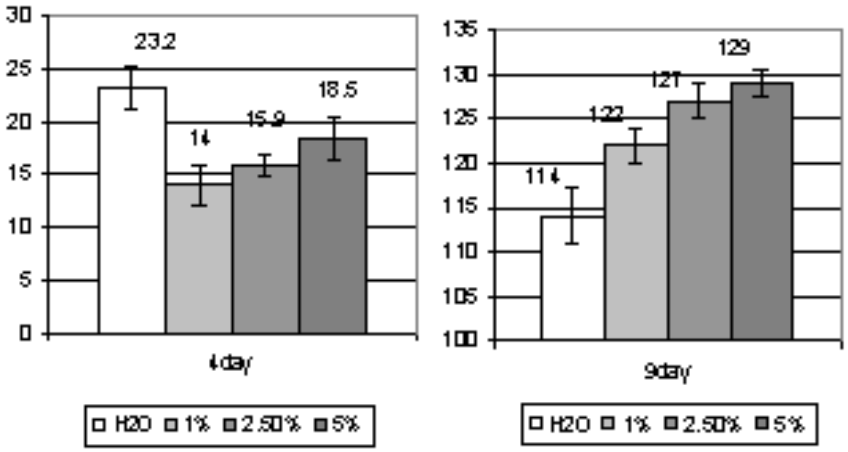

Fig. 3. Length of seedlings (mm) after four and nine days growth for different concentrations of encapsulation solutions (Control is H_2O only).

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Estimating different kinds and lines of spring bread wheat for total resistance to fungus diseases.

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Since 2005, we estimated the resistance of material for loose smut, powdery mildew, and leaf and stem rust in the city of Saratov, Russian Federation. The total resistance to all investigated pathotypes of loose smut have shown that the cultivars Zhigulevskaya and Saratovskaya 70 and lines L658-01 and L2040 are most resistant. The cultivars Lutescens 62, Dobrinja, L503, and L504 were susceptible to all the investigated patotypes. Other cultivars showed race-specific resistance.

A pedigree analysis of the cultivars with sources of resistance to any pathotype of loose smut included *T. turgidum* subsps. *durum, dicoccum,* and *turgidum, T. timopheevi* subsp. *timopheevii,* and *Elytrigia intermedia* and also the cultivars Krimka (a local winter wheat cultivar from Ukraine), Ostka Halisijskaza (a spring bread wheat from Poland),

Selivanovskij Rusak (a local spring bread wheat cultivar from the Volga region), and Beloturka (a local durum cultivar from the Volga region).

Resistance also was studied to leaf and stem rust and powdery mildew in spring bread wheat. Lines selected carrying alien genes that would ensure total resistance to leaf and stem rust and powdery mildew were L2166 and L784/03; for resistance to leaf and stem rust was L2075; for resistance to leaf rust and powdery mildew were Мульти 6R, L2505, L1059, L484/03, and L487/03; for resistance to leaf rust were L1078, L2608, and L2870; and for resistance to powdery mildew was L2032. The donors of resistance to these diseases are *Ae. speltoides, S. cereale, Th. intermedium,* and *T. turgidum subsps. durum* and *dicoccoides*.

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Novel antimicrobial peptides from seeds of Triticum kiharae and Leymus arenarius.

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To protect themselves against pathogens, plants produce a wide array of antimicrobial proteins and peptides (AMPs), some of which are synthesized constitutively, whereas others are induced upon challenge with pathogenic microorganisms (Selitrennikoff 2001; Garcia-Olmedo et al. 2001). Each plant genome encodes hundreds AMPs (Manners 2007). Such biodiversity ensures efficient defense against numerous invading and constantly evolving microorganisms. Most plant AMPs belong to cysteine-rich peptides and contain an even number of cysteine residues, all of which are involved in the formation of intrachain disulphide bridges providing their molecules with high structural stability. Based on cysteine spacing motifs and three-dimensional structures several families of antimicrobial peptides have been discriminated in plants (Broekaert 1997). Hevein-type peptides show structural similarity to the 43-amino-acid residue chitin-binding peptide isolated from the rubber tree *Hevea brasiliensis* L. (Van Parijs et al. 1991) and comprise the single-hevein-domain subfamily in a large group of chitin-binding proteins implicated in plant defense (Raikhel and Lee 1993). Despite sequence similarity, hevein-type AMPs differ in the number of disulphide bonds. Most of them possess 8 cysteine residues forming 4 disulphide bonds and in this respect are close to the chitin-binding domains of class I/IV chitinases (Beintema 1994). Truncated variants with only six cysteine residues also occur (Broekaert et al. 1992). AMPs are regarded as promising agents for plant transformation and production of resistant crops, therefore the search for new, highly potent AMPs is a rapidly developing area of research.

We focused on AMPs from seeds of two Poaceae species, *Leymus arenarius* and *Triticum kiharae*. In contrast to *T. kiharae*, *L. arenarius* grows in a narrow shore region of the White Sea at high soil salinity. We show that both species possess highly homologous hevein-type peptides of unusual structure, which effectively inhibits growth of a wide range of plant pathogens at micromolar concentrations.

Materials and methods. The species used in this study were *T. kiharae* Dorof. et Migush. and *L. arenarius*; the fungi and bacteria *Fusarium solani* VKM F-142, *F. verticillioides* VKM F-670, *F. oxysporum* TSA-4, *Botrytis cinerea* VKM F-85, *Neurospora crassa* VKM F-184, *Pseudomonas syringae* VKM B-1546, *Clavibacter michiganense* subsp. *michiganense* VKM Ac-1144, and *Erwinia carotovora* subsp. *carotovora* VKM B-1247 were obtained from the All-Russian Collection of Microorganisms.

Flour was extracted with 10% acetic acid for 1 h at room temperature and desalted on an Aquapore RP300 column. Freeze-dried acidic extract was subjected to chromatography on Heparin Sepharose. Proteins and peptides were

eluted with a stepwise NaCl gradient. The 100-mM NaCl fraction was collected, desalted as described above, and separated on a Superdex Peptide HR 10/30 column (Amersham, Pharmacia, Biotech, Uppsala, Sweden). Proteins and peptides were eluted with 0.05% TFA, containing 5% acetonitrile, at a flow rate of 250 µl/min and monitored by absorbance at 214 nm. The peptide fraction was further separated by RP-HPLC on a Vydac C18 column (4.6 x 250 mm, particle size 5 µm) with a linear acetonitrile gradient (10-50%) for 1 h at a flow rate of 1 mL/min and 40°C. Peptides were detected at 214 nm. Mass spectra were acquired on a model Reflex III mass spectrometer (Bruker Daltonics, Bremen, Germany). N-terminal amino acid sequences were determined by automated Edman degradation on a model 492 Procise sequencer (Applied Biosystems) according to the manufacturer's protocol.

The antifungal activity of the peptides was tested against several fungi using microtiter-plate assays. Wells were filled with 10 µl of two-fold serial dilutions of the peptide and mixed with 90 µl half-strength potato-glucose broth containing approximately 10^4 spores/mL. The inhibition of spore germination was evaluated by measuring the absorbance at 620 nm. The antibacterial activity of peptides was assayed against several Gram-positive and Gram-negative bacteria using radial diffusion assay. Petri dishes with LB agar were seeded with test bacteria. The peptide solutions (50 µl) were applied to the wells (5 mm in diameter) punched into the agar, and the Petri dishes were incubated at room temperature for 24-48 h. Antibacterial activity was evaluated by the size of the inhibition zone formed around the wells with the peptide solution. The antibiotic claforan and sterile water were used as controls.

Results and discussion. For the isolation of AMPs from *T. kiharae* and *L. arenarius*, we followed the procedure developed for the isolation of *T. kiharae* defensins (Egorov et al. 2005; Odintsova et al. 2006), which included acidic extraction of flour followed by subsequent separation of the protein-peptide extract by a combination of different types of HPLC (affinity, size-exclusion and reversed-phase). As a result, two novel peptides named WAMP and LAMP were isolated from seeds of *T. kiharae* and *L. arenarius*, respectively. The measured monoisotopic molecular masses of the peptides were 44,31 and 4,444 Da for WAMP and LAMP, respectively. Their amino acid sequences were determined by automated Edman degradation after reduction and alkylation.

Considerable sequence similarity with hevein and homologous peptides was revealed providing evidence that both peptides belong to hevein-type AMPs. However, in contrast to hevein, they possess ten cysteine residues and, thus, may be classified as 10-Cys hevein-like peptides. Only two 10-Cys hevein-like peptides have been described so far, isolated from the bark of the trees *Eucommia ulmoides* Oliv. (Huang et al. 2002) and *Euonymus europaeus* L. (Van den Bergh et al. 2002). Despite similarity in the number of cysteine residues, the cysteine motif in WAMP and LAMP differs remarkably from that of their 10-Cys homologues indicating that isolated peptides belong to a new subfamily of hevein-type peptides. Striking similarity with hevein-type domains of cereal class-I chitinases both in amino acid sequences and cysteine patterns was noticed.

Thiol-specific alkylation of unreduced native WAMP and LAMP peptides did not result in molecular mass changes pointing to the involvement of all 10 SH-groups in the formation of 5 disulphide bridges in each peptide. The measured molecular masses of the peptides were in good agreement with calculated values indicating the absence of post-translational modifications except disulphide bridges. Based on sequence similarity with hevein, for which the cysteine connectivities are known, disulphide bridges in WAMP were predicted as follows: C^4–C^{19}, C^1–C^{25}, C^{18}–C^{32}, C^{37}–C^{41}. An additional fifth disulphide bond is likely to be formed between C^{16} and C^{44}. Because chitin is the main component of fungal cell walls and exoskeleton of insects, chitin-binding activity is assumed to be indicative of the ability of polypeptides to inhibit growth of phytopathogenic fungi or pests. The chitin-binding properties of WAMP and LAMP peptides were assayed *in vitro* . Purified peptides were applied to a chitin column and the bound fraction was eluted with 0.1% TFA. RP-HPLC and mass measurements of unbound and bound fractions showed that both peptides eluted only in the bound fraction thus providing evidence that they bind to chitin. Thus both peptides WAMP and LAMP bind chitin. The inhibitory activity of both peptides towards several pathogens was assayed directly. The results for WAMP are presented in Table 1.

Table 1. Antifungal activity of the WAMP peptide (IC_{50} is the concentration necessary for 50% growth inhibition).

Fungus	IC_{50} (µg/ml)
Fusarium solani	5
Fusarium verticillioides	30
Fusarium oxysporum	15
Botrytis cinerea	20
Neurospora crassa	10

Testing of the biological activity of the recombinant peptide WAMP against several fungi including deiteromycetes and ascomycetes showed marked inhibition of spore germination at micromolar concentrations with an IC_{50} ranging from 5 to 30 µM depending on the fungus (Table 1). The highest inhibitory activity was achieved against *F. solani*; the

IC_{50} for this fungus was 5 µM. The WAMP peptide was also tested for inhibition of bacterial growth against both Gram-positive (*C. michiganense*) and Gram-negative bacteria (*P. syringae* and *E. carotovora*); for the Gram-positive bacterium *C. michiganense* the effect was most pronounced (Table 2). The antifungal activity of WAMP is likely to be associated with its chitin-binding activity, whereas the inhibitory effect on bacteria, which are devoid of chitin, implies the existence of some other mechanism.

Table 2. Antibacterial activity of the WAMP peptide.

Peptide concentration (µg/50 µl)*	Inhibition zone in cm including the size of the peptide application zone**		
	P. syringae	*E. carotovora*	*C. michiganense*
10	1.3 (1.4)	1.5 (3.4)	1.7 (3.6)
5	1.2 (1.2)	1.3 (2.7)	1.5 (3.2)
2.5	0.9 (1.0)	1.1 (1.1)	1.3 (3.0)

* Sample volume was 50 µl.
** Size of the peptide application zone was 0.5 cm. The size of the inhibition zone caused by claforan is shown in parentheses.

In summary, two novel, highly homologous, hevein-type and chitin-binding AMPs, WAMP and LAMP, which share sequence similarity with chitin-binding domains of cereal class-I chitinases, were purified from *T. kiharae* and *L. arenarius* seeds. To the best of our knowledge, this is the first report on the occurrence of 10-Cys hevein-type peptides in plant seeds. The cysteine motif in WAMP and LAMP is new and distinct from those of other previously characterized hevein-type AMPs providing evidence that they belong to a new structural type of AMPs. The peptides showed potent antifungal and antibacterial activities at micromolar concentrations and, thus, may be used in genetic transformation of plants to enhance resistance to pathogenic microorganisms.

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Influence of bacterial lipopolysaccharide on the morphogenetic and morphometric parameters of cultivation of wheat somatic callus.

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A major challenge in cultivating plants is ensuring that the cells preserve their morphogenetic potential. The capacity of plant explants for morphogenesis depends on the plants' genotypic peculiarities and on nutrient-medium composition and culture conditions (Yezhova 2003). In addition, plant-associated methylobacteria promote accelerated seed germination and the further seedling growth *in vivo* (Fall 1996), and they also stimulate plant growth and morphogenesis *in vitro* (Kalyayeva et al. 2001). N_2-fixing bacteria promote plant growth only *in vivo* (Steenhoudt and Vanderleyden 2000). Inoculation *in vitro* of plants with these bacteria is technically difficult (Korzhenevskaya 1990). In this context, it is important to treat explants not with a bacterial suspension but with bacterial-cell components that determine the plant-bacterium interaction. The outer-membrane lipopolysaccharide (LPS) of N_2-fixing bacteria of the genus *Azospirillum* is an active bacterial component that not only determines contact bacterium-plant root interactions (Fedonenko et al. 2001) but also is involved in the processes inducing plant responses to these interactions (Matora et al. 1995). The aim of this work was to examine the influence of LPS on the morphometric and morphogenetic parameters of cultivation of wheat somatic callus.

Immature embryos of two model near-isogenic lines (genetic background of cultivar Saratovslaya 29), differing in the *Rht-B1c* alleles were placed on a callus-initiation nutrient medium that contained 2.5, 5, and 10 mg/l LPS. The resulting morphogenic callus were transferred to a regeneration medium with the same LPS content. A study of callus initiation and the cultures' regeneration ability showed that the LPS at the concentrations used did not have a significant effect on the formation of morphogenic callus or on the ability of the *Rht-B1c* gene to increase this parameter, found by us previously (Tkachenko and Lobachev 2008). LPS slightly increased the mass of morphogenic and nonmorphogenic callus. The regeneration ability of the callus and the dynamics of formation of regenerated plants did not change in the presence of the LPS. In summary, the LPS at 2.5, 5, and 10 mg/l did not have a significant effect on the morphogenetic parameters of *in vitro* cultivation of wheat somatic cells. A search further for effective concentrations or for a method of introducing LPS into a nutrient medium for cultivation of wheat somatic embryos will be necessary.

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Influence of bacterial lipopolysaccharide on the functional activity of wheat-seedling-root meristems.

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During the past several decades, plant-growth-promoting rhizobacteria of the genus *Azospirillum* have been used as a model object for study of plant-microbial associativeness owing to their abilities to fix atmospheric nitrogen, to synthesize phytohormones, and to influence plant water status and also owing to other positive factors. In studying associative symbioses, it is important to reveal the associated partners' active components that characterize the effectiveness of this interaction. The outer-membrane lipopolysaccharide (LPS) of gram-negative bacteria of the genus *Azospirillum* has an important role in the formation of associative bacterium-cereal root interaction. In particular, *Azospirillum* LPS induces specific deformation of the wheat-seedling root-hairs, as happens in the presence of whole bacterial cells (Fedonenko et al. 2001). In addition, *Azospirillum* LPS causes an increase in the synthesis of major proteins in the wheat-root cell apoplast, comparable with the action of intact bacterial cells (Matora et al. 1995).

Currently, few data exist on the functional activity of plant-root apical meristems during plant interaction with the associated micropartners, although it is these organs that serve as formative and regulatory centers in the host plant and are a major site of localization of associative bacteria. This work examined the functional activity of wheat-seedling-root meristems during treatment with the LPS isolated from the outer membrane of *A. brasilense* strain Sp245, as compared with inoculation with whole bacterial cells.

Etiolated 3-day-old wheat seedlings were incubated for 24 h either in a solution of 10 mg/l LPS or in a bacterial suspension (cell density, 10^9 cells/ml). The control was noninoculated plants grown in water culture. Samples were taken at 2 days after inoculation. The functional activity of the seedling-root-tip meristem cells was assessed by using two parameters: (1) the results of determination of the cells' mitotic index and (2) comparative estimation of the content of the proliferative antigen of initials (PAI) – a molecular marker of wheat-meristem cells (Evseeva et al. 2007). For determination of the mitotic index of the root-apex meristematic cells, the material was fixed in acetic-acid-ethanol (1:3), stained with acetohematoxylin, macerated with the cytase enzyme, and visualized at 400X magnification. PAI was revealed with an immunochemical test-system developed by us on the basis of the enzyme immunoassay using rabbit monospecific anti-PAI antibodies.

Inoculation of the wheat-seedling roots with whole bacterial cells led to a 2-fold increase in the root-cell mitotic index and to an approximately 1.5-fold increase in PAI content in the cells, as compared with the noninoculated plants. When the wheat-seedling-root system was treated with the isolated LPS, the mitotic index of the root-meristem cells was increased 2.4-fold and PAI content was increased 1.4-fold.

In summary, the increase in PAI content recorded after root inoculation with whole bacteria and also after root treatment with the isolated bacterial LPS is associated with the fact that the cell divisions in the root meristems of inoculated plants proceed more intensively. This possibly facilitates the formation of new adventitious roots and leads to the well-known growth-promoting effects exerted by associative bacteria. Possibly, LPS may be considered to be an active component of the *Azospirillum* cell surface that determines contact bacterium-wheat root interactions and also is involved in the processes inducing plant responses to these interactions.

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Localization of two class-III peroxidase genes expressed in the roots of a Heterodera avenae-resistant wheat line.

The cereal cyst nematode is a pest that seriously affects cereal crops in many of the world's wheat-growing areas. The *H. avenae* resistance gene *Cre2* from *Ae. ventricosa* present in the *Ae. ventricosa*/wheat introgression line H-93-8, was shown to confer a high level of resistance to the Spanish pathotype Ha71 (Delibes et al. 1993). The infection of H-93-8 line with *H. avenae* resulted in a hypersensitive reaction, with syncytial cells deteriorating in a few days. Following nematode infection, peroxidase, esterase, and superoxide dismutase activities increased in H-93-8 roots compared with the parental, susceptible cultivar Almatense, H-10-15 (Andrés et al. 2001). Twenty peroxidase genes were characterized from 211 ESTs and 259 genomic DNA clones of this resistant line. The alignment of deduced amino-acid sequences and phylogenetic clustering with peroxidases from other plant species showed that these enzymes fall into seven different groups (designated TaPrx108 to TaPrx114) that represent peroxidases secreted into the apoplast by a putative N-terminal peptide signal. The expression levels of groups *TaPrx112* and *TaPrx113* in roots of the H-93-8 resistant line increase in response to nematode infection. The maximum peroxidase levels were reached four days post-inoculation. Moreover, the expression of groups *TaPrx112* and *TaPrx113* always was much higher in H-93-8 line (4- and 100-fold, respectively) than in their susceptible parental. This fact may be related to a constitutive mechanism of defense in this resistant line. The chromosomal assignment of peroxidases of both groups was done using Sears' aneuploid wheat lines (Sears 1954; Kimber and Sears 1968) and PCR-specific primers from peroxidases. Two PCR fragments obtained from peroxidases *TaPrx112-F* and *TaPrx113-F* were absents in nulli-tetrasomic and ditelosomic lines N2BT2D and Dt2BL, respectively. Therefore, both peroxidase genes would be located in 2B short arm chromosome of wheat.

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Cooperation with other institutions.

We are coöperating with 'Agrosa Semillas Selectas SA'.

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ITEMS FROM TURKEY

TURKEY–CIMMYT–ICARDA
CIMMYT International Winter Wheat Improvement Center (IWWIP), Turkey Regional Office.

Alex Morgounov, Beyhan Akin, Mesut Keser, and Yuksel Kaya.

The overall objective of IWWIP remained the same: development of high-yielding and drought-tolerant winter/facultative wheat cultivars resistant to prevailing diseases with suitable grain quality as well as facilitation of the global winter wheat germ plasm exchange. The 2007–08 season was characterized by further transition of the IWWIP towards a more focused research and cultivar development for irrigated and semiarid environments on one hand. On the other hand, substantial efforts continued for the program to be more responsive to the clients, more transparent, and more efficient. The recommendations of 2008 IWWIP Traveling Seminar served as a guide for focusing the program and restructuring the international nursery system. The IWWIP global survey was completed in 2008 (report available on request) demonstrating that out of 49 programs responding to survey, 95% were satisfied with the germ plasm provided and appreciated the diversity of the traits. Two important practical suggestions were made, provide the data with the international nurseries (implemented) and increase the amount of seed distributed for Facultative and Winter Wheat Observation Nursery (FAWWON; implemented). The IWWIP governing mechanism, including coördinators from Turkey, CIMMYT, and ICARDA; a technical committee; a steering committee; and an annual meeting, functioned well and contributed substantially to streamlining the program. The weather conditions of 2007–08 season were not as dry as in previous year but quite variable across locations some with excellent yield potential (Konya and Edirne), whereas others suffering almost complete failure due to drought (Dyiarbakir and Haymana). In general, the season was interesting and productive from the breeding point of view.

International nurseries. The new system of international nurseries is in place since 2007 and proved to serve the IWWIP community well. One important modification was made for the 2008–09 international nurseries. All the entries entering the IWWYT nursery were repeated in the respective FAWWON as the first block essentially under the same numbers, which provided the best germ plasm to FAWWON coöperators who did not receive the IWWYT. Table 1 lists the nurseries that have been distributed for 2008–09 season. For the 2009–10 season, the program plans to expand the IWWYT trials to 30–40 entries also including the best introduced germ plasm.

Table 1. The International Winter Wheat Improvement Program international nurseries distributed for the 2008–09 season.

Nursery	Number of entries	Reps	Amount of seed per entry (g)	% of introduced germ plasm	Number of sets distributed (Turkey/OSU)
16th Facultative and Winter Wheat Observation Nursery for Irrigated conditions (16th FAWWON–IRR)	90	1	30	67	86/30
16th Facultative and Winter Wheat Observation Nursery for Semiarid conditions (16th FAWWON–SA)	65	1	30	25	50/30
12th International Winter Wheat Yield Trial for Irrigated conditions (12th IWWYT–IRR)	20	2	180	0	35
11th International Winter Wheat Yield Trial for Semiarid conditions (12th IWWYT–SA)	20	2	160	0	30

Cultivars released. The collection of the data on released cultivars is challenging and only possible through coöperation and feedback from the region. Table 2 (p. 190) presents the list of winter facultative wheat germ plasm originating from the IWWIP and released in the region.

Table 2. The list of winter/facultative wheat varieties originating from International Winter Wheat Improvement Program and released in the CWANA region (* – the area is being updated presently).

Country	Cultivar	Year	Pedigree	Area* (ha)
Afghanistan	Pamir 94	1994	YMH/TOB//MCD/3/LIRA	150,000
Afghanistan	Gul 96	1996	ID800994.W/VEE	
Afghanistan	Sultan 95	n.a.	AGRI/NAC	
Afghanistan	Solh 02	2002	OK 82282//BOW/NKT	
Armenia	Armcim	2006	1D13.1/MLT	300
Georgia	Mtshetskaya 1	2002	TAST/SPRW//ZAR	100
Iran	Tous	2002	SPN/MCD//CAMA/3/NZT	25,000
Iran	Zarrin	1996	NAI60/HEINE VII//BUC/3/F59.71/GHK	200,000
Kazakhstan	Egemen	2007	BHR/AGA//SNI/3/TRK13	500
Kyrghyzstan	Almira	2005	F.474S10.1	50
Kyrghyzstan	Azibrosh	2004	OK82282//BOW/NKT	3,000
Kyrghyzstan	Djamin	2005	NS55-58/VEE	3,000
Kyrghyzstan	Zubkov	2004	1D13/MLT//KAUZ	1,000
Tajikistan	Alex	2007	PYN/BAU	2,500
Tajikistan	Norman	2007	OR F1.158/FDL//BLO/3/SHI4414/CROW	2,500
Tajikistan	Ormon	2008	NWT/3/TAST/SPRW//TAW12399.75	1,700
Turkey	Alpaslan	2001	TX69A509-2//BLUEBOY II/FOX	6,500
Turkey	Alpu 2001	2001	ID800994.W/VEERY	20,000
Turkey	Bagci 02	2002	HN7/OROFEN//BEIJING 8/3/SERI M 82/4/ 74CB462/ TRAPPER//VONA	1,500
Turkey	Kinaci 97	1997	YMH/TOB//MCD/3/LIRA	20,000
Turkey	Cetinel 2000	2000	MALCOLM/4/VPM 1/MOISSON 951//HILL 81/3/ STEPHENS	1
Turkey	Daphan	2002	JUPATECO F 73/4/COLLAFEN/3/II14.53/ ODIN// CI13431/WA00477	26,000
Turkey	Goksu 99	1999	AGRI/NACOZARI F 76	100
Turkey	Gün 91	1999	FUNDALEA 35.70/MOCHIS 73	350,000
Turkey	Izgi	2001	CA8055/KUTLUK 94	1
Turkey	Karasu 90	1990	LOVRIN 11/BOLAL 2973// MIRONOVSKAYA 264	32,800
Turkey	Nenehatun	2001	NORD DEPREZ/PULLMAN SELECTION 101//BLUE-BOY	16,000
Turkey	Ozcan	2004	K8/MM2	50
Turkey	Sakin	2002	PITIC 62/FUNO*2//VALDIVIA/3/ CO723595	600
Turkey	Soyer	2002	ATAY 85/GALVEZ S 87	0
Turkey	Sultan 95	1995	AGRI/NACOZARI F 76	50,000
Turkey	Yildirim	2002	ID800994.W/VEERY	6,500
Turkey	Yildiz 98	1998	55.1744/PULLMAN SELECTION 101//MAYA 74/3/MUS-ALA/PRIMO//MAYA 74/ALONDRA	10,000
Turkey	Ekiz	2004	F885 K1.1/SXL	5,000
Turkey	Canik 2003	2003	ANZA/VRZ	250
Turkey	Hanli	2007	OK82282//BOW/NKT/3/F4105	0
Turkey	Beskopru	2007	362K2.111/6/NKT/5/TOB/CNO67// TOB/8156/3/CAL//BB/ CNO67/4/TRM	0
Turkey	Müfitbey	2006	NGDA146/4/YMH/TOB//MCD/3/LIRA/5/F130L1.12	1
Turkmenistan	Bitarap	2004	SN64//SKE/2*ANE/3/SX/4/BEZ/5/SERI	25,000
Uzbekistan	Dostlik	2002	YMH/TOB//MCD/3/LIRA	40,000

Table 3. Stem rust reaction of selected Internation Wheat Wheat Improvement Program entries in Njoro, Kenya, 2008. Rust reactions were recorded on two dates, 20 October 2008 and 31 October, 2008.

Nursery	Entry	Cname	Origin	Sr 20.10.08	Sr 31.10.08
08CBWF	19	VORONA//MILAN/SHA7/3/MV17	TCI	20MRMS	15MR, 30S
08CBWF	20	MOTAH/BOUHOUTH6	TCI	15MR	15MR
08CBWF	28	VORONA/OPATA//PYN/BAU	TCI	20MRMS	20MRMS
08CBWF	32	KS82W409/SPN//TAM106/TX78V3630	TCI	10MR	10MR
08CBWF	57	STARSHINA	RUS	20MRMS	20MRMS
08CBWF	72	NEMURA/CRDN//78014-40	OR–TCI	20MR	20MR
08CBWF	73	PYN/BAU	MX	RV	20MRMS
08CBWF	76	AGRI/BJY//VEE/3/BUL6687.12	TCI	RV	20MRMS
08CBWF	91	CITARI-9	TCI	20MR	20MRMS
08CBWF	98	POBEDA 50	RUS	RV	20MRMS
08CBWF	107	UN-49	UN	20MRMS	20MRMS
08CBWF	124	LC 909 MIMA	BG–KC	20MRMS	20MR, 40S
08CBWF	188	ICDW-9246	AFG	20MR	20MR
08CBWF	194	338-K1-1//ANB/BUC/3/GS50A	TCI	20MRMS	20MRMS
08CBWF	195	338-K1-1//ANB/BUC/3/GS50A	TCI	10MR	10MS
08CBWF	201	BILINMIYEN96.7	TCI	RV	10MRMS
08CBWF	269	DMN//SUT/AG(ES86-7)/3/OPATA/ 4/ TX71A1039-VI*3/AMI	TCI	20MRMS	20MRMS
10th EYT-SA	9,909	SABALAN/4/VRZ/3/OR F1.148/ TDL// BLO	TCI	10MS	10MS, 10M
10th EYT-SA	9,920	AGRI/BJY//VEE/3/GUN91/4/ CHAM6//1D13.1/MLT	TCI	30MS	100S
10th EYT-SA	9,923	SUBEN-7	SY	20MR	20MR
11th IWWYT-IRR	9,819	ID800994.W/KAUZ//ROLLER/4/ WN158/ NSD//4105W/3/TAM200	TCI	10MR	10MR
15th FAW-IRR	9	AGRI/NAC//KAUZ/3/1D13.1/MLT	TCI	20MS	20MRMS
15th FAW-IRR	34	KAUZ//ALTAR 84/AOS/3/F10S-1	TCI	20MR	20MR
15th FAW-IRR	39	ID800994.W/KAUZ//ROLLER/4/ WN158/ NSD//4105W/3/TAM200	TCI	15MR	15MR
15th FAW-IRR	40	SULTAN95	TCI	5MS	10MR
15th FAW-IRR	51	BONITO//KAREE/TUGELA	TCI	10MRMS	10MRMS
15th FAW-IRR	56	B.YAPEYU/P.QUINTAL	ARG	20MR	20MRMS
15th FAW-IRR	59	CONA/KLCRI/3/BPON/W000015//KL-CRI	ARG	10MRMS	10MRMS
15th FAW-IRR	61	CONA/KLCRI/3/BPON/W000015//KL-CRI	ARG	10MS	10MS
15th FAW-IRR	67	KL. ESCUDO	ARG	5MRMS	20M
15th FAW-IRR	97	F99419G4-1A12	RO	10MR	20MR
15th FAW-IRR	98	Od.Krasnok/DOR	RO	10MRMS	20MR
15th FAW-IRR	109	INIA TORCAZA	URU	10MR (1 PL-20S)	10MRMS
15th FAW-SA	10	ZARGANA-6	TCI	20MR	20MR
15th FAW-SA	16	MAHON DEMIAS/3/HIM/ CNDR// CA8055	TCI	10MR (1 PL-30S)	10MR
15th FAW-SA	28	PYN/BAU//VORONA/HD2402	TCI	20MR	20MR
15th FAW-SA	36	SUBEN/4/PKG16/OLV13// JSW3/3/ KVZ/./IDH2	TCI	RV	10MRMS
15th FAW-SA	43	UNKNOWN-3	IR	10MRMS	10MSMR
15th FAW-SA	48	059E//Jagger/Pecos	US–Agripro	10MS	10MS
15th FAW-SA	49	TAM 105/3/NE70654/BBY// BOW"S"/4/ Century*3/TA2450	US–AgriPro	10MRMS	10MRMS
16th FAW-IRR	63	MV-TALTOS	HUN	0	10MR
16th FAW-IRR	72	F00429GP1	ROM	TR	10MR
16th FAW-SA	121	TIRCHMIR1//71ST2959/CROW/4/ NWT/3/TAST/SPRW//TAW12399.75	TCI	15MS	20MRMS

Stem rust evaluation in Kenya. During the off-and regular season of 2008 a good evaluation of resistance to stem rust in Kenya was conducted. The previous two years failed to produce reliable data. In 2008, more than 700 IWWIP entries were evaluated and approximately 120 entries were identified that possess variable degrees of resistance (a sample is presented in Table 3, p. 191). Personally conducting the evaluation in Kenya was very important, because it allowed a good feel for the germ plasm and confidence in selection. The data singled out F_2 and F_3 segregating populations, tracing their pedigree to resistant parents. Respectively, a stem rust Ug99-resistant F_3 was assembled and distributed in Turkey and outside (Iran, Azerbaijan, and Kazakhstan). The selected entries are being multiplied in Turkey and Oregon, USA, for international distribution. Subsets were sent to Cornell University for haplotyping and to the Cereal Disease Laboratory for seedlings tests to identify possible genes. The selected entries will be used for targeted crosses.

ITEMS FROM THE UKRAINE

INSTITUTE OF PLANT PRODUCTION N.A. V.YA. YURJEV OF UKRAINIAN ACADEMY OF AGRARIAN SCIENCES
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Change in the climate and sowing dates of winter wheat.

Yu.G. Krasilovets and N.V. Kuzmenko.

The best conditions for winter wheat yields are at emergence during the 55–60 days in autumn. Winter wheat, planted at both early and late sowing dates, have insufficient winter hardiness and considerably reduced yield ability. When sown earlier than the optimal date, plants develop a heavy aboveground mass and, thus, loose more moisture and nutrients in the autumn than those sown at the optimal date. On the contrary, late-sown plants fail to develop sufficient vegetation and root systems and can not fully use water and nutrients (Zubets MV 2004). The sowing date also influences the phytosanitary state of the wheat crop.

Early sown plants are damaged by Hessian and other flies, cereal aphids, cicadas, and also, to a greater degree, by root rots, brown leaf rust, powdery mildew, Septoria, and virus diseases (Rakhmaninov 1925; Bockman and Knout 1971; Pavlov 1976; Susidko et al. 1976). At the same time, later sown plants are damaged more severely by spring generations of flies (Zagovora 1953) and wheat sawflies (Begzadyan 1984; Peresypkin 1976).

The dependence of winter wheat yield on sowing date was studied at the Plant Production Institute nd. a. V. Ya. Yuriev of the UAAS (the eastern Forest-Steppe of Ukraine) from 1914-17, 1937-41 (Solodkyi 1959), 1970-72 (Matushkin 1985), 1987-90 (Budyennyi et al. 1992), and 2001-07 (Krasilovets et al. 2007). According to these multi-year studies, particularly 1914-90 in the latitude of Kharkov, maximum grain yield in winter wheat after fallow forecrops was obtained when sown on the 25 August (Table 1). When the sowing took-place on 15-18 August, crop yield was 94–96 % compared to the 25th. Sowing on 1, 10, and 20 September reduced this index to 97–99%, 90–92%, and 75–81%,

Table 1. Average yield of winter wheat on fallow at different sowing dates in experiments at the Plant Production Institute nd. a. V. Ya. Yuriev, Ukraine, % of maximum (* maximum yield, t/ha).

Sowing date	1914–17	1937–41	1970–72	1987–90	2001–04	2004–07
15–18 August	94	99	—	97	—	—
25 August	100 (2.55)*	100 (2.20)*	100 (4.54)*	100 (5.21)*	—	—
1 September	—	97	98	99	—	96
10 September	92	90	92	92	96	100 (5.36)*
20 September	75	—	78	81	100 (6.51)*	9-6
25 September	50	—	—	68	98	—

respectively. These studies indicate the optimal sowing dates for winter wheat were 25 August–10 September for the southern Forest-Steppe of the Eastern Ukraine.

Studies between 1987–90 have shown that, for such forecrops as annual grasses, maize for silage, and barley, the highest winter wheat yield was achieved when the crop had been sown from 25 August and 10 September (Budyennyi et al. 1992). Starting roughly from 2001, the highest winter wheat yield was obtained when sown between 10–20 September or 15 days later than in previous years. This phenomenon is conditioned by a rise in temperature. The average yearly temperatures in the latitude of Kharkov rose from 69°C during 1910–66 to 8.1°C between 1981–2000, and to 9°C between 2001–07. This index, compared to the previous period, increased by 1.2°C betweem 1981–2000 and 21°C between 2001–07.

In the latitude of Kharkov between August–October 1969–71 and 1986–89, the average monthly temperatures came nearer to the climatic norm. From August–October 1969–71, the average air temperature was 0.3°C higher and 0.1°C higher in 1986–89 compared to the climatic norm. Since 2001, the average monthly temperature in the Kharkov latitude has risen considerably (August–October, see Table 2). On average during 2001–08, this index exceeded the climatic norm by 1.7°C.

Table 2. Hydrothermal conditions in the latitude of the Plant Production Institute nd. a. V. Ya. Yuriev, Kharkov, Ukraine.

Month	Average montly air temperature (°C)			Total monthly precipitation (mm)			Hydrothermal coefficient		
	2001–08	Climatic norm	± norm	2001–08	Climatic norm	± norm	2001–08	Climatic norm	± norm
April	9.6	8.2	+1.2	32.6	35.7	–3.1	—	—	—
May	16.5	15.4	+1.1	44.9	47.9	–3.0	0.9	1.0	–0.1
June	19.4	19.4	0.0	81.0	63.5	+17.5	1.3	1.1	–0.2
July	22.7	21.3	+1.4	80.2	64.2	+16.0	1.2	1.0	+0.2
August	22.2	20.0	+2.2	44.9	55.2	–10.3	0.8	0.9	–0.1
September	15.7	14.2	+1.5	51.7	38.0	+13.7	—	—	—
October	8.8	7.3	+1.5	47.1	35.0	+12.1	—	—	—
7-month index	16.4	15.1	+1.3	382.4	339.5	+42.9	1.1	1.0	+0.1

These studies have shown that between 2003–05, the planting of winter wheat on both black fallow and after peas between 10–20 September, when compared to 1 September, favor a considerable improvement of the phytosanitary state. Planting winter wheat on black fallow on 20 September reduced damage by flies in the autumn by 91.5%, and after a pea forecrop by 96.0 %, compared to the planting on 1 September; the biological efficiency of root rot development with these forecrops in this period was 53.1 and 90.7 %, respectively. The yield increase of winter wheat sown on black fallow on 20 September was 1.42 t/ha after a pea forecrop and 0.64 t/ha after sowing on 1 September (Krasilovets et al. 2006).

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ITEMS FROM UNITED KINGDOM

JOHN INNES CENTRE
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Genetic biodiversity for stripe and stem rust resistance in African wheat genotypes.

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This new program, launched in February 2008, involves the genetic and phenotypic characterisation of over 500 African wheat genotypes for resistance to the new virulent stem rust, *P. graminis* Ug99-derived strains, and to stripe rust, *P. striiformis*. Stem rust resistance will be assessed in field trials in Njoro, Kenya, the first trial taking place in March 2009, and by seedling tests. This collection also will be assessed for stripe rust resistance in South Africa and the UK. The population is being assessed for molecular diversity using SSR and AFLP markers. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK; Prof. Zakkie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA; Dr. Ruth Wanyera, KARI, Njoro, Kenya; and Dr. Susanna Dreisigacker, CIMMYT, Mexico. The student working on this project is Mr. Turnbull Chama. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative.

Fine mapping of durable resistance to stripe rust in the South African wheat cultivar Kariega.

Gloudi Agenbag, Ruth MacCormack, Zakkie Pretorius, Debbie Snyman, Denise Liebenberg, Lesley A. Boyd, and Renée Prins.

The objective of this study is to use an EST marker strategy to fine map previously identified QTL for effective adult-plant resistance to stripe rust in the cultivar Kariega. Two major QTL have been identified, *QYr.sgi-7D* and *QYr.sgi-2B.1*, as well as minor QTL, which included *QYr.sgi-4A* and *QYr.sgi-2B.2*. All evidence indicates that the 7D QTL is the *Lr34/Yr18* complex. To date, one EST-derived marker has mapped to each of the 2BS intervals, and one marker has mapped to 4AL in the target QTL interval. These ESTs provide anchors for further EST-derived marker development within the QTL intervals. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK and Profs. Zak-

kie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA. The student working on this project is Miss Gloudi Agenbag. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative.

Genetic mapping of adult-plant stripe rust resistance within the European wheat cultivar Cappelle Desprez.

Gloudi Agenbag, Zakkie Pretorius, Debbie Snyman, Denise Liebenberg, Lesley A. Boyd, and Renée Prins.

Cultivar Cappelle Desprez was grown in Western Europe throughout the 1960s and 1970s, being a known source of durable adult-plant resistance (APR) to stripe rust. The stripe rust resistance in Cappelle Desprez has remained effective under South African conditions since 2001, and programs are underway to select for this APR in a cross to the South African cultivar Palmiet. Zakkie Pretorius is currently developing an RIL population derived from this cross that will be used to genetically map the resistance QTL for stripe rust resistance in Cappelle Desprez. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK and Profs. Zakkie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA. The student working on this project is Miss Gloudi Agenbag. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative.

Biological and transcriptional defence responses of wheat to nonadapted and adapted species of the blast fungus Magnaporthe.

Hale A. Tufan, Graham R.D. McGrann, Andreas Magusin, Jean-Benoit Morel, Lucie Miché, and Lesley A. Boyd.

The *Magnaporthe* species complex infects over 50 Graminaeceous plant species, and rice blast, caused by *Magnaporthe oryzae*, is one of the most economically important diseases worldwide. *M. oryzae* tends to colonise cultivated grasses, whereas *M. grisea* attacks wild grass species. Recently in Brazil, *M. oryzae* has become a problem to local wheat production and could potentially become a threat to global wheat production. We have investigated the resistance present in the wheat cultivar Renan against species of *Magnaporthe* that are either adapted or nonadapted to wheat. Confocal microscopy demonstrated that the early defence response against both adapted and nonadapted species involves the production of a diffuse autofluorescent HALO structure around the site of attempted fungal penetration. A high proportion of HALOs were associated with penetration events over time in response to the nonadapted *M. grisea*, with very few infection attempts being able to progress beyond the HALO stage. In contrast, the adapted *M. oryzae* was frequently able to infect past the HALO stage and develop further into the leaf. In these cases whole cell autofluorescence was often observed, indicative of a hypersensitive response to prevent further pathogen colonisation.

Microarray analysis of the transcriptome 24 hours post inoculation indicated that wheat undergoes extensive transcriptional reprogramming during interactions with both adapted and nonadapted species. Comparison between the differentially expressed transcripts responding to the adapted and nonadapted *Magnaporthe* species revealed both conservation and diversification in the type of transcripts that were regulated, suggesting some common mechanisms in the defence response against adapted and nonadapted *Magnaporthe* species, while highlighting potential differences that may result in the observed biological phenotypes. Functional genomic approaches are currently being used to examine the roles of candidate transcripts in innate immunity of wheat against different species of the blast fungus. This program was part of a collaboration with Drs. Jean-Benoit Morel and Lucie Miché at UMR BGPI INRA/CIRAD, Montpellier, France, and was funded by a CGIAR, Generation Challenge project, Cereal Immunity.

Publications.

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ITEMS FROM THE UNITED STATES OF AMERICA

GEORGIA / FLORIDA

GEORGIA EXPERIMENT STATION / UNIVERSITY OF GEORGIA
Griffin, GA 30223-1197, USA.

J.W. Johnson, J.W. Buck, G.D. Buntin, and Z. Chen.

The 2008 Georgia winter wheat crop was grown on about 380,000 planted acres. Yields of wheat grown by top producers were around 6,000 kg/ha on resistant cultivars to stripe rust. Average yield for the state was 3,200 kg/ha. The growing season was characterized by drought conditions in the autumn that delayed planting and in the spring by very dry conditions during the grain-filling period.

Breeding.

Two high-yielding, broadly adapted wheat cultivars, GA981621-5E34 and GA981622-5E35, were released by the University of Georgia in 2008 for growers in the Southeast. These two SRWW cultivars are high yielding with excellent test weight and disease and insect resistance and will offer new sources of resistance to both pathogens and insects. GA981621-5E34 and GA981622-5E35 have excellent stripe rust resistance derived from PIO26R61 and Hessian fly. The cultivars are medium-maturing, soft wheats with good resistance to wheat soil-borne mosaic virus.

GA 981621-5E34 (AGS 2485 / PIO 26R61) is a medium-late maturity SRWW that combines high yield, high test weight, and good straw strength. The cultivar has resistance to leaf rust, stripe rust, and soil-borne mosaic virus and is moderately resistance to powdery mildew. GA 981621-5E34 is resistant to Hessian fly. Maturity averages about 4 days later than that of AGS 2000 in Georgia.

GA 981622-5E35 (AGS 2000 / PIO 26R61) is a medium-late maturity SRWW that combines high yield, high test weight, and good straw strength. The cultivar has resistance to leaf rust, stripe rust, and soil-borne mosaic virus, and is moderately resistance to powdery mildew. GA 981622-5E35 is resistant to Hessian fly. Maturity averages similar to that of AGS 2000 in Georgia.

Hessian Fly.

Forty-six elite lines were field evaluated for Hessian fly resistance at Plains and Griffin, GA. Twenty-seven lines had good levels of resistance at both locations. BC_3F_2 and subsequent generation wheat lines of more recent crosses that were segregating for Hessian fly resistance were screened to select progeny with resistance. Lines containing *H13* or *H21* resistance genes have been selected and carried forward into elite lines.

Entries in the Georgia State Wheat Variety trial also were evaluated for Hessian fly resistance at Plains and Griffin, GA. A total of 65 entries, including 24 advanced University of Georgia (UGA) lines, were evaluated. A total of 22 entries were rated as moderately or highly resistant at Plains. About 83% (20/24) of the resistant entries were either released cultivars or advanced lines from the UGA small grain breeding program. Three triticale entries also were evaluated. Infestations at Griffin were lower but also provided useful results. Results of State Wheat Variety trial were published in the 2007/2008 Georgia Small Grain Performance Tests. Results of these evaluations have been critically important in informing Georgia county agents and farmers about which varieties are resistant to Hessian fly.

Samples of Hessian fly populations were collected near Griffin and Plains, GA in January 2007, and shipped to Sue Cambron at Purdue University for biotype determination and gene resistance evaluation. Hessian fly biotype preva-

lence has shifted over the last 20 years. In 1986, the prevalent biotype throughout the state was biotype E. Since then, Hessian fly populations have rapidly shifted to biotype O in southern GA (Fig. 1) and only the *H7H8* gene combination remains effect in southern GA. Currently populations in southern GA about 50% biotype O and L. The population in northern GA has rapidly progressed to 100% Biotype L (Table 1) indicating that none of the older deployed resistance genes are effect. Despite this result, several cultivars from the Georgia breeding program continue to exhibit good levels of field resistance. The virulence of the Griffin population also was assessed for 19 other genes (Table 1). Genes *H12*, *H18*, *H21*, *H24*, and *H26* had high levels of virulence against this population. In similar evaluations, *H13* was virulent at most locations in the southern region but not in the Griffin population. Nevertheless *H13* is now deployed in several commercial cultivars and is in a number of elite lines from the Georgia program. These cultivars show high levels of Hessian fly resistance in the field throughout the state. *H21* shows high levels of virulence to Hessian fly populations throughout the Southeast and also is in several elite lines in the Georgia program.

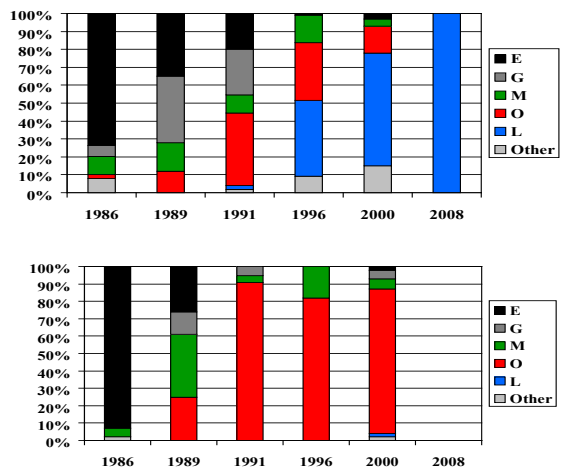

Fig. 1. Proportion of Hessian fly biotypes from 1986–2000 in northern (left) and southern (right) Georgia.

Table 1. Hessian fly virulence to a population from Pike County (near Griffin) Georgia, USA, to selected Hessian fly-resistance genes; biotypes are based on the differentials (*H3*, *H5*, *H6*, and *H7H8* highlighted in yellow; R = plants with resistance reaction; S = plants with a susceptible reaction).

Hessian fly gene	Source	Pike County, GA	
		R-S	% R
No gene	Newton	0–20	0
H3	Monon	0–24	0
H5	Magnum	0–18	0
H6	Caldwell	0–18	0
H7H8	Seneca	0–19	0
H9	Iris	13–7	65
H10	Joy	10–9	53
H11	Karen	0–18	0
H12	Lola	19–0	100
H13	Molly	4–18	18
H14	921676A3-5	0–15	0
H15	81602C5-3-3-8-1	0–4	0
H16	921682A4-6	2–13	13
H17	921680D1-7	0–12	0
H18	Marquillo	18–1	95
H19	84702B14-1-3-4-3	0–1	0
H21	Hamlet	23–3	88
H22	KS85WGRC01	15–5	75
H23	KS89WGRC03	4–20	17
H24	KS89WGRC6	19–0	100
H25	PI 592732	12–6	11
H26	KS92WGRC26	14–0	100
H28	PI 59190	3–1	75
H31	P921696A1-15-2-1	19–1	95

Scab.

Fusarium head blight is a potential devastating disease in the Southeast region in the United States where low temperature and misted weather occurs frequently during soft red winter wheat flowering. Several diverse native sources of type-II resistance from other breeding programs (Coker 9511, Truman, Roane, Ernie, OH 02-12686, IL01-11934, and IL 00-8530) are being incorporated into GA scab-resistant lines. Breeding for type-I resistance is also in progress. Populations are derived from Truman (GA 061209 (Truman / 2*AGS 2000 sib) and Frontana. FHB resistance from derivatives of Sumai 3 (INW 0411 (P97397E1-11), INW 0412, VA02W-713, VA01W-476, and VA 04W-433) and derived lines from Futai8944 and W14 will be crossed with our best yielding lines.

Marker-assisted backcrossing of QTL from Sumai 3 (3BS and 5AS), Goldfield (2BS), and Ernie (5AS, 3BS, and 4BL) will be performed using high-yielding and moderately resistant lines as recurrent parents. Pyramiding QTL (3BS and 5AS) will greatly facilitate development of cultivars that have more effective FHB resistance from native and exotic sources. Derived lines from Futai8944, and W14, VA01W-461 (Roane / W14), and VA FE24 (Ernie *2 // Futai 8944

2* Ernie) will be evaluated and validated for the presence of two major FHB resistance QTL on chromosome 3BS and 5AS among elite lines and backcross populations. Populations of BC_1F_2 and BC_1F_3 plants with AGS 2000 as the recurrent parent will be screened with markers for *Fhb1* (3BS) and *Xbarc117*, *Xgwm156*, *Xbarc100*, and *Xbarc186* for 5AS.

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KANSAS

KANSAS AGRICULTURAL STATISTICS
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Overley recaptures number one.

Overley became the leading cultivar of wheat seeded in Kansas for 2009. Jagalene held this position last year. Accounting for 13.7% of the state's wheat, Overley was the most popular cultivar in three of the nine districts. New to the top ten is Fuller, ranking second with 10.9% of the acreage. Santa Fe moved up to third place with 9.5% of the states acreage. Jagalene moved down to fourth place with 9.1% of the acreage. Jagger came in fifth at 8.5% down 6.2 points from last year. TAM 111 moved down to sixth place at 6.8% New to the top ten is Postrock, ranking seventh with 6.0% of the acreage. The KSU-maintained cultivar 2137 down to eighth place at 2.9%; T81 moved down to ninth place at 2.5%. TAM 112, rounded out the top ten at 2.0%. Acres planted with blended cultivars were not included in the rankings by cultivar. Blends accounted for 10.7% of the state's planted acres and were used more extensively in the north-central, northwest, and central areas of the State. Out of the total acres planted with blends, 37.5% included Santa Fe in the blend, and 33.1% had Jagalene in the blend. Hard white cultivars accounted for 1.0% of the state's acreage. Danby was the leading hard white cultivar, accounting for 70% of the state's white wheat. The majority of the white wheat was planted in the western third of the State. This Wheat Variety project is funded by the Kansas Wheat Commission.

Table 1. Top 10 cultivars grown in the state of Kansas in 2009 and their percent of seeded acreage.

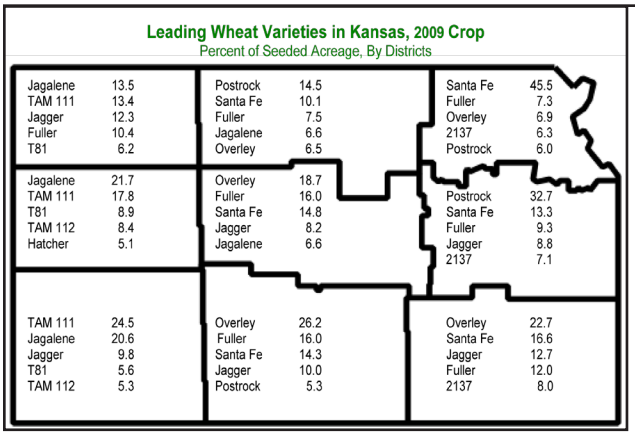
#	Cultivar	% of acerage
1.	Overley	13.7
2.	Fuller	10.9
3.	Santa Fe	9.5
4.	Jagalene	9.1
5.	Jagger	8.5
6.	TAM 111	6.8
7.	Postrock	6.0
8.	2137	2.9
9.	T81	2.5
10.	TAM 112	2.0

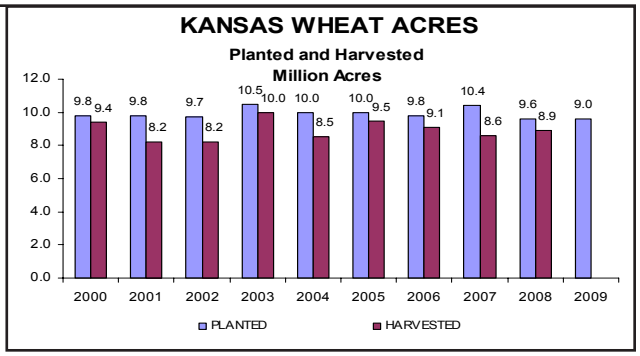
Table 2. Distribution of Kansas winter wheat cultivars, 2009 crop (— = cultivar not reported in this district; 0 = < 1%).

Cultivar	Agricultural Statistics Districts									
	NW	WC	SW	NC	C	SC	NE	EC	SE	State
Overley	1.5	0.3	0.1	6.5	18.7	26.2	6.9	4.7	22.7	13.7
Fuller	10.4	1.6	0.7	7.5	16.0	16.0	7.3	9.3	12.0	10.9
Santa Fe	—	—	—	10.1	14.8	14.3	45.5	13.3	16.6	9.5
Jagalene	13.5	21.7	20.6	6.6	6.6	2.7	1.5	2.3	7.5	9.5
Jagger	12.3	4.6	9.8	4.2	8.2	10.0	3.2	8.8	12.7	8.5
TAM 111	13.4	17.8	24.5	1.5	2.3	0.4		0.4	—	6.8
Postrock	4.9	1.9	2.0	14.5	6.3	5.3	6.0	32.7	0.7	6.0
2137	1.7	4.4	2.2	3.0	4.0	2.2	6.3	7.1	8.0	2.9
T81	6.2	8.9	5.6	1.4		0.5	—	—	—	2.5
TAM 112	2.6	8.4	5.3	0.3	1.4	—	0.1	—	—	2.0
Hatcher	4.0	5.1	3.0	0.3	0.0	—	—	—	—	1.3
Shocker	—	—	—	0.2	2.0	1.7	—	1.6	0.1	1.0
Karl / Karl 92	0.2	0.9	0.1	4.3	0.3	—	5.0	0.9	—	0.8
Ike	2.3	0.3	4.4	0.1	0.2	—	0.3	—	—	0.8
Art	—	—	—	0.2	1.2	1.5	0.8	0.7	0.6	0.8
2174	—	—	—	—	0.4	1.6	—	0.1	3.6	0.7
Danby – HWWW	1.7	1.6	2.7	0.1	—	0.1	—	0.5	—	0.7
T136	—	3.6	1.5	0.0	—	0.5	—	—	—	0.7
TAM 107	1.2	1.5	0.6	0.1	—	0.7	—	—	—	0.6
Bullet	—	—	—	—	—	1.4	—	—	—	0.5
Endurance	—	—	0.3	—	0.1	0.9	—	1.3	3.7	0.4
Larned	1.1	0.7	1.1	—	0.3	—	—	—	—	0.4
Above	0.4	3.6	0.2	—	—	—	—	—	—	0.4
Stanton	2.5	1.0	0.6	0.1	—	—	—	—	—	0.4
Smokey Hill	0.5	0.1	—	0.8	0.5	—	0.2	—	—	0.3
Thunderbolt	0.7	1.0	0.1	0.2	0.0	0.2	—	—	—	0.3
Cutter	—	—	—	0.1	1.0	0.4	0.3	—	—	0.3
Dominator	—	—	—	0.6	1.0	—	0.1	2.2	—	0.3
Coronado	—	—	—	0.5	0.1	0.4	—	—	—	0.2
Hawk	0.2	—	—	1.3	—	—	0.0	—	0.2	0.2
Keota	1.2	—	—	—	0.1	—	—	—	0.8	0.2
2145	—	—	—	1.2	0.2	—	2.1	0.2	—	0.2
Protection	—	—	0.2	0.0	0.7	0.2	—	0.2	—	0.2
Scout / Scout66	—	—	0.5	—	—	—	—	—	—	0.2
Blends	11.6	2.8	6.4	29.1	11.5	7.1	3.3	4.4	0.2	10.7
Other hard white cultivars	0.1	0.7	1.6	0.0	—	0.0	—	0.6	—	0.3
Other hard red cutlivars	5.7	7.5	4.9	5.2	2.1	5.7	11.1	8.4	6.4	5.1
All soft red cultivars	—	—	—	—	—	—	—	0.1	4.2	0.1
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

Table 3. Distribution of Kansas winter wheat cultivars, 2000–2009. (— = cultivar not reported in this district; 0 = < 1%).

Cultivar	By crop year									
	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
Overley	—	—	—	—	0.1	2.2	15.3	23.3	17.3	13.7
Fuller	—	—	—	—	—	—	—	—	0.3	10.9
Santa Fe	—	—	—	—	—	—	0.2	1.3	5.8	9.5
Jagalene	—	—	—	—	3.0	21.2	27.2	23.1	18.0	9.1
Jagger	34.0	35.8	42.8	45.2	40.9	28.2	19.7	17.1	14.7	8.5
TAM 111	—	—	—	—	—	0.2	2.2	4.0	7.3	6.8
Postrock	—	—	—	—	—	_	—	—	0.9	6.0
2137	23.1	22.3	15.5	13.3	8.6	5.7	3.1	2.9	2.8	2.9
T81	0.2	0.2	0.8	0.6	1.8	1.6	2.6	2.0	2.8	2.5
TAM 112	—	—	—	—	—	—	—	0.4	1.6	2.0
Hatcher	—	—	—	—	—	—	—	—	0.3	1.3
Shocker	—	—	—	—	—	—	—	—	0.2	1.0
Karl / Karl 92	3.5	3.3	3.6	3.2	2.3	1.5	1.1	1.0	0.8	0.8
Ike	4.1	3.6	2.6	2.1	2.0	1.4	1.1	1.2	0.5	0.8
Art	—	—	—	—	—	—	—	—	0.1	0.8
2174	1.1	3.0	3.1	3.1	2.8	3.0	1.2	1.1	0.9	0.7
Danby – HWWW	—	—	—	—	—	—	—	0.7	1.2	0.7
T136	—	—	—	—	—	—	—	—	0.3	0.7
TAM 107	6.3	5.3	2.9	2.3	1.3	1.0	0.4	0.1	0.2	0.6
Bullet	—	—	—	—	—	—	—	—	0.0	0.5
Endurance	—	—	—	—	—	—	—	—	0.1	0.4
Larned	1.2	1.0	0.9	0.8	0.4	0.3	0.2	0.3	0.2	0.4
Above	—	—	—	—	0.2	0.1	0.1	0.0	0.2	0.4
Stanton	—	—	0.1	0.6	1.4	1.4	0.8	0.2	0.3	0.4
Smokey Hill	—	—	—	—	—	—	—	—	0.1	0.3
Thunderbolt	—	0.2	0.6	0.8	1.4	1.7	1.1	0.4	0.9	0.3
Cutter	—	—	—	—	0.7	1.7	1.6	2.1	0.9	0.3
Dominator	1.4	1.5	2.0	2.2	1.5	1.1	0.8	0.4	0.2	0.3
Coronado	1.0	1.1	0.7	0.8	0.5	0.4	0.4	0.2	0.1	0.2
Hawk	—	—	—	—	—	—	—	0.0	0.0	0.2
Keota	—	—	—	—	—	—	—	0.0	0.2	0.2
2145	—	—	—	—	1.5	2.2	0.8	0.5	0.6	0.2
Protection	—	—	—	—	—	—	0.2	0.3	0.4	0.2
Scout / Scout66	0.3	0.1	0.2	0.2	0.2	0.1	0.2	0.1	0.1	0.2
Blends	7.5	7.0	11.5	12.8	15.2	11.3	10.0	10.4	10.4	10.7
Other hard white cultivars	0.2	0.8	1.1	2.7	4.9	3.9	1.7	1.0	0.7	0.3
Other hard red cutlivars	16.1	14.8	11.5	9.2	9.3	9.8	7.9	5.8	8.5	5.1
All soft red cultivars	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.1	0.1	0.1
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0





KANSAS STATE UNIVERSITY
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M.B. Kirkham.

Increasing atmospheric carbon dioxide (CO_2) and water use efficiency.

The Environmental Physics Group (formerly the Evapotranspiration Laboratory) at Kansas State University was the first to carry out experiments with winter wheat under elevated levels of carbon dioxide (CO_2) in the field. For three years (1984–87), we grew winter wheat under elevated levels of CO_2 in closed top chambers at the Rhizotron Facility of the Evapotranspiration Laboratory, located at the Ashland Experimental Field Site, about eight miles south of the Kansas State University campus in Manhattan, Kansas. The research was funded by the Department of Energy (DOE), and the detailed data were published in three reports to the DOE (Chaudhuri et al. 1986, 1987, 1989). The results were summarized in two journal articles (Chaudhuri et al. 1990a, 1990b).

When we started the experiments, the concentration of CO_2 in the atmosphere was 330 ppm. Our control (the ambient CO_2 concentration) was 330 ppm. The four atmospheric CO_2 concentrations that we used were 330, 485, 660, and 825 ppm. The CO_2 concentration in the air in 2007, the last year for which data are compiled, was 382.7 ppm (Schnell 2008) or, rounding off, 383 ppm. Because the concentration of CO_2 in the atmosphere has increased 53 ppm since we started our experiments, it is time to revisit the earlier data, in particular the data that dealt with water use efficiency, to determine how much the water use efficiency has increased as a result of increased levels of CO_2 in the atmosphere. Elevated CO_2 increases water-use efficiency because it closes the stomata, and this conserves water.

The closed-top chambers, which we used to control the CO_2 concentration, were placed over underground boxes (rhizotrons) that could be pulled out of the ground and weighed to determine water lost. Water in half of the boxes, which contained a silt loam soil, was maintained at a high water level (field capacity; 0.38 m^3/m^3) and the other half was maintained at a low-water level (half field capacity). The amount of

Table 1. Water requirement (mL/g) for winter wheat grain grown under high and low water levels as affected by CO_2 concentrations during a three-year study (1984–87) (* = estimated).

CO2 concentration (ppm)	Well watered				Drought stressed			
	84–85	85–86	86–87	Average	84–85	85–86	86–87	Average
330	680	530	710	640	860	670	870	800
383 (surrent)				599*				739*
485	510	470	570	517	810	450	590	617
660	490	450	460	467	730	440	530	567
825	500	430	440	457	670	450	520	547

water required to produce a gram of grain was calculated from water used and grain yield for each CO_2 level (Chaudhuri et al. 1990a). The water requirement, which is the reciprocal of water use efficiency, decreased as CO_2 concentration increased (Table 1, p. 201; reproduced from Fig. 3 in Chaudhuri et al. 1990a).

The greatest reduction in water requirement occurred between the control (330 ppm CO_2) and the first increment of CO_2 added to the air (485 ppm CO_2). That increment is 155 ppm CO_2. We already are one-third of the way to reaching that first increment (53 ppm divided by 155 ppm = 0.34 or about one-third). In Table 1, I have estimated what the water requirement of wheat now is, based on the data collected for wheat grown 1984-1987. For the well-watered and dry conditions, wheat is using 41 mL and 61 mL less water, respectively, to produce a gram of grain than it was in the 1984-1987 period. This will benefit farmers. That is, increases in atmospheric CO_2 apparently have allowed production of more wheat grain for the same amount of water applied.

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News.

Graduate student Nicole A. Rud (nrud@ksu.edu) continues with research on her Master's degree, which she is getting jointly under Professor Kimberly A. Williams (kwilliam@ksu.edu) in the Department of Horticulture, Forestry, and Recreational Resources and M.B. Kirkham (mbk@ksu.edu). Nicole is studying the causes of the physiological disorder, edema, which affects a wide range of greenhouse-grown agronomic and horticultural plant species. The disorder is thought to occur when roots absorb water faster than it is transpired by a plant, which results in small blisters of fluid on a leaf that burst and leave corky lesions. Edema is of great concern to the protected-agricultural industry, because of its economic damage.

Graduate student Prasanna Ayyaru Thevar (prasan@ksu.edu) has finished his research on his master's degree, which he is getting jointly under M.B. Kirkham and Dr. Robert M. Aiken (raiken@ksu.edu) of the Kansas State University Northwest Research-Extension Center, Colby, Kansas. He graduated in May, 2009. The title of his thesis is 'Transpiration Efficiency of Eight Grain Sorghum Lines [*Sorghum bicolor* (L.) Moench].'

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THE WHEAT GENETIC & GENOMIC RESOURCES CENTER
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Notice of release of KS09WGGRC51-J and KS09WGGRC51-C Hessian fly-resistant hard red winter wheat and KS09WGGRC51-P Hessian fly-resistant spring wheat germ plasm.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS09WGGRC51-J and KS09WGGRC51-C hard red winter wheat (*Triticum aestivum* L.) and KS09WGGRC51-P spring wheat germ plasm with resistance to Hessian fly for breeding and experimental purposes. Scientists participating in this development were B.S. Gill, B. Friebe, J.C. Cainong, D.L. Wilson, and W.J. Raupp, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506; A.K. Fritz, Department of Agronomy, Kansas State University, Manhattan, KS 66506; M.S. Chen and M.O. Pumphrey, USDA–ARS Plant Science and Entomology Research Unit, Department of Agronomy, Kansas State University, Manhattan, KS 66506; J. Johnson, Griffin Campus, University of Georgia, Griffin, GA 30223; and L.E. Zavatsky and A.J. Lukaszewski, Department of Botany and Plant Sciences, Batchelor Hall, University of California, Riverside, CA 92507.

KS09WGGRC51-J, KS09WGGRC51-J, and KS09WGGRC51-P are improved derivatives of Hamlet (KS89WGRC08, PI 549276) with the resistance gene *H21* in the form of a wheat-rye (*Secale cereale*) recombinant chromosome T2BS·2BL-2R#2L. The recombinant chromosome consists of the short arm of wheat chromosome 2B, most of the long arm of 2B, and a shortened distal segment derived from the long arm of the *S. cereale* chromosome 2R#2 harboring *H21*. KS09WGGRC51-J is derived from the cross Hamlet (T2BS·2R#2L)/2B(L)+20 (T2BS·2BL-2R#5L)/2*Jagger. KS09WGGRC51-C is derived from the cross Hamlet (T2BS·2R#2L)/2B(L)+20 (T2BS·2BL-2R#5L)/2*Culver. KS09WGGRC51-P is derived from the cross Hamlet (T2BS·2R#2L)/2B(L)+20 (T2BS·2BL-2R#5L)/2*Pavon. The F_4-derived families are homozygous for *H21* but are segregating for other traits.

Small quantities (3 grams) of seed of KS09WGGRC51 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506. Genetic material of this release will be deposited in the National Plant Germplasm System where it will be available for research purposes, including the development of new cultivars.

Development and characterization of wheat–Leymus racemosus translocation lines with resistance to Fusarium head blight.

Lili Qi, Mike Pumphrey, Bernd Freibe, Bikram Gill, and P.D. Chen.

Fusarium head blight can be a significant disease in Kansas in a year with a wet spring. Working with scientists at Nanjing Agricultural University in China, we have identified a new source of resistance from a perennial grass relative *L. racemosis* (Lr). A chromosome segment (called 7Lr#1S) from this grass specifying resistance to FHB has been transferred to a chromosome arm of wheat (called 7AL) in the form of a translocation T7AL·7Lr#1S. Using *ph1*-induced homoeologous method, we identified three putative recombinants. Putative recombinants were confirmed by genomic in situ hybridization (GISH), and we identified one proximal recombinant (rec124) with the proximal 80% derived from 7Lr#1S and the distal 20% derived from 7AL, and two distal recombinants (rec679 and rec989) with the proximal 80% derived from 7AL and the distal 20% of the arm derived from 7Lr#1. We presently are backcrossing these recombinants with adapted Kansas winter wheats and selecting homozygous recombinant stocks. Once these have been obtained, they will be evaluated for their resistance to FHB.

Another new source of resistance is derived from the perennial relative *Elymus tsutushiense*. We identified a wheat-Elymus addition translocation stock with 42 wheat chromosomes plus a pair of translocation chromosomes in which the short arm of chromosome 1Ets#1 was transferred to an unknown wheat chromosome. This line was highly resistant to FHB in both greenhouse and under field conditions. Further chromosome engineering aimed at producing compensating translocation lines is underway.

Development of wheat–Thinopyrum intermedium recombinant lines resistant to wheat streak mosaic virus.

Bernd Friebe, Lili Qi, Duane L. Wilson, Zhijian Chang, Dallas L. Seifers, T. Joe Martin, Alan K. Fritz, and Bikram S. Gill.

Wheat streak mosaic is a devastating virus disease of bread wheat in the Great Plains of the U.S. and Canada and in most spring and winter wheat-producing areas worldwide. Only one gene conferring resistance to WSM has been designated, *Wsm1*. Previously, we released WGRC27 with resistance to WSMV controlled by *Wsm1*, a gene transferred from *Th. intermedium* to wheat in the form of a wheat–*Th. intermedium* T4Ai#2S.4D translocation, which was redesignated as T4DL·4J^{s}S. Using *ph1*-induced homoeologous pairing we identified five recombinants using molecular markers and confirmed them by GISH.

All recombinants were evaluated for their reaction to WSMV and *Triticum* mosaic virus (TMV). The distal recombinants rec45, rec64, rec87, and rec213 were free of symptoms and had low virus titers to both viruses at 18°C by ELISA. The proximal recombinant rec36 reacted susceptible to both viruses, which mapped the *Wsm1* gene in the distal 20% of the 4DS-4JsS arm.

The recombinant rec213 in the 'Overley/Amadina' background was released as a new germ plasm, KSWG-GRC50, with resistance to wheat streak and *Triticum* mosaic viruses in 2008.

A second source of WSMV resistance was mapped to the long arm of a *Th. intermedium* group-7 chromosome that is available in the form of a ditelosomic 7Ai#2L chromosome addition line. This germ plasm requires further chromosome engineering before it can be used in cultivar improvement. To speed up this process, we have developed three PCR-based STS markers that detect the 7Ai#2L-specific fragment in a wheat background, from screening 120 primer pairs designed from mapped wheat EST sequences. Five plants with a chromosome number of 2n = 40 +7D +7Ai#2L and homozygous for ph1b have been obtained. In the homozygous *ph1b* condition, the 7Ai#2L telosome is expected to pair and recombine with 7DL. Presently, we are screening these progenies using molecular markers for putative recombinants, which will be verified by GISH. Once homozygous recombinants have been obtained they will be screened for their resistance to WSMV and TMV.

Development of wheat–Elymus trachycaulus translocation lines with resistance to barley yellow dwarf virus.

Bernd Friebe and Bikram S. Gill.

Barley yellow dwarf virus is a devastating disease of bread wheat worldwide and is vectored by several aphid species. Average yield losses are between 1 and 3%, although yield losses higher than 10% have been reported. Only two genes conferring resistance to BYDV have been reported in wheat. *Bvd1* confers reduced infection to BYDV and was mapped to the short arm of wheat chromosome 7D, and *Bvd2* was derived from *Th. intermedium* and was transferred to wheat in the form of a T7DS·7DL-7Ai#1L translocation. Our previous work identified a new source of BYD resistance derived from *E. trachycaulus*, which is a tetraploid wild relative of bread wheat (2n=4x=28, S^{t}S^{t}H^{t}H^t). In 1992, we produced an alloplasmic wheat–*E. trachycaulus* translocation T7AL·7AS-1StS translocation consisting of the long arm of wheat chromosome 7A, a proximal part of 7AS and a distal segment derived from 1S^{t}S that confers resistance to BYDV. However, the 1S^{t}S segment cannot compensate for the missing 7AS segment in this translocation, causing duplications and deficiencies and, thus, is agronomically undesirable. From the cross 'CSM1B/TA5534', we have selected plants with 2n = 41 chromosomes that were monosomic for 1B and heterozygous for 7A and T7AL·7AS-1S^{t}S that were crossed

with *ph1b*. In the next growing season, we will select plants with 2n = 41 chromosomes that are homozygous for *ph1b*, monosomic for 1B, and heterozygous for chromosomes 7A and T7AL·7AS-1S^{t}S. Targeted homoeologous recombinantion between 1S^{t}S and 1BS can occur in these genotypes. We have also crossed the T7AL·7AS-1S^{t}S translocation stock directly with *ph1b*. The F1 was backcrossed with *ph1b* and in the next season, we will identify plants that homozygous for *ph1b* and heterozygous for chromosomes 7A and T7AL·7AS-1S^{t}S. In these genotypes, homoeologous recombination between the 1StS segment and the homoeologous short arm segments of group-1 chromosomes can occur.

Stripe rust and leaf rust resistance from Ae. geniculata.

Vasu Kuraparthy, Shilpa Sood, Deven R. See, and Bikram S. Gill.

This goatgrass is widespread in the eastern Mediterranean and southwest Asia region from western Iraq, Syria, and Jordan, through Israel and Lebanon, and the island of Cyprus. The grass is common in southern Europe and Africa north of the Sahara Desert. This species has been introduced into parts of northwest and central Europe and the United States. Aegilops geniculata has immunity to most of the diseases and pests that attack wheat, including the powdery mildew and leaf rust fungi, Hessian fly, and greenbug. WGGRC scientists have been introgressing genetic material from this grass for over 12 years. Recently, we transferred new leaf rust resistance genes *Lr57* and stripe resistance gene *Yr40* that are inherited as a single block. Cleaved amplified polymorphic sequence (CAPS) markers were developed as diagnostic PCR-based markers for marker-assisted transfer of the *Lr57* and *Yr40* genes into hard red winter wheats. Two different CAPS markers were developed based on the EST marker XBF200555 diagnostically detecting the alien introgressed segment in T5DL·5DS-5MgS(0.95). BC_3F_2 plants segregating for rust resistance were evaluated in the field at two locations in Manhattan in 2008 but were still segregating. We have now isolated homozygous $BC_3F_{2:3}$ and BC_3F_4 lines for the two rust-resistance genes and these will be further evaluated in the field in 2009 for subsequent germ plasm release.

Production of compensating Robertsonian Haynaldia villosa D-genome translocations.

Bernd Friebe, Lili Qi, Jamie J. Wilson, and Bikram S. Gill.

Haynaldia villosa is a diploid, annual wild relative of bread wheat and a promising source for agronomically important traits including disease and pest resistance and grain-quality characteristics. Resistance to powdery mildew, curl mite colonization, and spindle streak mosaic virus has been transferred from *H. villosa* and used in wheat improvement. Resistance to stem rust, an emerging threat to wheat production, also has been identified (Pumphrey MO, unpublished results). We have initiated a project aimed at producing a complete set of 14 compensating, whole-arm, Robertsonian translocations involving V- and D-genome chromosomes of wheat. The strategy involves crossing the wheat D-genome monosomic stocks (20''+D') with the disomic chromosome addition lines (DA) DA1V to DA7V (21''+V'). The F_1 plants with the chromosome constitution of 20"+D'+V', double monosomic for a D-genome and a V-genome chromosome, will be selected and allowed to self. In such plants, monosomic chromosomes frequently misdivide at the centromere and broken chromosomes fuse to form translocation chromosomes at a rate of 5 % or even higher. Progenies of such plants will be screened by molecular markers, C-banding, and GISH analyses to identify plants with compensating translocations, which will be selfed and screened for homozygous translocation stock. To date, we have produced Robertsonian translocations involving chromosomes 1D/1V (T1DL·1VS, T1DS·1VL), 4D/4V (T4DL·4VS, T4DS·4VS), 5V/5D (T5DL·5VS), 6A/6V (T6AL·6VS, T6AS·6VL), and 7D/7V (T7DS·7VL). Once complete, this set will provide a useful and efficient tool to sample the genetic variability of this species.

Chromosome specific bacterial artificial chromosome libraries for wheat physical mapping.

Sunish K. Sehgal, Wanlong Li, Pablo Rabinowicz, Jaroslav Dolezel, Ming-Cheng Luo, and Bikram S. Gill.

We are working with Dr. J. Dolezel, Czech Republic, to make chromosome-specific libraries for physically mapping the wheat genome. Twenty thousand seeds of all double ditelosomic stocks of Chinese Spring wheat and several ditelosomic stocks (3A, 1A, 1D, 3D, 4A, and 2A) were sent to the Dolezel laboratory. Using flow cytometry, we have developed two BAC libraries each for chromosome arm 3AS (110,592 clones) and 3AL (110,592 clones) and three BAC libraries (294,912 clones) for chromosomes 1D, 4D, and 6D (size fraction 1) of Chinese Spring wheat.

The BAC library for chromosome arm 3AS (55,296 clones) has been fingerprinted with a SNaPshot-based, high-throughput technique. After removing the clones with very small inserts and cross contamination, 47,063 fingerprinted BACs were used for contig assembly with the FPC computer program. There are 1,677 contigs and 11,939 singletons providing 7.5-fold coverage of 3AS. The largest contig has 417 BAC clones and is ~2.7 MB in length. We now are fingerprinting two BAC libraries, the second BAC library for 3AS (55,296 clones) and the first BAC library for chromosome arm 3AL (55,296 clones) to complete the physical map of chromosome 3A with 15x coverage. Simultaneously, fingerprinting of the first 1D, 4D, and 6D libraries (26,112 clones) also has been initiated, and a 15x physical map of these chromosomes will be developed.

Six-dimensional BAC pools were developed to integrate the genetic and physical maps in an efficient and cost-effective manner. This pooling strategy involved constructing a block of 68 (384-wells) plates in a '32x24x34' plate array creating 190 pools of BAC DNA (~6.0 chromosome arm equivalents). ESTs showing high homology with the corresponding regions in rice, Brachypodium, and barley were used to design 1,240 EST–STS markers. Nearly 400 EST–STS markers have been mapped to individual BAC clones and BAC contig(s).

Personnel.

Dr. Lili Qi joined the USDA–ARS Northern Crop Science Laboratory in November, 2008. Dr. Wanlong Li is now an assistant professor at South Dakota State University, Brookings. Two graduate students completed their thesis work in December, 2008. Shilpa Sood, Ph.D., dissertation title 'Molecular characterization of threshability genes in wheat' and Jamie J. Wilson, M.S. thesis title 'Production of wheat–*Haynaldia villosa* Robertsonian translocations'. New visiting scientists in the WGGRC laboratories include Sundeep Kumar, Sardar Vallabh Bhai Patel University of Agriculture & Technology, Meerut, India, and Cheng Liu, University of Electronic Science and Technology, Chengdu, Sichuan, PR China.

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GRAIN MARKETING AND PRODUCTION RESEARCH CENTER

U.S. Grain Marketing Research Laboratory, USDA, Agricultural Research Service, Manhattan, KS 66502, USA.

M. Tilley, F. E. Dowell, B.W. Seabourn, J.D. Wilson, E.B. Maghirang, S.R. Bean, Y.R. Chen, K.H. Peiris, M.O. Pumphrey, and R.C. Kaufman.

The Grain Marketing and Production Research Center welcomes Dr. Thomas Herald as the new Research Leader for the Grain Quality and Structure Research Unit. Dr. Herald joins us from Kansas State University, where he served as a professor in the Food Science Institute. Dr. Herald was raised in Michigan. He earned his B.S. degree in Food Science from Michigan State University, East Lansing, in 1980. He served as a Peace Corps volunteer from 1980–83 in Swaziland, Southern Africa. Dr. Herald completed his M.S. and Ph.D. degrees in Food Science at Michigan State University in the area of food chemistry. Dr. Herald worked in the food industrial sector with Yoplait USA and Kellogg's. He recently completed a 16+ year career at Kansas State University holding the rank of professor. Dr. Herald's research focus was on the chemical and physical properties of food and food ingredients. He has 63 peer-reviewed publications and numerous invited presentations at national and international meetings. As Research Leader for the Grain Quality and Structure Research Unit, Dr. Herald will integrate his technical background into the identification and utilization of wheat cultivars and sorghum hybrids for use in value-added systems that will include both food and non-food applications.

Environmental events affecting starch size distribution in developing hard red winter wheat caryopsis.

J. D. Wilson and R. C. Kaufman.

Starch constitutes the greatest weight portion of the wheat endosperm (65–75%) and contributes its own unique functional qualities such as texture, volume, consistency, aesthetics, moisture, and shelf stability to various baked products. Starch particle size has long been recognized as an important variable in the efficiency of a range of processes including predicting rheology and flow behavior. Although genetics is the dominant determinant in caryopsis development, the environment also has a critical role in quality variability. The objective of this work is to study starch size distribution in identical varieties of developing hard red winter wheat grown in the same location over seven consecutive years and correlate differences to various environmental factors. The samples were collected from the Kansas State University Agronomy field plots in Manhattan, KS. Heads were tagged as to flowering dates and samples were collected starting at 7 days-after-flowering (DAF) and regularly sampled until harvest. Starch was isolated, then freeze-dried and starch size distribution was analyzed on a laser diffraction particle-size analyzer. Trends were observed within cultivars between starch size distribution and temperature as well as total precipitation in 10, 17, and 28 DAF and just prior to harvest. These trends included total volume fluctuations and shifts in peak diameters of 10–20% of the A-type granules. Studying starch size distribution during development of the wheat caryopsis may provide needed insight into critical environmental growth phases.

Progress on development and application of single kernel NIR sorting technology for assessment of FHB resistance in wheat germ plasm.

K.H.S. Peiris, M.O. Pumphrey, Y. Dong, S. Wegulo, W. Berzonsky, P.S. Baenziger, and F.E. Dowell.

Plant breeders working on developing *Fusarium*-resistant wheat cultivars need to evaluate kernels coming from a multitude of crosses for *Fusarium*-damaged kernels (FDKs). We are developing near-infrared (NIR) spectroscopic methods to sort FDKs from sound kernels and to determine DON levels of FDKs nondestructively to facilitate rapid varietal screening for *Fusarium* resistance by assessing proportions of sound and FDKs and estimating their DON levels. We report the progress and research highlights of the development and use of our single-kernel NIR (SKNIR) scab sorting and deoxynivalenol (DON) estimation techniques since January, 2008.

We have improved the SKNIR scab sorting technique and its feasibility as an objective, rapid, and nondestructive method for assessment of FDKs of wheat germ plasm demonstrated. Depending on the kernel DON level, FDKs can be sorted into 2–3 fractions, making it possible to get an understanding of what fraction and how much each fraction contributes to the final DON level of a composite sample. Moreover, our studies with sorting of North Dakota State University (NDSU) germ plasm showed that proportions of SKNIR sorted FDKs in wheat lines affected by FHB correlated fairly well with field FHB assessment indices. Therefore, this technique can be used by wheat breeders as a nondestructive, rapid, and objective method for comprehensive analysis of FDKs when wheat germ plasm are screened for *Fusarium* resistance. Since April 2008, we have sorted 108 samples for NDSU and 405 samples for University of Nebraska, Lincoln (UNL), wheat breeders. Another set of samples from the above two institutions will be sorted in November–December, 2008.

A calibration was developed for estimation of DON concentration in single wheat kernels by the SKNIR system, which can estimate DON levels in single kernels having more than 60 ppm DON. Experiments will be carried out in collaboration of UNL researchers to further test and refine this calibration to estimate DON levels of FHB-affected wheat samples. NIR spectra of pure DON also were studied, and DON absorption peaks identified. A SKNIR wheat moisture calibration also was developed that will be integrated to determine moisture content of kernels concurrently when DON levels are estimated so that it is possible to compare DON levels of kernels having different moisture contents or to express DON content of kernels with specific moisture content.

Automated single-kernel sorting to enhance end-use quality in wheat breeding lines.

F.E. Dowell, E.B. Maghirang, and P.S. Baenziger.

An automated, single-kernel, near-infrared system was used to select kernels to enhance the end-use quality of hard red wheat breeder samples. Twenty breeding populations and advanced lines were sorted for hardness index, protein content, and kernel color. To determine if the phenotypic sorting was based upon genetic or environmental differences, the progeny of the unsorted control and sorted samples were planted at two locations two years later to determine if differences in the sorted samples were transmitted to the progeny (e.g., based on genetic differences). The average hardness index of the harvested wheat samples for segregating populations improved significantly by seven hardness units. For the advanced lines, hardness index was not affected by sorting indicating little genetic variation within these lines. When sorting by protein content, a significant increase from 12.1% to 12.6% was observed at one location. Purity of the red samples was improved from about 78% (unsorted control) to about 92% (sorted samples), whereas the purity of the white samples improved from 22% (control) to about 62% (sorted samples). Similar positive results were found for sorting red and blue kernel samples. Sorting for kernel hardness, color, and protein content is effective and based upon genetic variation.

Modified omega gliadins as chain terminators in Pegaso near-isogenic lines.

R. Jonnala, S. R. Bean, D. Lafiandra, and F. MacRitchie.

Unextractable polymeric protein (UPP) is a parameter that gives a relative measure of the molecular weight distribution (MWD) of the polymeric protein, based on solubility. For any glutenin subunit to participate in a growing polymer, it has to have at least two cysteine residues. Modified (mutated) gliadins of LMW-GS having an odd number of cysteines or LMW compounds having one thiol group can act as chain terminators and this should shift the MWD towards lower values that in turn would be reflected in lower UPP values. Thus, a higher number of omega-gliadins cross-linked to glutenins should correlate with UPP. Twenty-four NILs in the background of Pegaso bread wheat with variation at the *Glu-1*, *Gli-1*/*Glu-3*, and *Gli-2* loci were used for investigation. The goal of the study was to seek evidence for the role of chain terminators in decreasing UPP values and to examine the influence of chain terminators on the MWD of gluten proteins. A novel method was developed to extract the omega-gliadins. Capillary electrophoresis (CE) and SEC-MALLS were used to quantify the omega-gliadins and to estimate the MWD, respectively. The moderately high negative correlation (R squared = 0.65) between reduced (SDS-RA) polymeric protein and modified omega-gliadins in CE suggests that these omega-gliadins act as chain terminators, resulting in smaller polymers, thus causing a reduction of UPP values. Results from SEC-MALLS indicated the significant differences among Pegaso NILs for MWD of the SDS-insoluble fraction.

Wheat starch size distribution and its impact on quality

J.D. Wilson and S.H. Park.

Starch constitutes the greatest weight portion of the wheat endosperm (65–75%) and contributes its own unique functional qualities such as texture, volume, consistency, aesthetics, moisture, and shelf stability to various baked products. Wheat gluten proteins have received the greatest amount of attention due to their unique properties of extension and elasticity, which gives them their unique dough forming properties and are what allows wheat to be such a unique and versatile raw material for so many food products. Cereal starches have been well studied in dilute aqueous systems, but the functionality of starch in concentrated water-limiting systems such as that in dough and breads is far from understood. Particle size and shape have long been recognized as important variables in the efficiency of a range of processes including predicting rheology and flow behavior. A feature of the endosperm of mature Triticeae is the multimodal starch granule size population. The larger-sized granules are called the A-type granules, are thought to form soon after anthesis, and may continue to grow throughout grain filling. The intermediate sized (B-type) and the smallest (C-type) granules are thought to be initiated a number of days after anthesis, depending on cultivar, growing location, and isolation method, and both classes of granules remain smaller than A-type granules. Different size starch granules have different physical, chemical, and functional properties. However, limited research has been conducted to find relationships of starch granules size distribution to final product quality. The objectives of this work were to investigate and correlate starch size distribution to flour, dough mixing, and bread-making properties of hard red winter, hard red spring, and spelt wheat.

A modified extensigraph test method feveloped for wheat breeding lines and vommercial wheat.

Y. R. Chen, B. W. Seabourn, and F. Xie

Dough rheological characteristics, resistance to extension and extensibility, are very important wheat flour quality traits for the milling and baking industries and for new wheat varietal selection in wheat-breeding programs. Current available techniques or test methods, such as the AACCI Extensigraph standard method or the small-scale TA-XT2 Kieffer method, have some limitations with respect to flour sample size, testing time, water absorption, sample throughput, data interpretation, and results. A modified extensigraph test method utilizing 100-g flour and 2-g salt and adapting 50-g Farinograph optimum water absorption for dough prepared in a 100-g mixer with an orbital speed of 86 rpm was developed to measure dough rheological characteristics. The dough is mixed until fully developed. Mix time was much shorter and dough preparation much easier in the 100-g mixer than that in the 300-g Farinograph. Data generated by the modified method is highly correlated with data obtained by the standard extensigraph method (AACC method 54-10). The correlation coefficients (r) for 93 pairs of each of six extensigraph dough characteristics of 31 different tested wheat samples, grown in Texas, Oklahoma, Kansas, Colorado, Nebraska, South Dakota, and Montana were 0.95 for resistance to extension, 0.93 for maximum resistance to extension, 0.80 for extensibility, 0.93 for ratio of resistance to extension to extensibility, 0.92 for ratio of maximum resistance to extension to extensibility, and 0.81 for the area under the curve. There also were significant correlation coefficients for the data of extensigraph dough characteristics evaluated at each of three tests (30, 60, and 90 min) between the modified and standard methods. Therefore, the modified extensigraph test method is a useful and valuable alternative for wheat-breeding programs, milling and baking industries, crop quality surveys, and wheat quality research due to its smaller flour sample requirement and the reduced time required for dough preparation.

Selecting and sorting waxy wheat kernels using near-infrared spectroscopy.

F.E. Dowell, E.B. Maghirang, R.A. Graybosch, W.A. Berzonsky, and S.R. Delwiche.

An automated, single kernel, near-infrared (NIR) sorting system was used to separate single wheat kernels with amylose-free (waxy) starch from reduced-amylose (partial waxy) or wild-type wheat kernels. Waxy kernels of hexaploid wheat are null for the granule-bound starch synthase alleles at all three *Wx* gene loci; whereas, partial-waxy kernels have at least one null and one functional allele. Wild-type kernels have three functional alleles. Our results demonstrate that automated single-kernel NIR technology can be used to select waxy kernels from segregating breeding lines or to purify advance breeding lines for the low-amylose kernel trait. Calibrations based on either amylose content or the waxy trait performed similarly. Also, a calibration developed using the amylose content of waxy, partial waxy, and wild-type

durum wheat enabled adequate sorting for hard red winter and hard red spring wheat with no modifications. Regression coefficients indicated that absorption by starch in the NIR region contributed to classification models. Single-kernel NIR technology offers significant benefits to breeding programs developing wheat with amylose-free starches.

Comparison of waxy vs. nonwaxy wheats in fuel ethanol fermentation.

R. Zhao, X. Wu, B.W. Seabourn, S. Bean, L. Guan, Y. Shi, J.D. Wilson, R. Madl, and D. Wang.

Fermentation performance of eight waxy, seven nonwaxy soft, and 15 nonwaxy hard wheat cultivars was compared in a laboratory dry-grind procedure. With nitrogen supplemented into the mash, the range of ethanol yields was 368–447 L/ton. Nonwaxy soft wheat had an average ethanol yield of433 L/ton, higher than nonwaxy hard and waxy wheat. Conversion efficiencies ranged from91.3–96.2%. Despite having higher levels of free sugars in grain, waxy wheat had higher conversion efficiency than nonwaxy wheat. Although there was huge variation in protein content between nonwaxy hard and soft wheat, no difference in conversion efficiency was observed. Waxy cultivars had extremely low peak viscosity during liquefaction. Novel mashing properties of waxy cultivars were related to unique pasting properties of their starch granules. With nitrogen supplementation, waxy wheat had a faster fermentation rate than nonwaxy wheat. Fermentation rates for waxy cultivars without nitrogen supplementation and nonwaxy cultivars with nitrogen supplementation were comparable. Ethanol yield was highly related to both total starch and protein content, but total starch was a better predictor of ethanol yield. We saw strong negative relationships between total starch content of grain and both yield and protein content of distillers dried grains with solubles.

Investigating the effect of dough preparation using hot water and pregelatinized starch on tortilla quality.

F. Xie, B.W. Seabourn, M. Tilley, and Y.R. Chen.

One of the traditional ways to make Lao Bing, a Chinese tortilla-like flatbread, is to mix dough in which one-half of the added water is heated to 60~80°C. The product is preferred due to its softness, but the reason for this increased softness is unknown. Our hypothesis is that addition of hot water gelatinizes part of the starch, which could hold more moisture, and, hence, increase the softness. The objective of this study was to determine if pregelatinized (pre-g) starch could improve tortilla quality. A complete randomized block design was applied. Tortillas were made using a commercial tortilla flour with the addition of 0%, 10%, 20%, and 30% pre-g starch. To examine the effects of hot water on tortilla quality, tortillas were prepared using the commercial flour and 50% of the total water at 75°C. Samples were kept in plastic ziplock bags at room temperature immediately after cooling. A rollability test was conducted on days 1, 7, and 14 of storage, and samples were rated on a 1–5 scale with 5 the best. Stretchability (maximum force (MF) and distance) was analyzed on days 0, 1, 7,, and 14 after baking using a Texture Analyzer (TA-XT2; Texture Technology Corp., Scarsdale, NY). At least six replicates were tested for rollability, and 12 were tested for stretchability. The control had the lowest rollability compared to the others at all timepoints. At day 14, the rollability of the 30% pre-g was 3.85, which was 1.71 times of that of the control. The MF of all the samples was about the same at day 0 and increased during storage. However, the 30% pre-g had the lowest rate of increase. On day 14, the control had the highest MF, which was 1.5 times that of the 30% pre-g. The results indicated that pr-gelatinized starch could improve tortilla quality. Increasing water temperature could easily gelatinize starch and, hence, improve tortilla quality with minimal cost. This method would largely benefit the commercial tortilla producer.

Mechanism of gas cell stabilization in breadmaking. II. The primary gluten-starch matrix.

B.S. Sroan, S.R. Bean, and F. MacRitchie.

A key parameter in the primary stabilizing dough film (gluten-starch matrix) is thought to be the property of strain hardening. The hard red winter wheat,Jagger gave a higher test-bake loaf volume than a soft wheat and higher strain hardening index for the dough. Rheological properties of the doughs were varied by the addition of flour protein fractions prepared by pH fractionation. Fractions were characterized by SE-HPLC and MALLS. The molecular weight distribution (MWD) of fractions progressively shifted to higher values as the pH of the fractionation decreased. Changes

in mixograph peak development time paralleled the changes in MWD. However, the strain-hardening index and the test-bake loaf volume increased with increasing MWD up to a point (optimum), after which they declined. At a given strain rate, the behavior at the optimum is thought to result from slippage of the maximum number of statistical segments between entanglements, without disrupting the entangled network of polymeric proteins. The shift of MWD to s molecular weight higher than the optimum results in a stronger network with reduced slippage through entanglement nodes, whereas a shift to lower molecular weights will decrease the strength of the network due to a lesser number of entanglements per chain.

Effect of frying conditions and yeast fermentation on the acrylamide content in you tiao, a traditional Chinese fried twisted-dough roll.

W. Huang, S. Yu, Q. Zou, and M. Tilley.

The effects of frying temperature, frying time, and dough pH on the formation of acrylamide in the processing of you tiao, a traditional Chinese fried twisted-dough roll, were analyzed using response surface methodology. The results obtained showed that the frying temperature and time had a notable impact on the formation of acrylamide. Dough pH also had a significant effect on the amount of acrylamide resulting in the products. Lowering the frying temperature to 175°C, prolonging the frying time to 86 seconds, and adjusting the dough pH to 6.0 with citric acid reduced the acrylamide content by 71% in the finished products. T he addition of different levels of yeast ranging from 0.1% to 1.2% to the traditional formulation was examined. We found that dough, with the addition of 0.8% yeast fermented for 1 h, could significantly reduce the amount of acrylamide formed in the fried twisted-dough roll by 66.7%. An examination of the influence of yeast fermentation on the free asparagine and reducing sugars revealed that when the reducing sugars reach the maximum content, the acrylamide content was reduced, and the free asparagine was decreased. As a result, the asparagine reduced by yeast fermentation is more important than the rise in reducing sugar in the reduction of acrylamide content in you tiao.

NIR optical characteristics of deoxynivalenol.

K.H.S. Peiris and F.E. Dowell.

We have developed rapid, near-infrared (NIR) techniques for nondestructive automatic sorting of *Fusarium*-damaged wheat kernels and for estimating deoxynivalenol (DON) levels in single wheat kernels. We studied NIR optical characteristics of DON to identify NIR absorption bands and to assess the applicability of NIR technique for direct measurement of DON in order to improve the calibrations. The NIR transmission spectra of DON (0.5–2,000 ppm) dissolved in acetonitrile and that of water (0–640 ppm) in acetonitrile were studied to identify NIR absorption bands of DON and water and to see how strong NIR absorption bands of water interact with DON NIR absorption bands.

Deoxynevalenol crystals were dissolved in acetonitrile to prepare a 2,000-ppm stock solution, which was serially diluted to prepare a series of DON solutions up to 0.5 ppm. The solutions in IR quartz (10-mm path length) cuvettes were scanned using an ASD spectrometer. Solutions were scanned three times to collect three different spectra per each DON concentration. Likewise, water was added to acetonitrile and spectra were recorded. The collected DON spectra were used to develop a calibration to predict DON levels in an acetonitrile solution. Two spectra from each concentration were used for developing the calibration by the PLS regression method, and the other spectra used to validate the calibration. The optical density spectra of DON and water in various concentrations were used to study DON and water absorption peaks. Difference spectra and second derivative spectra of DON and water were used to identify and resolve absorption peaks.

In the 95–2,200 nm range, two DON absorption bands were identified at 1,390–1,440 nm and 1,880–1,950 nm having peaks at 1,410 and 1,905 nm, respectively. The absorbance at 1,905 nm is approximately one magnitude stronger than the absorbance at 1,10 nm. Water absorption bands were found around 970 and 1,420 nm in increasing intensity. The water absorption bands above 1,850 nm were much stronger being unable to measure even at 40 ppm using 10 mm path length.

The calibration developed for DON in acetonitrile (R^2=0.995 SECV=38.8 with six PLS factors) predicted DON levels in acetonitrile with an R^2=0.998 and shows that NIR absorbance can be used to accurately estimate DON levels in acetonitrile. However, when it comes to predicting DON in cereal grains, such an accuracy is difficult to achieve due to interference with stronger water absorption bands that overlap DON absorption bands. Our present SKNIR technique for scab sorting and DON estimation use a 950–1,650 nm waveband. Based on the observations of this study, it may be possible to further improve calibrations by extending NIR scanning range above 1,950 nm to include the stronger DON absorption band at 1,905 nm.

Measuring grain and insect characteristics using NIR laser-cluster technology

F.E. Dowell, E.B. Maghirang, and V. Jayaraman.

The potential of using an eight-wavelength, near-infrared (NIR), laser-cluster spectrometer for measuring wheat quality (hardness index, protein content, moisture content, and waxy character) and determining tsetse fly pupae sex was investigated and compared to a commercial single-kernel, near-infrared (SKNIR) system. Wheat hardness was predicted accurately by both NIR systems and results were in close agreement with reference values. Predicted protein content followed the same trend as the reference values, but the laser cluster system over predicted low protein content values and under predicted high values by about 1 percentage point. The accuracy of predicting moisture content by either system was similar with predicted values within 0.5% moisture content of the reference values. the waxy character was predicted by the laser system with less accuracy than the SKNIR system, but tsetse fly pupae sex was predicted with similar accuracies for both systems. Prediction equations derived from the laser spectra show that wavelengths influencing classification models generally agree with published literature. Thus, this research shows that a NIR laser-cluster system can be used to predict some grain and insect traits with acceptable accuracy, and some predictions can likely be improved if other wavelengths are used in the laser cluster system.

An NIRS method for the precise identification of Fusarium-damaged wheat kernels.

K.H. Peiris, M.O. Pumphrey, Y. Dong, and F.E. Dowell.

Development of FHB-resistant wheat cultivars may be enhanced by nondestructive evaluation of kernels for *Fusarium*-damaged kernels (FDKs) and deoxynivalenol (DON) levels. *Fusarium* infection generally affects kernel appearance, but insect damage and other fungi can cause similar symptoms. Also, some kernels may have high DON levels but appear asymptomatic. We are developing technology to correctly identify FDKs using an automated, single-kernel NIR (SKNIR) system. A calibration developed to select sound kernels from scabby kernels had an accuracy of more than 99%, but the fraction sorted as FDKs contained kernels that were not totally scabby or sound (grey kernels). Comparison of the NIR spectra of sound and FDKs (both tombstones and grey kernels) showed distinguishable NIR absorption patterns at 960–985, 1,110–1,180, 1,210–1,230, and 1,310–1,350 nm wavebands. These differences may be due to changes in food (carbohydrates and proteins) reserves and/or DON levels. Additional research is ongoing to determine DON levels of grey kernels and to assess the accuracy of sorting FDKs. We also are developing a calibration to estimate DON levels of single wheat kernels. Kernels from artificially inoculated and control wheat spikes were used for the collection of spectra in order to get a concentration gradient of DON for calibration and validation samples. Analysis of single-kernel DON by wet chemical methods also will yield additional information regarding the changes in DON kevels in kernels above and below the point of infection . The findings of these studies will be helpful to develop a rapid and automated single-kernel evaluation technology to correctly identify sound and FDKs in wheat samples and/or to sort wheat kernels based on DON level. This will facilitate quick evaluation of a large number of breeding lines for scab resistance to identify better FHB-resistant cultivars or parent materials for crossing. Furthermore, this technique may be extended as a cost-effective and environmentally friendly technique for analysis of DON in wheat samples for grading commercial grain lots by replacing the time-consuming and expensive methods that use various other chemicals for extraction of DON. This technique may also be extended to other grains such as barley.

NIR absorbance characteristics of deoxynivalenol and of sound and Fusarium-damaged wheat kernels.

K.H.S Peiris, M.O. Pumphrey, and F.E. Dowell.

The near-infrared (NIR) absorption spectra of deoxynivalenol (DON) and single wheat kernels with or without DON were examined. The NIR absorption spectra of 0.5–2,000 ppm of DON in acetonitrile were recorded in the 350–2500 nm range. A second derivative processing of the NIR spectra and spectral subtractions showed DON absorption bands at 1,408, 1,904, and 1,919 nm. The NIR spectra of sound and *Fusarium*-damaged scabby kernels also were acquired using two instruments. Subtraction of average absorption spectra and second derivative spectra were evaluated to identify different NIR signatures of the two types of kernels. Differences in peak heights and positions of the NIR absorption bands of the kernels were noted. At 1,204, 1,365, and 1700 nm, the differences were in the heights of the absorption peaks. Such differences may be attributed to changes in the levels of grain food reserves and other structural compounds. Shifts in absorption peak positions between the two types of kernels were observed at 1,425–1,440 nm and 1,915–1,930 nm. These differences may arise from other NIR active compounds, such as DON, which are not common for the two types of grains. Because the NIR absorption of DON may have contributed to the shifts between sound and *Fusarium*-damaged kernels, this study indicates the potential for NIR spectrometry to evaluate *Fusarium* damage in single kernels based on the DON levels.

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Wheat rusts in the United States in 2008.

Wheat stem rust (*Puccinia graminis f. sp. tritici*). The first report of wheat stem rust in 2008 was from a plot of the susceptible soft wheat McNair 701 in South Texas at Castroville on 3 April. The pustules developed from spores that were likely rain deposited approximately a week earlier and the severity of the infections was low. On 9 April, wheat stem rust was found scattered throughout plots in south central Louisiana at Crowley. One soft wheat cultivar, CK 9553, had significant stem rust infection. Hot dry weather accelerated the crop to maturity in these plots.

On 22 April, low levels of wheat stem rust were found scattered throughout susceptible cultivars and experimental lines at Castroville in south Texas. On 24 April, low levels of wheat stem rust were found on the susceptible variety McNair 701 in plots at College Station in central Texas. On 28 April, traces of wheat stem rust were found in plots of McNair 701 and an unknown cultivar at Bardwell in central Texas. In late April, low levels of wheat stem rust were found in plots at Prosper in northern Texas. Traces of wheat stem rust were also found in a field near Abilene, Texas.

On 24 April, traces of stem rust were found at Baton Rouge, Louisiana. On 29 April, low levels of stem rust were found in plots at Quincy in the panhandle of Florida. In both cases, the wheat was near maturity and, therefore, rust did not increase much more.

The first wheat stem rust identifications of 2008 from Castroville, Texas, and Crowley, Louisiana, were identified as race QFCS. This race has been the most commonly identified race from U.S. collections in the past few years, and is avirulent to most of the winter and spring wheats in the U.S.

In mid May, low levels of stem rust were found on stems in plots of the cultivars Winmaster and Deliver at College Station, Texas. Uredinia were found on only 4–5 stems. In mid-May, low levels of stem rust were found in plots of McNair 701 at Stillwater, Oklahoma, and 40 miles west at Marshall. On 24 May, low levels of wheat stem rust were found in the susceptible McNair 701 plot at Lahoma in north-central Oklahoma. In late May, stem rust was severe in some wheat head-rows of a late planted nursery at Chillicothe in north Texas.

In late May, wheat stem rust was found in east-central and northeastern Arkansas. The disease developed too late to cause much damage, but these are the first reports of stem rust in Arkansas in the past 10 years.

On 8 May, low levels of stem rust were found in a wheat nursery at Blackville in south-central South Carolina. In late May, during harvest, wheat stem rust was found in a breeding nursery at Plains and in early June stem rust was found in a Pike County plot in west-central Georgia.

In summary, during the spring of 2008, low levels of stem rust were found in susceptible plots of soft and hard red winter wheat in the southern U.S. and in one field at Abilene, Texas.

On 10 June, a center of wheat stem rust infection was observed in a research plot at Owensboro in northwestern Kentucky. In early June, low levels of stem rust were found on the susceptible line Bezostaya at Hutchinson in south-central Kansas and on McNair 701 at Manhattan, Kansas. In mid-June, low levels of wheat stem rust were found in a plot at Lexington, Kentucky. In late June, high levels of wheat stem rust were found in varietal plots at Belleville in north-central Kansas. This was the most stem rust observed in these plots in the last 10 years. Also in late June, high levels of wheat stem rust were observed in the southern part of Nebraska in plots at Lincoln to low levels at North Platte and Sidney. In all cases, no wheat stem rust found on the commonly grown cultivars.

On 30 June, low levels of wheat stem rust were found in entries in the stripe rust winter wheat nursery at Brookings, South Dakota. The pustules had developed in the previous seven days. Pustules were primarily on the stems although some also were found on the leaves.

On 1 July, light levels of wheat stem rust were found on the leaves and stems of susceptible winter wheat cultivars (e.g., McNair 701) at the Rosemount, Minnesota nursery.

On 21 June, several infection sites of wheat stem rust were found in plots at Delphos in west-central Ohio.

In early July, low levels of stem rust were found in winter wheat plots at Lancaster in southwestern Wisconsin and Urbana, Illinois. On 10 July, low levels of wheat stem rust were found in a soft red winter wheat field and plots in Door County in northeastern Wisconsin.

High levels of wheat stem rust were found on flag leaves of susceptible spring wheats (e.g., Baart) in plots at Rosemount in southeastern Minnesota on 16 July. Wheat stem rust was also found on susceptible winter wheat, which had not reached maturity. During the week of 21 July, high levels of stem rust were found on the susceptible spring wheat cultivar Baart at Waseca, Lamberton, and Morris experiment stations in Minnesota.

During the second week in July, low levels of stem rust were detected on the winter wheat cultivar Radiant in a Ransom County plot in southeastern North Dakota and on a winter wheat line at the Waseca plots in south-central Minnesota. On 13 July, low levels of stem rust were found in plots of a rust-spreader mix (highly susceptible lines) at Groton and Redfield in northeastern South Dakota.

In summary, during the month of July, low levels of wheat stem rust were found in susceptible winter wheat and spring wheat plots from northeastern Wisconsin through Minnesota to northeastern South Dakota. Stem rust was not observed on any current wheat cultivars in research plots or in fields in this area.

In early August, trace levels of stem rust were found on susceptible spring wheats (Baart and Little Club) at Carrington in east-central North Dakota and at Crookston in northwestern Minnesota.

In early July, significant levels of wheat stem rust were found in a field of irrigated winter wheat in east central Colorado. In the second week of July, there were low levels of wheat stem rust in northeastern Colorado plots.

In early July, low levels of stem rust were found in winter wheat plots near Pullman, Washington. This was the only report of stem rust in the Palouse region of eastern Washington in 2008.

In 2008 there were more stem rust reports on susceptible cultivars in the northern winter wheat growing area than usual. The crop matured slower than normal, which allowed more stem rust than normal to develop.

The wheat stem rust observation maps are available on the CDL website (http://www.ars.usda.gov/SP2UserFiles/ad_hoc/36400500Cerealrustbulletins/2008wsr.pdf).

Stem rust race identifications. From collections made from the above locations race QFCS was identified as the predominant race. This is a common race that has been found in the U.S. the past several years. This race is relatively avirulent - the majority of the U.S. cultivars are resistant to QFCS.

Stem rust on barberry (Alternate host for stem rust). In early May, light pycnial infection were found on susceptible barberry (*Berberis vulgaris)* bushes growing in south central Wisconsin. The infection was lighter than in years past. In late May, severe aecial infection was found on susceptible barberry bushes growing in southeastern Minnesota. The infection was heavier than 2007.

Aecial collections from southeastern Minnesota and south-central Wisconsin were identified as rye stem rust, *P. graminis* f. sp. *secalis*. *P. graminis* f. sp. *tritici*, and *P. graminis* f. sp. *avenae* were not isolated from barberry samples**.**

Wheat leaf rust (*Puccinia triticina*). Southern Plains – Texas. In late February, low levels of leaf rust were reported in central Texas wheat plots. Moisture had been limited from late January to mid-March in western Texas. In mid-March, 30% leaf rust severities were found on the susceptible cultivars, Cutter (*Lr24* resistance), Jagger (*Lr17* resistance), Overley (*Lr41* resistance), and TAM 110 in the nursery at Castroville, Texas. During the fourth week in March in College Station plots, leaf rust severities ranged from 30% on TAM 110 to traces on Fuller (*Lr17*+*Lr41*).

In early April, susceptible cultivars TAM 110, Jagalene (*Lr24*), and Jagger (*Lr17*) in nurseries at Castroville and College Station, Texas, had 60% leaf rust severities on lower leaves. On the highly resistant cultivars Fannin and Endurance, no infections were found. In the first week in April, light to moderate levels of leaf rust were noted in fields in north central Texas. In early April, no rust was found in the Rolling Plains, Texas Panhandle, or North Texas High Plains fields (Fig. 1).

By the third week of April, the susceptible cultivars TAM 110, Jagalene (*Lr24*), and Jagger (*Lr17*) had 60% leaf rust severities on flag leaves in nurseries at Castroville Texas. In northeastern Texas, leaf rust was beginning to appear on susceptible wheat varieties (Pio 25R78, Terral 8558, Coker 9553). Most of the fields received a foliar fungicide application. In 2008, leaf rust appeared much earlier than normal in this area. In late April, plots of susceptible wheat cultivars had leaf rust severities up to 80%, in central Texas.

In early May, fields of Jagger (*Lr17*) and Jagalene (*Lr24*) in northern Texas had severities up to 30% (Fig. 1), while the majority of the fields had traces of leaf rust.

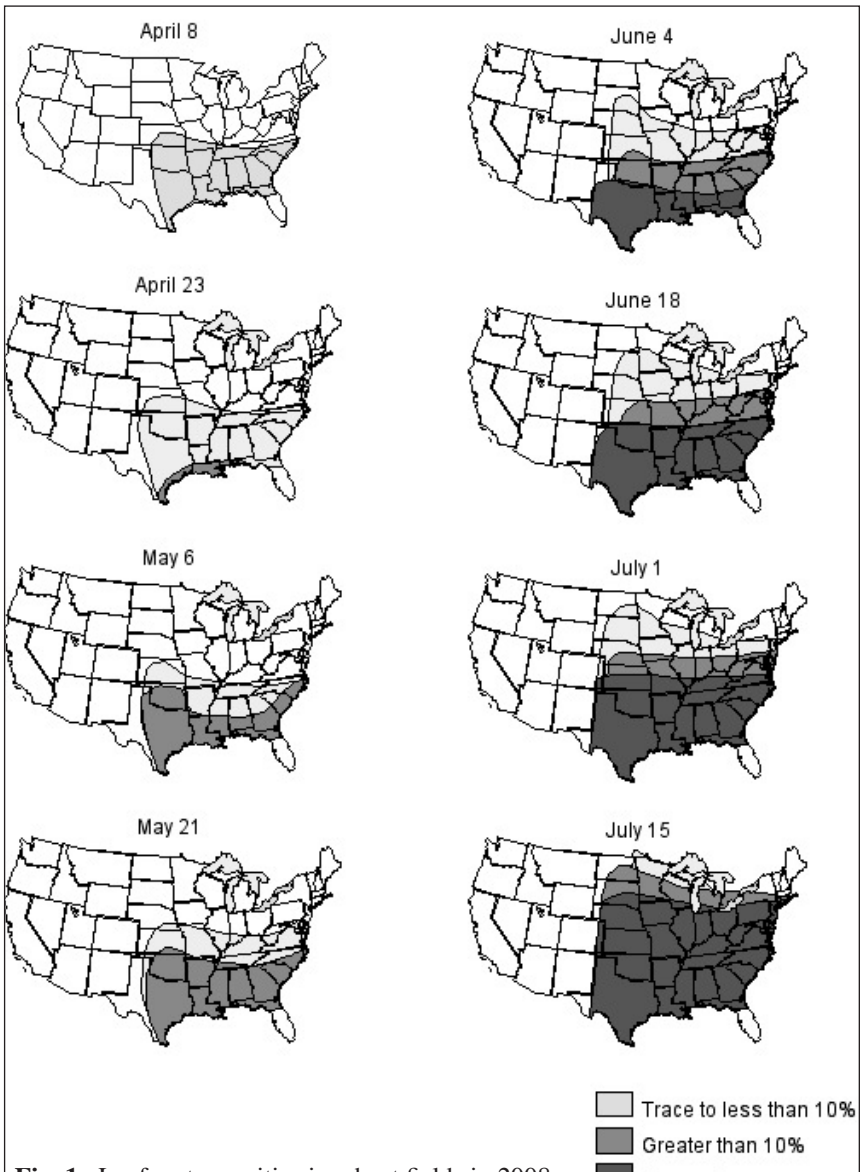

Fig. 1. Leaf rust severities in wheat fields in 2008.

Oklahoma. In mid-March, no leaf rust was found in the Stillwater, Oklahoma plots. In mid-April, scattered pustules of leaf rust were found on susceptible cultivars in central Oklahoma and the highest severity (10–20%) was found on the lowest leaves in plots at Minco. On 21 April, leaf rust was found in many fields in southwestern Oklahoma. The rust was visible on most of the lower leaves with flecking occurring on the upper leaves. In central Oklahoma, widely scattered pustules of leaf rust were found on lower yellowing/dying leaves.

In late April, leaf rust was observed on Jagalene and Jagger in commercial fields and cultivar evaluations in northern Oklahoma. By early May, leaf rust was increasing rapidly in plots near Stillwater and Lahoma, Oklahoma, with severity levels of 65% on flag leaves of Jagger and Jagalene.

During early May, wheat leaf rust was severe on susceptible varieties in plots, trials and fields in Oklahoma where conditions (moisture and temperature) have favored rust development. In 2008, 5% losses to leaf rust were reported in Oklahoma (Table 3, p. 225). In central Oklahoma, leaf rust was covering the flag leaves of unsprayed fields of Jagger. In western Oklahoma, the incidence and severity of rust decreased dramatically.

Central Plains – Kansas. In late February, leaf rust infections that had overwintered were found in plots at Manhattan, Kansas. In mid-March, traces of leaf rust were found in central Kansas fields. The leaf rust pustules were actively producing spores.

In early April, low levels of rust were found in a wheat field of Jagger in south-central Kansas. In fields near Manhattan, Kansas, leaf rust was increasing. Leaf rust was actively producing spores at both locations. The top three wheat cultivars in the state (Jagalene (*Lr24*), Overley (*Lr41*), and Jagger (*Lr17*)) are susceptible to leaf rust. Severe levels of rust were observed in south Texas plots of these three cultivars, which provided inoculum for wheat further north. The susceptibility of these cultivars, the apparent over wintering of leaf rust, and delay in crop maturity all increased the risk of severe disease in Kansas in 2008.

In early May, leaf rust was observed in additional counties from south-central Kansas to north-central Kansas. The highest rust severities were found on Jagger and Jagalene with traces levels on Overley (*Lr41*) and Fuller (*Lr17, Lr41*). The rust on Fuller was not completely unexpected because small hot spots of rust were found on Fuller the last two years.

In mid-May, wheat leaf rust was increasing in fields of susceptible cultivars (e.g. Jagger and Jagalene) throughout the state of Kansas. Many fields were sprayed with fungicide to control the rust.

In late May, high severity (60%) levels of wheat leaf rust were found in fields of Jagalene (*Lr24*), Jagger (*Lr17*), and Overley (*Lr41*) throughout north-central Oklahoma and southeastern and south-central Kansas (Fig. 1, p. 217). In some fields of susceptible cultivars there was a significant loss to leaf rust. In 2008, 4.7% losses where reported to leaf rust in Kansas (Table 3, p. 225). In varietal plots in south-central Kansas, leaf rust was light in the resistant cultivars Fuller, Santa Fe, and Duster. In north-central Kansas fields of Jagger, etc., leaf rust severities on flag leaves were much lower, but with continued favorable conditions for rust development, leaf rust increased throughout this area. Only trace levels of leaf rust were reported in western Kansas because of the drought-like conditions.

In mid-June, leaf rust was increasing in north-central and northwestern Kansas where environmental conditions were conducive for rust increase.

Central Plains – Nebraska. In mid-May, traces levels of leaf rust were found in south-central Nebraska fields in counties that border Kansas. During the fourth week in June, plots of susceptible winter wheat cultivars such as Jagalene in southern Nebraska had high levels of rust severities, whereas resistant cultivars had 0 to trace levels of infection on the upper leaves. In late June, high levels of wheat leaf rust were found in fields of susceptible cultivars in southern Nebraska. Throughout this area, fungicide usage on winter wheat was very common in 2008 with many fields receiving multiple applications.

Northern Plains – Minnesota, South Dakota, North Dakota, Montana. In late May, light levels of leaf rust were reported in a field of Jagalene at Reliance, in central South Dakota. In mid-June, low levels of leaf rust were found in the winter wheat nursery at Brookings in east-central South Dakota on older susceptible varieties (e.g., Scout 66). On 13 June, low levels of leaf rust were found in winter wheat plots at Lamberton in southwestern Minnesota and in spring wheat plots at St. Paul. Minnesota.

On 16 June, low levels of leaf rust were found in two spring wheat fields in Richland County in southeastern North Dakota. Scouts in North Dakota found wheat leaf rust in 11 of the 117 fields they surveyed the fourth week of June. Five of the fields with wheat leaf rust were winter wheat fields; the other six were spring wheat fields. The spring wheat fields were in east-central North Dakota and had severities of 1% or less; the winter wheat fields were in southeastern and south-central North Dakota and had severities as high as 25%.

In late June, high levels of wheat leaf rust were found in plots of susceptible winter wheat cultivars in east-central South Dakota and east-central Minnesota (e.g. Jagalene 60%). In late June, susceptible spring wheat cultivars had leaf rust severities of trace to 5% on lower leaves in southern Minnesota and southern South Dakota fields (Fig. 1).

During the second week in July, leaf rust was increasing in spring wheat fields and plots throughout southern Minnesota, eastern South Dakota and southeastern North Dakota. In susceptible winter wheat fields in southeastern North Dakota, average severities were close to 10%. Many of the wheat fields in the spring wheat region were treated with fungicide, which helped prevent losses due to leaf rust and FHB. High levels of wheat leaf rust were found on susceptible spring wheats at Rosemount, Minnesota, on 16 July.

Wheat leaf rust was widespread in 2008, but the rust was at lighter levels than 2007 in the northern plains on both spring and winter wheat. High amounts of rust inoculum arrived from the southern plains winter wheat region, but because the crop matured slower than normal the rust also developed at slower rate.

More leaf rust was expected since some of the northern spring wheat cultivars currently grown have less effective resistance to leaf rust than those commonly grown 10-15 years ago. Therefore, many of the wheat fields in the spring wheat region were treated with fungicide, which prevented losses due to leaf rust and FHB.

In early July, low levels of leaf rust were found in irrigated spring wheat plots near Billings in south central Montana.

Louisiana. In mid-February, leaf rust was increasing on susceptible varieties, McCormick (*Lr24* resistance) in Baton Rouge, Louisiana, plots. In early March, leaf rust was active and at significant levels in the Baton Rouge plots and growers were starting to apply fungicides in fields that were infected with leaf rust.

During the first week in April, wheat plots in south-central Louisiana had high levels of leaf rust on the lower leaves. In the plots at Baton Rouge leaf rust was moderately heavy on susceptible lines. In mid-April, leaf rust was increasing in plots and fields throughout southern and central Louisiana. In late April, plots of susceptible wheat cultivars had leaf rust severities up to 80%, in northern Louisiana.

Arkansas. In mid-March, low levels of leaf rust were found on susceptible cultivars in southeastern Arkansas fields. Rust was severe in susceptible cultivars in disease-management plots that were planted very early and were more mature than most of the wheat in the state.

In early April, leaf rust was heavy on the lower leaves of early-planted wheat fields (early October) and traces on late-planted fields (early November) and plots in central and southern Arkansas. In west-central Arkansas, 10% severity levels were reported on lines in a nursery.

A significant amount of leaf rust over wintered in southern Arkansas. Most of the commonly grown cultivars appear to have some resistance and by mid-April some fields had been sprayed with a fungicide. The leaf rust epidemic developed slowly in Arkansas.

In early May, a few very small pustules were found on older leaves, but upper leaves were free of leaf rust. In mid-May, the Arkansas wheat crop was in good shape, but high levels of leaf rust were found in many fields that were not sprayed with fungicide. In some fields the fungicides were applied too early and therefore they were not effective when the rust arrived. Wheat matured rapidly, so impact was minimal. On 20 May, severe levels of leaf rust were reported in varietal plots in northeastern Arkansas at Kibler.

Southeast – Mississippi, Georgia, Alabama, South Carolina. In mid-March, low levels of leaf rust were found in southern Mississippi fields.

In mid-April, plots of susceptible wheat cultivars in southern and central Alabama and southern Georgia had severe levels of infection on the lower leaves and a few pustules were noted on the flag leaves. Good rainfall in March and April made conditions more conducive for rust development in this area than in the past two years.

In late April, severities of 40% were observed on flag leaves in fields of susceptible cultivars from southern Alabama to southern Georgia. Many fields in the southern U.S. were sprayed with fungicide to control rust development. Dry conditions in early May slowed rust development throughout much of the southern U.S.

Mid-Atlantic – North Carolina, Virginia. In mid-March, leaf rust was widespread but not severe in plots at Kinston and Plymouth, North Carolina.

Leaf rust was present in lower canopies of susceptible varieties such as Saluda (*Lr*11) since late March at Plymouth in eastern North Carolina. In late April, rust moved up the canopy and covered 15% of the flag leaf area on cultivars such as Saluda, McCormick (*Lr24*), and USG 3209 (*Lr11, Lr26*). Rust covered approximately 1% of the mid-canopy of Tribute (*Lr9, Lr24*) and Coker 9511 (*Lr9*). Leaf rust likely over wintered in the region and developed faster than normal.

In early May, in the eastern soft red winter wheat region, leaf rust was found from South Carolina to Maryland. In South Carolina it was found in the Coastal Plain, where it was more severe at Blackville than at Florence, but mostly because Blackville was more advanced in maturity. In Maryland, a few widely scattered fields with leaf rust were found on the Delmarva Peninsula, in Caroline and Queen Anne counties. Only a few pustules developed on the flag leaves, but conditions were good for continued development. Much of the acreage was sprayed for wheat diseases. In late May, leaf rust was increasing in some Maryland fields.

In early May, leaf rust developed in the nurseries at Blacksburg (southwestern Virginia) and Warsaw (northeastern Virginia). In late May, trace to low levels of leaf rust were reported at the northern (Blackstone, VA) and southern (Orange, VA) Piedmont experiment stations. The heaviest rust was found at the eastern shore station (Painter, VA) where cultivars with *Lr26* (USG 3209, Sisson) and *Lr24* (McCormick) were heavily infected. At the Warsaw station leaf rust was light to moderate while severe leaf rust was observed at the Blacksburg (western Virginia) location. In early June, severe leaf rust was observed at the Blacksburg experiment station in western Virginia.

Pennsylvania. In mid-June, moderate levels of leaf rust were found in winter wheat plots in south-central Pennsylvania.

New York. In early July, wheat leaf rust was present at light to moderate levels on flag leaves across western and central New York. The crop matured rapidly.

Kentucky. In late May, leaf rust was light in central and western Kentucky wheat fields. In much of this area, many of the fields were sprayed with fungicide to control the rust. In early June, leaf rust levels ranged from low to severe in western Kentucky plots.

Midwest – Ohio, Indiana, Illinois, and Wisconsin. In early June, wheat leaf rust was found in fields from northeastern Missouri to southern Illinois to southern Indiana to west central Ohio at 20 to 60% severities on flag leaves. There were yield losses to leaf rust in the soft red winter cultivars in this area. In early June, light levels of leaf rust were found on flag leaves in wheat fields and plots from northwestern Ohio, northwestern Indiana, to south-central Wisconsin.

In mid-June, low to moderate levels of leaf rust were found in a winter wheat plots in east-central and southwestern Wisconsin. In early July, high levels of leaf rust were found in winter wheat plots in Grant County in southwestern Wisconsin. On 10 July, high levels of wheat leaf rust were found in soft red winter wheat fields and plots in Door County in northeastern Wisconsin.

California. In mid-May, a foci of leaf rust (50% severity) was found in wheat plots near Fresno, California.

Washington. In late April, leaf rust was observed on the lower wheat leaves in a field in Horse Heaven Hills in southeastern Washington.

Canada. In early June, leaf rust infection levels ranged from trace to 30% in plots in southwestern Ontario, Canada. In early July, low levels of leaf rust were found on hard red spring wheat in the Red River Valley in Southern Manitoba, Canada.

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2008 identified by virulence to 20[a] lines of wheat with single genes for leaf rust resistance.

Phenotype	Virulences	AL, AR, FL, GA, LA, MS, SC		NY, PA, VA		IL, IN, KY, MO, OH, WI		OK, TX		KS, NE		MN, ND, SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBDB	14a	1	0.4	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
BBBGB	10	2	0.9	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
FLBDB	2c,3,9,14a	1	0.4	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
MBBJG	1,3,10,14a,28	2	0.9	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MBDSB	1,3,17,B,10,14a	3	1.3	2	3.6	0	0	0	0	0	0	0	0	0	0	5	0.7
MBGJG	1,3,11,10,14a,28	1	0.4	1	1.8	2	3.6	0	0	0	0	0	0	0	0	4	0.5
MBPTB	1,3,3ka,17,30,B,10,14a,18	5	2.2	0	0	0	0	0	0	0	0	0	0	0	0	5	0.7
MBSNB	1,3,3ka,11,17,B,14a	2	0.9	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MCBGG	1,3,26,10,28	0	0	0	0	0	0	0	0	0	0	0	0	2	100	2	0.3
MCDSB	1,3,26,17,B,10,14a	9	3.9	2	3.6	2	3.6	0	0	3	3	0	0	0	0	16	2.2
MCGJG	1,3,26,11,10,14a,28	2	0.9	0	0	1	1.8	0	0	0	0	0	0	0	0	3	0.4
MCPSB	1,3,26,3ka,17,30,B,10,14a	2	0.9	0	0	0	0	2	1	0	0	0	0	0	0	4	0.5
MCPTB	1,3,26,3ka,17,30,B,10,14a,18	4	1.8	0	0	0	0	0	0	0	0	0	0	0	0	4	0.5
MCRJG	1,3,26,3ka,11,30,10,14a,28	2	0.9	0	0	2	3.6	0	0	0	0	0	0	0	0	4	0.5
MCRKG	1,3,26,3ka,11,30,10,14a,18,28	4	1.8	0	0	0	0	0	0	1	1	0	0	0	0	5	0.7
MCTSB	1,3,26,3ka,11,17,30,B,10,14a	3	1.3	4	7.3	0	0	0	0	0	0	0	0	0	0	7	1
MFGJG	1,3,24,26,11,10,14a,28	5	2.2	5	9.1	0	0	0	0	0	0	0	0	0	0	10	1.4
MFGJH	1,3,24,26,11,10,14a,28,42	0	0	8	14.5	1	1.8	0	0	0	0	0	0	0	0	9	1.2
MFPSC	1,3,24,26,3ka,17,30,B,10,14a,42	30	13.2	0	0	1	1.8	13	6.6	7	7.1	2	2.2	0	0	53	7.3
MFRJH	1,3,24,26,3ka,11,30,10,14a,28,42	1	0.4	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
MLDSD	1,3,9,17,B,10,14a,41	4	1.8	0	0	0	0	32	16.2	24	24.2	20	21.5	0	0	80	11
MLNSD	1,3,9,3ka,17,B,10,14a,41	0	0	0	0	0	0	6	3	0	0	0	0	0	0	6	0.8
TBDGH	1,2a,2c,3,17,10,28,42	0	0	0	0	0	0	0	0	2	2	0	0	0	0	2	0.3
TBDSB	1,2a,2c,3,17,B,10,14a	2	0.9	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
TBJDG	1,2a,2c,3,11,17,14a,28	0	0	2	3.6	0	0	0	0	0	0	0	0	0	0	2	0.3
TBRJG	1,2a,2c,3,3ka,11,30,10,14a,28	0	0	0	0	2	3.6	0	0	0	0	0	0	0	0	2	0.3
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	25	11	12	21.8	9	16.1	0	0	2	2	1	1.1	0	0	49	6.7

Table 1. Number and frequency (%) of virulence phenotypes of *Puccinia triticina* in the United States in 2008 identified by virulence to 20[a] lines of wheat with single genes for leaf rust resistance.

Phenotype	Virulences	AL, AR, FL, GA, LA, MS, SC		NY, PA, VA		IL, IN, KY, MO, OH, WI		OK, TX		KS, NE		MN, ND, SD		WA		Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
TCBJG	1,2a,2c,3,26,10,14a,28	2	0.9	0	0	0	0	4	2	0	0	0	0	0	0	6	0.8
TCDSB	1,2a,2c,3,26,17,B,10,14a	9	3.9	2	3.6	1	1.8	1	0.5	0	0	0	0	0	0	13	1.8
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	69	30.3	8	14.5	2 5	44.6	14	7.1	6	6.1	0	0	0	0	122	16.7
TCSBB	1,2a,2c,3,26,3ka,11,17	2	0.9	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
TDBGG	1,2a,2c,3,24,10,28	0	0	0	0	0	0	0	0	0	0	7	7.5	0	0	7	1
TDBGH	1,2a,2c,3,24,10,28,42	15	6.6	3	5.5	6	10.7	59	29.9	3 1	31.3	34	36.6	0	0	148	20.3
TDBJG	1,2a,2c,3,24,10,14a,28	0	0	0	0	0	0	0	0	5	5.1	6	6.5	0	0	11	1.5
TDBJH	1,2a,2c,3,24,10,14a,28,42	10	4.4	2	3.6	0	0	29	14.7	0	0	11	11.8	0	0	52	7.1
TDRKG	1,2a,2c,3,24,3ka,11,30,10,14a,18,28	0	0	0	0	4	7.1	0	0	0	0	0	0	0	0	4	0.5
TFBDB	1,2a,2c,3,24,26,14a	1	0.4	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
TFBGG	1,2a,2c,3,24,26,10,28	0	0	0	0	0	0	0	0	0	0	3	3.2	0	0	3	0.4
TFBGH	1,2a,2c,3,24,26,10,28,42	1	0.4	0	0	0	0	2	1	2	2	0	0	0	0	5	0.7
TFBJH	1,2a,2c,3,24,26,10,14a,28,42	1	0.4	0	0	0	0	17	8.6	3	3	3	3.2	0	0	24	3.3
TFDSB	1,2a,2c,3,24,26,17,B,10,14a	2	0.9	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
TFRJG	1,2a,2c,3,24,26,3ka,11,30,10,14a,28	4	1.8	0	0	0	0	0	0	0	0	0	0	0	0	4	0.5
TJBGH	1,2a,2c,3,16,24,10,28,42	0	0	0	0	0	0	6	3	7	7.1	0	0	0	0	13	1.8
TJBJH	1,2a,2c,3,16,24,10,14a,28,42	0	0	0	0	0	0	3	1.5	3	3	4	4.3	0	0	10	1.4
TJDSC	1,2a,2c,3,16,24,17,B,10,14a,42	0	0	0	0	0	0	2	1	1	1	0	0	0	0	3	0.4
TLBFJ	1,2a,2c,3,9,14a,18,28,41	0	0	0	0	0	0	2	1	2	2	0	0	0	0	4	0.5
TLBJJ	1,2a,2c,3,9,10,14a,28,41	0	0	0	0	0	0	1	0.5	0	0	0	0	0	0	1	0.1
TLGJG	1,2a,2c,3,9,11,10,14a,28	0	0	0	0	0	0	0	0	0	0	2	2.2	0	0	2	0.3
TLMJD	1,2a,2c,3,9,3ka,30,10,14a,41	0	0	2	3.6	0	0	0	0	0	0	0	0	0	0	2	0.3
TNBJJ	1,2a,2c,3,9,24,10,14a,28,41	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0.3
TNRJF	1,2a,2c,3,9,24,3ka,11,30,10,14a,41,42	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0.3
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,14a,28,41	2	0.9	2	3.6	0	0	0	0	0	0	0	0	0	0	4	0.5
Total		228		55	5	6		197	9	9		93		2		730	

[a] Lines tested were Thatcher lines with genes *Lr1*, *Lr2a*, *Lr2c*, *Lr3a*, *Lr9*, *Lr16*, *Lr24*, *Lr26*, *Lr3ka*, *Lr11*, *Lr17*, *Lr30*, *LrB*, *Lr10*, *Lr14a*, *Lr18*, *Lr21*, *Lr28*, and winter wheat lines with genes *Lr41*, and *Lr42*.

Wheat leaf rust race identifications. In 2008, 52 races of wheat leaf rust were described in the United States (Table 1, pp. 221-222). Races TDBGH (20.3%), TCRKG (16.7%), MLDSD (11.0%), TDBJH (7.1%) and TBRKB (6.7%) were the five most common races. Races TDBGH and TDBJH with virulence to *Lr24* were most common in the Great Plains region. Races TCRKG (*Lr26*, *Lr11*, and *Lr18* virulence) and TBRKB (*Lr11*, and *Lr18* virulence) increased in 2008 and were found mostly in the southeastern states. Race MLDSD (*Lr9*, *Lr17*, *Lr41*/*Lr39* virulence) was found mostly in the Great Plains region. Races with virulence to genes *Lr24*, *Lr26*, *Lr17*, and *Lr41*/*Lr39* that are present in the hard red winter wheats were common in the Great Plains region (Table 2). Races with virulence to *Lr24*, *Lr26*, *Lr11*, and *Lr18* that are present in the soft red winter wheats were common in the southeastern states. Races with virulence to *Lr16* that is present in the hard red spring wheats were at low frequencies in the Great Plains region. Races with virulence to *Lr21* that is present in hard red spring wheats were not detected. The 2008 wheat leaf rust survey results may be found at http://www.ars.usda.gov/Main/docs.htm?docid=10493.

Table 2. Number and frequency (%) of isolates of *Puccinia triticina* in the United States in 2008 virulent to 20 lines of wheat with single resistance genes for leaf rust resistance.

Resistance gene	AL, AR, FL, GA, LA, MS, SC		NY, PA, VA		IL, IN, KY, MO, OH, WI		OK, TX		KS, NE		MN, ND, SD		WA		Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	224	98.2	55	100	56	100	197	100	99	100	93	100	2	100	726	99.5
Lr2a	145	63.6	33	60	47	83.9	144	73.1	64	64.6	71	76.3	0	0	504	69
Lr2c	146	64	33	60	47	83.9	144	73.1	64	64.6	71	76.3	0	0	505	69.2
Lr3	225	98.7	55	100	56	100	197	100	99	100	93	100	2	100	727	99.6
Lr9	7	3.1	4	7.3	0	0	45	22.8	26	26.3	22	23.7	0	0	104	14.2
Lr16	0	0	0	0	0	0	11	5.6	11	11.1	4	4.3	0	0	26	3.6
Lr24	72	31.6	20	36.4	12	21.4	135	68.5	59	59.6	70	75.3	0	0	368	50.4
Lr26	153	67.1	29	52.7	33	58.9	53	26.9	22	22.2	8	8.6	2	100	300	41.1
Lr3ka	155	68	28	50.9	43	76.8	37	18.8	16	16.2	3	3.2	0	0	282	38.6
Lr11	122	53.5	42	76.4	46	82.1	16	8.1	9	9.1	3	3.2	0	0	238	32.6
Lr17	77	33.8	12	21.8	4	7.1	56	28.4	37	37.4	22	23.7	0	0	208	28.5
Lr30	151	66.2	28	50.9	43	76.8	31	15.7	16	16.2	3	3.2	0	0	272	37.3
LrB	75	32.9	10	18.2	4	7.1	56	28.4	35	35.4	22	23.7	0	0	202	27.7
Lr10	221	96.9	53	96.4	56	100	195	99	97	98	93	100	2	100	717	98.2
Lr14a	208	91.2	52	94.5	50	89.3	130	66	57	57.6	49	52.7	0	0	546	74.8
Lr18	107	46.9	20	36.4	38	67.9	16	8.1	11	11.1	1	1.1	0	0	193	26.4
Lr21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lr28	146	64	43	78.2	52	92.9	139	70.6	64	64.6	71	76.3	2	100	517	70.8
Lr41	6	2.6	4	7.3	0	0	45	22.8	26	26.3	20	21.5	0	0	101	13.8
Lr42	58	25.4	13	23.6	8	14.3	133	67.5	56	56.6	54	58.1	0	0	322	44.1
Total	228		55		56		197		99		93		2		730	

Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*). ***Southern Plains.*** As of mid-March, no stripe rust had been reported in Texas or Oklahoma. In early April, low amounts of stripe rust were found on flag leaves of wheat in south central Texas plots at Castroville (Fig. 2). The pustules developed from spores that were likely rain deposited approximately 7–14 days earlier. In early April, traces to high levels of stripe rust were found in north Texas plots. As of early April, no stripe rust had been found in Oklahoma or states to the north. In late April, hot spots of stripe rust were found in a breeder line planted at the Lahoma and Stillwater experiment stations in Oklahoma. They appeared to be limited to a relatively small area of rust at each of these stations. These were the first reports of stripe rust in Oklahoma in 2008.

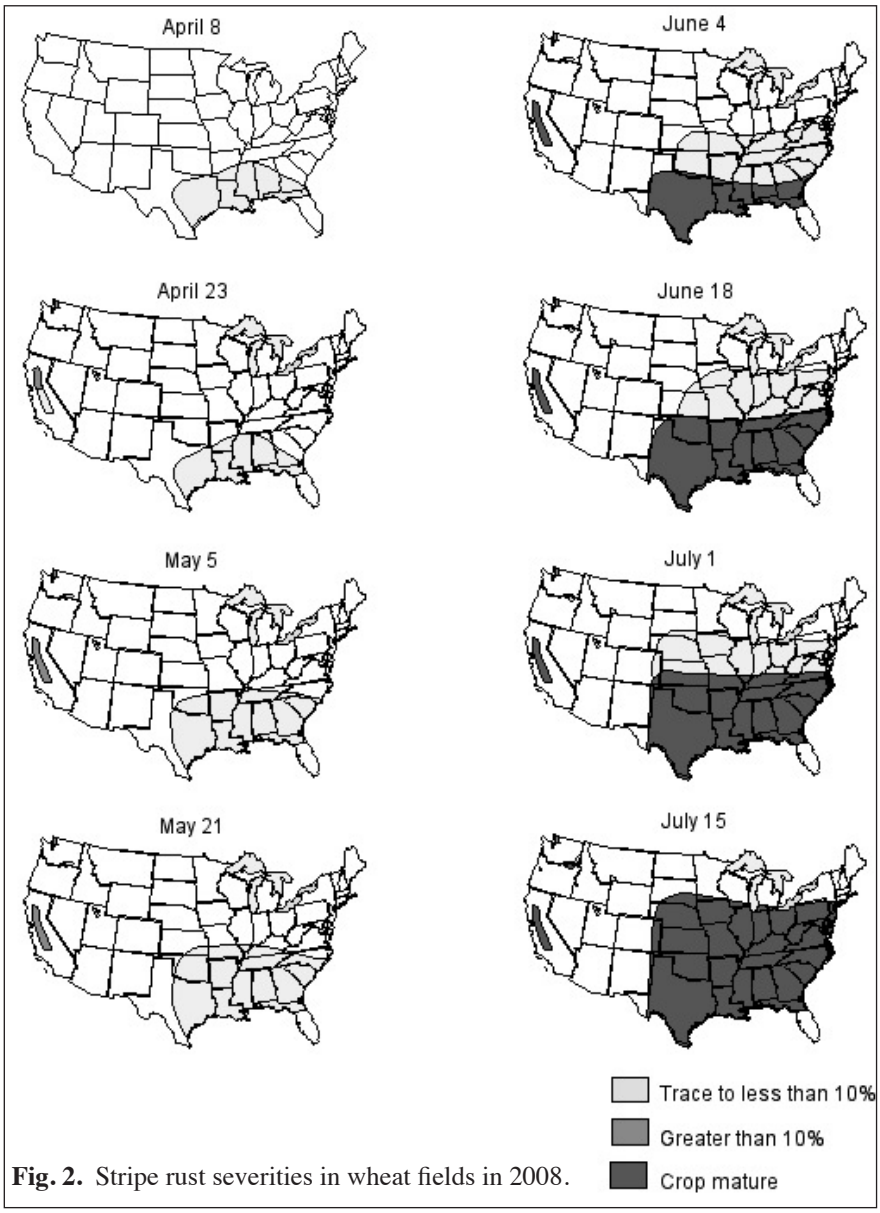

Fig. 2. Stripe rust severities in wheat fields in 2008.

Central Plains. On 8 May, wheat stripe rust was found for the first time this season in Kansas in Sedgwick County in the south central part of the state. The rust was light on the cultivar 2137, which is known to be susceptible to the disease. Most cultivars of wheat grown in Kansas are resistant to stripe rust and, as the weather got warmer and drier, the disease did not cause any major losses in the state. In late May, low to moderate levels of stripe rust were found in cultivar demonstration plots in south-central and central Kansas. The disease was limited to susceptible cultivars such as 2137, 2174, and Above which are grown on limited acreage. In a few fields in central Kansas near Lincolnville, hot spots of 60–80% severity were observed. In 2008, stripe rust arrived too late to cause widespread infections and yield loss in Kansas. In mid-June, low levels of stripe rust were found in susceptible entries in northeastern Colorado plots. In late June, light levels of wheat stripe rust were found at Sidney in the southern Panhandle of Nebraska.

Northern Plains. In early June, light levels of stripe rust were found in one plot at Aberdeen in east-central South Dakota. In late June, light levels of wheat stripe rust were found south central South Dakota winter wheat plots. By late June, hot temperatures slowed stripe rust infections to almost a complete remission in the Great Plains states.

In mid-June, low levels of stripe rust were found in field plots near Bozeman, Montana, in the southwestern part of the state. In early July, stripe rust was found on susceptible winter wheat cultivars in fields at Bozeman, Montana. There were low severities (<10% of leaf area) on flag leaves and incidences were high in infection sites but low through the field.

Louisiana. In mid-March, stripe rust was increasing in Baton Rouge and Winnsboro plots. Growers applied fungicides in fields that were infected with rust. In Louisiana, stripe rust epidemics usually develop in the first half of March and

Table 3. Estimated losses in winter wheat due to rust in 2008 (T = trace).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to: Stem rust %	Stem rust 1,000 bu	Leaf rust %	Leaf rust 1,000 bu	Stripe rust %	Stripe rust 1,000 bu
AL	200	71.0	14,200	0.0	0.0	1.0	143.4	T	T
AR	980	57.0	55,860	T	T	0.5	280.7	T	T
CA	400	85.0	34,000	0.0	0.0	0.0	0.0	2.0	693.9
CO	1,900	30.0	57,000	T	T	1.0	575.8	T	T
DE	79	77.0	6,083	0.0	0.0	T	T	0.0	0.0
FL	23	55.0	1,265	0.0	0.0	1.0	12.8	0.0	0.0
GA	400	56.0	22,400	0.0	0.0	1.0	226.3	T	T
ID	800	75.0	60,000	0.0	0.0	T	T	T	T
IL	1,150	64.0	73,600	0.0	0.0	3.0	2,276.3	T	T
IN	560	69.0	38,640	0.0	0.0	1.0	3,903.0	T	T
IA	35	48.0	1,680	0.0	0.0	T	T	0.0	0.0
KS	8,900	40.0	356,000	0.0	0.0	4.7	17,557.2	T	T
KY	460	71.0	32,660	0.0	0.0	0.1	32.7	0.1	32.7
LA	385	57.0	21,945	T	T	1.0	225.1	1.5	337.6
MD	180	73.0	13,140	0.0	0.0	0.5	66.0	0.0	0.0
MI	710	69.0	48,990	0.0	0.0	2.0	999.8	0.0	0.0
MN	70	52.0	3,640	0.0	0.0	2.0	74.3	0.0	0.0
MS	485	62.0	30,070	0.0	0.0	1.0	303.7	T	T
MO	1,160	48.0	55,680	0.0	0.0	2.0	1,136.3	T	T
MT	2,420	39.0	94,380	0.0	0.0	T	T	T	T
NE	1,670	44.0	73,480	0.0	0.0	1.0	742.2	0.0	0.0
NJ	33	61.0	2,013	0.0	0.0	0.0	0.0	0.0	0.0
NM	140	30.0	4,200	0.0	0.0	0.0	0.0	0.0	0.0
NY	122	63.0	7,686	0.0	0.0	1.0	77.6	0.0	0.0
NC	720	60.0	43,200	0.0	0.0	0.5	217.1	0.0	0.0
ND	550	41.0	22,550	0.0	0.0	2.0	460.2	0.0	0.0
OH	1,090	68.0	74,120	T	T	1.0	748.7	0.0	0.0
OK	4,500	37.0	166,500	0.0	0.0	5.0	8,763.2	T	T
OR	775	58.0	44,950	0.0	0.0	T	T	T	T
PA	185	64.0	11,840	0.0	0.0	0.5	59.5	0.0	0.0
SC	205	54.0	11,070	0.0	0.0	0.5	55.6	0.0	0.0
SD	1,890	55.0	103,950	0.0	0.0	1.0	1,050.0	T	T
TN	520	63.0	32,760	0.0	0.0	T	T	T	T
TX	3,300	30.0	99,000	T	T	1.8	1,822.1	0.4	404.9
UT	120	41.0	4,920	0.0	0.0	0.0	0.0	0.0	0.0
VA	280	71.0	19,880	0.0	0.0	0.5	99.9	0.0	0.0
WA	1,720	56.0	96,320	T	T	T	T	0.3	289.8
WV	8	60.0	480	0.0	0.0	T	T	0.0	0.0
WI	335	66.0	22,110	T	T	2.0	451.2	0.0	0.0
Total	39,595	41.7	1,866,042		T		42,360.7		1,758.9
U.S. % loss				T		2.22		0.09	
U.S. total	39,614	47.2	1,867,903						

peak by early April when temperatures surpass the optimum for stripe rust development. In mid-March, traces of stripe rust were found in wheat plots at Crowley in south central Louisiana but by late March no stripe rust was found.

Arkansas. In mid-March, stripe rust was confirmed in southeastern Arkansas plots. By early April, stripe rust was found in plots and fields in central Arkansas. Stripe rust was scattered with little evidence of hot spots and most of the commonly planted cultivars have some resistance. One hot spot of stripe rust was found in a plot in west-central Arkansas. Stripe rust over wintered in Arkansas in 2008, but at a much lower level than leaf rust. Very susceptible cultivars are no longer grown, and the acreage planted to susceptible cultivars is small. Most cultivars have adult-plant resistance to the current pathogen population. The combination of resistance and fungicides controlled stripe rust. By early May, conditions were still favorable for stripe rust development north of I-40 in Arkansas. Most cultivars have some resistance, except for a few fields in northeast Arkansas that were planted with susceptible cultivars. Stripe rust was still active in plots at Fayetteville.

Southeast. In mid-March, very low levels of stripe rust were found in a southern Mississippi field. In late March, hot spots of stripe rust were reported in Griffin, Georgia fields and low levels were reported in the Tifton, Georgia area. In mid-April, in southern Alabama and southwestern Georgia low levels of wheat stripe rust were found in a few plots (Fig. 2, p. 224). In these locations most of the stripe rust infections had occurred earlier in mid to late winter when temperatures were cooler**.** As day and nighttime temperatures continued to increase, the conditions for stripe rust development were less favorable. This lead to a reduced amount of stripe rust inoculum for the northern wheat growing regions of the U.S. In late April, hot and dry conditions slowed stripe rust development in plots and fields throughout the southern U.S. (Fig. 2, p. 224). Hot spots of severe stripe rust were observed in late maturing susceptible cultivars in nurseries in southwestern Georgia and north central Louisiana. Most of the infections had occurred when conditions were cooler. In early May, stripe rust levels were fairly high in many fields in western Tennessee.

Midwest. In early May, a field in southwest Kentucky had very low levels of stripe rust. In late May, stripe rust was at low levels in central and western Kentucky wheat fields. In much of this area many of the fields had been sprayed with fungicide to control the rust.

On 20 May, a few stripe rust hot spots were found in research plots at Mount Vernon, Illinois. In late May, low levels of stripe rust were found in southwestern Missouri fields. In early June, low levels of stripe rust were found in northeastern Missouri and west-central Indiana fields and plots. On 10 June, a center of wheat stripe rust infection was observed in a research plot at Napoleon in northwestern Ohio. In mid-June, low levels of stripe rust were found in susceptible entries in plots in southwestern Wisconsin (Fig. 2, p. 224).

Virginia. Trace amounts of stripe rust were found in wheat breeding nurseries at Blacksburg and Warsaw, Virginia in early June.

California. On 27 February, two infection foci of 25 ft^2 and 50 ft^2 were detected in plots of D6301 in Davis, California. The foci were severely diseased, so the initial infections probably occurred at least two weeks previous to detection. In mid-March, stripe rust was confirmed in a few commercial fields in the Yolo and Colus counties in the Sacramento Valley on susceptible cultivars (Blanca Grande, Summit) and on the previously resistant cultivar Cal Rojo. Disease severity was relatively light overall, but within the infection foci severity was up to 50%. In early April, stripe rust was found in the Central Valley of California.

By the second week in April, wheat stripe rust was increasing in the northern part of the Central Valley of California (Sacramento Valley and the Sacramento/San Joaquin Delta), but the rust was not uniformly severe. Only a few commercial fields were not treated with a fungicide and these fields had severe infection levels (80%). Only light infections were observed in the southern part of the Valley (San Joaquin Valley).

Cool conditions were favorable for continued development of wheat stripe rust in California's Central Valley and surrounding areas through the middle of May. Several cultivars that were not infected earlier in the season had susceptible infection types in mid-May, possibly indicating that new races have become established. With few exceptions, fungicides were applied to fields of known susceptible cultivars, so yield losses were minimal. Five consecutive days of extremely hot weather (high 90s and 100s) beginning on 15 May terminated the epidemic and hastened the Central Valley's crop toward maturity. Many entries in the wheat stripe rust screening nurseries at the UC Davis Agronomy Farm had final disease severities of 60–100%.

Table 4. Estimated losses in spring and durum wheat due to rust in 2008 (T = trace).

SPRING WHEAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
CO	36.0	75.0	2,700.0	0.0	0.0	T	T	0.0	0.0
ID	520.0	72.0	37,440.0	0.0	0.0	T	T	T	T
MN	1,800.0	56.0	100,800.0	0.0	0.0	T	T	0.0	0.0
MT	2,480.0	24.0	59,520.0	0.0	0.0	T	T	T	T
NV	4.0	95.0	380.0	0.0	0.0	0.00	0.0	0.0	0.0
ND	6,400.0	38.5	246,400.0	0.0	0.0	T	T	0.0	0.0
OR	170.0	45.0	7,650.0	0.0	0.0	T	T	0.0	0.0
SD	1,520.0	45.0	68,400.0	0.0	0.0	1.00	690.9	0.0	0.0
UT	19.0	44.0	836.0	0.0	0.0	0.00	0.0	0.0	0.0
WA	505.0	42.0	21,210.0	T	T	T	T	1.5	323.0
WI	22.0	41.0	902.0	0.0	0.0	T	T	0.0	0.0
WY	11.0	46.0	506.0	0.0	0.0	0.00	0.0	0.0	0.0
Total	13,487.0	40.5	546,744.0		T		690.6		323.0
U.S. % Loss				T		0.13		0.1	
U.S. Total	13,487.0	40.5	546,744.0						
DURUM WHEAT									
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
AZ	149.0	98.0	14,602.0	0.0	0.0	0.0	0.0	0.0	0.0
CA	155.0	105.0	16,275.0	0.0	0.0	0.0	0.0	0.0	0.0
ID	10.0	73.0	730.0	0.0	0.0	0.0	0.0	0.0	0.0
MT	570.0	19.0	10,830.0	0.0	0.0	0.0	0.0	0.0	0.0
ND	1,690.0	25.0	42,250.0	0.0	0.0	0.0	0.0	0.0	0.0
SD	10.0	19.9	190.0	0.0	0.0	0.0	0.0	0.0	0.0
Total	2,584.0	32.8	84,877.0		0.0		0.0		0.0
U.S. % Loss				0.0		0.0		0.0	
U.S. Total	2,584.0	32.8	84,877.0						

Pacific Northwest. In early April, wheat stripe rust had not been found in the major eastern wheat-growing areas of the Pacific Northwest. In the first week in April, susceptible cultivars in winter wheat nurseries in northwestern Washington had 50% levels of stripe rust infection. Similar levels of rust severities were observed in commercial fields that were planted with susceptible cultivars. In the second week of April, low levels of stripe rust were found in central Washington fields, which was much less rust than was found in 2007 in the same area. In late April, stripe rust was found in southeastern Washington. Some early-planted fields had severities up to 10% incidence and 5% severity. In general, stripe rust developed slowly in eastern Washington. In the Mount Vernon area in western Washington, stripe rust had developed up to 100% severity on highly susceptible entries by 24 April.

On 14 May, trace levels of stripe rust were found on a susceptible spreader row in a winter wheat nursery near Pullman, Washington. This was the first observation of stripe rust in the Washington/Idaho Palouse region in 2008.

On 10 June, no stripe rust was found in the Mosses Lake area in central Washington. Low levels of stripe rust were found in the susceptible spreader rows in the rust-monitoring nursery at the Lind Dryland Experiment Station in east central Washington. In mid-June, wheat stripe rust was severe on susceptible spreader rows in the winter wheat nurseries near Pullman, Washington but few winter wheat entries in the nurseries had stripe rust. No stripe rust was found in the spring wheat and barley nurseries or fields near Pullman. In general, stripe rust infections were low in the eastern Pacific Northwest.

In early July, wheat stripe rust was developing at a slow pace in the Pacific Northwest due to the dry and hot weather conditions. No rust was found in winter wheat fields in the Palouse area. Low levels of stripe rust were found in spring wheat fields in east central Washington. On 1 July, highly susceptible winter wheat entries in experimental fields at Walla Walla in southeastern Washington had 80% stripe rust severities.

In mid-June, high levels of wheat stripe rust were reported on susceptible winter wheat and low levels on spring wheat plants in nurseries at the Pendleton Experiment Station in northeastern Oregon. In late June, high levels of stripe rust were found in susceptible winter wheat entries in nurseries at Corvalis, Oregon, and Moscow, Idaho. In Pendleton and Hermiston, Oregon, nurseries susceptible spring wheat entries had stripe 20% rust severities.

NEBRASKA

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Wheat production.

In 2008, 1,750,000 acres of wheat were planted in Nebraska and 1,670,000 were harvested with an average yield of 44 bu/acre for a total production of 73,500,000 bu. The autumn generally was conducive to good emergence in these parts of the state. Planting in eastern Nebraska was subject to heavy rains that delayed planting and hurt emergence after planting. Hence, the eastern wheat crop got off to a bad start that unfortunately carried forward through the rest of the growing season. The winter was relatively mild and winterkilling was minor. The spring growing season began and stayed on the dry side in parts of western Nebraska, thus reducing diseases other than viruses, but did cause concerns for drought damage. However, much of eastern Nebraska had ample moisture during flowering and grainfill leading to leaf diseases, and Fusarium head blight, which again was a major concern. In the south-central and eastern parts of the state, early season diseases included powdery mildew, tan spot, and Septoria leaf blotch. Despite the wetness, leaf rust did not develop to damaging levels (except in some susceptible lines or cultivars) because the inoculum (rust spores) blown into Nebraska from southern states was limited. In western Nebraska, wheat streak mosaic virus was present as was loose smut and common bunt (syn. stinking smut). For the first time, *Triticum* mosaic virus was confirmed in Nebraska. Wheat stem sawfly in the panhandle continued to expand its presence with severe infestations being found for the first time in central Box Butte County.

In 2009, the most popular and most widely grown wheat cultivar was Agripro Jagalene (13.8% of the state) followed by Millennium (13.2%), Pronghorn (12.1%), TAM 111 (6.5%), Alliance (6.1%), Goodstreak (5.0%), and Wesley (4.8%). Pronghorn and Goodstreak are tall (conventional height) wheat cultivars that have consistently done well in the drought prone areas of western Nebraska where tall wheat cultivars are increasingly being planted.

Increase of new experimental lines.

P.S. Baenziger.

Two lines are under increase NE01481 and NI04421. NE01481 is being evaluated for the Southeastern NE and the organic market. It has superior end use quality, soilborne wheat mosaic virus resistance (a rarity among our lines), and very high grain yield for Southeast NE. We view it as an excellent new experimental line with a trait that is valuable to a part of our state that we have had difficulty finding good new cultivars with the right disease resistances. NI04421 is targeted for irrigated production systems where it has preformed extremely well. It has acceptable end-use quality and disease resistance with one exception. It is very susceptible to stinking smut. Additional information about our breeding program can be found at http://agronomy.unl.edu/grain/WHTANN08F.PDF.

Winter triticale nursery.

P.S. Baenziger and K. Vogel.

In 2008, no new triticale lines were recommended for release; however, we selected nine lines for increase (five small and four large) as possible replacements or to complement NE426GT and NE422T, which continue to perform well. Because triticale is a small market crop, we are carefully deciding how best to release new triticale cultivars so as to not cause inventory problems with the previously released cultivars. We now are beginning to move to higher and more consistent grain yield levels, but identifying excellent forage types requires forage harvesting, which is expensive and difficult for widespread trials. Although the markets for biofuels fluctuate with the price of oil and other geologically based fuels, we believe that there is a future for triticale in a biobased energy system. Triticale can be grown over the winter as forage or grain crop in areas where maize cannot be grown successfully. The grain will substitute for maize in animal rations and the forage can be used as forage, cellulosic ethanol feed stocks, or as a ground cover.

Wheat transformation and tissue culture studies.

N. Mengistu, T. Clemente, S. Sato, S. Wegulo, J. Counsells, and P.S. Baenziger.

Wheat transformation continues to be a key strategic effort in the wheat improvement overall effort. Mr. Neway Mengistu, a graduate student on the project, is genetically characterizing and evaluating some lines with possible Fusarium head blight resistance genes. In addition, Dr. Clemente is adding some new transgenes with novel sweetener and fiber characteristics that may enhance end-use quality as a potential value added trait.

Chromosome substitution lines.

M.D. Ali, N. Mengistu, A. Bakhsh, P.S Baenziger, I. Dweikat, K. Eskridge, K. Gill, and M. Kazi.

This research was undertaken with the expectation as we learn more about the wheat genome; we would be able to develop better breeding strategies. Dr. Md. Liakat Ali is currently summarizing data on 223 recombinant inbred chromosome lines in a Cheyenne background for chromosome 3A (CNN(RICL3A)) in a four-replicated trial in six trials (Mead, 2005, 2006, and 2007; Sidney, 2005; Lincoln, 2006, North Platte, 2007). this research. We continue testing in replicated trials recombinant chromosome lines involving both chromosomes 3A and 6A in a Cheyenne background (CNN(RICL3A+6A)) to study epistasis (led by Mr. Ali Bakhsh, a new student in our project). Mr. Neway Mengistu is studying in replicated trials at Lincoln, Mead, and North Platte, 90 WI(RICL3A)s to compare to our CNN(RICL3A)s and CNN(RICL3A+6A)s studies. Preliminary results suggest that the yield reducing QTL from CNN in the WI background maps to the same location and the yield increasing QTL from WI mapped in the CNN background. Dr. Mujeeb Kazi created these lines for us using doubled haploid techniques and we are very appreciative of his efforts.

Collaborative research on wheat diseases.

J. Sidiqi, N. Mengistu, S. Wegulo, F. Dowell, and P.S. Baenziger.

The major event in stem rust research is the emergence of a new race Ug99 that can overcome most of the previously very durable resistance genes in wheat, which were the main genes used in our program. Hence, this is a huge potential loss for our breeding efforts. *Sr2* (found in Scout 66 but is associated with false or pseudo black chaff), appears to be one of the few commonly used genes available. We are rapidly incorporating new stem rust genes (*Sr25, Sr26, Sr39, and Sr40*), but the rapid loss of so many resistance genes in unprecedented in my lifetime. Interestingly Sr_{Tmp}, which is found in many of our lines, including NE01643 is resistant to Ug99, but not to some of the races found in the United States. Mr. Javed Sidiqi, a Fulbright scholar from Afghanistan, screened 505 lines from Central Asia (430 from Afghanistan, 25 from Pakistan, 25 from Iran, and 25 from Tajikistan) and only two modern lines from Afghanistan were resistant to stem rust race TPMK (a surrogate race that is present in the U.S.). Working with Dr. Yue Jin, the four most resistant lines were screened to Ug99 in his carefully confined testing facility and all were found to be susceptible to Ug99. This result confirms the extreme vulnerability of the Central Asian wheat crop to this new race.

Molecular markers are becoming an important aspect of our research on developing Fusarium head blightresistant lines. This year we began screening all three way cross F_1 seed to identify those carrying FHB QTL so as to enhance the frequency of the QTL in our populations. In the F_2 and possibly F_3 bulk generations, we are using optical sorting to enrich the populations for kernel hardness (remove the soft kernel genotypes). Currently, experiments to determine the efficacy of optical sorting for hardness and protein content are underway with Dr. Floyd Dowell of the USDA–ARS, Manhattan, KS. In this approach, at the minimum, we should create populations that are fixed for the 3BS QTL (*Fhb1*), enriched for other FHB QTL, and selected for hardness prior to visual selection for plant type. The FHB research is supported by a grand from the USDA–National Wheat and Barley Scab Initiative program, which also funds part of Mr. Mengistu's research.

Plant height and diversity in wheat.

Z. Al-Ajlouni, I. Dweikat, G. Bai, K. Eskridge, and P.S. Baenziger.

We are interested in knowing if Rht_1 or Rht_2 may have better height characteristics in our tall and short plant height environments. Virtually all of our lines have the Rht_1 gene and only two lines may have had Rht_2. The most surprising result was that although many of lines have markers associated major dwarfing genes, the gene effects were missing (hence the markers were not diagnostic of the gene in our populations). None was more surprising than Cheyenne having the marker for *Rht8*, a gibberellic-sensitive dwarfing gene. There are many different responses to the environment for lines with Rht_1, which we believe can best be explained by unknown modifier genes in the background that affect of Rht_1.

Coordinated agriculture project: Applied Wheat Genomics.

N. Crowley, I. Dweikat, K. Eskridge, and P.S. Baenziger.

We are genotyping and phenotyping a mapping population of 154 F_6-derived recombinant inbred lines of 'TAM 107-R7/Arlin' in collaboration with Pat Byrne and Scott Haley of Colorado State University. We submitted our marker data set and linkage map including 436 markers, a mixture of SSR, DArT, HMW- and LMW-glutenins, and morphological markers in June 2008. The linkage map covers approximately 2,120 cM, with a density of 6.44 cM/marker. The population has been submitted into the National Small Grains Collection with the accession numbers in GRIN: GSTR 11601–11756 and is available upon request. We harvested our first field trails in 2008 and have repeated the field experiments in 2008–09, which includes two sites in Texas. This research is supported by a grand from the USDA–CSREES–NRI (Proj. No. 2006-55606-16629) competitive grants program.

Genetic diversity in Turkish and Nebraska cultivars.

A. Auvuchananon, I. Dweikat, K. Eskridge, S. Dere (deceased), and P.S. Baenziger.

Ms. Anyamanee Auvuchanon is studying the relationship between U.S. and Turkish wheat lines. In her study, she is evaluating 23 U.S. Great Plains wheat and 22 Turkish wheat lines. In 1874, Turkey red winter wheat was brought to the Great Plains and became the most widely grown wheat in the United States. Since then, the Turkish and U.S. breeding programs have interacted, but often used different germ plasm. This study suggests that modern Great Plains wheat cultivars diverged from Turkish wheat cultivars by breeding for adaptation since only historic Great Plains wheat cultivars had a close relationship with Turkish wheat cultivars using the various clustering programs to determine similarity. For Great Plains wheat improvement, it may be possible to use those Turkish wheat cultivars that have agronomic merit and are most closely related to the Great Plains wheat cultivars as parents to add new alleles without adding so much genetic diversity as to make it hard to find the useful alleles.

Genetics of white flour and noodle color in wheat.

P.S. Baenziger, R.A. Graybosch, and Somrudee Onto.

Ms. Somrudee Onto, PhD student, is studying the genetics grain polyphenol oxidases (PPO), enzymes involved in discoloration of white flour and noodle color. Most Nebraska-bred hard white wheats have been found to carry wild-type alleles at the *Ppo-2A* and *Ppo-2D* loci. A newly released HWW, Anton, was found to carry both low levels of grain PPO, and, based on results with the STS marker PPO18, a mutant allele at *Ppo-2A*.

Breeding wheat for organic production systems.

R. Little, P.S. Baenziger, L. Xu, and V. Schegel.

Wheat breeding research for organic systems was initiated in 2008 through a USDA–CSEERS grant (Proj. No. 2007–51300–03785) on certified organic land at four Nebraska research stations. An additional component of this project is to develop production systems utilizing cover crops and winter wheat in organic systems. Testing in organic environments at UNL begins at the F_6 generation with unreplicated yield trials. The F_6 nursery plus F_7 (early replicated yield trial) and F_8–F_{12} (Nebraska interstate Nursery—NIN) nurseries are grown on organic land at two locations, Mead and Sidney. The F_{10}–F_{12} (Organic State Cultivar Trial) nursery is grown at four locations of which three also have conventional State Cultivar Trials for comparison: Mead, Clay Center, and Sidney. Concord (Haskell) has only an organic cultivar trial. Based on discussions with organic small grains producers, an initial list of ideal winter wheat cultivar traits was used as the basis for screening in 2008: 1) competitive grain yield, 2) excellent end-use quality, 3) the ability to extract soil nutrients, 4) excellent disease and insect resistance, and 5) the ability to provide early season ground cover to suppress or tolerate weeds.

Yield. Many yield rank changes were expressed between organic and conventional lines in the NIN trials. Ironically, the line that did best in our elite trial grown in organic conditions was NH03614 (released as Settler CL), an herbicide-resistant wheat that is unlikely to be used in organic production. For the three locations with both organic and conventional plots, 2145 and NI04421 (most likely due to its being very susceptible to common bunt (or stinking smut) yielded much lower in organic plots than in conventional plots, whereas Overland was consistently high in both systems. This change of ranks is reflected in a highly significant system by entry interaction ($P<.0001$). In the three eastern locations, the long, cool, early summer seemed to favor tall cultivars including Goodstreak and Pronghorn. Goodstreak consistently outyielded all other cultivars at all three locations. Darrell was the most consistent in yield rank next to Goodstreak and performed the best for canopy cover (light bar readings) at jointing stage across locations. One new line with an excellent yield record in eastern Nebraska, NE01481, that also has great baking quality (yet poor milling quality) and very good disease resistance (including soilborne mosaic virus resistance, rare in our releases), is being increased for conventional and organic production.

Quality. Good USDA–ARS milling, mixing, and baking ratings from previous years were supported in 2008 for Pronghorn, Wesley, Alice, and Millennium. The promising USDA milling and baking quality for three experimental lines

(NW03681, NE04424, and NE04490) was supported. High protein content was responsible for all good mixing and baking lines, except for NE04490. NE04490 baked well and Hatcher, Harry, Alliance, and NE03490 had acceptable baking quality in 2008 despite low protein, which indicates good protein quality.

Breeding and characterization of waxy wheats.

R. Graybosch, L.E. Hansen, and D. Jackson.

A winter waxy (amylose-free) wheat breeding line, NX04Y2107 was entered both in the USDA–ARS cördinated Northern Regional Performance Nursery and in the University of Nebraska Wheat Variety Trial. In trials in nine Nebraska counties, grain yield of NX04Y2107 was equal to or greater than that of Jagalene, the most widely grown wheat in Nebraska over the past five years. In Lancaster and Clay Counties in Eastern Nebraska, NX04Y2107 was the highest yielding entrant and was entered in these trials again for 2009. Three additional waxy wheat breeding lines were selected from 2008 field trials and were advanced to regional and statewide trials for further testing. Using starch derived from waxy and partial waxy (reduced amylose) durum wheats, we discovered that cross-linked waxy starches have much greater final viscosity after cooking than normal or partial waxy starches, and that mechanical blends of waxy and normal starch produces final viscosities different than both types alone.

Tolerance to preharvest sprouting.

R.A. Graybosch.

Populations based on the sprout-tolerant hard white winter wheat RioBlanco were used, in collaboration with USDA–ARS scientists at Manhattan, KS, to identify potential new quantitative trait loci linked to preharvest-sprouting tolerance. A highly efficient technique of screening for resistance to preharvest sprouting was developed, incorporating readings of treated spikes via use of a Li-Cor Leaf Area Meter. To verify the effect of the identified QTL, samples from five additional breeding populations were obtained from 2007 and 2008 field plantings. Evaluation of 2007 samples has been completed and 2008 evaluations are commencing.

Comings and goings.

Mr. Javed Sidiqi successfully completed his M.S. degree. Mr. Zakaria Aj-Alouni successfully completed his Ph.D. degree. We welcome Ms. Kayse Onweller as a new graduate student to our program. Finally, we welcome Dr. Dipak Santra, who is the new proso millet breeder in western Nebraska and who will be an invaluable coöperator on wheat research. Three visiting scientists joined our project: Dr. Munir Turk from Jordan, Dr. Xianming Chen from the Peoples Republic of China, and Dr. Xiyue Song from the Peoples Republic of China.

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Wheat extension and wheat management research.

Jeff T. Edwards.

The 2007–08 wheat production year was outstanding for most Oklahoma wheat producers. Average yield was 2,486 kg/ha on 1.82 x 10^6 total harvested hectares, resulting in total crop value of $1.082 billion. In most of the state, wheat yields were 50 to 75% higher than historical averages. Many producers reported dryland wheat yields in excess of 5,000 kg/ha, and several variety-trial test plots exceeded 6,000 kg/ha. These record yields were present despite a lackluster environment for wheat emergence and growth during autumn 2007. In fact, many fields did not emerge until late winter. Timely spring rainfalls, adequate soil nitrogen mineralization, and moderate temperatures throughout late spring and early summer, however, allowed wheat plants to tiller and recover from a late start.

One interesting phenomenon that emerged in 2008 was a yield increase associated with grazing in some of our experiments. Winter wheat in the southern Great Plains is commonly grazed by cattle from late autumn through late winter, but a yield penalty, not increase, is generally associated with this practice. In 2008, grazed treatments yielded as much as 600 kg/ha more than nongrazed treatments when both were sown in mid-September. Nongrazed treatments, however, yielded approximately 500 kg/ha more than grazed treatments when nongrazed plots were sown at an optimal mid-October date. These data reinforce a hypothesis shared among many dual-purpose wheat researchers that the earlier-than-optimal sowing date in dual-purpose wheat production system probably has equivalent or greater impact on grain yield than grazing by cattle.

Cultivar development and breeding research.

Brett F. Carver.

Proposals submitted by the Oklahoma Wheat Improvement Team have been accepted by the Oklahoma Agricultural Experiment Station for the release of **OK Rising** hard white wheat in early 2008 and **Billings** and **Pete** hard red winter wheat in early 2009.

OK Rising was tested as experimental line OK02522W in the Southern Regional Performance Nursery (SRPN) in harvest years 2006 and 2007. The naming of this cultivar was intended to coincide with the 100th anniversary of Oklahoma's statehood (1907–2007); the cultivar's namesake is a contemporary musical piece composed specifically for the centennial by Oklahomans Jimmy Webb and Vince Gill, entitled 'Oklahoma Rising'. The name OK Rising also was intended to show linkage with its closely related HRWW counterpart and sister line, OK Bullet. Both OK Bullet and OK Rising came from the cross 'Jagger/KS96WGRC39'.

Substantial genetic improvement has been realized in the US HWWW class in the past decade, such that HWWW wheat lacks nothing for yield and quality compared with its sister class HRWW. What the HWWW class does

lack is genetic depth, or to the wheat producer, varietal choice. With a restricted genetic base often comes a restricted adaptation range. The current state of HWWW is that superior cultivars are available to producers, but primarily in the High Plains area of the U.S. Great Plains region. The primary driver for release of OK Rising was its greater adaptation range, extending from the High Plains to lower-elevation and higher-rainfall regions of Oklahoma and the southern and central Plains, where previous releases such as Intrada and Guymon were not adapted. Its capability is derived from a yield-performance history and disease resistance package comparable, if not identical, to OK Bullet, substantially improved straw strength and standability, and improved tolerance to pre-harvest sprouting over Intrada and Guymon.

Preharvest-sprouting tolerance has been observed by germination tests of seed harvested from field plots at physiological maturity or falling number determination from grain samples collected after harvest maturity. OK Rising has demonstrated the ability to maintain falling number values in excess of 350 to 400 sec when harvested two to three weeks after harvest maturity in extreme high-rainfall environments (years 2007 and 2008). OK Rising also shows heat-sensitive germination much like the cultivars 2174 and Cimarron. This type of seed dormancy pattern causes delayed germination in hot soils when planting early for the purpose of forage production in grazed or dual-purpose systems. OK Rising produces the same band pattern as 2174 at the SSR marker locus, *Xbarc310*, which is tightly linked to a QTL for heat-sensitive germination, *QGhs.osu-3A* (Liuling Yan and Shuwen Wang, personal communication).

The OSU wheat-improvement program continues to emphasize dual development of HWWW and HRWW cultivars. Currently, we allocate 80% of our resources in the latter stages of selection to HRWW inbred line development. In the past three crossing cycles, 49% (2007), 37% (2008), and 26% (2009) of the crosses made each year involved HWWW parentage to varying degrees, and our program tends to produce about 900 hybrid combinations per year. In those same years, the percentage of crosses involving strictly HW parentage decreased from 19% in 2007 to 15% in 2008 to 12% in 2009. These declining numbers do not indicate a declining interest in HW cultivar development but instead a more concerted focus on parentage with suitable agronomic and sprout-tolerant patterns.

Two new HRWW cultivars will be introduced to certified seed producers during fall 2009. Having appeared in the SRPN in harvest years 2007 and 2008, **Billings** was tested as OK03522, and **Pete** was tested as OK03305. Billings is a $F_{4:5}$ line from the cross 'N566/OK94P597', which N566 is 'Eritrospermum 2755-91'/'Odisseya' and OK94P597 is 'HBY359A/Fundulea 133//TAM 200'. Pete also is a $F_{4:5}$ line from the cross 'N40/OK94P455'; N40 was derived from 'Lutestens 11291 Vumpel/Istok' and OK94P455 was derived from a double-cross of Pioneer and Kansas State University experimental lines (W0405D/KS831957//W3416/KS831957). Both N40 and N566 were germ plasm lines graciously provided by the Institute of Plant Breeding, Odessa, Ukraine, made possible through a germ plasm exchange program in the early 1990s between the Institute and USDA–ARS (ARS oversight provided by Jim Peterson).

Both cultivars were produced through our ***GRAZE***n***GRAIN*** breeding system, though Pete is better adapted to dual-purpose management systems. Pete is awnless but has produced excellent test weight patterns, with acceptable milling and break baking quality. The cultivar is projected to replace some of the acreage currently occupied by Deliver, an awnless HRWW cultivar released by OSU in 2004, because Pete offers improved yield potential throughout the state, has slightly improved aluminum tolerance in acidic soils, and shows much improved straw strength. Pete is resistant to *wheat soilborne mosaic virus* and *wheat spindle streak mosaic virus*, and it has shown effective adult-plant resistance to leaf rust and powdery mildew. Pete's resistance to stripe rust is classified as intermediate and similar to that of Endurance.

Billings will be positioned for the northern half Oklahoma, including irrigated production in the Oklahoma panhandle (High Plains areas), and its range of adaptation extends into southern Kansas. The foliar disease package is similar to Pete, except that Billings provides excellent adult-plant resistance to stripe rust. Billings also is more tolerant of low pH conditions. Milling quality is outstanding, as kernel size typically exceeds 32 g in 1,000-kernel weight and 2.40 mm in kernel diameter based on the single-kernel characterization system. Mixing tolerance is above average for the HRWW class, with reasonably a good combination of dough strength and extensibility, at an intermediate level of wheat protein (12.0–13.0% on a 12% moisture basis). Billings is considered a suitable replacement for HRWW cultivars Endurance, OK Bullet, or Overley, all of which occupy significant acreage in Oklahoma in 2009.

Marker-assisted selection is playing an increasing role in our wheat improvement program, primarily for the purpose of gene enrichment in early segregating generations. This activity is tied directly to participation in the multi-institutional CAP project funded by USDA–CSREES (award no. 2006-55606-16629), in conjunction with the Hard Winter Wheat Genotyping Laboratory (USDA–ARS, Manhattan, KS) supervised by Dr. Guihua Bai and in cooperation with Dr.

Liuling Yan (Oklahoma State University molecular geneticist). Target traits currently under watch are Hessian fly resistance, acid-soil tolerance, and resistance to leaf rust, *wheat streak mosaic virus*, and *barley yellow dwarf virus*.

Wheat genomic research: genetic regulation of reproductive development in winter wheat.

Liuling Yan.

Central to the research mission of the OSU Wheat Improvement Team is to use molecular tools to regulate the reproductive development process in winter wheat to maximize adaptation to specific management systems, with an emphasis on dual-purpose production systems in the southern Great Plains.

When sown in the autumn, winter wheat cultivars show variation in developmental processes, including the initiation of stem elongation, heading, and physiological maturity. Phenotypic variation in the timing of a specific developmental stage can be subtle, spanning only a few days due to adaptive responses and synchronization with changes in photoperiod and low temperature in seasonal climates; however, this minor variation is important to final productivity. Delayed reproductive development may be optimized to generate more biomass for cattle grazing in dual-purpose production systems. Additionally, a relatively later stem-elongation time is desired to avoid frost damage frequently occurring during early spring, whereas a relatively early maturity time is desired to avoid the hot and dry summer season, or as global climate shifts toward warmer temperature.

In recent studies, we generated two populations of RILs that were used to map genetic loci controlling developmental processes in winter wheat. One was generated from a cross between two winter wheat cultivars, Jagger (early stem elongation) and 2174 (late stem elongation), and the other was generated from a cross between Intrada (undergoing stem elongation earlier but reaches heading later) and Cimarron (undergoing stem elongation later but reaches heading earlier). We mapped SSR markers and known genes related to vernalization and photoperiod responses in these two populations. We concluded that segregation in arrival time of stem elongation is mainly controlled by a major QTL on chromosome 5A associated with the vernalization gene *VRN-A1* (=*AP1*). When *VRN-A1* was fixed for the same allele, segregation in heading date and maturity time was controlled by QTL associated with the photoperiod gene *PPD-D1* and the vernalization gene *VRN-D3* (=*FT*). Several other genomic regions were associated with variation in these developmental traits. In addition to direct application of these molecular tools to winter wheat breeding populations, we are further pursuing the molecular mechanism of the developmental adaptation of winter wheat.

Personnel.

The Wheat Improvement Team at OSU currently has nine members Brett Carver (team leader, wheat breeder), Liuling Yan (molecular genetics), Bob Hunger (disease resistance), Tom Royer and Kris Giles (Hessian fly resistance), Art Klatt (prebreeding and germ plasm development), Jeff Edwards (extension, management), Patricia Rayas-Duarte (cereal chemistry), and Bjorn Martin (stress physiology). The team services of David Porter, formerly USDA–ARS (aphid resistance), were lost in 2007 to his assuming the position of Department Head, Department of Plant and Soil Sciences, OSU.

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Bob Hunger.

Wheat diseases in Oklahoma in 2008.

Until the month of May, 2008 was a fairly quiet year for diseases in Oklahoma. Prior to May, powdery mildew, leaf rust, stripe rust, septoria, tan spot, wheat streak mosaic, high plains, and barley yellow dwarf were all confirmed in the state. However, at the end of the first week of May, leaf rust exploded across central and north-central Oklahoma, and hot spots of stripe rust were observed. As May progressed, other diseases observed included dryland root rot, stem rust, and Fusarium head blight. Leaf rust did not hit the southern, northwestern, or panhandle regions of Oklahoma because of drought; however, in the central and north-central regions of Oklahoma, fungicide use was much greater than normal due to severe leaf rust.

Breeding for wheat disease resistance.

Regional nurseries, including the Southern Regional Performance Nursery, the Northern Regional Performance Nursery, and the Regional Germplasm Observation Nursery, were tested for reaction to wheat soilborne mosaic/wheat spindle streak mosaic in the field, and to leaf rust in the greenhouse (seedling) and field. Results from these and other trials conducted on winter wheat are summarized at http://www.ars.usda.gov/Research/docs.htm?docid=11932.

Tan spot research.

Three isolates of *P. tritici-repentis* were compared for hyphal growth, sporulation, reproduction, and virulence on wheat. These isolates, OKD-1, RBB6 and OK06-1, were collected in Oklahoma in 1983, 1996, and 2006, respectively. Greatest radial growth was observed for OK06-1, which also produced significantly ($P<0.05$) more conidia. Isolates were similar in number of pseudothecia formed; OK06-1 produced the highest percent of mature pseudothecia (22.0%), followed by OKD-1 and RBB6. RBB6 produced significantly less conidia than OKD-1 but was more virulent in the field. Maximum disease severity was recorded for OK06-1 in both greenhouse and field studies. In the field, OK06-1 reduced yield by 20.7% compared to the control, whereas RBB6 and OKD-1 reduced yield by 13.8 and 4.9%, respectively. Similar testing with additional isolates currently is ongoing.

Karnal bunt testing.

Commercial wheat produced in Oklahoma in 2008 was examined for the presence of teliospores of *Tilletia indica*. Testing was conducted using methods and following protocols approved by the Animal and Plant Health Inspection Service (APHIS). In 2008, 52 samples collected from elevators representing 14 counties were tested, which satisfied APHIS's National Karnal Bunt Testing Program. Testing has been conducted every year since 1996 in Oklahoma, with no positive samples being found.

Personnel.

Faculty conducting research in wheat pathology has been greatly reduced in the past 5 years because of retirements in 2004 by Mr. Ken Jackson, Dr. Larry Singleton, and Dr. Larry Littlefield. Bob Hunger's efforts are now primarily directed toward screening wheat breeder lines for disease reaction, incorporating disease resistance into wheat germ plasm, and fulfilling the extension wheat pathology responsibilities including foliar fungicide and seed treatment testing on wheat. He also advises two Ph.D. students, Mr. Kazi Kader (Bangladesh), who is comparing isolates of the tan spot pathogen collected over the last 25 years, and Mr. Ahmed Abd-Elmajid (Egypt – Dr. Hassan Melouk, co-advisor), who is investigating the effect of water potential on diseases of peanut and wheat.

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2008 wheat production in the Commonwealth of Virginia.

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Growing Conditions. The autumn of 2007 presented challenging planting conditions for many growers due to dry soil conditions with over half the state reported to be very short of soil moisture. Growers needing to perform primary tillage waited for rain, whereas some small grain was planted into these dry seedbeds. Rains in late October improved conditions dramatically and by the end of the first week of November, wheat planting reached 53 percent of intended

acres, which is the same as the five-year average. Early winter was relatively dry (Fig. 1) and although there were still concerns over subsoil moisture, most of the small-grain crop was rated good or better. Warm and favorable conditions in April resulted in wheat heading approximately 5 days earlier than the long-term average. However, generally cool conditions in May resulted in longer grain fill and an on-time harvest (Fig. 2). These cool conditions during grain fill helped produce plump kernels and generally good yields across the Commonwealth.

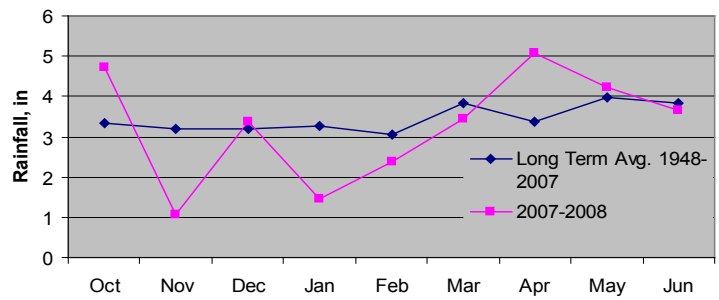

Fig. 1. Long-term mean and 2008 growing season statewide rainfall.

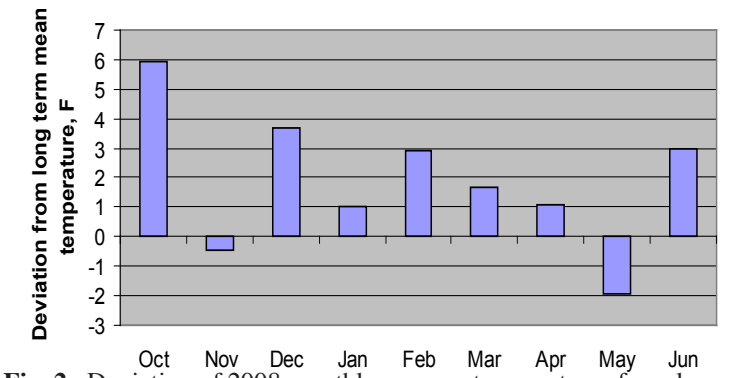

Fig. 2. Deviation of 2008 monthly average temperatures from long term average (1948–2008).

Disease and insect incidence and severity. Following four consecutive years (2004–07) of relatively low incidence of powdery mildew in Virginia, the disease reëmerged with susceptible cultivars having disease severities ranging from 50–80% at Blacksburg, Painter, and Warsaw, VA. For the first time, significant mildew infection was noted on isolated plots of the cultivars McCormick at Warsaw and Tribute at Painter both of which possess gene *Pm17*. Leaf rust infection and severity was high on susceptible cultivars (60–80%) grown in research yield trials at Blacksburg, Warsaw, and Painter, VA. Cultivars such as Sisson and USG3209 having gene *Lr26* and McCormick having gene *Lr24* were very susceptible to leaf rust. Race surveys conducted by the USDA–ARS Cereal Disease Lab on 21 samples from six regions in Virginia indentified six races (MBDSB, MFGJH, TBRKG, TCDSB, TCRKG, and TNRJJ) at Blacksburg (southwest), race TDBGH at Blackstone (southern Piedmont), race TLMJD at Orange (northern Piedmont), race TBRKG at Holland (southeast), races MFGJH and TDBGH at Painter (eastern shore), and four races (MCDSB, MCTSB, MFGJH, and TCRKG) at Warsaw (coastal plain). Virulence for the widely deployed genes *Lr24* and *Lr26* was common, whereas virulence for *Lr9* was only identified at Blacksburg and Orange, VA. Stripe rust was only found at one of the seven Official Variety Test sites in 2008. Isolated infection foci were observed in wheat headrows at Warsaw, VA, and rust samples sent to Xianming Chen at Washington State University were identified as race PST100. *Fusarium* head blight was moderately severe in no-till plots of the state variety trial at Holland, VA, with susceptible cultivars having severities exceeding 50% and DON toxin levels up to 2.8 ppm. *Barley yellow dwarf virus* infection was moderate at Blacksburg, and *Stagonospora* leaf blotch was moderate at Holland.

Production. According to the United States Department of Agriculture's National Agriculture Statistical Service (http://www.nass.usda.gov/Statistics_by_State/Virginia/index.asp), in 2007–08 Virginia wheat producers planted 310,000 acres (125,453 ha), up 80,000 acres (32,375 ha) from the previous year. The estimated area harvested was 280,000 acres (113,312 ha), a 37 percent increase over the 2006–07 total of 210,000 acres (113,312 ha). The 2008 state average grain yield of 71 bu/acre (4,771 kg/ha) was 7 bu/acre (4,771 kg/ha) higher than that in 2007, and set a new state record that was 3 bu/acre (202 kg/ha) higher than the previous record set in 2006. Overall wheat production in 2008 was 19.9 million bushels (541,000 metric tons).

State cultivar tests. In the 2007-08 tests, there were a total of 91 entries planted at seven locations across Virginia (http://www.grains.cses.vt.edu/). The test included 46 experimental lines and 45 released cultivars. No-till tests were conducted at Warsaw, Holland, and Shenandoah Valley with the Warsaw and Holland tests being planted after corn. The released cultivars Shirley, USG 3555, Branson, Pioneer 26R15, SS 560, SS 548, Renwood 3434, USG 3665, USG 3725, SS 5205, and SS 8641 all produced significantly higher yields than the overall trial average of 88 bu/acre (5,913 kg/ha). Average grain yields among the 91 lines ranged from 71 bu/acre (4,770 kg/ha) to 93 bu/acre (6,249 kg/ha). Average test weight ranged from 56.5 lb/bu (727 kg/m^3) to 61.5 lb/bu (792 kg/m^3) with an overall trial average of 59.2 lb/bu (762 kg/m^3).

2008 Virginia Small Grain Yield Contest results. The 2008 contest was divided into three separate regions and also included a statewide ranking. The results are presented in Table 1.

Table 1. Results of the 2008 Virginia Small Grain Yield Contest.

STATEWIDE			
Place	**Farm**	**Area**	**Yield (bu/acre)**
1	Grainfield Farm / Chuck McGhee	3	131.70
2	Turner Family Farms / Donald & Jamie Turner	1	130.05
3	Corbin Hall Farm / Ronnie Russell	3	111.07

Place	Farm	County	Yield (bu/acre)	Planting date	Cultivar
Area 1 – Southern Piedmont and Southern Coastal Plain					
1	Turner Family Farms / Donald & Jamie Turner	Dinwiddie	130.05	11/13/07	SS 560
Area 2 – Ridge & Valley and Northern Piedmont					
1	Alvis Farms / George Alvis	Goochland	107.11	11/07/07	SS 520
Area 3 – Northern Coastal Plain					
1	Grainfield Farm / Chuck McGhee	King William	131.7	11/03/07	USG 3665
2	Corbin Hall Farm / Ronnie Russell	Middlesex	111.07	10/12/07	Pioneer 26R15
3	Jason Benton	Middlesex	105.89	11/02/07	USG 3665
Additional entries					
	Oakland Farm / Randolph Aigner	Henrico	103.20	10/26/07	SS 8302
	Clifton "Boogie" Davis	New Kent	103.25	10/31/07	Vigoro 9510
	Heritage Farms LLC / David Black	Charles City	96.85	10/28/07	Vigoro 9553

Seeding rate effects on grain yield and yield components of winter durum wheat cultivars.

W.E. Thomason, C.A. Griffey, S. Liu, R.M. Pitman, W.S. Brooks, B. Will, J. Seago, and M.E. Vaughn.

Grain yield is the product of three components; heads/unit area, kernels/head, and weight/kernel. Yield improvement of winter durum wheat cultivars, through enhanced management, will increase the acceptance of this alternative crop by farmers. Current durum wheat lines yield approximately 80% of the best soft red winter wheat lines, but little is known about how intensive wheat management techniques affect these durum lines. Among durum lines alone, there was a significant linear increase in head density with increased seeding rate (Fig. 3). This often results in either fewer kernels per head or in lighter kernels. In this case, we did find fewer kernels/head when seeding rate was increased for VA05WD42, but we saw an increase in number of kernels/head for XVAD99147-1 (Fig. 4).

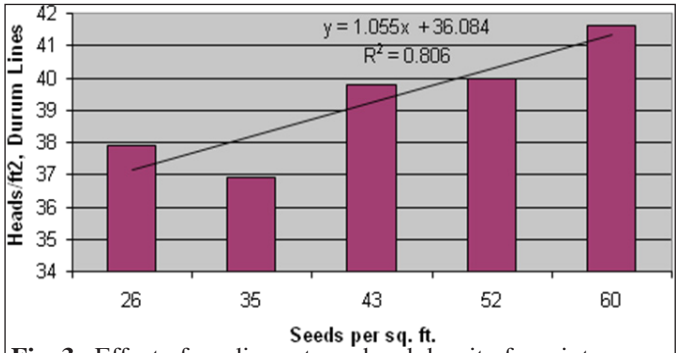

Fig. 3. Effect of seeding rate on head density for winter durum wheat lines.

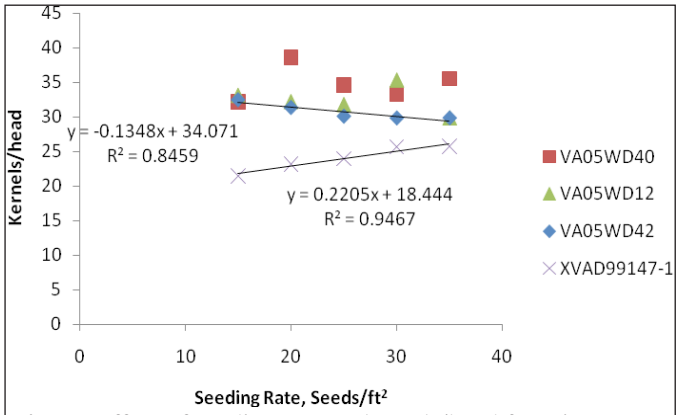

Fig. 4. Effect of seeding rate on kernels/head for winter durum wheat lines.

Update on quantitative trait loci for adult-plant resistance to powdery mildew in soft red winter wheat.

M.D. Hall, S. Liu, D. Van Sanford, J. Costa, G. Brown-Guedira, D. Marshall, and C.A. Griffey.

Three QTL for adult-plant resistance (APR) to powdery mildew were previously mapped on chromosomes 1B, 2A, and 2B in the soft red winter wheat cultivar Massey and later confirmed in a 'USG3209/Jaypee' population. A whole-genome linkage analysis was not conducted during the initial identification of these three QTL, but subsequently has been completed. Averaged over 11 environments, four genomic regions on chromosomes 1B, 2A, 2B, and 5A were associated with APR to powdery mildew. The new QTL for APR to powdery mildew identified on chromosome 5A of USG3209 is located near BARC056 and explains 9.75% of the phenotypic variation. The 5A QTL identified in USG3209 is located in the same chromosome region as a QTL conferring Fusarium head blight resistance identified in the cultivars Ernie and Massey. The relationship between these QTL controlling resistance to two different fungal pathogens is unknown at this time. However, Massey is a parent of USG3209, and we are currently mapping APR to powdery mildew and FHB resistance in a 'Becker/Massey' population to further understand this relationship on chromosome 5A.

A QTL for APR to powdery mildew located on chromosome 1B was identified in Massey and USG 3209 and is located near marker SCM09, which is the diagnostic marker for the T1RS·1AL and T1RS·1BL translocations. Although USG3209 contains the defeated major gene *Pm8* located on T1RS·1BL, which may have a residual effect on powdery mildew, Massey lacks this gene. The effect of this QTL is small accounting for only 8% of the total variation in powdery mildew severity.

Chromosome 2A has a QTL for APR to powdery mildew located near the centromere and marker GWM122. This QTL explained approximately 9% of the total phenotypic variation. The QTL for APR to powdery mildew on chromosome 2B is located near marker GWM047 and explained the most phenotypic variation (19.1%) of the four identified QTL. This QTL also had the highest LOD score of approximately 8. Markers GWM047 and GWM501 flank this QTL region, which spans approximately 6 cM.

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Identification and saturation mapping of QTL for Fusarium head blight resistance in the Virginia wheat cultivar Massey.

Shuyu Liu, Marla D. Hall, Carl A. Griffey, Anne L. McKendry, Jianli Chen, Patricia G. Gundrum, Gina Brown-Guedira, and David Van Sanford.

Massey, a cultivar released by Virginia Tech in 1985, has adult-plant resistance to powdery mildew and is moderately resistant to Fusarium head blight. A set of 589 Diversity Array Technology (DArT) markers were mapped onto all 21 chromosomes in a 'Becker/Massey' mapping population comprised of 152 RILs. Phenotypic data for FHB severity were obtained from a greenhouse test conducted in Virginia and FHB incidence, severity, index, toxin (DON) concentration, and Fusarium-damaged kernels (FDK) were collected from field tests conducted in Virginia (2007, 2008), Missouri (2008), and Kentucky (2008). Within each test, FHB incidence was significantly correlated to FHB severity ($P < 0.001$), and correlations between FHB severity and FHB index were the highest. After preliminary QTL analysis based on DArT markers, 58 simple sequence repeat (SSR) markers were mapped onto those target regions. Mapping results indicated that Massey has QTL on chromosomes 2B and 3BS centromere conferring resistance to fungus spread, which is close to the two QTL in Ernie. Two major QTL on chromosomes 4B and 4D are associated with field FHB resistance measured by incidence, severity, index, and FDK. The 4B QTL explained 8%, 6%, 12%, and 30% of phenotypic variation whereas the 4D QTL explained 21%, 33%, 28%, and 10% of phenotypic variation of corresponding FHB traits averaged over four environments. Two genes, *Rht1* and *Rht2*, were mapped onto the target QTL regions on chromosomes 4B and 4D, respectively. This result confirmed that *Rht2* gene is associated with FHB susceptibility. Another minor QTL associated with field incidence, severity, index, and DON reduction is on chromosome 2D, which explained 7% of phenotypic vari-

ation averaged over four environments. This QTL is close to the *Rht8* gene. Another QTL on chromosome 2D is close to the *Ppd1* gene and explained 8% of phenotypic variation in DON measured at Blacksburg, VA, in 2008.

These QTL and their relationship with *Rht* genes and *Ppd1* will be further validated with field data from two locations in Virginia in 2009. The similarity between QTL mapped in Massey with other known QTL will be compared and potentially novel QTL and/or tightly linked markers will be reported.

Acknowledgments. This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0790-4-102. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

Saturation mapping of FHB-resistance QTL in Ernie and the identification and application of diagnostic markers for breeding.

Shuyu Liu, Carl A. Griffey, Anne L. McKendry, Marla D. Hall, Patricia G. Gundrum, and Gina Brown-Guedira.

Fusarium head blight decreases wheat yields and quality significantly under epidemics in the eastern and southern U.S. Many QTL for FHB resistance have been mapped in exotic and native sources. However, only a few QTL have been widely deployed in breeding programs using marker-assisted selection due to the lack of diagnostic and tightly linked markers for most QTL. Four major QTL for type-II resistance were mapped on chromosomes 5A, 4B, 3BS, and 2B of the SRW wheat cultivar Ernie. A set of 243 RILs were evaluated in inoculated, mist-irrigated FHB nurseries at Columbia, MO, and Blacksburg, VA, in 2008. Phenotypic data were obtained for resistance to initial infection, to severity, to DON toxin accumulation and to Fusarium-damaged kernels (FDK) in irrigated and inoculated field experiments.

Fifty-five new microsatellite markers were mapped to saturate these four QTL target regions and other regions based on field scab resistance. Overlapping and distinct QTL were identified for different types of resistances in Ernie. The major QTL on chromosome 4B conditioning type-II FHB resistance explained 12.2% of the phenotypic variation for greenhouse severity based on point inoculation. This same QTL also explained 4%, 4.6%, 4.4%, 6.5%, and 8% of phenotypic variation in field incidence, severity, index, FDK, and grain weight, respectively. The awn-suppresser gene B_1 explained 5.8%, 7.9%, 7.5%, of the phenotypic variation in field incidence, severity, and index in two environments, respectively. One major QTL for DON reduction on chromosome 3A explained more than 20% of phenotypic variation. All these field FHB resistance QTL will be further validated in two experiments in Virginia in 2009.

Tightly linked markers were tested in a wide range of Chinese, European, and America resistance sources. The most diagnostic markers were used to screen top-cross breeding populations to pyramid scab resistance QTL from Ernie and Ning7840. Lines with native and exotic sources of scab resistance are being evaluated in the field.

Acknowledgments. This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0790-4-102. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

Release of the soft red winter wheat cultivar Shirley.

Shirley is a broadly adapted, high-yielding, short-stature, full-season soft red winter wheat cultivar developed and released in March 2008 by the Virginia Agricultural Experiment Station. The cultivar was derived from the three-way cross 'VA94-52-25/Coker 9835//Sisson sib'. The cultivar name Shirley was selected in commemoration of the Shirley Plantation, which is Virginia's first plantation founded in 1613 and the oldest family-owned business in North America dating back to 1638. The name also was selected in honor and memory of the cultivar developer's grandmother Nannie Jane Shirley. The cultivar Shirley provides producers and end users in the mid-South, mid-Atlantic, Corn Belt, and Northeastern regions of the U.S. with a cultivar that has very high-yield potential and good milling and pastry-baking qualities. In Virginia's State Variety Trial, Shirley had the highest three year (2006–08) average grain yield (6,316 kg/ha) and an average grain volume weight of 75 kg/hl. Shirley is notably resistant to leaf rust, stem rust, and powdery mildew. Certified seed of Shirley will be available to producers beginning in autumn 2009.

Release of the soft red winter wheat cultivar 3434.

Wheat cultivar **3434** was derived from the three-way cross 'Roane/Coker 9835//VA96W-270' and released by the Virginia Agricultural Experiment Station in March 2008. The cultivar provides producers and end users in the mid-South, mid-Atlantic, northeast, and southern Corn-Belt regions of the U.S. with a high-yielding, full-season cultivar that is very short in stature with stiff-straw and good milling and baking qualities. In Virginia's State Variety Trial, 3434 had a three year (2006–08) average grain yield of 5,980 kg/ha and an average grain volume weight of 76 kg/hl. The cultivar is resistant to powdery mildew and moderatley resistant to leaf rust. Certified seed of cultivar 3434 will be available to producers beginning in autumn 2009.

Release of the soft red winter wheat cultivar 5205.

Cultivar **5205** was derived from the three-way cross 'Pioneer Brand 2684/VA93-54-185//Pocahontas' and released by the Virginia Agricultural Experiment Station in March 2008. The cultivar provides producers and end users in the Deep South, mid-South, and mid-Atlantic regions of the U.S. with a high-yielding, mid-season cultivar that is short in plant height and has excellent milling and baking qualities. In Virginia's State Variety Trial, wheat cultivar 5205 had a three year (2006–08) average grain yield of 6,114 kg/ha, and an average grain volume weight of 77 kg/hl. Cultivar 5205 is notably resistant to leaf rust and stripe rust, and moderately resistant to Fusarium head blight. Certified seed of cultivar 5205 will be available to producers beginning in autumn 2009.

Release of the winter durum wheat cultivar Snowglenn.

Snowglenn was derived from the three-way cross 'N1291-86/N1439-83//Alidur' and is the first winter durum cultivar developed and released in March 2008 by the Virginia Agricultural Experiment Station. Snowglenn is a full-season, medium-height cultivar that has consistently expressed resistance to Fusarium head blight with low DON toxin accumulation. The three year (2006–08) average grain yield of Snowglenn in Virginia is 4,898 kg/ha with a grain-volume weight of 80.4 kg/hl. Snowglenn provides identity preserved producers in Virginia with a high-value specialty wheat cultivar that purveys to millers and end-users in the eastern U.S. locally grown durum wheat for pasta production.

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

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National Small Grains Collection activities.

H.E. Bockelman, C.A. Erickson, and B.J. Goates.

Table 1. Wheat descriptors with data currently in GRIN (February 2009).

Descriptor	Years	Location	Accessions evaluated
DISEASE DESCRIPTORS			
Barley Yellow Dwarf Virus	1985–92	Davis, CA	2,287
Barley Yellow Dwarf Virus	1988–94	Urbana, IL	17,517
Soilborne Mosaic Virus	1985–89	Urbana, IL	6,587
Soilborne Mosaic Virus	2000	Manhattan, KS	4,998
Leaf Rust	1983–89, 1991–95	Manhattan, KS	38,751
Leaf Rust – Adult	2000	Manhattan, KS	5,000
Stripe Rust – Adult	1984–2005	Mt. Vernon, WA	47,540
Stripe Rust – Adult	1984–2005	Pullman, WA	37,676
Stripe Rust – PST 17	1984–2005	Pullman, WA	24,662
Stripe Rust – PST 20	1984–95	Pullman, WA	12,508
Stripe Rust – PST 25	1984–95	Pullman, WA	1,682
Stripe Rust – PST 27	1984–95	Pullman, WA	14,511
Stripe Rust – PST 29	1984–95	Pullman, WA	14,259
Stripe Rust – PST 37	1984–2005	Pullman, WA	17,252
Stripe Rust – PST 43	1984–2005	Pullman, WA	16,285
Stripe Rust – PST 45	1984–2005	Pullman, WA	17,217
Stripe Rust – PST 78	2000–05	Pullman, WA	4,277
Stripe Rust – PST 80	2004–05	Pullman, WA	2,998
Stripe Rust – PST 100	2004–05	Pullman, WA	5,892
Stem Rust – Adult	1987–94	Rosemount, MN	8,078
Stem Rust – Adult	1987–94	St. Paul, MN	19,141
Stem Rust – HJCS	1987–92	St. Paul, MN	4,342
Stem Rust – QFBS	1987–92	St. Paul, MN	8,639
Stem Rust – QSHS	1987–92	St. Paul, MN	4,455
Stem Rust – RHRS	1987–92	St. Paul, MN	4,312
Stem Rust – RTQQ	1987–92	St. Paul, MN	8,973
Stem Rust – TNMH	1987–92	St. Paul, MN	4,402
Stem Rust – TNMK	1987–92	St. Paul, MN	8,938
Stem Rust – HNLQ	1987–92	St. Paul, MN	4,705
Stem Rust – RKQS	1987–92	St. Paul, MN	4,682
Stem Rust – Genes	1987–92	St. Paul, MN	1,018
Common Bunt	1981–2004	Aberdeen, ID & Pendleton, OR	25,245
Dwarf Bunt	1978–2006	Logan, UT	19,295

Descriptor	Years	Location	Accessions evaluated
DISEASE DESCRIPTORS			
Stagonospora nodorum blotch	1970–78	Bozeman, MT	8,095
Powdery Mildew	1996–2005	Kinston, NC	13,973
Fusarium Head Blight/Scab	1998–2002	Brookings, SD	4,084
INSECT DESCRIPTORS			
Hessian Fly – B	1983–94	W. Lafayette, IN	449
Hessian Fly – C	1983–94	W. Lafayette, IN & Manhattan, KS	24,165
Hessian Fly – E	1983–94	W. Lafayette, IN & Manhattan, KS	24,149
Hessian Fly – GP	1983–94	W. Lafayette, IN & Manhattan, KS	14,441
Hessian Fly – L	1983–97	W. Lafayette, IN & Manhattan, KS	8,315
Russian Wheat Aphid – Biotype 1	1988–95, 2005	Stillwater, OK & Ft. Collins, CO	41,160
Russian Wheat Aphid – Biotype 2	2003–08	Ft. Collins, CO	14,186
Cereal Leaf Beetle	1963–70	Indiana, Michigan	16,347
AGRONOMIC–QUALITY DESCRIPTORS			
Growth Habit	1987–07	Aberdeen, ID	54,803
Lysine Content	1966–69	Lincoln, NE	10,367
Awn Color	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	25,582
Awn Type	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	28,615
Glume Color	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	25,839
Glume Pubescence	1983–97	Aberdeen, ID & Maricopa, AZ	24,312
Heading Date	1983–94	Aberdeen, ID & Maricopa, AZ	18,365
Heading Date – related to check	1999–2004	Maricopa, AZ	46,831
Kernel Color	1983–94, 2005–09	Aberdeen, ID & Maricopa, AZ	34,273
Kernels/Spike	1983–94	Aberdeen, ID & Maricopa, AZ	3,666
Kernel Weight	1983–94, 2005–09	Aberdeen, ID & Maricopa, AZ	29,717
Leaf Pubescence	1983–94	Aberdeen, ID & Maricopa, AZ	20,888
Plant Height	1983–97	Aberdeen, ID & Maricopa, AZ	21,841
Plant Height – related to check	1999–2004	Maricopa, AZ	46,841
Rachis Length	1995	Maricopa, AZ	2,512
Shattering	1983–94	Aberdeen, ID & Maricopa, AZ	10,637
Spike Density	1983–98, 2007–09	Aberdeen, ID & Maricopa, AZ	21,426
Spikelets/Spike	1995	Maricopa, AZ	2,502
Spike Type	1983–97, 2007–09	Aberdeen, ID & Maricopa, AZ	21,194
Straw Breakage	1983–94	Aberdeen, ID & Maricopa, AZ	16,829
Straw Color	1983–97	Aberdeen, ID & Maricopa, AZ	24,142
Straw Lodging	1983–94	Aberdeen, ID & Maricopa, AZ	23,075

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Passport and descriptor data for these new accessions can be found on the Germplasm Resources Information Network (GRIN): http://www.ars-grin.gov/npgs. Certain accessions may not be available from the National Small Grains Collection due to intellectual property rights, quarantine, or insufficient inventories. Accessions registered in the *Journal of Plant Registrations* or *Crop Science* are available by contacting the developers.

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
652450	*Triticum aestivum* subsp. *aestivum*	8641	United States	Georgia
652451	*Triticum aestivum* subsp. *aestivum*	USG 3295	United States	Georgia
652452	*Triticum aestivum* subsp. *aestivum*	AGS 2031	United States	Georgia
652453	*Triticum aestivum* subsp. *aestivum*	S-24	Pakistan	Punjab
652923	*Triticum aestivum* subsp. *aestivum*	Samson	United States	North Dakota
652924	*Triticum aestivum* subsp. *aestivum*	Blade	United States	North Dakota
652926	*Triticum aestivum* subsp. *aestivum*	Aspen	United States	Kansas
652927	*Triticum aestivum* subsp. *aestivum*	Winterhawk	United States	Kansas
652930	*Triticum aestivum* subsp. *aestivum*	RB07	United States	Minnesota
652933	*Triticum aestivum* subsp. *aestivum*	INW0731	United States	Indiana
653260	*Triticum aestivum* subsp. *aestivum*	Bill Brown	United States	Colorado
653509	*Triticum aestivum* subsp. *aestivum*	Fineway	United States	Washington
653518	*Triticum aestivum* subsp. *aestivum*	Vantage	United States	North Dakota
653521	*Triticum aestivum* subsp. *aestivum*	Fuller	United States	Kansas
653527	*Triticum aestivum* subsp. *aestivum*	Cromwell	United States	Minnesota
653530	*Triticum aestivum* subsp. *aestivum*	Jedd	United States	Montana
653535	*Triticum aestivum* subsp. *aestivum*	Lassik	United States	California
653707	*Triticum aestivum* subsp. *aestivum*	Harry/H13	United States	Washington
653708	*Triticum aestivum* subsp. *aestivum*	Wahoo/H13	United States	Washington
653709	*Triticum aestivum* subsp. *aestivum*	Wesley/H13	United States	Washington
653710	*Triticum aestivum* subsp. *aestivum*	Alliance/*Wsm1*	United States	Washington
653711	*Triticum aestivum* subsp. *aestivum*	Arrowsmith/*Wsm1*	United States	Washington
653712	*Triticum aestivum* subsp. *aestivum*	Goodstreak/*Wsm1*	United States	Washington
653713	*Triticum aestivum* subsp. *aestivum*	Harry/*Wsm1*	United States	Washington
653714	*Triticum aestivum* subsp. *aestivum*	Millennium/*Wsm1*	United States	Washington
653715	*Triticum aestivum* subsp. *aestivum*	Wahoo/*Wsm1*	United States	Washington
653716	*Triticum aestivum* subsp. *aestivum*	Wesley/*Wsm1*	United States	Washington
653726	*Triticum aestivum* subsp. *aestivum*	Hat Trick	United States	Minnesota
653731	*Triticum aestivum* subsp. *aestivum*	Jamestown	United States	Virginia
653832	*Triticum aestivum* subsp. *aestivum*	Camelot	United States	Nebraska
653833	*Triticum aestivum* subsp. *aestivum*	NH03614 CL	United States	Nebraska
653841	*Triticum aestivum* subsp. *aestivum*	Whit	United States	Washington
653842	*Triticum aestivum* subsp. *aestivum*	Kelse	United States	Washington
654142	*Triticum aestivum* subsp. *aestivum*	TJK04-3	Tajikistan	
654143	*Triticum aestivum* subsp. *aestivum*	TJK04-4	Tajikistan	
654144	*Triticum aestivum* subsp. *aestivum*	TJK04-5	Tajikistan	
654145	*Triticum aestivum* subsp. *aestivum*	TJK04-10	Tajikistan	
654146	*Triticum aestivum* subsp. *aestivum*	TJK04-30	Tajikistan	
654147	*Triticum aestivum* subsp. *aestivum*	TJK04-32	Tajikistan	
654148	*Triticum aestivum* subsp. *aestivum*	TJK04-35	Tajikistan	
654149	*Triticum aestivum* subsp. *aestivum*	TJK04-42	Tajikistan	

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
654150	*Triticum aestivum* subsp. *aestivum*	TJK04-45	Tajikistan	
654151	*Triticum aestivum* subsp. *aestivum*	TJK04-46	Tajikistan	
654152	*Triticum aestivum* subsp. *aestivum*	TJK04-59	Tajikistan	
654153	*Triticum aestivum* subsp. *aestivum*	TJK04-60	Tajikistan	
654154	*Triticum aestivum* subsp. *aestivum*	TJK04-63	Tajikistan	
654155	*Triticum aestivum* subsp. *aestivum*	TJK04-64	Tajikistan	
654156	*Triticum aestivum* subsp. *aestivum*	TJK04-65	Tajikistan	
654157	*Triticum aestivum* subsp. *aestivum*	TJK04-66	Tajikistan	
654158	*Triticum aestivum* subsp. *aestivum*	TJK04-78	Tajikistan	
654159	*Triticum aestivum* subsp. *aestivum*	TJK04-90	Tajikistan	
654160	*Triticum aestivum* subsp. *aestivum*	TJK04-91	Tajikistan	
654161	*Triticum aestivum* subsp. *aestivum*	TJK04-92	Tajikistan	
654162	*Triticum aestivum* subsp. *aestivum*	TJK04-99	Tajikistan	
654163	*Triticum aestivum* subsp. *aestivum*	TJK04-105	Tajikistan	
654164	*Triticum aestivum* subsp. *aestivum*	TJK04-106	Tajikistan	
654165	*Triticum aestivum* subsp. *aestivum*	TJK04-107	Tajikistan	
654166	*Triticum aestivum* subsp. *aestivum*	TJK04-112	Tajikistan	
654167	*Triticum aestivum* subsp. *aestivum*	TJK04-129	Tajikistan	
654168	*Triticum aestivum* subsp. *aestivum*	TJK04-138	Tajikistan	
654169	*Triticum aestivum* subsp. *aestivum*	TJK04-142	Tajikistan	
654170	*Triticum aestivum* subsp. *aestivum*	TJK04-151	Tajikistan	
654171	*Triticum aestivum* subsp. *aestivum*	TJK04-153	Tajikistan	
654172	*Triticum aestivum* subsp. *aestivum*	TJK04-155	Tajikistan	
654173	*Triticum aestivum* subsp. *aestivum*	TJK04-170	Tajikistan	
654174	*Triticum aestivum* subsp. *aestivum*	TJK04-180	Tajikistan	
654175	*Triticum aestivum* subsp. *aestivum*	TJK04-184	Tajikistan	
654176	*Triticum aestivum* subsp. *aestivum*	TJK04-188	Tajikistan	
654177	*Triticum aestivum* subsp. *aestivum*	TJK04-189	Tajikistan	
654178	*Triticum aestivum* subsp. *aestivum*	TJK04-190	Tajikistan	
654179	*Triticum aestivum* subsp. *aestivum*	TJK04-192	Tajikistan	
654180	*Triticum aestivum* subsp. *aestivum*	TJK04-197	Tajikistan	
654181	*Triticum aestivum* subsp. *aestivum*	TJK04-204	Tajikistan	
654182	*Triticum turgidum* subsp. *durum*	TJK04-205	Tajikistan	
654183	*Triticum aestivum* subsp. *aestivum*	TJK04-216	Tajikistan	
654184	*Triticum aestivum* subsp. *aestivum*	TJK04-223	Tajikistan	
654185	*Triticum aestivum* subsp. *aestivum*	TJK04-235	Tajikistan	
654186	*Triticum aestivum* subsp. *aestivum*	TJK04-237	Tajikistan	
654187	*Triticum aestivum* subsp. *aestivum*	TJK04-242	Tajikistan	
654188	*Triticum aestivum* subsp. *aestivum*	TJK04-243	Tajikistan	
654189	*Triticum turgidum* subsp. *durum*	TJK04-245	Tajikistan	
654190	*Triticum aestivum* subsp. *aestivum*	TJK04-249	Tajikistan	
654191	*Triticum aestivum* subsp. *aestivum*	TJK04-284	Tajikistan	
654192	*Triticum aestivum* subsp. *aestivum*	TJK04-287	Tajikistan	
654193	*Triticum aestivum* subsp. *aestivum*	TJK04-296	Tajikistan	
654194	*Triticum aestivum* subsp. *aestivum*	TJK04-298	Tajikistan	
654195	*Triticum aestivum* subsp. *aestivum*	TJK04-299	Tajikistan	
654196	*Triticum aestivum* subsp. *aestivum*	TJK04-310	Tajikistan	

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
654197	*Triticum aestivum* subsp. *aestivum*	TJK04-321	Tajikistan	
654198	*Triticum aestivum* subsp. *aestivum*	TJK04-238	Tajikistan	
654199	*Triticum aestivum* subsp. *aestivum*	TJK04-330	Tajikistan	
654200	*Triticum aestivum* subsp. *aestivum*	TJK04-345	Tajikistan	
654201	*Triticum aestivum* subsp. *aestivum*	TJK04-369	Tajikistan	
654202	*Triticum aestivum* subsp. *aestivum*	TJK04-379	Tajikistan	
654203	*Triticum aestivum* subsp. *aestivum*	TJK04-383	Tajikistan	
654204	*Triticum aestivum* subsp. *aestivum*	TJK04-384	Tajikistan	
654205	*Triticum aestivum* subsp. *aestivum*	TJK04-385	Tajikistan	
654206	*Triticum aestivum* subsp. *aestivum*	TJK04-386	Tajikistan	
654207	*Triticum aestivum* subsp. *aestivum*	TJK04-396	Tajikistan	
654208	*Triticum aestivum* subsp. *aestivum*	TJK04-397	Tajikistan	
654209	*Triticum aestivum* subsp. *aestivum*	TJK04-403	Tajikistan	
654210	*Triticum aestivum* subsp. *aestivum*	TJK04-404	Tajikistan	
654211	*Triticum aestivum* subsp. *aestivum*	TJK04-407	Tajikistan	
654212	*Triticum aestivum* subsp. *aestivum*	TJK04-420	Tajikistan	
654213	*Triticum turgidum* subsp. *durum*	TJK04-71	Tajikistan	
654214	*Triticum turgidum* subsp. *durum*	TJK04-77	Tajikistan	
654215	*Triticum turgidum* subsp. *durum*	TJK04-300	Tajikistan	
654216	*Triticum turgidum* subsp. *durum*	TJK04-324	Tajikistan	
654217	*Triticum aestivum* subsp. *aestivum*	TJK2006:003	Tajikistan	Khujand
654218	*Triticum aestivum* subsp. *aestivum*	TJK2006:016	Tajikistan	Khujand
654219	*Triticum aestivum* subsp. *aestivum*	TJK2006:020	Tajikistan	Khujand
654220	*Triticum aestivum* subsp. *aestivum*	TJK2006:027	Tajikistan	Khujand
654221	*Triticum aestivum* subsp. *aestivum*	TJK2006:028	Tajikistan	Khujand
654222	*Triticum aestivum* subsp. *aestivum*	TJK2006:029	Tajikistan	Khujand
654223	*Triticum aestivum* subsp. *aestivum*	TJK2006:031	Tajikistan	Khujand
654224	*Triticum aestivum* subsp. *aestivum*	TJK2006:032	Tajikistan	Khujand
654225	*Triticum aestivum* subsp. *aestivum*	TJK2006:033	Tajikistan	Khujand
654226	*Triticum aestivum* subsp. *aestivum*	TJK2006:034	Tajikistan	Khujand
654227	*Triticum aestivum* subsp. *aestivum*	TJK2006:035	Tajikistan	Khujand
654228	*Triticum aestivum* subsp. *aestivum*	TJK2006:037	Tajikistan	Khujand
654229	*Triticum aestivum* subsp. *aestivum*	TJK2006:038	Tajikistan	Khujand
654230	*Triticum aestivum* subsp. *aestivum*	TJK2006:045	Tajikistan	Khujand
654231	*Triticum aestivum* subsp. *aestivum*	TJK2006:050	Tajikistan	Khujand
654232	*Triticum aestivum* subsp. *aestivum*	TJK2006:052	Tajikistan	Khujand
654233	*Triticum aestivum* subsp. *aestivum*	TJK2006:054	Tajikistan	Khujand
654234	*Triticum aestivum* subsp. *aestivum*	TJK2006:056	Tajikistan	Khujand
654235	*Triticum aestivum* subsp. *aestivum*	TJK2006:098	Tajikistan	Khujand
654236	*Triticum aestivum* subsp. *aestivum*	TJK2006:077	Tajikistan	Khujand
654237	*Triticum aestivum* subsp. *aestivum*	TJK2006:083	Tajikistan	Khujand
654238	*Triticum aestivum* subsp. *aestivum*	TJK2006:084	Tajikistan	Khujand
654239	*Triticum aestivum* subsp. *aestivum*	TJK2006:085	Tajikistan	Khujand
654240	*Triticum aestivum* subsp. *aestivum*	TJK2006:094	Tajikistan	Khujand
654241	*Triticum aestivum* subsp. *aestivum*	TJK2006:102	Tajikistan	Khujand
654242	*Triticum aestivum* subsp. *aestivum*	TJK2006:103	Tajikistan	Khujand
654243	*Triticum aestivum* subsp. *aestivum*	TJK2006:107	Tajikistan	Khujand

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
654244	*Triticum aestivum* subsp. *aestivum*	TJK2006:120	Tajikistan	Khujand
654245	*Triticum aestivum* subsp. *aestivum*	TJK2006:124	Tajikistan	Khujand
654246	*Triticum aestivum* subsp. *aestivum*	TJK2006:125	Tajikistan	Khujand
654247	*Triticum aestivum* subsp. *aestivum*	TJK2006:126	Tajikistan	Khujand
654248	*Triticum aestivum* subsp. *aestivum*	TJK2006:136	Tajikistan	Khujand
654249	*Triticum aestivum* subsp. *aestivum*	TJK2006:137	Tajikistan	Khujand
654250	*Triticum aestivum* subsp. *aestivum*	TJK2006:138	Tajikistan	Khujand
654251	*Triticum aestivum* subsp. *aestivum*	TJK2006:139	Tajikistan	Khujand
654252	*Triticum aestivum* subsp. *aestivum*	TJK2006:140	Tajikistan	Khujand
654253	*Triticum aestivum* subsp. *aestivum*	TJK2006:158	Tajikistan	Khujand
654254	*Triticum aestivum* subsp. *aestivum*	TJK2006:169	Tajikistan	Khujand
654255	*Triticum aestivum* subsp. *aestivum*	TJK2006:171	Tajikistan	Khujand
654256	*Triticum aestivum* subsp. *aestivum*	TJK2006:172	Tajikistan	Khujand
654257	*Triticum aestivum* subsp. *aestivum*	TJK2006:182	Tajikistan	Khujand
654258	*Triticum aestivum* subsp. *aestivum*	TJK2006:183	Tajikistan	Khujand
654259	*Triticum aestivum* subsp. *aestivum*	TJK2006:184	Tajikistan	Khujand
654260	*Triticum aestivum* subsp. *aestivum*	TJK2006:186	Tajikistan	Khujand
654261	*Triticum aestivum* subsp. *aestivum*	TJK2006:201	Tajikistan	Khujand
654262	*Triticum aestivum* subsp. *aestivum*	TJK2006:202	Tajikistan	Khujand
654263	*Triticum aestivum* subsp. *aestivum*	TJK2006:203	Tajikistan	Khujand
654264	*Triticum aestivum* subsp. *aestivum*	TJK2006:204	Tajikistan	Khujand
654265	*Triticum aestivum* subsp. *aestivum*	TJK2006:205	Tajikistan	Khujand
654266	*Triticum aestivum* subsp. *aestivum*	TJK2006:215	Tajikistan	Khujand
654267	*Triticum aestivum* subsp. *aestivum*	TJK2006:217	Tajikistan	Khujand
654268	*Triticum aestivum* subsp. *aestivum*	TJK2006:218	Tajikistan	Khujand
654269	*Triticum aestivum* subsp. *aestivum*	TJK2006:219	Tajikistan	Khujand
654270	*Triticum aestivum* subsp. *aestivum*	TJK2006:220	Tajikistan	Khujand
654271	*Triticum aestivum* subsp. *aestivum*	TJK2006:222	Tajikistan	Khujand
654272	*Triticum aestivum* subsp. *aestivum*	TJK2006:223	Tajikistan	Khujand
654273	*Triticum aestivum* subsp. *aestivum*	TJK2006:224	Tajikistan	Khujand
654274	*Triticum aestivum* subsp. *aestivum*	TJK2006:239	Tajikistan	Khujand
654275	*Triticum aestivum* subsp. *aestivum*	TJK2006:240	Tajikistan	Khujand
654276	*Triticum aestivum* subsp. *aestivum*	TJK2006:241	Tajikistan	Khujand
654277	*Triticum aestivum* subsp. *aestivum*	TJK2006:242	Tajikistan	Khujand
654278	*Triticum aestivum* subsp. *aestivum*	TJK2006:243	Tajikistan	Khujand
654279	*Triticum aestivum* subsp. *aestivum*	TJK2006:244	Tajikistan	Khujand
654280	*Triticum aestivum* subsp. *aestivum*	TJK2006:246	Tajikistan	Khujand
654281	*Triticum aestivum* subsp. *aestivum*	TJK2006:248	Tajikistan	Khujand
654282	*Triticum aestivum* subsp. *aestivum*	TJK2006:250	Tajikistan	Khujand
654283	*Triticum aestivum* subsp. *aestivum*	TJK2006:274	Tajikistan	Khujand
654284	*Triticum turgidum* subsp. *durum*	TJK2006:285	Tajikistan	Khujand
654285	*Triticum aestivum* subsp. *aestivum*	TJK2006:286	Tajikistan	Khujand
654286	*Triticum aestivum* subsp. *aestivum*	TJK2006:290	Tajikistan	Khujand
654287	*Triticum aestivum* subsp. *aestivum*	TJK2006:291	Tajikistan	Khujand
654288	*Triticum aestivum* subsp. *aestivum*	TJK2006:292	Tajikistan	Khujand
654289	*Triticum aestivum* subsp. *aestivum*	TJK2006:294	Tajikistan	Khujand
654290	*Triticum turgidum* subsp. *durum*	TJK2006:296	Tajikistan	Khujand
654291	*Triticum aestivum* subsp. *aestivum*	TJK2006:298	Tajikistan	Khujand

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
654292	*Triticum aestivum* subsp. *aestivum*	TJK2006:304	Tajikistan	Khujand
654293	*Triticum aestivum* subsp. *aestivum*	TJK2006:305	Tajikistan	Khujand
654294	*Triticum aestivum* subsp. *aestivum*	TJK2006:309	Tajikistan	Khujand
654295	*Triticum aestivum* subsp. *aestivum*	TJK2006:310	Tajikistan	Khujand
654296	*Triticum aestivum* subsp. *aestivum*	TJK2006:322	Tajikistan	Khujand
654297	*Triticum aestivum* subsp. *aestivum*	TJK2006:323	Tajikistan	Khujand
654298	*Triticum aestivum* subsp. *aestivum*	TJK2006:324	Tajikistan	Khujand
654299	*Triticum aestivum* subsp. *aestivum*	TJK2006:325	Tajikistan	Khujand
654300	*Triticum aestivum* subsp. *aestivum*	TJK2006:326	Tajikistan	Khujand
654301	*Triticum aestivum* subsp. *aestivum*	TJK2006:328	Tajikistan	Khujand
654302	*Triticum aestivum* subsp. *aestivum*	TJK2006:334	Tajikistan	Khujand
654303	*Triticum aestivum* subsp. *aestivum*	TJK2006:335	Tajikistan	Khujand
654304	*Triticum aestivum* subsp. *aestivum*	TJK2006:348	Tajikistan	Khujand
654305	*Triticum aestivum* subsp. *aestivum*	TJK2006:352	Tajikistan	Khujand
654306	*Triticum aestivum* subsp. *aestivum*	TJK2006:354	Tajikistan	Khujand
654307	*Triticum aestivum* subsp. *aestivum*	TJK2006:359	Tajikistan	Khujand
654308	*Triticum aestivum* subsp. *aestivum*	TJK2006:361	Tajikistan	Khujand
654309	*Triticum aestivum* subsp. *aestivum*	TJK2006:362	Tajikistan	Khujand
654310	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-008	Turkey	Urfa
654311	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-009	Turkey	Urfa
654312	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-061	Turkey	Diyarbakir
654313	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-068	Turkey	Diyarbakir
654314	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-072	Turkey	Diyarbakir
654315	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-077	Turkey	Diyarbakir
654316	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-083	Turkey	Diyarbakir
654317	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-090	Turkey	Diyarbakir
654318	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-095	Turkey	Urfa
654319	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-097	Turkey	Urfa
654320	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-099	Turkey	Urfa
654321	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-102	Turkey	Urfa
654322	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-103	Turkey	Urfa
654323	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-104	Turkey	Urfa
654324	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-106	Turkey	Urfa
654325	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-107	Turkey	Urfa
654326	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-110	Turkey	Urfa
654327	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-114	Turkey	Urfa
654328	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-120	Turkey	Adiyaman
654329	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-127	Turkey	Adiyaman
654330	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-138	Turkey	Urfa
654331	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-152	Turkey	Gaziantep
654332	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-155	Turkey	Gaziantep
654333	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-157	Turkey	Gaziantep
654334	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-160	Turkey	Gaziantep
654335	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-162	Turkey	Gaziantep
654336	*Triticum turgidum* subsp. *dicoccoides*	TUR-05-BJS-HB-163	Turkey	Gaziantep
654337	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-164	Turkey	Gaziantep
654338	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-171	Turkey	Gaziantep
654339	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-177	Turkey	Gaziantep
654340	*Triticum timopheevii* subsp. *armeniacum*	TUR-05-BJS-HB-181	Turkey	Gaziantep

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
654341	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-182	Turkey	Gaziantep
654342	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-189	Turkey	Gaziantep
654343	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-194	Turkey	Gaziantep
654344	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-201	Turkey	Maras
654345	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-207	Turkey	Maras
654346	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-212	Turkey	Maras
654347	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-220	Turkey	Maras
654348	*Triticum monococcum* subsp. *aegilopoides*	TUR-05-BJS-HB-222	Turkey	Maras
654367	*Triticum aestivum* subsp. *aestivum*	TC 67	Canada	Ontario
654384	*Triticum aestivum* subsp. *aestivum*	Jensen	United States	New York
654419	*Triticum aestivum* subsp. *aestivum*	Doans	United States	Kansas
654420	*Triticum aestivum* subsp. *aestivum*	Coker 9804	United States	Arkansas
654421	*Triticum aestivum* subsp. *aestivum*	9700	United States	Arkansas
654422	*Triticum aestivum* subsp. *aestivum*	Culpepper	United States	Kansas
654423	*Triticum aestivum* subsp. *aestivum*	AP503 CL2	United States	Kansas
654424	*Triticum aestivum* subsp. *aestivum*	AP700 CL	United States	Washington
654425	*Triticum aestivum* subsp. *aestivum*	Salute	United States	Washington
654426	*Triticum aestivum* subsp. *aestivum*	AP402 CL2	United States	Kansas
654454	*Triticum aestivum* subsp. *aestivum*	USG 3555	United States	Virginia
654514	*Triticum aestivum* subsp. *aestivum*	25R39	United States	Indiana
654518	*Triticum aestivum* subsp. *aestivum*	Carter	United States	Montana
654519	*Triticum aestivum* subsp. *aestivum*	Tiller	United States	North Dakota
654520	*Triticum aestivum* subsp. *aestivum*	Golaith	United States	North Dakota
654521	*Triticum aestivum* subsp. *aestivum*	Breaker	United States	North Dakota
654526	*Triticum aestivum* subsp. *aestivum*	Crystal	United States	Michigan
655029	*Triticum aestivum* subsp. *aestivum*	Goetze	United States	Oregon
655030	*Triticum aestivum* subsp. *aestivum*	Norwest 553	United States	Oregon
655031	*Triticum aestivum* subsp. *aestivum*	WB 1020M	United States	Washington
655032	*Triticum aestivum* subsp. *aestivum*	Blanca Fuerte	United States	California
655033	*Triticum aestivum* subsp. *aestivum*	Blanca Royale	United States	California
655034	*Triticum aestivum* subsp. *aestivum*	Lariat	United States	California
655035	*X Triticosecale* sp.	888	United States	California
655036	*Triticum turgidum* subsp. *durum*	RSI 59	United States	California
655037	*Triticum turgidum* subsp. *durum*	Volante	United States	California
655038	*X Triticosecale* sp.	Pacheco	Germany	Baden-Wurt-temberg
655039	*Triticum aestivum* subsp. *aestivum*	Volt	Germany	Baden-Wurt-temberg
655042	*Triticum aestivum* subsp. *aestivum*	Bitterroot	United States	Idaho
655073	*Triticum aestivum* subsp. *aestivum*	Willow Creek	United States	Montana
655074	*Triticum aestivum* subsp. *aestivum*	AGS 2060	United States	Louisiana
655233	*Triticum aestivum* subsp. *aestivum*	ND901CL	United States	North Dakota
655234	*Triticum aestivum* subsp. *aestivum*	TAM 304	United States	Texas
655242	*Triticum aestivum* subsp. *aestivum*	Settler CL	United States	Nebraska
655244	*Triticum aestivum* subsp. *aestivum*	Sunburst	United States	Ohio
655291	*Triticum aestivum* subsp. *aestivum*	LA95135	United States	Louisiana

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
655312	*Triticum aestivum* subsp. *aestivum*	Biointa 2004	Argentina	Cordoba
655352	*Triticum turgidum* subsp. *durum*	OR948927	United States	Oregon
655353	*Triticum turgidum* subsp. *durum*	OR971856	United States	Oregon
655354	*Triticum turgidum* subsp. *durum*	OR971881	United States	Oregon
655355	*Triticum turgidum* subsp. *durum*	OR924696	United States	Oregon
655356	*Triticum turgidum* subsp. *durum*	OR971849	United States	Oregon
655357	*Triticum turgidum* subsp. *durum*	OR971886	United States	Oregon
655358	*Triticum turgidum* subsp. *durum*	OR971894	United States	Oregon
655359	*Triticum turgidum* subsp. *durum*	OR971895	United States	Oregon
655360	*Triticum turgidum* subsp. *durum*	OR9801900	United States	Oregon
655361	*Triticum turgidum* subsp. *durum*	OR9801915	United States	Oregon
655362	*Triticum turgidum* subsp. *durum*	OR9801887	United States	Oregon
655363	*Triticum turgidum* subsp. *durum*	OR9801890	United States	Oregon
655364	*Triticum turgidum* subsp. *durum*	OR9801891	United States	Oregon
655365	*Triticum turgidum* subsp. *durum*	OR924696	United States	Oregon
655366	*Triticum turgidum* subsp. *durum*	OR2000001	United States	Oregon
655367	*Triticum turgidum* subsp. *durum*	OR2000002	United States	Oregon
655368	*Triticum turgidum* subsp. *durum*	OR2000003	United States	Oregon
655369	*Triticum turgidum* subsp. *durum*	OR2000004	United States	Oregon
655370	*Triticum turgidum* subsp. *durum*	OR2000007	United States	Oregon
655371	*Triticum turgidum* subsp. *durum*	OR2000008	United States	Oregon
655372	*Triticum turgidum* subsp. *durum*	OR2000009	United States	Oregon
655373	*Triticum turgidum* subsp. *durum*	OR2000011	United States	Oregon
655374	*Triticum turgidum* subsp. *durum*	OR2000015	United States	Oregon
655375	*Triticum turgidum* subsp. *durum*	OR2000018	United States	Oregon
655376	*Triticum turgidum* subsp. *durum*	OR2000020	United States	Oregon
655377	*Triticum turgidum* subsp. *durum*	OR2000021	United States	Oregon
655378	*Triticum turgidum* subsp. *durum*	OR2000022	United States	Oregon
655379	*Triticum turgidum* subsp. *durum*	OR2000024	United States	Oregon
655380	*Triticum turgidum* subsp. *durum*	OR2000025	United States	Oregon
655381	*Triticum turgidum* subsp. *durum*	OR2000026	United States	Oregon
655382	*Triticum turgidum* subsp. *durum*	OR2001209	United States	Oregon
655383	*Triticum turgidum* subsp. *durum*	OR2001212	United States	Oregon
655384	*Triticum turgidum* subsp. *durum*	OR2001217	United States	Oregon
655385	*Triticum turgidum* subsp. *durum*	OR2001218	United States	Oregon
655386	*Triticum turgidum* subsp. *durum*	OR2001220	United States	Oregon
655387	*Triticum turgidum* subsp. *durum*	OR2001223	United States	Oregon
655388	*Triticum turgidum* subsp. *durum*	OR2001224	United States	Oregon
655389	*Triticum turgidum* subsp. *durum*	OR2001229	United States	Oregon
655390	*Triticum turgidum* subsp. *durum*	OR2001232	United States	Oregon
655391	*Triticum turgidum* subsp. *durum*	OR2001233	United States	Oregon
655392	*Triticum turgidum* subsp. *durum*	OR2001234	United States	Oregon
655393	*Triticum turgidum* subsp. *durum*	OR2001236	United States	Oregon
655394	*Triticum turgidum* subsp. *durum*	OR2001239	United States	Oregon
655395	*Triticum turgidum* subsp. *durum*	OR2001586	United States	Oregon
655396	*Triticum turgidum* subsp. *durum*	OR2001243	United States	Oregon

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
655397	*Triticum turgidum* subsp. *durum*	OR2001245	United States	Oregon
655398	*Triticum turgidum* subsp. *durum*	TU991561	United States	Oregon
655399	*Triticum turgidum* subsp. *durum*	TU991621	United States	Oregon
655400	*Triticum turgidum* subsp. *durum*	TU991622	United States	Oregon
655401	*Triticum turgidum* subsp. *durum*	TU991627	United States	Oregon
655402	*Triticum turgidum* subsp. *durum*	TU991628	United States	Oregon
655403	*Triticum turgidum* subsp. *durum*	TU991632	United States	Oregon
655404	*Triticum turgidum* subsp. *durum*	TU991637	United States	Oregon
655405	*Triticum turgidum* subsp. *durum*	TU991640	United States	Oregon
655406	*Triticum turgidum* subsp. *durum*	TU991643	United States	Oregon
655407	*Triticum turgidum* subsp. *durum*	TU991644	United States	Oregon
655408	*Triticum turgidum* subsp. *durum*	TU991645	United States	Oregon
655409	*Triticum turgidum* subsp. *durum*	TU991646	United States	Oregon
655410	*Triticum turgidum* subsp. *durum*	TU991647	United States	Oregon
655411	*Triticum turgidum* subsp. *durum*	OR2010478	United States	Oregon
655412	*Triticum turgidum* subsp. *durum*	OR2010483	United States	Oregon
655413	*Triticum turgidum* subsp. *durum*	OR9801890	United States	Oregon
655414	*Triticum turgidum* subsp. *durum*	OR2010485	United States	Oregon
655415	*Triticum turgidum* subsp. *durum*	OR2010491	United States	Oregon
655416	*Triticum turgidum* subsp. *durum*	OR2010496	United States	Oregon
655417	*Triticum turgidum* subsp. *durum*	OR2010498	United States	Oregon
655418	*Triticum turgidum* subsp. *durum*	OR2010502	United States	Oregon
655419	*Triticum turgidum* subsp. *durum*	OR2010504	United States	Oregon
655420	*Triticum turgidum* subsp. *durum*	OR2010505	United States	Oregon
655421	*Triticum turgidum* subsp. *durum*	OR2010506	United States	Oregon
655422	*Triticum turgidum* subsp. *durum*	OR2010507	United States	Oregon
655423	*Triticum turgidum* subsp. *durum*	OR2010509	United States	Oregon
655424	*Triticum turgidum* subsp. *durum*	OR2010510	United States	Oregon
655425	*Triticum turgidum* subsp. *durum*	OR2010514	United States	Oregon
655426	*Triticum turgidum* subsp. *durum*	OR2010518	United States	Oregon
655427	*Triticum turgidum* subsp. *durum*	OR2010519	United States	Oregon
655428	*Triticum turgidum* subsp. *durum*	OR2010520	United States	Oregon
655429	*Triticum turgidum* subsp. *durum*	OR2010521	United States	Oregon
655430	*Triticum turgidum* subsp. *durum*	OR2010534	United States	Oregon
655431	*Triticum turgidum* subsp. *durum*	OR2010537	United States	Oregon
655432	*Triticum turgidum* subsp. *durum*	OR2010539	United States	Oregon
655433	*Triticum turgidum* subsp. *durum*	OR2010540	United States	Oregon
655434	*Triticum turgidum* subsp. *durum*	OR2010542	United States	Oregon
655435	*Triticum turgidum* subsp. *durum*	OR2010543	United States	Oregon
655436	*Triticum turgidum* subsp. *durum*	OR2010547	United States	Oregon
655437	*Triticum turgidum* subsp. *durum*	OR2010548	United States	Oregon
655438	*Triticum turgidum* subsp. *durum*	OR2010554	United States	Oregon
655439	*Triticum turgidum* subsp. *durum*	OR2010555	United States	Oregon
655440	*Triticum turgidum* subsp. *durum*	OR2010556	United States	Oregon
655441	*Triticum turgidum* subsp. *durum*	OR2010558	United States	Oregon
655442	*Triticum turgidum* subsp. *durum*	OR2010567	United States	Oregon

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
655443	*Triticum turgidum* subsp. *durum*	OR2010569	United States	Oregon
655444	*Triticum turgidum* subsp. *durum*	OR2010578	United States	Oregon
655445	*Triticum turgidum* subsp. *durum*	OR2010579	United States	Oregon
655446	*Triticum turgidum* subsp. *durum*	OR2010582	United States	Oregon
655447	*Triticum turgidum* subsp. *durum*	OR2010586	United States	Oregon
655448	*Triticum turgidum* subsp. *durum*	OR2010587	United States	Oregon
655449	*Triticum turgidum* subsp. *durum*	OR2010596	United States	Oregon
655450	*Triticum turgidum* subsp. *durum*	OR2000008	United States	Oregon
655451	*Triticum turgidum* subsp. *durum*	OR2010599	United States	Oregon
655452	*Triticum turgidum* subsp. *durum*	OR2010601	United States	Oregon
655453	*Triticum turgidum* subsp. *durum*	OR2010606	United States	Oregon
655454	*Triticum turgidum* subsp. *durum*	OR2010608	United States	Oregon
655455	*Triticum turgidum* subsp. *durum*	OR2010609	United States	Oregon
655456	*Triticum turgidum* subsp. *durum*	OR2010610	United States	Oregon
655457	*Triticum turgidum* subsp. *durum*	OR2010611	United States	Oregon
655458	*Triticum turgidum* subsp. *durum*	OR2010627	United States	Oregon
655459	*Triticum turgidum* subsp. *durum*	OR2010628	United States	Oregon
655460	*Triticum turgidum* subsp. *durum*	OR2010634	United States	Oregon
655461	*Triticum turgidum* subsp. *durum*	OR2010635	United States	Oregon
655462	*Triticum turgidum* subsp. *durum*	OR2010637	United States	Oregon
655463	*Triticum turgidum* subsp. *durum*	OR2010643	United States	Oregon
655464	*Triticum turgidum* subsp. *durum*	OR2010644	United States	Oregon
655465	*Triticum turgidum* subsp. *durum*	OR2010645	United States	Oregon
655466	*Triticum turgidum* subsp. *durum*	OR2010658	United States	Oregon
655467	*Triticum turgidum* subsp. *durum*	OR2000011	United States	Oregon
655468	*Triticum turgidum* subsp. *durum*	OR971897	United States	Oregon
655469	*Triticum turgidum* subsp. *durum*	OR9801888	United States	Oregon
655470	*Triticum turgidum* subsp. *durum*	OR9801889	United States	Oregon
655471	*Triticum turgidum* subsp. *durum*	OR2000005	United States	Oregon
655472	*Triticum turgidum* subsp. *durum*	OR2000012	United States	Oregon
655473	*Triticum turgidum* subsp. *durum*	OR2000014	United States	Oregon
655474	*Triticum turgidum* subsp. *durum*	OR9800646	United States	Oregon
655475	*Triticum turgidum* subsp. *durum*	OR2001208	United States	Oregon
655476	*Triticum turgidum* subsp. *durum*	OR2001235	United States	Oregon
655477	*Triticum turgidum* subsp. *durum*	OR2010497	United States	Oregon
655478	*Triticum turgidum* subsp. *durum*	OR2010503	United States	Oregon
655479	*Triticum turgidum* subsp. *durum*	OR2010515	United States	Oregon
655480	*Triticum turgidum* subsp. *durum*	OR2010516	United States	Oregon
655481	*Triticum turgidum* subsp. *durum*	OR2010517	United States	Oregon
655482	*Triticum turgidum* subsp. *durum*	OR2010525	United States	Oregon
655483	*Triticum turgidum* subsp. *durum*	OR2010535	United States	Oregon
655484	*Triticum turgidum* subsp. *durum*	OR2010557	United States	Oregon
655485	*Triticum turgidum* subsp. *durum*	OR2010559	United States	Oregon
655486	*Triticum turgidum* subsp. *durum*	OR2010580	United States	Oregon
655487	*Triticum turgidum* subsp. *durum*	OR2010581	United States	Oregon
655488	*Triticum turgidum* subsp. *durum*	OR2010583	United States	Oregon

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxonomy	Cultivar name or identifier	Country	State/Province
655489	*Triticum turgidum* subsp. *durum*	OR2010585	United States	Oregon
655490	*Triticum turgidum* subsp. *durum*	OR2010600	United States	Oregon
655491	*Triticum turgidum* subsp. *durum*	OR2010607	United States	Oregon
655492	*Triticum turgidum* subsp. *durum*	OR2010624	United States	Oregon
655493	*Triticum turgidum* subsp. *durum*	OR2010625	United States	Oregon
655494	*Triticum turgidum* subsp. *durum*	OR2010629	United States	Oregon
655495	*Triticum turgidum* subsp. *durum*	OR2010630	United States	Oregon
655496	*Triticum turgidum* subsp. *durum*	OR2010631	United States	Oregon
655497	*Triticum turgidum* subsp. *durum*	OR2010632	United States	Oregon
655498	*Triticum turgidum* subsp. *durum*	OR2010633	United States	Oregon
655499	*Triticum turgidum* subsp. *durum*	OR2010636	United States	Oregon
655500	*Triticum turgidum* subsp. *durum*	OR2010642	United States	Oregon
655501	*Triticum turgidum* subsp. *durum*	OR2010647	United States	Oregon
655502	*Triticum turgidum* subsp. *durum*	OR2010648	United States	Oregon
655503	*Triticum turgidum* subsp. *durum*	OR2010649	United States	Oregon
655504	*Triticum turgidum* subsp. *durum*	OR2010650	United States	Oregon
655505	*Triticum turgidum* subsp. *durum*	OR2010652	United States	Oregon
655506	*Triticum turgidum* subsp. *durum*	OR2010653	United States	Oregon
655507	*Triticum turgidum* subsp. *durum*	OR2010654	United States	Oregon
655508	*Triticum turgidum* subsp. *durum*	OR2010655	United States	Oregon
655509	*Triticum turgidum* subsp. *durum*	OR2010656	United States	Oregon
655510	*Triticum turgidum* subsp. *durum*	OR2010657	United States	Oregon
655511	*Triticum turgidum* subsp. *durum*	OR2010659	United States	Oregon
655512	*Triticum turgidum* subsp. *durum*	OR2010660	United States	Oregon
655513	*Triticum turgidum* subsp. *durum*	OR2010662	United States	Oregon
655514	*Triticum turgidum* subsp. *durum*	OR2010663	United States	Oregon
655515	*Triticum turgidum* subsp. *durum*	OR2010664	United States	Oregon
655516	*Triticum turgidum* subsp. *durum*	OR2010668	United States	Oregon
655517	*Triticum turgidum* subsp. *durum*	OR2010669	United States	Oregon
655518	*Triticum turgidum* subsp. *durum*	OR2010670	United States	Oregon
655528	*Triticum aestivum* subsp. *aestivum*	Thunder CL	United States	Colorado

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2009 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11Th International Wheat Genetics Symposium held in Brisbane, Australia, is available from 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. The Wheat Gene Catalog is not included as part of the proceedings and, therefore, cannot be cited as part of them.

INTRODUCTION

9. Laboratory Designators

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Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1. Squarehead/spelt

Q. **bin:** 5AL-17 {10541}.

1.2. Club/Compact spike

C. Add to chromosome location: , probably 2DL {10578}.
bin: C-2DS1 – C-2DL3, markers flanking *C* were located on either side of the centromere {10578}.
v: Coda {10578}; Corrigin {10578}.
ma: Coda / Brundage: *Xwmc144-2D* – 1 cM – *C* – 8 cM – *Xwmc18-2D*; Corrigin / CS (*Ae. tauschii* 2D) {10578}: *Xwmc245-2D* – 1 cM – *Xcfd116-2D / Xgwm358-2D / C / Xcfd-2D* – 1 cM – *Xbarc145-2D* {10578}.

Add note:
C may be orthologous to gene *Sog* for soft glumes on chromosome $2A^m$ {10578}.
Add at the end of the section:
Tetraploid wheat: A compact spike gene C^{17648} in mutant line MA 17648 was located in chromosome 5AL {10541}. *Xbarc319-5A* – 9.7 cM – C^{17648} – 24.8 cM – *Xgwm179-5A* {10541}. C^{17648} was distal to the *Q* locus {10541}.

1.3. Sphaerococcum

S ***B1b.*** Add: […, s^{16219} {10541}]. **tv:** MA 16219 {10541}.

1.4. Branched spike

Replace the previous entry with the following:
Synonyms: branched spike, four-rowed spike, multi-rowed spike, supernumerary spikelet, tetrastichon spikelet.
Branched spike and multi-rowed spike are phenotypes involving the presence of supernumerary spikelets or the presence of additional spikelets at rachis nodes. A similar condition in rye is known as 'monstrosum ear' (reviewed in {10637}). Genetic studies of branched spike in tetraploid and hexaploid wheats indicate that the phenotype is recessive, involves one or more genes, and is strongly influenced by environmental effects. Comparative genetic studies suggest an orthologous gene series in homoeologous group 2 {10637}.

bh-A1 {10637}. *bh* {665}. 2AS {665}. **tv:** PI 349056 {665}.
bh-D1 {10637}. *mrs* {10637}. 2DS {10637}. **bin:** 2DS-5 0.47-1.0 {10637}.
v: Ra1 {10637}; Ruc163-1-02 = 'Ra1 / ZGK242-81' {10637}; RUC163167-1-02 = 'Alana /3/ Ra1/ ZGK242-82 // Ra1' {10637}.
ma: *Xwmc453-2D/ bh-D1* – 7.8 cM – *Xgwm988-2D* {10637}; *Xwwm484-2D* – 3.3 cM – *Xwmc453-2D/bh-D1* – 3 cM – *Xgwm988-2D* {10637}.

Ra1 is a mutant stock maintained at the NI Vavilov Research Institute of Plant Industry, St Petersburg, Russian Federation.

A chromosome 2B gene of minor effect was identified {9907}. In a monosomic analysis of the hexaploid line LYB with supernumerary spikelets, Peng et al. {9908} located recessive genes on chromosomes 2A and 4A that promote the development of supernumerary spikelets and a gene on chromosome 2D that prevents their expression.

bh-R1 {10637}. *mo* {see 10637}. 2R {10637}. **al:** *S. cereale* D40 {10637}.
ma: *Xrms056-2R* – 15.7 cM – *bh-R1* – 10.7 cM – *Xcfe209-2R* {10637}.

1.7. Multi-gynoecium

Synonym: three pistils (TP)

This trait describes a dominant phenotype consisting of three kernels within each wheat floret; that is, the flower consists of three separate ovaries, three anthers, and two lodicules.

Pis1 {10636}. 2DL {10636}. **Bin:** C-2DL3-0.49 {10636}.
v: TP Mutant {10636}.
ma: *Xgwm539-2D* – 17.6 cM – *Pis1* – 19.5 cM – *Xgwm349-2D* {10636}.

4. Aluminium Tolerance

QTL:

FSW (Al tolerant) / ND35 (Al sensitive): Three QTL for tolerance, *Qalt.pser-4DL* co-segregating with *Xups4*, a marker for the promoter of the *ALMT1* gene; *Qalt.pser-3BL* (*Xbarc164-3B – Xbarc344-3B*); and *Qalt.pser-2A (Xgwm515-2A – Xgwm296-2A* {10605}.

Add at end of section:

In D-genome introgression lines of Chinese Spring, a major QTL was located in the interval *Xgwm125-4D – Xgwm976-4D*, $R^2 = 0.31$ {10598}, probably coinciding with *Alt2*. A second QTL from CS, $Qalt_{cs}$*.ipk-3B*, $R^2 = 0.49$, occurred in interval *Xgwm1029-3BL – Xgwm1005-3BL* in a 'CS / CS (Synthetic 3B)' population (10598}.

6. Awnedness

6.1. Dominant inhibitors.

6.1.2. Tipped 1

B2. **tv:** LD222 {10541}. **matv:** *Xgwm291-5A* - 8.0 cM - *B1* {10541}.

ma: *Xcfd71-4A* – 10.3 cM – *Ba* – 16.5 cM – *Xcfa2173-4A* {0802}[3].

17. Dormancy (Seed)

Vivipary

Following the present material add:

Alleles of *Vp-B1* were recognized using STS marker Vp1B3 {10615,10621}.

Vp-B1a {10615}. Sequence AJ400713 {10615}.
v: Charger {10616}; Zhongyou 9507 {10615}; 271 accessions {10616}.
Vp-B1b (10615}. 193-bp insertion in third intron relative to *Vp-A1a*.
v: Altria {10616}; Recital; {10616}; Yongchuanbaimai {10615}; 2 accessions {10616}.
Vp-B1c {10615}. 83-bp deletion relative to *Vp-B1a*.
v: Scipion {10616}; Xinong 979 {10615}; 101 others {10616}.
Vp-B1d {10616}. 25-bp deletion relative to *Vp-A1a*.
v: Cezanne {10616}; Jason {10616}; 97 others {10616}.
Vp-B1e {10621}. 83-bp deletion, 4-bp insertion, and 2 SNPs relative to *Vp-B1a* {10621}.
v: Hongheshangtou {10621}.

There was a suggestion of a relationship between alleles and PHS response {10615}. *Vp-B1* allelic identifications for Chinese landraces, historical and current wheat cultivars are listed in {10621}.

Pre-harvest sprouting:
QTL:
Insert as the third line in paragraph 2:
In 'AC Domain (red seeded, PHS resistant) / RL4137 (white seeded, PHS moderately resistant)' most measures of PHS occurred as clusters at the *R* loci. However, *QSi.crc-5D* for sprouting index, $R^2 = 0.44$, was independent of seed color {10626}.
Inset before the last paragraph:
'CN10955 (PHS resistant white seeded) / Annuello (PHS susceptible, white seeded)' F_8 RIL population: *QPhs.dpivic-4A.2* in the *Xgwm637-4AS – Xgwm937/Xgwm894-4AL* region and *QPhs.dpivic-4A.1* in the *Xwmc48-4AS – Xgwm397-4AS* region {10599}.

'Rio Blanco (white seeded, PHS resistant) / NW97S186 (white seeded, PHS susceptible)' RIL population: *QPhs.pseru-3AS*, $R^2 = 0.41$, *Xgwm369-3A – Xbarc12-3A*, and one minor QTL (10634}. This major QTL was confirmed in a Blanco / NW98S079 RIL population, R^2 up to 0.58 {10634}.

20. Flowering Time
Insert above the entry for *QFlt.ipk-3A*:
Spring wheat cross: 'Nanda 2419 / Wangshuibai': Seven QTL for flowering time identified with earlier alleles for five coming from Nanda 2419: *QFlt.nau-1B* (closest marker *Xbarc80-1B*, $R^2 = 11\%$), *QFlt.nau-1D* (*Xbarc62-1D*, *Xgwm232-1D*, $R^2 = 6–13\%$), *QFlt.nau-2B* (*Xwmc35-2B*, $R^2 = 10\%$), *XFtl.nau-2D* (*Xwmc601-2D*, $R^2 = 10\%$), *XFtlnau.4A.1* (*Xcfd2-4A, Xmag1353-4A*, $R^2 = 10\%$), *XFtl.nau-4A.2* (*Xmag3386-4A, Xwmc161-4A*, $R^2 = 18–19\%$), and *XFlt.nau7B* (*Xmag2110-7B, Xmag1231-7B, Xgwm537-7B, Xwmc218-7B*, $R^2 = 18\%$) {10566}.

Following the *QFlt.ipk-3A* entry list the following gene:
QFt.cri-3B.1 {10567}. Nearest marker *Xbarc164-3B*; identified in crosses of substitution lines of Ceska Presivka and Zlatka or Sandra (10567}.

26. Glaucousness (Waxiness/Glossiness)
26.2. Epistatic inhibitors of glaucousness
Iw2 **bin:** 2DS5-0.47-1.00 {10578}.
ma: *Xcfd56-2D* – 6 cM – *Iw2* – 10 cM – *Xcfd51-2D* {10578}.

Add at end of section:
A dominant gene (*Vir*) for nonglaucousness was located in chromosome 2BL of cultivar Shamrock, a derivative of *T. turgidum* subsp. *dicoccoides* (10543). This gene mapped 2 cM distal to *Xgwm614-2B* {10543}, whereas the *W1/Iw1* locus was placed distal to *Xgwm614-2B* in {10189}. Lines with *Vir* had delayed senescence ('staygreen') and an average yield advantage over their glaucous sibs {10543}.

27. Glume Colour and Awn Colour
27.1. Red (brown/bronze/black) glumes

Rg-A1b.	**ma:**	Add: *Xgmw1223-1A/Rg-A1/Hg* - 2.2 cM - *Xgwm136-1A* - 4.2 cM - *Xgwm33-1A* {10635}.
Rg-A1c.	**v:**	TRI 14341 {10638}.
	v2:	Sears Synthetic *Rg-D1c* {10638}.
	ma:	*Rg-A1c* – 0.7 cM – *Xgwm1223-1A* {10638}.
Rg-B1b.	**v:**	Golubka {10635}.
	ma:	Add: *Xgwm1078-1B* – 4.6 cM – *Rg-B1* – 2.0 cM – *MW1B002 (Gli-B1)* – 4.1 cM – *Xgwm550-1B* {10635}.
Rg-D1b.	**v:**	ITMI Synthetic W7984 {10635}.
	v2:	Sears Synthetic *Rg-A1c* {10638}.
	ma:	*Xgwm1223-1D* – 6.6 cM – *Rg-D1/Xksud14-1D* – 13.9 cM – *Xgwm33-D1* {10635}; *Rg-A1c* – 3.9 cM – *Xgwm1223-1D* {10638}.

28. Grain Hardness/Endosperm Texture
Add at end of section:
'Neixiang 188 (hard) / Yanshan 1 (medium hard)' RIL population: *QGh.caas-1B.1* with hardness allele from Yanshan 1, $R^2 = 0.28$, *Xwms153-1BL – Xbarc81-1BL* {10640}.

29. Grain Quality Parameters
Add at the end of the preamble:
'Neixing 188 / Yanshan 1' RIL population: 75 QTL for five quality-related traits are reported in {10640}.

29.2. Flour, semolina, and pasta colour

Add:
'Huapei 3 / Yumai 57': DH lines: 18 additive QTL and 24 pairs of epistatic QTL affected flour colour parameters; *qa-1B*, closely linked with *Xbarc372-1B* was associated with variation of a*, $R^2 = 0.256$ {10625}.

29.8. Loaf volume
QTL: Add:
A total of 30 QTL were located on 12 chromosomes, each of which explained between 5.85 and 44.69% of the phenotypic variation; the QTL of largest effect were located on chromosomes 6B and 6D {10659}.

29.10. Grain fructan content
Add:
Fructans are nondigestible carbohydrates considered to have health benefits to consumers.
QTL:
'Berkut (high fructan concentration) / Krickauff (low fructan concentration)': QTL detected on chromosomes 2B, 3B, 5A, 6D, and 7A of which *QGfc.aww-6D.2* ($R^2 = 0.17$, nearest marker, *Xbarc54-6D*) and *QGfc.aww-7A.1* ($R^2 = 0.27$, *Xgwm681-7A*) had the largest effects {10631}.

29.11. Water absorption
'Neixiang 188 / Yanshan 1' RIL population: *XAbs.caas-5D.1* with positive effects from Yanshan 1, $R^2 = 0.3$, *Xcfd189-5DS – Xcfd189-5DS* {10640}.

29.12. Chinese dry noodle quality
'Chuan 35050 / Shannong 483' RIL population: three QTLs for noodle palate, elasticity, and smoothness clustered near *Glu-D1* with beneficial effects associated with subunits 5+10 coming from Chuan 35050. A very significant taste QTL, *QStas.sdau-4A.1*, and positive QTL for stickiness and total score also on chromosome 4A came from Shannong 483 {10647}.

40. Height
40.1. Reduced height: GA-insensitive
Rht-D1b. **v:** Biscay {10574}; Pirat {10574}; Rubens {10574}.

40.2. Reduced height: GA-sensitive
Rht12. **bin:** 5AL-23, based on co-segregation with *B1* {1606}.

42. Hybrid Weakness
42.1. Hybrid necrosis
Ne2ms. **v:** Mironovskaya {0995}.
Add references ',10627, 0995' to the genotype list.

46. Leaf Tip Necrosis
Ltn1. **c:** See *Lr34*.
This gene is identical to *Yr18, Pm38*, and *Ltn* and confers stem rust resistance in some genetic backgrounds.

48. Male Sterility
48.1. Chromosomal
ms1g {10546}. **v:** Male sterile line 257A {10546}.

62. Response to Photoperiod

Ppd-A1. The present listing for *Ppd-A1a* should be entered as *Ppd-A1*.

ma: *Xwmc177-2A – Ppd-A1*, 2.2 and 2.8 cM in GS100/GS101 and GS105/GS104, respectively {10612}.

Ppd-A1a {10612}. **tv:** GS100 {10612}; GS105 {10612}.

GS100 and GS105 had different deletions relative to GS101 and GS104, respectively, and both were consistently a few days earlier flowering than their near-isogenic counterparts with *Ppd-A1b*{10612}.

Ppd-A1b {10612}. **tv:** GS101 {10612}; GS104 {10612}.

Ppd-B1.

Ppd-B1a. **i:** H(C) = 'Haruhikari*5 / Fukuwasekomugi' {10611}, H(D) = 'Haruhikari*/ 5 / Fukuwasekomugi' *Ppd-D1a* {10611}.

v2: Fukuwasekomugi *Ppd-D1a* {10611}.

Ppd-B1b [{10611}]. **v2:** Haruhikari *Ppd-D1b*[{10611}].

Ppd-D1.

Ppd-D1a. **i:** H(A) = 'Haruhikari*5 / Fukuwasekomugi' {10611}; 'Haruhikari*5 / Saitama 27' {10611}, H(D) = 'Haruhikari*/5 /Fukuwasekomugi' *Ppd-B1a* {10611}

v: Akagomughi {10622}: Mazhamai {10622}; Youzimai {10622}.

v2: Fukuwasekomugi *Ppd-B1a* {10611}.

Ppd-A1a was present in 39% of Chinese landraces and 97% of improved cultivars{10622}.

Ppd-D1b [{10611}]. **v:** Haruhikari *Ppd-B1b* [{10611}].

According to {10611} the *Ppd-B1* allele from Japanese wheats has a stronger effect than the allele from CS.

Ppd-B2 {10628}. 7BS {10628}. **su:** Favorit (F26-70 7B) {10628}.

v: F26-70 {0093}.

ma: *Xgwm255-7B* – 20.7 cM – *Ppd-B2* – 4.4 cM – *Xgwm537-7B* {10628}.

This gene confers earlier flowering under long photoperiod conditions {10628}.

65. Response to Vernalization

Add at the end of the *Vrn* section:

Allelic variations at the *Vrn-1* and *Vrn-B3* loci in Chinese wheat cultivars are summarized in {10617}.

XX. New section: Soft Glumes

sog {10555}. 2AS {10555}. **dv:** *T. monococcum* subsp. *monococcum* var. *sinskajae* ID69 {10555}.

ma: Co-segregation with AFLP loci *Xe423204I and Xe373311* {10555}.

Sog {10555}. **dv:** *T. monococcum* subsp. *aegilopoides* ID49 {10555}.

sog was considered to be an homologue of *Tg1* and *Tg2*. See Tenaceous glumes.

73. Tenacious Glumes

Add note after *Tg2*

Tg1 and *Tg2* were considered to be homologues of *sog* for soft glumes in *T. monococcum*. See Soft glumes.

77. Yield and Yield Components

77.4. Grain yield

Nonglaucous (virescent) lines from a 'Shamrock/Shango' DH population had higher yields than glaucous sibs (10543}; see Glaucousness, subsection Epistatic inhibitors of glaucousness.

Proteins

79. Protein

79.1 Grain protein content

QGpc.ipk.7B {10628}. **su:** Favorit (F26-70 7B) {10628}.

v: F26-70 {10628}. Closely associated with *Ppd-B2* {10628}. See Response to Photoperiod.

79.2. Enzymes

79.2.33.1 Phytoene synthase 1 (EC 2.5.1.32)

This section is completely revised:

Homology with the same gene in rice (*Psy1*) {10230}.
Phytoene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Flour colour and Grain quality parameters: Flour, semolina and pasta colour). The gene *Psy-A1* was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents {10501}. Most hexaploid wheat cultivars have a 676-bp insertion in intron four that is absent in the Australian cultivars Dundee, Raven, and Aroona with high yellow pigment. The *Psy-B1b* allele from tetraploid wheat Kofa is the result of a B–A intergenomic conversion event that probably occurred in Cappelli *ph1c* mutant 1 {10530}. An EMS mutation in the *Psy-E1* gene is associated with whiter endosperm in lines carrying the *Th. elongatum* 7EL translocation.

Psy1-A1 {10230}. 7AL {10230}. **tv:** Kofa {10230}.
ma: *Xwmc809-7A* – 5.8 cM – *Yp7A* {10501}.

Psy1-A1a {10501}. **v:** Chinese Spring 10501}; CA 9648{10501}; Neixiang 188 {10501}; Chinese common wheats with high pigment content {10501}.
c: GenBank EF600063 {10501}, EU096091 {10530}, Eu649788 {10654}. No 37-bp insertion in intron 2 (194-bp fragment for marker Yp7A {10501}. 676-bp insertion in intron 4 {10530}.
tv: Blackbird {10653}. **c:** EF600063 {10653}.

Psy1-A1b {10501}. **v:** PH82-2 {10501}; Shaan 9314 {10501}; Xinong 336 {10501}. Chinese common wheats with low yellow pigment content {10501}.
c: GenBank EF600064 {10501}. 37-bp insertion in intron 2 (231-bp fragment for marker *Yp7A* {10501}. 676-bp insertion in intron 4 {10530}.

Psy1-A1c {10530}. **v:** M564 {10650}.
c: GenBank EU650391 {10650}; No 37-bp insertion in intron 2 and no 676-bp insertion in intron 4 {10530}. High yellow pigment cultivars: Aroona (PI 464647) {10530}; Dundee (PI 89424, PI 106125) {10530}; Raven (PI 303633, PI 330959) {10530}.

Psy1-A1d {10651}. **tv:** Langdon {10651}; *T. turgidum* subsp. *dicoccum* DM28 {10652}.
c: GenBank EU263018 {10651}; FJ 393515 {10652}.

Psy1-A1e {10651}. **v:** Sunco {10654}. **tv:** DR8 {10651}.
c: EU649791 {10654}; EU263019 {10651}.

Psy1-A1f {10652}. **dv:** *T. urartu* PI 428326 {10652}. **c:** FJ393516 {10652}.

Psy1-A1g {10652}. **dv:** *T. urartu* UR1 {10652}. c: FJ393517 {10652}.

Psy1-A1h {10652}. **dv:** *T. monococcum* subsp. *aegilopoides* BO1 {10652}; *T.monococcum* subsp. *monococcum* MO5 {10652}.
c: FJ393518 {10652}; FJ393519 {10652}.

Psy1-A1i {10652}. **dv:** *T. monococcum* subsp. *monococcum* MO1 {10652}.
c: FJ393520 {10652}.

Psy1-A1j {10652}. **dv:** *T. monococcum* subsp. *monococcum* MO2 {10652}.
c: FJ393521 {10652}.

Psy1-A1k {10652}. **v:** Spelt 167 {10652}.
tv: *T. turgidum* subsp. *dicoccoides* DS3 {10652}; *T. turgidum* subsp. *dicoccum* DM37 {10652}.
c: FJ293527 {10652}; FJ393522 {10652}; FJ393523 {10652}.

Psy1-A1l {10652}. **tv:** Kofa {10230,10530}; Strongfield {10653}; *T. turgidum* subsp. *dicoccoides* DS6 {10652}.
c: EU096090 {10230,10530}; FJ393524 {10652}.

Psy1-A1m {10652}. **tv:** *T. turgidum* subsp. *dicoccum* DM26 {10652}.
c: FJ393525 {10652}.

Psy1-A1n {10652}. **v:** Spelt SP9 {10652}. **c:** FJ393526 {10652}.

Psy1-A1o {10653}. **tv:** Commander {10653}. **c:** FJ234424 {10653}.

Psy1-A1p {10654}. **v:** Tasman {10654}. **c:** EU649792 {10654}.

Psy1-A1q {10654}. **v:** Cranbrook {10654}. **c:** EU649793 {10654}.
Psy1-A1r {10654}. **v:** Halberd {10654 }. **c:** EU649794 {10654}.
Psy1-A1s {10654}. **v:** Schomburgk{10654}. **c:** EU649795 {10654}.
Psy1-B1 {10230}. 7BL {10230}. **tv:** Kofa {10230}.
ma: *Xcfa2040-7B* – 12 cM – *Psy-B1* – 5 cM – *Xgwm146-7B* {10230}.
Psy1-B1a {10650}. **v:** Chinese Spring {10530,10650,10654}; Spelt SP9 {10652}.
tv: *T. turgidum* subsp. *dicoccoides* DS4 {10652}; FJ393529 {10652}; FJ393528 {10652}.
c: EU650392 {10650}; EU096094 {10530}; EU649789 {10654}.
Psy1-B1b{10650}. **v:** Neixiang 188 {10650}. **c:** EU650393 {10650}.
Psy1-B1c {10650}. **v:** CA 9648 {10650}. **c:** EU650394 {10650}.
Psy1-B1d {10650}. **v:** Ning 98084 {10650}. **c:** EU650395 {10650}.
Psy1-B1e {10650}. **v:** M484 {10650}. **c:** EU263021 {10650}.
tv: DR8 {10650}; *T. turgidum* subsp. *dicoccum* DM28 {10652}.
c: EU263021 {10650}; FJ393541{10652}.
Psy1-B1f {10651}. **tv:** Langdon {10651}. **c:** EU263020 {10651}.
Psy1-B1g {10651}. **tv:** DR1 {10651}; *T. turgidum* subsp. *dicoccoides* DS6 10652}.
c: EU650396 {10651}; FJ393530 {10652}.

Psy1-B1h {10652}. **tv:** *T. turgidum* subsp. *dicoccoides* DS3 {10652}.
c: FJ393531 {10652}.
Psy1-B1i {10652}. **tv:** *T. turgidum* subsp. *dicoccoides* DS8 {10652}.
c: FJ393532 {10652}.
Psy1-B1j {10652}. **tv:** T. *turgidum* subsp. *dicoccum* DM26 {10652}.
c: FJ393533 {10652}.
Psy1-B1k {10652}. **tv:** T. *turgidum* subsp. *dicoccum* DM33 {10652}.
c: FJ393534 {10652}.
Psy1-B1l {10652}. **tv:** T. *turgidum* subsp. *dicoccum* DM37 {10652}.
c: FJ393535 {10652}.
Psy1-B1m {10652}. **v:** Spelt 167 {10652}. **c:** FJ393540 {10652}.
tv: *T. turgidum* subsp. *dicoccum* DM47 {10652}.
c: FJ393539 {10652}.
Psy1-B1n {10530}. Previously designated *Psy1-B1b* {10656}.
tv: Kofa **c:** EU096092 {10530}; DQ642439 {10230}.
Psy1-B1o {10530}. Previously designated *Psy1-B1a* {10656}.
tv: UC1113 {10530}; W9262-260D3 {10230}.
c: EU096093 {10530}; DQ642440 {10230}.
Psy1-D1{10652}. 7DL{10652}.
Psy1-D1a {10652}. **v:** Chinese Spring {10652}. **c:** EU650397 {10652}; EU649790 {10654}.
Psy1-D1b {10652}. **dv:** *Ae. tauschii* Ae34 {10652}. **c:** FJ393542 {10652}.
Psy1-D1c {10652}. **dv:** *Ae. tauschii* Ae46 {10652}. **c:** FJ393543 {10652}.
Psy1-D1d {10652}. **dv:** *Ae. tauschii* Y99 {10652}. **c:** FJ393544 {10652}.
Psy1-D1e {10652}. **v:** Spelt SP9 {10652}. **c:** FJ393545 {10652}.
Psy1-D1f {10652}. **v:** Spelt217 {10652}. **c:** FJ393546 {10652}.
Psy1-D1g {10652}. **v:** Zhongliang 88375 {10652}. **c:** FJ807498 {10652}.
Psy1-D1h {10652}. **dv:** *Ae. tauschii* Ae37 {10652}. **c:** FJ807499 {10652}.
Psy1-D1i {10652}. **dv:** *Ae. tauschii* Ae38 {10652}. c: FJ807500 {10652}.
Psy1-D1j {10652}. **dv:** *Ae. tauschii* Ae42 {10652}. c: FJ807501 {10652}.
Psy1-D1k {10655}. **v:** Nongda 3291 {10655}. c: FJ807495 {10655}.
Psy1-D1l {10655}. **v:** E 86642 {10655}. c: FJ807496 {10655}.
Psy1-D1m {10655}. **v:** Ning 97-18 {10655}. c: FJ807497 {10655}.

Psy1-S1 {10652}. al: *Ae. speltoides* Ae48 {10652}.
Psy1-S1a {10652}. al: *Ae. speltoides* Ae48 {10652}. **c:** FJ393536 {10652}.
Psy1-S1b {10652}. al: *Ae. speltoides* Ae49 {10652}. **c:** FJ393537 {10652}.
Psy1-S1c {10652}. al: *Ae. speltoides* Y162 {10652}. **c:** FJ393538 {10652}.

79.2.34. Polyphenol oxidase

This section is completely revised:

High PPO activity in kernels and flour leads to a time-dependent discoloration of end products such as noodles, pasta and breads.

Primers different from those in {10386} were developed in {10504}, but their ability to distinguish phenotypic groupings (alleles) were similar. A null allele of *Ppo-D1* was identified for this locus using primer pair WP3-2 {10504}.

Ppo-A1 {10386}. *PPO-2A* {10385}. 2AL {10385}.
ma: Detected with STS markers PPO18 {10385} and PPO33 {10386}; *Xgwm321-2A* – 1.4 cM – *Ppo-A1* – 5.8 cM – *Xgwm294-2A* {10385}.
Ppo-A1a {10386}. *PPO-2Aa* {10385}.
v: Nongda 139 {10386}. Zhongyou 9507 {10385,10386,10504}; others {10386, 10504}.
c: EF070147 {10386}.
Wheats with this allele tend to have higher PPO activity {10385, 10386}.
Ppo-A1b {10386}. *PPO-2Ab* {10385}.
v: Chinese Spring {10386}. CA 9632 {10385,10386}; Nongda 183 {10504}; others {10386, 10504}.
tv: *T. turgidum* subsp. *dicoccoides* DS4 {10386}.
c: EF070148 {10386}.
Wheats with this allele tend to have lower PPO activity {10385,10386}.
Ppo-A1c {10657}. **dv:** *T. urartu* UR1 {10657}. **c:** EU371651 {10657}.

Ppo-A1d {10657}. **dv:** *T. monococcum* subsp. *aegilopoides* BO1 {10657}.
c: EU371652 {10657}.
Ppo-A1e {10657}. **tv:** DR8 {10657}. **dv:** *T. monococcum* subsp. *monococcum* MO1 {10657}.
c: EU371653 {10657}.
Ppo-A1f {10657}. **tv:** *T. turgidum* subsp. *dicoccoides* DS3 {10657}.
c: EU371654 {10657}.
Ppo-A1g {10657}. **tv:** Langdon {10657}. **c:** EU371655 {10657}.
Ppo-B1 {10658}. **v:** Chinese Spring {10658}.
Ppo-B1a {10658}. **v:** Chinese Spring {10658}. **c:** GQ303713 {10658}.
Ppo-D1 {10386}. **ma:** Detected with primers PPO16 and PPO29. *Xwmc41-2D* – 2.0 cM – *Ppo-D1*{10386}.
Ppo-D1a {10386}. **v:** Chinese Spring {10386}. Zhonghou 9507 {10386,10504}; others {10386,10504}.
c: EF070149 {10386}.
Wheats with this allele tend to have lower PPO activity {10386}.
Ppo-D1b {10386}. **v:** CA 9719 {10386}; CA 9632 {10386); Nongda 183 {10504}; others {10386,10504}.
c: EF070150 {10386}.
Wheats with this allele tend to have higher PPO activity {10386}.
Ppo-D1c {10657}. **dv:** *Ae. tauschii* Ae38 {10657}. **c:** EU371656 {10657}.
Ppo-D1d {10657}. **dv:** *Ae. tauschii* Y59 {10657}. **c:** EU371657 {10657}.
Ppo-D1e [{10504}]. [*Ppo-D1null* {10504}]; *Ppo-D1c* {10656}.
v: Gaiyuerui {10504}; Zm2851 {10504}. XM2855 {10504}; 9114 {10504}.
Wheats with this allele tend to have lower PPO activity {10504}.

79.2.36. Polygalacturonase-inhibiting proteins

PGIPs are leucine-rich repeat (LRR) proteins involved in plant defense.

Pgip-A1 [{10608}]. *Tapgip3*, AM180658 {10608}. **dv:** *T. monococcum* PI 538722 {10608}.
Not expressed in *T. urartu* PI 428315 (AM884191 {10608} or in polyploid wheat because of inactivation by an inserted copia transposon in the fourth LRR {10608}.

Pgip-B1 [{10608}]. *Tapgip1* {10610}. 7BS {10610, 10608}.
ma: *XS13M50-7B* – 5 cM – *Pgip-B1* – 11.7 cM – *Xmgb105s-7B* {10608}.
Pgip-B1a [{10608}] . *Tapgip1a* {10608}. **tv:** Messapia {10608}.
Pgip-B1b [{10608}]. *Tapgip1b,* AM884195 {10608}. **tv:** *T. turgidum* subsp. *dicoccoides* MG4343 {10608}.
This nonexpressed allele produces a large amplicon in Southern blots using the pgip sequence as probe due to an insertion of a Vacuna mutator element {10608}.

Pgip-D1 [{10608}]. *Tapgip2* {10610}. 7DS {10610}.
tv: Langdon 7D(7A) {10610}; Langdon 7D(7B) {10610}.

Endosperm Storage Proteins
77.3.1. Glutenins
77.3.1.1. *Glu-1*
Glu-A1
Glu-A1y
Correction: The subunit encoded by this allele should be 2 and not 2" as currently listed.

Add note to the end of the *Glu-A1* section:
Primers were designed that enabled Ax2* to be distinguished from Ax1 or Ax-null {10641}.

Glu-B1
Add:
Glu-B1bp {10643}. 7**+8 {10643}. **v:** XM1368-2 {10643}.
v: XM1404-2 {10643}.
Glu-B1bq {10643}. 7+8** {10643}.

Glu-D1
Glu-D1f
Add note:
Glu-D1f is present at high frequencies in wheats of southern Japan. Its presence may be associated with white salted noodle (Udon) quality {0936}.
Add:
Glu-D1bs {10642}. 1.6^t+12.3^t {10642}. **dv:** *Ae. tauschii* TD16 {10642}.
Glu-D1bt {10568}. 2.1^t+12^t {10568}. **v:** Syn 396 {10568}.

Add note to the end of the *Glu-D1* section:
Primers were designed that enabled Dx2 to be distinguished from Dx5 and Dy10 from Dy12 {10641}.

Glu-A1-1
Glu-A1-1x
The subunit encoded by this allele should read 2 and not 2" as currently listed.

Glu-B1-1
Add:
Glu-B1-1ag {10643}. 7** {10643}. **v:** XM1368-2 {10643}.

Glu-B1-2
Add:
Glu-B1-2ag {10643}. 8** {10643}. **v:** XM1404-2 {10643}.

Glu-D1-1
Add:
Glu-D1-1v {10642}. 1.6^t {10642}. **dv:** *Ae. tauschii* TD16 {10642}.

Glu-E1
Add:
Glu-E1a [{781}]. **ad:** CS/*L. elongatum* W0622 [{781}].
Glu-E1b [10644]. **ad:** Langdon/*L. elongatum* DGE-1 {10644}].
al: *L. elongatum* PI 531719 {10644}.
Add note to the end of the *Glu-E1* section:
Four {10660, 10661} and 11 {10662} alleles were observed in *Agropyron elongatum* (E^e genome, 2n = 10X = 70) and named *Aex1* to *Aex5* (producing x-type subunits) and *Aey1* to *Aey 10* (producing y-type subunits). *Aex4*, *Aey7*, and *Aey9*

were very similar to three alleles in the diploid progenitor *Lophopyrum elongatum* {10439, 10663}. The C-terminal regions of three of the y-type subunits (products of *Aey8*, *Aey9* and *Aey10*) were more similar to x-type subunits than to other y-type subunits {10662}. The subunit from *Aex4* contained an additional cysteine residue, which may be associated with good processing quality in wheat introgression lines {10662}. Allele *Aey4* was a chimeric gene formed by recombination of two other genes {10662}.

79.3.1.3. *Glu-3*
Glu-D3
Add:
Glu-D3f {10548}. **v:** Cheyenne {10548}.
Glu-D3g {10558}. **v:** Hira-1 {10558}.
Glu-D3h {10558}. **v:** India 115 {10558}.

Glu-D3i {10558}. **v:** Bolac {10558}.
Glu-D3j {10558}. **v:** Hira-2 {10558}.
Glu-D3k {10558}. **v:** Lincoln {10558}.

79.3.2. Gliadins
Add note to the end of the text appearing after the *Gli-DT1* locus:
A 1,200-bp *Dra*I RFLP was identified as a gene-specific probe for the T1 omega-gliadin {10645}.
Add:
79.3.2.7 *Gli-7*
Gli-A7 {10547}. 1DS {10547}. **dv:** AUS18913 {10547}.
The gamma-gliadin encoded by this locus co-segregated with the T1 omega-gliadin encoded by the *Gli-D^{t}T1* locus (currently included in the Catalogue as locus *Gli-DT1*). *Gli-A7* was located 0.69 cM from *Gli-D^{t}1* {10547}.

79.5.6. Waxy proteins
Wx-A1.
Wx-A1c. **v:** Pakistan Zairaishi selection {10629}.
Wx-A1e. **tv:** KU 3659 {10629}.
Wx-A1g. *Wx-A1'* {10587}. **v:** *T. aestivum* subsp. *spelta* accessions PI 348576 {10587}; PI 348476 {10587}; 2778 Epeautre Noir Velu {10587}.
Wx-B1.
Wx-B1c. **v:** Chousen 40 {0094}; Junguk 12 {10629}; Cikotaba {10629}; AF24 {10629}.
Wx-B1d. **tv:** KU4213D {10629}.
Wx-B^{S}1g {10587}. **al:** *Ae. speltoides 33* {10587}.
Wx-B^{SL}1h {10587}. **al:** *Ae. longissima* 12 {10587}.
Wx-D1.
Wx-D^{DN}1g {10587}. **al:** *Ae. ventricosa* 12 {10587}.

79.5.8. Puroindolines and grain softness protein
Pinb-D1ac 10570}. **v:** Kashibaipi {10570}; Red Star {10570}.
G to A substitution at position 257 and C to T substitution at position 382 {10570}.

Pathogenic Disease/Pest Reaction

81. Reaction to *Blumeria graminis* DC.
81.1. Designated genes for resistance
Pm4
Pm4b. **ma:** *STS241* – 4.9 cM – *Pm4b* – 7.1 cM – SRAP *Me8/Em7220* – 4.7 cM – *Xgwm382-2A* {10553}.
Pm4c {10583}. *Pm23* {1618}. 2AL {10583}; earlier reported on 5AL {1618}.
v2: 81-7241 *Pm8* suppressed {10583,1618}.
ma: *Xbarc122-2A* – 1.4 cM – *Pm4c* – 3.5 cM – *Xgwm356-2A* {10583}.

Pm5.

Pm5a. **v2:** Saar *Pm38 Pm39* {10481}.

Pm5d 7BL, FL 0.86 {10542}. **v:** Dream {10542}.

ma: *Xgwm611-7B* – 2.1 cM – *Pm5d* – 2.0 cM – *Xgwm577-7B* – 1.0 cM – *Xwmc581-7B* {10542}.

Pm6. **i:** Eight Prins derivatives {10576}.

ma: RFLP marker *Xbcd135-2B* was converted to STS markers *NAU/STSBCD135-1* and *NAU/STSBCD135-2*, which showed linkage of 0.8 cM with *Pm6* {10576}.

Pm23. Deleted, see *Pm4c*.

Pm36. **bin:** 5BL6-0.29-0.76 {10356}.

ma: Delete the present entry and replace with:
Xcfd7-5B – 10.7 cM – *Pm36* – 0.8 cM – *EST BJ261636* – 8.9 cM – *Xwmc75-5D* {10356}.

Pm38. **v:** Saar *Pm5a Pm39* {10481}.

c: See *Lr34*.

This gene is identical to *Yr18*, *Lr34*, and *Ltn* and confers stem rust resistance in some genetic backgrounds.

Pm39. Change **v:** to **v2:** and insert '*Pm5a*' in front of '*Pm38*'

Pm40 {10539}. Derived from *Th. intermedium* {10539}. 7BS {10539}.

v: GRY19 {10539}.

ma: Mapped relative to several SSR markers {10539}.

Pm41 {10551}. Derived from *T. turgidum* subsp. *dicoccoides*. 3BL {10551}.

v: XXX = '87-1*4//Langdon/IW2' {10551}.

tv: 'Langdon/IW2 Seln. XXX' {10551}; *T. turgidum* subsp. *dicoccoides* IW2 {10551}.

ma: *BE489472* – 0.8 cM – *Pm41* – 1.9 cM – *Xwmc687-3B* {10551}.

Pm41 and associated marker alleles showed strongly distorted inheritance with reduced frequencies relative to Langdon alleles {10551}.

Pm42 {10559}. Derived from *T. turgidum* subsp. *dicoccoides*. Recessive.

2BS {10559}. **bin:** 0.75-0.84.

v: P63 = Yanda 1817/G303-1M//3*Jing 411 {10559}.

tv: *T. turgidum* subsp. *dicoccoides* G303-1M {10559}.

ma: *BF146221* – 0.9 cM – *Pm42* – *Xgwm148-2B* {10559}.

Pm43 {10560}. Derived from *Th. intermedium*. 2DL {10560}.

v: Line CH5025 = '76216-96/TAI7045//2*Jing 411' {10560}; Partial amphiploid TAI7045 {10560}.

al: *Th. intermedium* Z1141 {10560}.

ma: *Xwmc41-2D* – 2.3 cM – *Pm43* – 4.2 cM – *Xbarc11-2D* {10560}.

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

PmLK906. After 'recessive' correct second reference to {10477}.

MlIw72 {0908}. 7AL {0908}. **bin:** FL 0.86 {0908}.

tv: *T. turgidum* subsp. *dicoccoides* IW72 {0908}.

ma: *Xmag1759-7A* – 8.2 cM – *MlIw72* – 3.3 cM – *Xmag2185-7A* – 1.6 cM – *Xgwm344-7A* {0908}.

PmYm66 {10619}. 2AL {10619}. **v:** Yumai 66 {10619}.

ma: *XKsum193-2A* – 2.4 cM & 3.6 cM – *PmYm66* {10619}.

Pm2026 [{10604}]. *pm2026* {10604}. Recessive {10604}. $5A^{m}L$ {10604}.

bin: 5AL17 – 0.78-1.00 {10604}.

dv: *T. monococcum* subsp. *monococcum* TA2026 {10604}.

ma: *Xcfd39-5A* – 1.8 cM – *Xcfd1493-5A/Xmg2170-5A* – 0.9 cM – *Pm2026* – 2.5 cM – *Xgwm126-5A* {10604}.

81.4. QTL for resistance to *Blumeria graminis*

'Avocet R (S) / Saar (R)' F_6 RILs: QTL located on chromosomes 1BL (close to *Xwmc44-1B*) (*Pm39*), 7DS (*Xgwm1220-7D*) (*Pm38*), and 4BL (*XwPt-6209*) (resistance allele from Avocet R {10481}.

86. Reaction to *Fusarium graminearum*

86.1. Disease: Fusarium head blight, Fusarium head scab, scab

Fhb3. Change 7D to 7DS.

ma: Three PCR markers, *Be586744-STS, BE404728-STS,* and *BE586111-STS*, were developed {10529}.

Following the entries 'Wuhan-1 / Maringa' in QTL section and under Resistance to Don Accumulation insert: (corrected to 'Wuhan / Nyubai' {10623}).'

Field resistance

After the present entry insert the following:

'G16-92 (R) / Hussar (S)': Two QTL for resistance to *F. culmorum* were identified on chromosomes 1A (resistance from Hussar) ($R^2 = 0.01$) and 2B (resistance from G16-92) ($R^2 = 0.14$) {10588}.

Under 'Nanda 2419 (S) / Wangshuiba (R)' and immediately above 'Wanshuibai / Seri 82' add the following:

Type IV resistance (proportion of Fusarium-damaged kernels) was attributed to five QTL, four from Wangshuibai. Those with the largest effects included *QFdk.nau-2B* (from Nanda 2419), *QFdk.nau-3B,* and *QFdk.nau-4B* {10577} with each accounting for more than 20% of the phenotypic variation.

'Pelikan (S) / G93010' (= 'Bussard / Ning 8026') (R). *Qfhs.Ifl-7BS*/5BL and Qfhs.*Ifl-6BS* (probably *Fhb2*) from Ning 8026 reduced disease severity by 30% and 24%, respectively, and by 46% when combined {10594}. Other resistance genes were located on chromosomes 1AS (*Qfhs.Ifl-1AS* from Pelikan) and 2AL and 7AL (from Ning 8026) {10594}.

'Spark (MR) / Rialto (S)' DH population: Of nine QTL identified across all environments, seven alleles for resistance came from Spark and two from Rialto. The largest effect on Type-1 resistance (*Xfhs.jic-4D.2*) was associated with the *Rht-D1b* allele in Rialto, which made lines more susceptible. Other QTL occurred on chromosomes 1B (T1B·1R), 4D (*Qfhs.jic-4D.2*), 2A, 3A (each, two QTL), 5A, and 7A. *Xfhs.jic-4d.2* had little effect on Type-2 resistance {10603}.

Add at end of section:

Associations between response to FHB caused by *F. culmorum* and the semidwarfing locus *Rht-D1* in crosses 'Apache / Biscay', 'Romanus / Pirat', and 'History / Rubens' (Biscay, Pirat, and Rubens carry *Rht-D1b*) were reported in {10574}. Genotypes with the semidwarf alleles tended to be more susceptible.

A review of 52 mapping studies is provided in {10593}.

Seedling resistance to *Fusarium graminearum* (FSB)

A QTL for FSB resistance in the 'Wuhan / Nyubai' population was associated with the *Qwmc75-5B* locus, $R^2 = 0.138$. The relationship of this resistance to crown rot resistance is unknown {10624} (see Reaction to *F. pseudograminearum*).

Tetraploid wheat

'Langdon / Langdon (DIC-2A)' RICL population: Increased susceptibility of the *T. turgidum* subsp. *dicoccoides* Israel A substitution line relative to Langdon was mapped to a 22-cM interval spanned by *Xgwm558-2A* and *Xgwm445-2A* {10613}.

88. Reaction to *Magnaporthe grisea* (Herbert) Barr

List following the note:

Rmg4 {10639}. 4A {10639}. **v:** Norin 4 {10639}; Norin 26 {10639}; Norin 29 {10639}; P168 {10639}; Shin-chunaga {10639}; *T. aestivum* subsp. *compactum* No. 24 {10639}.

Confers resistance to *Digitaria* isolate Dig41 at 26°C {10639}.

Mg5 {10639}. 6D {10639}. **s:** CS (Red Egyptian 6D) {10639}

v: Red Egyptain {10639}.

Confers resistance to *Digitaria* isolate Dig41 at 26°C {10639}.

91. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

Stb3. After the existing chromosome location, add:

According to {10556} this location is not correct. 7AS {10556}.

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

92.1. Genes for resistance

QTL:

Add at the end of the section:

'HRWSN125 (R) / WAWHT2074 (S)': Constant detection of *QSnl.daw-2DL* for flag leaf resistance and *QSng.daw-4BL* for glume resistance over two years {10584}.

Tetraploid wheat

'Langdon / Langdon' (*T. turgidum* subsp. *dicoccoides* Israel-A 5B): *QSnb.ndsu-5B* located 8.3 cM proximal to *tsn1* for tan spot resistance; $R^2 = 0.38$ {10597}.

92.2. Sensitivity to SNB toxins

Australian cultivars with *Tsn1* and *tsn1* are listed in {10540}.

94. Reaction to *Puccinia graminis*

Sr2 **v2:** HD2009 *Sr30* {10632}.

Sr8b. **tv2:** Arrivato *Sr9e Sr13* {10607}.
ma: *Sr8b* – 4.6 cM – *Xgwm334-6A* {10607}.

Sr9e. **tv2:** Arrivato *Sr8b Sr13* {10607}.
ma: *Xgwm191-2B* – 5.5 cM – *Sr9e* – 0.7 cM – *Xgwm47-2B* {10607}.

Sr13. **v2:** Machete *Sr2* {10607}. **tv2:** Arrivato *Sr8b Sr9e* {10607}.
ma: *Xwmc59-6A* – 5.7 cM – *Sr13* {10607}.

Sr17. 7BL {, 10565}. **v:** Forno (10511, 10565}.
ma: *Xwmc273-7B* – 15.3 cM – *Sr17* {10565}.

Sr30. **v2:** HD2009 *Sr2* {10632}.

Sr36 **v:** Others, add reference 10609, i.e., {572, 10609}.
ma: *Xgm429-2B* – 0.8 cM – *Sr36/Xstm773-2-2B/Xgwm31-2B/Xwmc477-2B* {10609}; *Xgwm319-2B* – 0.9 cM – *Sr36/Xstm773-2-2B/Xwmc477-2B* {10609}.

Sr47 {10549}. Derived from *Ae. speltoides*. 2B = T2BL-2SL·2SS {10549}.
tv: DAS15 {10549}. **al:** *Ae. speltoides* PI 369590 {10549}.

Sr48 {10564}. *SrAn1*{10565}. 2AL {10564, 10565}.
bin: 2AL1-0.85-1.00 {10564}. **v:** Arina {10511, 10564, 10565}.
ma: *Yr1* – 16.5 cM – *Sr48* {10564}. *Sr48* is considerably distal to the most distal of published markers, all of which are proximal to *Yr1*.

Add at end of section:

QTL:

'Arina / Forno': *Qsr.sun-5BL* {10565}; resistance contributed by Arina, associated with *Xglk356-5B*, $R^2 = 11$-12% {10565}. *Qsr.sun-7DS* {10565}; resistance contributed by Forno, associated with markers *XcsLV34* and *Xswm10* diagnostic for *Lr34/Yr18* {0828}.

'HD2009 / WL711' RILs: Three of several QTL gave consistent effects across environments, i.e., *QSr.sun-3BS*, $R^2 =$ 0.09-0.15, probably *Sr2*, *QSr.sun-5DL*; $R^2 = 0.2$-0.44, probably *Sr30*; and *QSr.sun-7A*, $R^2 = 0.07$-0.13, nearest marker *wPT-4515* {10632}.

95. Reaction to *Puccinia striiformis*

95.1. Designated genes for resistance to stripe rust

Yr1. **bin:** 2AL1-0.85-1.00 {10564}.
ma: *Xfba-2A* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* {10564}.

Yr9. At the end of section add:

Stripe rust resistant wheat–*S. africanum* derivatives G17 (substitution line with $1R^a$), L9-15 (T1BL·$1RS^a$) and L2-20 (putative cryptic translocation) are reported in {10596}.

Yr17. **v:** Apache {10554}; Bill {10554}; Caphorn {10554}; Clever {10554}; Clarus {10554}; Corsaire {10554}; Rapsodia {10554}; To Renan add reference, that is {0044,10554}; Rheia {10554}.

Yr18. **v2:** Saar *Yr29* {10481}.

Yr26. , 1BL {10544}. **Bin:** C-1BL6-0.32 {10544}.
v: Nannong 9918 {10544}; Nei 2938 {10544}; Nei 4221{10544}; Neimai 9 {10544}.
ma: *Xgwm11/18-1B* – 1.1 cM – *Xwe171/202/210-1B* – 0.4 cM – *Xwe177/201-1B* – 0.3 cM – *Xwe173-1B* – 1.4 cM – *Yr26* – 6.7 cM – *Xbarc181-1BL* – 3.0 cM – *Xwmc419-1BL* {10544}. According to {10544} the markers most closely associated with *Yr26* are actually located in chromosome 1BL.

Yr27. **v2:** Change 'Attila *Lr27*' to 'Attila *Yr27*'.

Yr29. **v2:** Saar *Yr18* {10481}.

Yr33. 7DL {10039}. **ma:** Linkage with *Xgwm111-7D* and *Xgwm437-7D* {10039}.

Yr42 {10537}. Derived from *Ae. neglecta*. 6A = T6AL-6^{Aen}L·6^{Aen}S {10537}.
v: Line 03M119-71A {10537}.
al: *Ae. neglecta* 155 {10537}.

Genotype list: Add:
European wheats {10579}.

95.2. Temporarily designated genes for resistance to stripe rust

YrCN17 {10562}. Derived from *S. cereale*. 1B, T1BL·1RS {10562}.
v: CN12 {10562}; CN17 {10562}; CN18 {10562}.
al: *S. cereale* L155 {10562}.

YrC591 {10606}. 7BL {10606}. **v:** C591 {10606}; Zhongzhi 1 {10606}.
ma: *Xcfa20-40-7B* – 8.0 cM – *YrC591* – 11.7 cM – *SC-P35M48* {10606}.

YrExp1 {10601}. 1BL {10601}. **v2:** Express *YrExp2* {10601}.
ma: *Xwgp78-1B* – 4.2 cM – *YrExp1* – 3.4 cM – *Xwmc631-1B* {10601}.

YrExp2 {10601}. 5BL {10601}. **v2:** Express *YrExp1* {10601}.
ma: *Xgwm639-5B* – 9.2 cM – *Xwgp81-5B* – 1 cM – *YrExp2* – 0.7 cM – *Xwgp82-5B* {10601}.

Based on the presence of the nearest flanking markers, *YrExp2* was postulated in Expresso, Blanca Grande, Buck Pronto, and 'Jeff / Pronto' {10601}.

YrR212{10562}. Derived from *S. cereale*. 1B, T1BL·1RS {10562}.
v: R185 {10562}**;** R205 {10562}; R212 {10562}.
al: *S. cereale* R212 {10562}.

YrS2199 {10618}. 2BL {10618}. **bin:** 2BL0.89-1.00 (10618}.
v: S2199 {10618}.
ma: *Xgwm120-3B* – 11.0 cM – *YrS2199* – 0.7 cM – *Xdp269-2B* {10618}.

95.3. Stripe rust QTL

Add at end of section:
'Luke (R) / Aquileja (R)': Two QTL for high-temperature adult-plant resistance, *QYRlu.cau-2BS.1* (distal, flanked by *Xwmc154-2B* and *Xgwm148-2B*, $R^2 = 0.366$) and *QYrl.cau-2BS.2* (proximal, flanked by *Xgwm148-2B* and *Xbarc167-2B*, $R^2 = 0.415$) from Luke, and *QYraq.cau-2BL* (flanked by *Xwmc175-2B* and *Xwmc332-2B*, $R^2 = 0.615$) in Aquileja for stripe number (10582}.
'Avocet S / Attila': QTL were located on chromosomes 2BS (probably *Yr27*), 2BL (a race-specific effect) and 7BL (*XP32/M59* – *Xgwm344-7B* {10586}.
'Guardian / Avocet S': F_3 lines. One major QTL, *QPst.jic-1BL* (*Xgwm818-1* – *Xgwm259-1B* , R^2 up to 0.45), and two minor resistance QTL on chromosomes 2D and 4B originating from Guardian {10589}. The major QTL was in the region of *Yr29*.
'Stephens / Michigan Ambe'r: Two QTL for high temperature APR were located in chromosome 6BS; *QYrst.wgp-6BS.1* located in a 3.9-cM region flanked by *Xbarc101-6B* and *Xbarc136-6B* and *QYrst.wgp-6BS.2* located in a 17.5-cM region flanked by *Xgwm132-6B* and *Xgdm113-6B* {10602}.

96. Reaction to *Puccinia triticina*

96.1. Genes for resistance

Lr1. **v:** Line 87E03-S2B1 {10561}. **ma:** Co-segegation with RGA567-5 {10561}.
c: *Lr1* is a member of a multigene family (PSR567), has a CC-NBS-LRR structure and produces a protein of 1,344 aa, EF567063 {10561}.

Lr11. **v2:** Ck9803 *Lr18* {10595}; FFR 524 *Lr18* {10595}; Pioneer 2684 *Lr18* {10595}; SS520 *Lr18* {10595}.

Lr13. **ma:** *Xbarc163-2B* – 5.1 cM – *Lr13* – 8.7 cM – *Xstm773b-2B* {0329}.

Lr14a. **v2:** Brambling *Lr23 Lr34* {10563}.

Lr14b **v:** Weebill 1 {10571}.

Lr17a. **bin:** 2AS-5 {10572}. **v:** TAM 111{10595}; Trego {10572}.

ma: *Xbarc123-2A* – 4.8 cM – *Xgwm636-2A* – 4.0 cM – *Lr17a* {10571}; *Xgwm614-2A* – 0.7 cM – *Lr17a* – *Xwmc407-2A* {10572}.

Lr18. **v2:** Ck9803 *Lr11* {10595}; FFR 524 *Lr11* {10595}; Pioneer 2684 *Lr11* {10595}; SS520 *Lr11* {10595}.

Lr19. 7AL. **tv:** This translocation was transferred to durum wheat and engineered to produce normally inherited secondary recombinants with smaller alien segments, such as R5-2-10, and tertiary recombinants such as R1 {10633}.

c: A candidate sequence, AG15, with a 1,258 amino-acid sequence and a CC-NBS-LRR structure was reported in {10575}.

Lr21. Add note at end of section:

A reconstituted, effective *Lr21* allele (designated *Lr21-b*) was obtained as a rare (1/5,872) recombinant (accession TA4446) between *Lr21* pseudogenes in common wheat cultivars Fielder and Wichita {10620}.

Lr23. **v:** IWP94 {10569}. **v2:** Brambling *Lr14a Lr34* {10563}

Lr24. **v:** Cutter {10595}; Jagalene {10595}; McCormick {10595}; Ogallala {10595}.

Lr26. **v:** AGS 2000 {10595}; Pioneer 26R61 {10595}.

Lr27. **tv:** Benimichi C2004 {10585}; Jupare C2001 {10585}.

Lr31. **tv:** Benimichi C2004 {10585}; Jupare C2001 {10585}.

Lr34. **v2:** Brambling *Lr14a Lr23* {10563}; Saar *Lr46* {10481}.

Lr34. **i:** Add: Arina + *Lr34* {10648}; Lalbahudar + Lr34 {10648}.

v: Ardito {10648}; Kavkaz {10648}; Pegaso {10648}; Penjamo 62 {10648}. To the following add reference: Bezostaya {, 10648}; Condor {, 10648}; Fukuko-Komugi {, 10648}.

v2: Anza = WW15 *Lr13* heterogeneous {10648}; Brambling *Lr14a Lr23* {10563}; Chris *Lr13*{10648}; Jupateco R *Lr17a,Lr27+Lr31* {10648}; Saar *Lr46* {10481}. To the following add reference: Chinese Spring *Lr12* {,10648}; Glenlea *Lr1* {,10648}; Mentana *Lr3b* {,10648}.

c: *Lr34* spanning 11,805 bp and producing a 1,401-aa protein belongs to the drug resistance subfamily of ABC reporters {10648}; contained within FJ436983 {10648}.

This gene is identical to *Yr18, Pm38* and *Ltn* and confers stem rust resistance in some genetic backgrounds.

Lr39. **v:** Fuller {10595}; Overley {10595}.

Lr42. **v:** Fannin {10595}.

Lr46. **v2:** Saar *Lr34* {10481}.

Lr48. Correct to 2BS {0329}. **i:** CSP44 / 5*Lal Bahadur {0329}.

ma: *Xgwm429b-2B* – 6.1 cM – *Lr48* – 7.3 cM – *Xbarc7-2B* {0329}.

Lr49. Add: ,4BL {0329}. **i:** VL404 / 5*Lal Bahadur *Lr34* {0329}.

ma: *Xbarc163-4B* – 8.1 cM – *Lr49* – 10.1 cM – *Xwmc349-4B*{0329}.

Lr59. Derived from *Ae. peregrina.* 1A, probably 1AS.alien centric fusion {10399}.

Lr60. **ma:** *Lr60* – 8.4 cM – *Xbarc149-1D*/*Lr21* {10400}; *Lr60* – 13 cM – *Lr21* {10400}.

Lr61. **ma:** Replace present entry with: *Lr61* – 2.2 cM – *P81*/*M70269*/*P87*/*M75131* – 4.6 cM – *P87*/*M76149* – 21.7 cM – *Xwmc487-6B* {10485}.

Lr62 {10537}. Derived from *Ae. neglecta*. 6A = T6AL-6^{Aen}L·6^{Aen}S {10537}.

v: Line 03M119-71A {10537}. **al:** *Ae. neglecta* 155 {10537}.

Lr63 {10550}. Derived from *T. monococcum* subsp. *monococcum*. 3AS {10550}.

i: RL 6137 = Thatcher*6/TMR5-J14-12-24 {10646,10550}.

v: TMR5-J14-12-24 {10646}. **dv:** *T. monococcum* subsp. *monococcum* {10646}.

ma: Very closely linked to *Xbarc321-3A* {10550}.

Lr64 {10550}. 6AL {10550}. **i:** RL 6149 = Thatcher*6/ *T. turgidum* subsp. *dicoccoides* 8404 {10550}.

tv: *T. turgidum* subsp. *dicoccoides* 8404 {10550}.

ma: *Xbarc104-6A* – 13.9 cM – *Lr64* – 21.9 cM {10550}.

Lr65. Tentatively approved subject to an allelism test and acceptance by a journal.

Lr66 {10591}. *LrS13* {10592}. 3A {10591}.

v: Line 07M101-127 = *Ae. speltoides* / 5*CS // 2*CS *ph1b* mutant /3/ 2* W84-17 /4/ CSN3AT3B {10591}.

al: *Ae. speltoides* Accession 691 {10591}.

ma: Most user-friendly marker, SCAR S15-t3 {10591}.

List after *LrW2*:

LrZH84 {10581}. 1BL {10581}. **v2:** Predgornaia 2 *Lr26* {10581}; Zhou 8425B *Lr26* {10581}.

ma: *Xbarc8-1B* (cent) – 5.2 cM – *LrZh84* – 3.9 cM – *Xgwm582-1B* {10581}.

96.2. Suppressor of genes for resistance to *P. triticina*

96.3. QTL for reaction to *P. triticina*

Add at end of section:

'Avocet S / Attila': At least two additive genes for slow rusting (10586}. In addition to *Lr46*, there were small effects on chromosomes 2BS, 2BL, and 7BL {10586}.

Tetraploid wheat

'Colosseo / Lloyd': A major QTL, *QLr.ubo-7B.2*, for seedling and adult-plant resistance from Colosseo, was located between *Xgwm344.2-7B* and DART 378059, bin 7BL10-0.78-1.00 {10600}.

97. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

97.1. Insensitivity to tan spot toxin (necrosis)

Add note following the *Tsn1* section:

Australian cultivars with *tsn1* and *Tsn1* are listed in {0903}.

97.3. Resistance to tanspot

***Tsr1*.** Add note:

The gene in Erik was allelic with resistance in a diverse set of genotypes including spelt and durum derivatives {10557}.

Add after *Tsr5*:

TsrHar {10590}. 3B {10590}. **v:** Dashen {10590}; HAR 604 {10590}; HAR 2562 {10590}.

Effective against races ASC1a (race 1) and DW-16{10590}.

QTL:

TA4152-60 (R) / ND495 (S) DH population. Five QTL for resistance, all from TA4152-60 (10580}, i.e., *QTs.fcu-2AS* and *QTs.fcu-5BL.1* conferring resistance to all races used; *QTs.fcu-5AL* conferring resistance to races 1, 2 and 5; *QTs.fcu-5B.2* conferring resistance to races 1 and 2; and *QTs.fcu-4AL* conferring resistance to race 3.

'WH542 (R) / HD29 (S)' RIL population: SIM indicated QTL on chromosomes 1B, 3AS, 3BL, 5B, and 6BS, but only two were confirmed by CIM, *Qts.ksu-3AS* flanked by *Xbarc45-3A* and *Xbarc86-3A* (LOD 5.4, $R^2 = 0.23$) and *Qts.ksu-5BL* (probably *Tsn1*) flanked by *Xgwm499-5B* and *Xest.stsbe968-5B* (LOD 6.5, $R^2 = 0.27$) {10552}.

100. Reaction to Soil-Borne Cereal Mosaic Virus

Vectored to the roots by the fungus, *Polymyxa graminis*.

Sbm1 {change reference to 10614}.

5DL {10614}. **v:** Tonic {10614}.

ma: *Xbarc110-5D* – 14.7 cM – *Sbm1* – 2.1 cM – *Xwmc765-5D* – 3.1 cM – *Xbarc144-5D/ Xwmc443-5D/RRES01-5D* {10614}. Caps marker RRESO1 was developed from an AFLP fragment {10614}.

Delete the paragraph beginning with *QSbv.ksu-5D* because the information duplicates the previous paragraph. Reference {10521} can be deleted because it duplicates {10273}.

Genetic linkages

Chromosome 2A

2AL

Yr1	–	*Sr48*	16.5 cM {10564}

Chromosome 2B

2BS

Lr48	–	*Lr13*	14.6 cM {0329}

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VI. ABBREVIATIONS USED IN THIS VOLUME.

PLANT DISEASES, PESTS, AND PATHOGENS:

BYDV = barley yellow dwarf virus
BMV = barley mosaic virus
CCN = cereal cyst nematode, *Heterodera avenae*
FHB = Fusarium head blight
RWA = Russian wheat aphid
SBMV = soilborne mosaic virus
SLB = Septoria leaf blotch
TMV = *Triticum* mosaic virus
WDF = wheat dwarf mosaic
WSBMV = wheat soilborne mosaic virus
WSMV = wheat streak mosaic virus
WSSMV = wheat spindle streak mosaci virus
WYMV = wheat yellow mosaic virus
E. graminis* f.sp. *tritici = *Erysiphe graminis* f.sp. *tritici* = the powdery mildew fungus
F. graminearum = *Fusarium graminearum* = head scab fungus
F. nivale = *Fusarium nivale* = snow mold fungus
H. avenae = *Heterodera avenae* = cereal cyst nematode
P. graminis = *Polymyxa graminis* = wheat soilborne mosaic virus vector
P. striiformis* f.sp. *tritici = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus
P. triticina = *Puccinia triticina* = *P. recondita* f.sp. *tritici* = leaf rust fungus
R. cerealis = *Rhizoctonia cerealis* = sharp eyespot
R. solani = *Rhizoctonia solani* = Rhizoctonia root rot
R. padi = *Rhonpalosiphum padi* = bird cherry-oat aphid
S. tritici = *Septorai tritici* = Septoria leaf spot fungus
S. graminearum = *Schizaphus graminearum* = greenbug
St. nodorum = *Stagonospora nodorum* = Stagonospora glume blotch
T. indica = *Tilletia indica* = Karnal bunt fungus

SCIENTIFIC NAMES AND SYNONYMS OF GRASS SPECIES (NOTE: CLASSIFICATION ACCORDING TO VAN SLAGEREN, 1994):

A. strigosa = *Avena strigosa*
Ae. cylindrica = *Aegilops cylindrica* = *Triticum cylindricum*
Ae. geniculata = *Aegilops geniculata* = *Aegilops ovata* = *Triticum ovatum*
Ae. 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. ventricosa = *Aegilops ventricosa* = *Triticum ventricosum*
S. cereale = *Secale cereale* = rye
T. aestivum* subsp. *aestivum = *Triticum aestivum* = hexaploid, bread, or common wheat
T. monococcum* subsp. *aegilopoides = *Triticum boeoticum*
T. turgidum subsp. dicoccum = *T. dicoccon* = *Triticum dicoccon* = *T. dicoccum*
T. turgidum* subsp. *durum = *Triticum durum* = durum, pasta, or macaroni wheat
T. aestivum* subsp. *macha = *Triticum macha*
T. militinae = *Triticum militinae*
T. aestivum* subsp. *spelta = *Triticum spelta*
T. timopheevii* subsp. *timopheevii = *Triticum timopheevii*
T. timopheevii* subsp. *armeniacum = *Triticum araraticum* = *T. araraticum*
T. turgidum* subsp. *dicoccoides = *Triticum dicoccoides* = wild emmer wheat
T. turgidum* subsp. *dicoccum = *Triticum dicoccum*
T. urartu = *Triticum urartu*

Th. bessarabicum = *Thinopyrum bassarabicum*
Th. elongatum = *Thinopyrum elongatum* = *Agropyron elongatum*
Th. intermedium = *Thinopyrum intermedium* = *Agropyron intermedium*

Scientific journals and publications:

Agron Abstr = Agronomy Abstracts
Ann Wheat Newslet = *Annual Wheat Newsletter*
Aus J Agric Res = *Australian Journal of Agricultural Research*
Cereal Res Commun = *Cereal Research Communications*
Curr Biol = *Current Biology*
Eur J Plant Path = *European Journal of Plant Pathology*
Funct Integ Genomics = *Functional Integrative Genomics*
Int J Plant Sci = *International Journal of Plant Science*
J Cereal Sci = *Journal of Cereal Science*
J Hered = *Journal of Heredity*
J Phytopath = *Journal of Phytopathology*
J Plant Phys = *Journal of Plant Physiology*
Mol Gen Genet = *Molecular and General Genetics*
Nat Genet = *Nature Genetics*
PAG = Plant and Animal Genome (abstracts from meetings)
Phytopath = *Phytopathology*
Plant Breed = *Plant Breeding*
Plant, Cell and Envir = *Plant, Cell and Environment*
Plant Cell Rep = *Plant Cell Reporter*
Plant Dis = *Plant Disease*
Plant Physiol = *Plant Physiology*
Sci Agric Sinica = *Scientia Agricultura Sinica*
Theor Appl Genet = *Theoretical and Applied Genetics*
Wheat Inf Serv = *Wheat Information Service*

Units of measurement:

bp = base pairs
bu = bushels
cM = centimorgan
ha = hectares
kDa = kiloDaltons
m^2 = square meters
m^3 = cubic meters
μ = micron
me = milli-equivalents
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
AUDPC = area under the disease progress curve
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
kD = kilodalton
LMW = low molecular weight (glutenins)
MAS = marker-assisted selection
NSF = National Science Foundation
NILs = near-isogenic lines
NIR = near infrared
NSW = New South Wales, region of Australia
PAGE = polyacrylamide gel electrophoresis
PCR = polymerase chain reaction
PFGE = pulsed-field gel electrophoresis
PMCs = pollen mother cells
PNW = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada)
PPO = polyphenol oxidase
QTL = quantative trait loci
RAPD = random amplified polymorphic DNA
RCB = randomized-complete block
RFLP = restriction fragment length polymorphism
RILs = recombinant inbred lines
RT-PCR = real-time polymerase-chain reaction
SAMPL = selective amplification of microsatellite polymorphic loci
SAUDPC = standardized area under the disease progress curve
SCAR = sequence-characterized amplified region
SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis
SE-HPLE = size-exclusion high-performance liquid chromatography
SH = synthetic hexaploid
SNP = single nucleotide polymorphism
SRPN = Southern Regional Performance Nursery
SRWW = soft red winter wheat
SRSW = soft red spring wheat
STMA = sequence tagges microsatellite site
SWWW = soft white winter wheat
SSD = single-seed descent
SSR = simple-sequence repeat
STS = sequence-tagged site
TKW = 1,000-kernel weight
UESRWWN = Uniform Experimental Soft Red Winter Wheat Nursery
VIGS = virus-induced gene silencing

VII. ADDRESSES OF CONTRIBUTORS.

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X. VOLUME 56 MANUSCRIPT GUIDELINES.

Manuscript guidelines for the *Annual Wheat Newsletter*, volume 55. The required format for Volume 55 of the *Annual Wheat Newsletter* will be similar to previous editions edited from Kansas State University.

CONTRIBUTIONS MAY INCLUDE:

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

FORMATTING & SUBMITTING MANUSCRIPTS:

Follow the format in volume 44–55 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Limited editing is done. Use Microsoft Word™ or send an RTF file that can be converted. Use Times 12 CPI and 1.0" (2.5 cm) margins. DO NOT use the table or column setting functions, create tables with tabs and spaces. Double space the text of your contribution if you must use a typewriter.

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In the interest of remaining solvent, the NWIC has approved future distribution primarily by computer diskette. We are asking that you renew your contribution or, if you have not contributed in the past, to join the list of contributors. Contributions from individuals in the range of $25 to $50 play a significant role in financing the *Newsletter*. An increase in the number of individual contributors is very important and, with continued support, we hope to meet our financial obligations in 2008. The address for contibutions is Dr. Brett Carver, Department of Agronomy, Oklahoma State University, Stillwater, OK 74078, U.S.A.