ANNUAL WHEAT NEWSLETTER

Volume 53

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IN DEDICATION TO DR. BENT SKOVMAND DIRECTOR, NORDIC GENE BANK, SWEDEN

Director Dr. Bent Skovmand passed away peacefully during the night between Monday and Tuesday, 5 February, 2007, after a short period of illness. A few glimpses of characteristic situations from Bent's rich life are provided by Ebbe Schiøler, consultant, formerly with Danida, the Danish Ministry of Foreign Affairs, and originally were published in the Danish daily *Politiken*. Dr. Schiøler worked with Bent for a number of years in the capacity as administrator of funds to international research at Danida (the Danish 'USAID'), including his time at the Nordic Gene Bank. His relationship with Bent went back to long before his years at the Gene Bank. Bent was a highly respected and well-liked person internationally. His great engagement in his work within plant genetic resources and his participation in many aspects of Nordic and international work. With his great scientific knowledge and unique personality, he especially has left his mark in the scientific world within his two favorite areas, wheat breeding and plant genetic resources. Bent is a person who will be remembered for who he was and what he stood for.

He took good care of plants.

Bending down in the middle of an experimental wheat plot at the international research center CIMMYT in Mexico. The plant breeder is absorbed in a conversation with a younger colleague on the robustness of a new line against drought and disease. How would it cope with growing conditions in the developing world, the center of his attention for such a long part of his working life.

Listening constructively in the middle of a staff group meeting in Alnarp, Sweden, during discussions and decision making on how to organize an expedition to collect grasses in the last few corners of Nordic wilderness to make sure that no material from our vital heritage of wild plants disappears in the continued development of our societies and while climate changes in our part of the world, as well.

With a modest smile and immense happiness, surrounded by his Danish-Mexican family, which has no fear of using genuine, honest, and direct words while celebrating the silver wedding of Eugenia and Bent. Young and old declare the family's love for them both in a manner that is somewhat strong, especially for guests from other parts of the world used to putting up a shield of modesty in personal relations.

Bent with a symbol of the new Svalbard Global Seed Vault (SGSV), which based on the experiences of the safety deposit since 1984, is being constructed now. The SGSV will be ready to receive seeds from all of the world in February 2008, making it the safety deposit of seeds for the world.

Here you have the wide span governing Bent's life. The professional person with his strong commitment to big and central scientific issues; the empathic and rewarding colleague and boss; and the man with the energy and warmth for friends and – for him, the heart of the matter – a close and warm family life.

He gave a lot, and he received a lot in return. Traveling from Denmark to U.S. on an exchange program, he spent some hard years financing his undergraduate studies in Minnesota on income from whatever job he could come across. But hard working, he advanced in biology and specialized in plant diseases, obtaining his Ph.D. in 1976. Throughout his university years, jobs became more sophisticated, and his last years were financed through a Rockefeller scholarship.

His first assignment was as a plant breeder at CIMMYT in Mexico working on the then novel triticale cereal. He became head of the program but later specialized in wheat and was in charge of the breeding program for wheat in Turkey, a UNDP project. Back at CIMMYT, he became head of wheat breeding and the gigantic gene bank with its

thousands of accessions. In this capacity, he developed into a leading figure fostering expansive international coöperation in wheat breeding.

For him it was a logical next step – and a great dream of his – to continue his work with plant genes in a Nordic context, closer to Denmark and to give his family a closer relationship with this part of the world. When the opportunity arose in 2003, he was more than happy to grasp it. For the last four years of his working life, he was the director of the Nordic Gene Bank, situated in the southern part of Sweden, for agricultural and horticultural plants and, more importantly for him and his staff, their wild relatives. Close to his heart were endeavors to secure the international dimension of the Gene Bank's work; development work for Southern Africa, the Baltic countries, and central Asia. He took a genuine pride in each step forward, most recently leading a very exciting effort to secure Nordic aromatic and herbal plants, collected by the Gene Bank in their natural habitat and at old and nearly forgotten spots in the cultural landscape in far away villages.

Inside the mine not far from Longyer-Byen, Bent is about to place some seeds to be stored in the safety deposit store of the Nordic Gene Bank. This safety deposit has been running since 1984, and the temperature never exceeds –4°C. The seeds can, therefore, be kept in permafrost and in excellent condition for many, many years.

He was repaid handsomely for his high professional standard by the international scientific community. For a number of years, prestigious awards in the U.S. for his publications; a long list of honors from his *alma mater* the University of Minnesota; and the most recent award this year, membership in the most impressive scientific academies and a number of medals. In 2005, he received the international Crop Science Award. That same year, the Agricultural University of Copenhagen, Denmark, awarded him an honorary post as professor. This recognition was, for him, a moment of joy, to be recognized, although in some sense 'a foreigner', by peers back in Denmark. You will come across few people who enjoyed his Danish Knighthood more than Bent. He was knighted by the queen in 2003 and this, for him, was a wonderful signal that his work had been noted although his career was abroad.

But, again, his innermost and greatest happiness and pride were centered around his family; towards his older daughters from an earlier marriage and towards the two now nearly adult children from his long marriage – and very strong partnership – with Eugenia.

It was heart breaking to follow how Bent was worn-out during the last few months of his disease. But it was so good to see that his Nordic colleagues, his warm family, and many international friends stood by and supported him in each their way. Bent will stay with us for long, professionally – and as a very special personality.

The Skovmand family has established the "Bent Skovmand Fellowship" for support of a graduate student at the University of Minnesota.

I. SPECIAL REPORTS

MINUTES OF THE NATIONAL WHEAT IMPROVEMENT COMMITTEE (NWIC) MEETING.
13 December, 2006.
Raleigh, NC, USA.

Attendence.

NWIC Members and Proxies: Jim Anderson, Joe Anderson, Harold Bockelman, Bob Bowden (proxy Secretary for Bob Graybosch), Kim Campbell, Brett Carver, Xianming Chen, Jose Costa, Benjamin Edge, Elias Elias, David Garvin, Jim Peterson (Chair), Jackie Rudd, and Luther Talbert.

Guests: Daren Coppock, Paul Murphy, Kay Simmons, Dave van Sanford, Olin Anderson, P. Stephen Baenziger, Larry Brown, Marty Carson, Mike Davis, Jane DeMarchi, Ruth Dill-Macky, Floyd Dowell, Ved Malik, Dave Marshall, Dave Matthews, Tom Payne, Scott Redlin, Jay Romsa, and Anne Marie Thro.

Approval of minutes.

Minutes from the January 2006 meeting in San Diego, as published in the *Annual Wheat Newsletter*, were approved without revision.

NWIC report, legislative update.

Jim Peterson. Appreciation was expressed to members of several groups that visited or will soon visit many federal agency and Congressional offices to support NWIC legislative priorities. These groups included a broad sample of stakeholders from the small grains industry. Much of the effort was directed toward restoration of small grains programs that were not included in the proposed FY07 federal budget. Another major effort centered on the Cereal Rust Initiative. Research priorities for the NWIC for 2006, 2007, and 2008 are listed at: http://cropandsoil.oregonstate.edu/wheat/reports/NWIC/.

NBIC and NOIC reports.

Mike Davis (Chair, National Barley Improvement Committee). This year was frustrating due to confusion about the status of Congressional earmarks and CSREES Special Grants. Progress on several joint legislative priorities was discussed.

Paul Murphy (Chair, National Oat Improvement Committee). NOIC supports re-instatements of earmark terminations. Funding at Aberdeen, Idaho is a priority . Others priorities are the Rust Initiative, molecular markers, and oat virus research. Need to keep closer contact with ASA Science Policy Director to assure we are not at cross purposes.

USDA–ARS update.

Kay Simmons. Discussed several ARS initiatives including the Rust Initiative and a bioenergy initiative. ARS is working to respond to demands for greater accountability from Congress and stakeholders. The U.S. Wheat and Barley Scab Initiative is undertaking a thorough review and re-organization to bring greater focus, efficiency, and accountability.

USDA–CSREES update.

Ann Marie Thro. CSREES National Research Initiative funding opportunities were discussed. Funding rates are decreasing due to limited resources and programs are becoming more focused. A portion of NRI funding is being directed to integrative projects with research, education, and extension components. A National Plant Breeding Workshop is planned for Raleigh, NC, for 8-9 February, 2007.

NAWG update.

Daren Coppock and Galen Afelt. The National Association of Wheat Growers (NAWG), North American Millers Association (NAMA), U.S. Wheat Associates (USW), and Wheat Export Trade Education Committee (WETEC) are working together on a position paper to address the economic competitiveness of wheat in the U.S. NAWG and U.S. Wheat Associates are working together on biotechnology issues. Both organizations are supportive of biotechnology in order to maintain the long-term competitiveness of wheat versus other crops. Reports entitled 'Addressing the Competitiveness Crisis in Wheat' and 'Wheat Summit Report' are both posted at http://cropandsoil.oregonstate.edu/wheat/reports/NWIC/.

NAMA update.

Jane DeMarchi. The North American Millers Association supports a coördinated national research agenda. It is important for NWIC to keep NAMA and the American Baking Association informed of issues.

CIMMYT update.

Tom Payne. Several staff changes and transfers at CIMMYT were discussed. Hans Braun relocated to El Batan as Director of the Global Wheat Program. Yann Manes is a new wheat breeder based in Mexico. Etienne Duveiller is the Head of Wheat Pathology, based in Mexico. Rick Ward is based in Mexico and is directing the Global Rust Initiative. There is continuing concern about cuts in funding to CGIAR centers.

USDA–APHIS update on regulations impacting germ plasm introduction and exchange.

Scott Redlin. Issues surrounding deregulation of flag smut were discussed. Efforts toward Karnal bunt deregulation also were discussed, including recognition of KB-free areas in Mexico. The NWIC conveyed desire to streamline inspection requirements for seed shipments to avoid costly delays.

Wheat CAP.

Jim Anderson. The Wheat Coordinated Agricultural Project (CAP) has been active for less than one year. It looks like milestones will be met for the first year. Jamie Sherman is coördinating the educational portion of CAP. Shiaoman Chao is managing the wheat marker database used to document progress.

CREATE-21.

Mike Mullen (by phone). CREATE-21 is designed to increase the funding for agricultural research for both competitive and intramural capacity programs. Another goal is to streamline programs and avoid duplication. Management would be closer to the NIH or NSF model. Proposed legislative language is being drafted. Concern was expressed regarding the proposed merger and reorganization of ARS and CSREES and the increased focus on competitive grants over core funding for ag research.

NWIC subcommittee on genomics.

Stephen Baenziger and Jim Anderson. The goal of the subcommittee is to facilitate communication, assess needs, develop strategies, and organize research efforts on wheat genomics. A set of by-laws for the subcommittee was proposed and discussed. An annual report to the NWIC was requested of the committee by Jim Peterson. Jose Costa moved that the subcommittee be approved with the provision that the by-laws be revised as Jim Peterson requested. Joe Anderson seconded. The motion was approved unanimously.

The 2007 National Wheat Genomics Conference sponsored by the subcommittee will take place 30 November–2 December, 2007 preceding the USWBSI National Head Blight Forum. See the following website for details: http://wheat.pw.usda.gov/NWIC/NWG07meet.html.

Graingenes update.

Dave Matthews. Graingenes 2.0 is up and running and has many new features, maps, markers, and QTL in the database. The Graingenes Liaison Committee is helping to define the future development priorities for Graingenes.

Rust – status and updates.

Stem rust. Marty Carson and Yue Jin (by phone), Kay Simmons. The CIMMYT/Kenya agreement with the USDA–ARS for stem rust nurseries has been renewed. There were some problems with vernalization in the Kenyan nursery this past year. A list of effective genes for the Ug99 strain was presented. Virulence to *Sr24* appears to have appeared in Ug99. This is troubling because *Sr24* was one of the few undefeated genes available in North America. *Sr36* may be the best short-term source of resistance for many U.S. programs, especially soft red winter wheats. Much more effort is needed on stem rust resistance screening, gene discovery, introgression. An international stem rust nursery set has been established and distributed. Concern was expressed about reëstablishment of barberries in the U.S. Malik indicated that fungicides would be fast-tracked if needed in an emergency situation. Phenotyping, prebreeding, and germ plasm exchange are top priorities.

Stripe rust. Xianming Chen. Stripe rust levels across the USA were lower than average in 2006. This made screening for field resistance difficult and highlighted the need for more phenotyping capacity. FY06 Stripe Rust Initiative funds were allocated according to recommendations of NWIC, the Stripe Rust working group, and ARS national program staff.

Leaf rust. Robert Bowden. Leaf rust remains the most important rust disease across the U.S. Race shifts continue to erode the resistance of commercial cultivars. Durable resistance from CIMMYT germ plasm is being introgressed in many programs.

Prioritization of needs.

Participants were asked by Jim Peterson to prioritize various needs for cereal rust research . Results are posted at this website: http://cropandsoil.oregonstate.edu/wheat/reports/NWIC/.

Wheat quality initiative.

Jim Peterson and Floyd Dowell. A strategic rewrite of the NWIC Wheat Quality Initiative was presented and discussed. The need to more effectively position and promote the Wheat Quality Initiative was discussed in light of federal budget constraints. Input and political support of the milling and baking industries will be critical if we are to increase federal funding of regional quality labs. The revised Initiative highlights the need for additional research on measures of functional quality and need to coordinate research with needs of USDA–FGIS.

Annual Wheat Newsletter.

Brett Carver. The AWN volume 52 was published in August 2006. There were 1 corporate, 19 country, and 9 U.S. State contributions. Fifty hard copies and 68 CDs were produced and distributed. Both HTML and PDF files are available for viewing on Graingenes. Monetary contributions were down this year.

Regional reports.

Pacific Northwest region. Kim Garland Campbell. Kelly Richardson joined the Wheat Genetics, Quality Physiology and Disease Research Unit in Pullman as a CAT4 Scientist for stripe rust. Deven See joined the same unit as a CAT4 Scientist in the molecular genotyping lab. The vice-Souza position at the University of Idaho will be refilled. Scot Hulbert joined Washington State University at Pullman in cropping systems research. Eric Jackson was hired for barley and oat molecular genetics at USDA-ARS in Aberdeen, ID.

Hard winter wheat region. Jackie Rudd and Floyd Dowell. Don Koeltzow recently retired as Center Director, GMPRC, Manhattan. His successor is Tom Shanower. Texas A&M will hire a new wheat breeder at College Station. Monica Menz, Texas A&M, departed for Syngenta.

Spring wheat region. Jim Anderson and Shiaoman Chao. Vice-Stack position being refilled at NDSU is in interviewing stage. The CAT3 Scientist position in the genotyping lab is vacant. An Illumina SNP detection system was purchased primarily for barley work.

Eastern soft wheat region. Joe Anderson. Michigan State University will refill the vice-Ward position.

Research priorities.

The NWIC voted to endorse, in order of preference, the following research priority areas. Increased emphasis and funding for these areas is encouraged.

a. Maintain existing USDA funding
b. Cereal Rust Disease Initiative
c. Regional Small Grains Molecular Genotyping Labs
d. Wheat Quality, Competitiveness, and Security Initiative
e. Small Grains Germplasm Enhancement, Aberdeen, ID

The NWIC also voted to encourage the State Department and U.S. Agency for International Development to increase support for CGIAR, including CIMMYT and ICARDA.

Upcoming events.

a. National Plant Breeding Workshop, Raleigh, NC, 8–9 February, 2007.
b. North American Wheat Workers Workshop, Saskatoon, 12–14 March, 2007.
c. The 2007 National Wheat Genomics Conference will take place 30 November–2 December, 2007 preceeding the USWBSI National Head Blight Forum.
d. The next NWIC annual meeting will be held 5 December, 2007, in Kansas City, KS, after the USWBSI National Head Blight Forum.

Prepared by R.L. Bowden, proxy for Bob Graybosch, Secretary, National Wheat Improvement Committee.

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December 2006.

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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 F1 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.

II. ANNOUNCEMENTS

INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM (IWGSC) www.wheatgenome.org

The mission of the International Wheat Genome Sequencing Consortium is to advance agricultural research for wheat production and utilization by developing DNA-based tools and resources that result from the complete sequence of the common (hexaploid) wheat genome and to ensure that these tools and the sequence are available for all to use without restriction and without cost. Information in this report can be found at the IWGSC website: www.wheatgenome.org.

Purpose of the IWGSC.

The International Wheat Genome Sequencing Consortium (IWGSC) is a collaboration focused on building the foundation for advancing agricultural research for wheat production and utilization by developing DNA-based tools and resources that result from the complete genome sequence of common (hexaploid) wheat. The IWGSC was established to facilitate and coördinate international efforts toward obtaining the complete sequence of the common wheat genome. To this end, the IWGSC will continue to refine the strategic roadmap, integrate existing international resources, and develop a sequencing strategy that will capture international participation and a broad funding base.

Membership in the IWGSC is open to any individual, laboratory, or entity with an active interest in meeting the objectives of the IWGSC; that can contribute substantially to this effort in resource development, sequence activity, annotation, scientific expertise, or funding; and that agrees to comply with the guidelines and spirit of this agreement.

Update on principal activities related to the IWGSC.

Overall project goals.

The goals of the IWGSC project are to advocate internationally for sequencing the wheat genome; to facilitate international cooperation; to coördinate the scientific efforts to position wheat as the next major species for sequencing; and to secure funding from various international and domestic sources for the sequencing of the wheat genome. Eversole Associates provides leadership, strategic planning, coördination, management, and advocacy activities for the IWGSC.

Project progress.

Progress has continued towards meeting the objectives of the IWGSC strategic roadmap to lay the foundation for sequencing the hexaploid wheat genome with a major focus on constructing the physical maps. Over the past few months, the following events were held:

- April 2007 – An IWGSC business meeting was held in conjunction with the International Triticeae Mapping Initiative (ITMI) in Israel.
- April 2007 – Several co-chairs and the Executive Director attended the inauguration of the extension of the chromosome sorting facilities at the Institute of Experimental Botany in the Czech Republic led by Jarsolav Dolezel.
- April 2007 – The Executive Director met with officials from the Czech Republic to solicit funding support for wheat genomics and for the IWGSC.
- May 2007 – The Executive Director attended a meeting in Montpellier with the board of directors of the AACC International (cereal chemists organization comprised mostly of industry).

- May 2007 – The Executive Director attended a meeting in Montpellier with the board of directors of the AACC International (cereal chemists organization comprised mostly of industry).
- May 2007 – IWGSC co-chair, C. Feuillet, and the Executive Director attended the Biology of Genomes meeting at Cold Spring Harbor and met with the leaders of the major international sequencing centers.
- May 2007 – Brief meetings with the President/CEO of GenomeCanada and with the Chief Scientific Officer of Genome Alberta.
- June 2007 – The 'Genomics in Business' meeting in Europe for potential partners and for meetings with developers of the new sequencing technologies.

In the previous report, we covered the proposals that were coördinated and funded through February 2007. Over the past 18 months, we have secured $7.18 million USD for IWGSC sponsored and coördinated projects. The following is an update of the March report of the proposals that have been coördinated by the IWGSC:

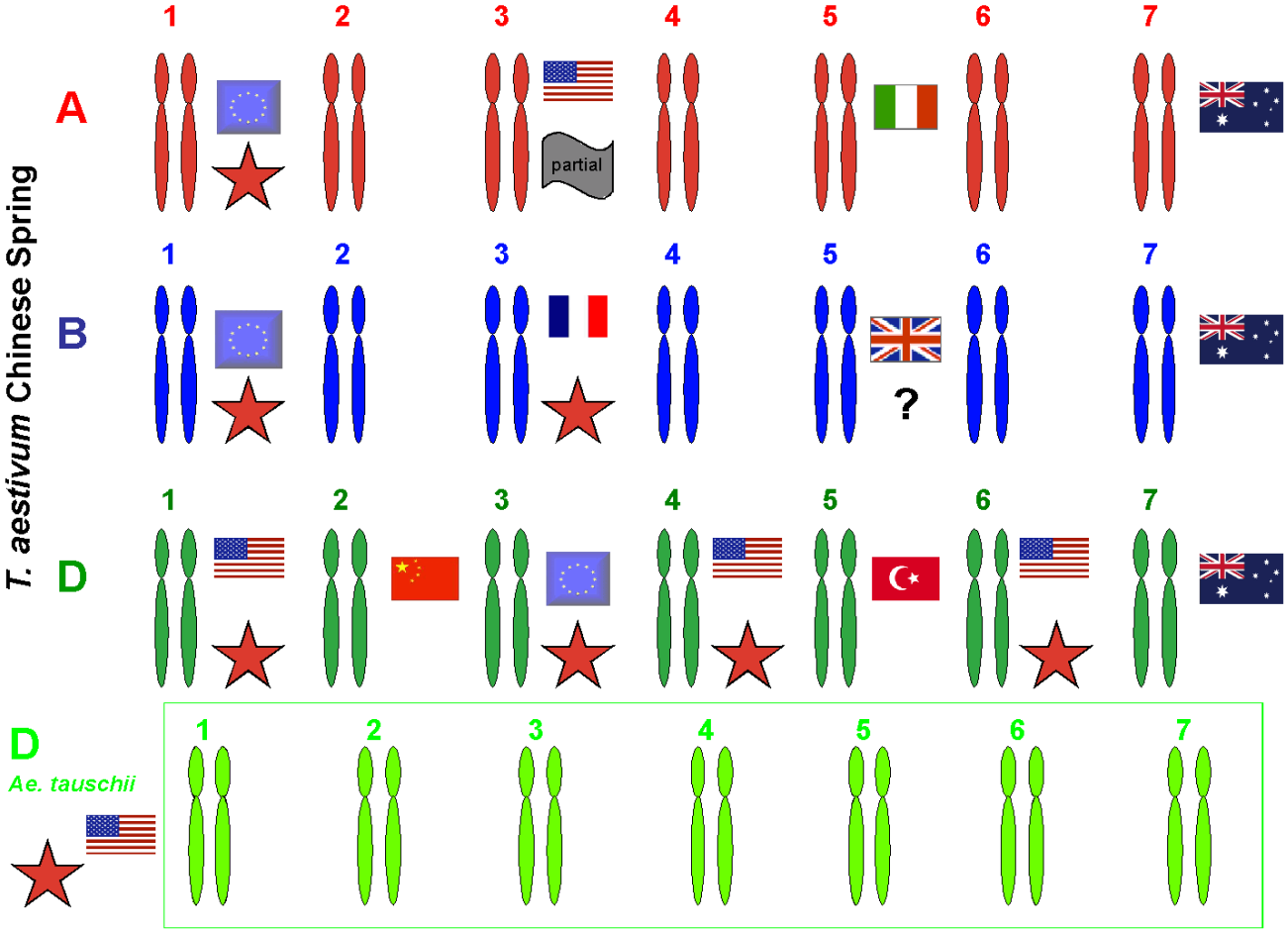
- Ministry of Agriculture, Turkey. Project to sequence 50 BACs on the short arm of chromosome 3B was funded at 1.5 million ($1.9 million USD).
- IWGSC pilot project to make a physical map of chromosome 3AS of Chinese Spring wheat was funded by the USDA–CSREES for $1 million USD from 2006–08.
- IWGSC proposal submitted to the US–NSF for $5.6 million to complete the map of the D-genome, diploid wild wheat *Ae. tauschii*; develop a physical map of chromosomes 1D, 4D, and 6D of hexaploid wheat; and test the feasibility of assembling A, B, and D genomes in a single experiment. The prospects for this project remain good although final approval is pending. We expect a final decision by October 2007.
- A proposal from the ETGI (17 EU partners) was finalized and submitted in May to the first call of the European FP7 and requests 5.7 million ($7.6 million USD). This project has been funded and seeks to develop physical maps of chromosomes 1A, 1B, and 3D of wheat and 1H and 3H of barley that will complement ongoing projects on 3A and 3B and the proposed project in the U.S. on chromosome 1D to achieve complete physical maps of the group-1 and -3 chromosomes.
- Australian Initiative for developing physical maps of the group-7 chromosomes. Funding expected to equal as much as $3 million USD with a decision in 2007. A successful workshop with industry, State governments, federal governmental departments, and federal funding agencies was held in May 2007 to ensure strong support for an Australian initiative. We continue to expect the development of the initiative to be finalized by the end of 2007.
- A proposal submitted to the Turkish government to develop a physical map of chromosome 5D was approved and the proposal was forwarded to the European Young Investigators program. Unfortunately, it was not funded at the European level. Efforts will now focus on seeking funding for the project directly from funding agencies of the Turkish government.
- Proposal in progress for submission to the Italian government for funding to develop the physical map of chromosome 5A, continuing.
- Efforts are underway to develop a Chinese proposal and secure funding for a project to make a physical map of chromosome 2D.

The following is a list of the IWGSC meetings and workshops that will be held or attended during the remainder of 2007:

- October 2007 – IWGSC business meeting held in conjunction with the PlantGEM meeting in Spain.
- Late autumn 2007 – IWGSC coördinating committee meeting (location to be determined) with focus on sponsors and industry.

The international collaboration of countries working on sequencing the wheat genome.

IWGSC scientists from Australia, France, Italy, the People's Republic of China, Turkey, the United States, the United Kingdom, and the European Union are resposible for constructing physical maps of individual chromosomes or chromosome arms of the wheat genome.



III. CONTRIBUTIONS

ITEMS FROM ARGENTINA

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

Effects of plant breeding on spike characteristics of bread wheat.

S.P. Gil, C.S. Perrone, M.M. Cerana, and R.H. Maich.

We are analyzing eight cycles of recurrent selection in bread wheat, C_0 (initial) C_1, C_2, C_3, C_4, C_5, C_6, and C_7 (intermediate); and C_8 (advanced) cycles. Plants were grown in the semiarid conditions of the central region of Argentina, at the Experimental Farm of the College of Agriculture in Córdoba (31°29'S and 64°00'W) during 2005. Five main shoot spikes divided in thirds (lower third: spikelets 4 and 5; middle third: spikelets 9 and 10; and upper third: subterminal) from each of the S-derived families/population were studied. Data were evaluated with ANOVA and Duncan's Multiple Range Test ($p < 0.05$).

The results did not show significant differences between cycles, although the more advance C_8 cycle presented a lot of floral primordia and fertile florets in the lower third.

Genetic progress for grain number/spike after eight cycles of recurrent selection.

M. N. Casanova, V. Davidenco, and R. H. Maich.

Changes in agronomic characteristics were measured after eight cycles of a recurrent selection program. Forty-five S_1-derived families (five/cycle) were grown during 2006 under the rainfed conditions of the central semiarid region of Argentina. A significant positive linear regression between the grain number/spike and cycles of recurrent selection was observed. Several workers have found positive associations between grain number/spike and grain number/m^2, the principal grain yield component. After eight cycles of a recurrent selection program in bread wheat conducted in the central semiarid region of Argentina, genetic progress for grain yield begins to be observed.

ITEMS FROM AUSTRALIA

UNIVERSITY OF ADELAIDE
Grain Biochemistry Group, Waite Campus, School of Agriculture, Food and Wine, Glen Osmond SA 5064, Australia.

Daryl Mares, Kolumbina Mrva, Robert Asenstorfer, Imelda Soriano, Judith Rathjen, and Michael Quinn.

Research interests.

1. Biochemistry and genetic control of factors that cause deterioration of wheat quality prior to harvest (preharvest sprouting and tolerance to preharvest sprouting, grain dormancy, late-maturity α-amylase, and black point).
2. Biochemical and genetic control of color and color stability in Asian noodles (grain and flour constituents involved in color of wheat flour and color and color stability Asian noodles, xanthophylls, flavonoids, polyphenol oxidase, peroxidase, lipoxygenase, and nutritive aspects of cereal xanthophylls, lutein and lutein esters).
3. Durum germ plasm with tolerance to hostile soils and root diseases and better adaptation to southern Australia.

Recent research.

We have focused on synthetic hexaploid wheats derived by crossing *T. turgidum* subsp. *durum* with *Ae. tauschii*. Over the past 4–5 years, around 400 synthetics have come into Australia primarily from the CIMMYT program in Mexico. This material is seen as a rich source of new genetic variation particularly for resistance to biotic and abiotic stresses. The lines have been screened for a range of biochemical traits related to color and color stability of Asian noodles (polyphenol oxidase, lipoxygenase, peroxidase, and flavonoid content) and for late-maturity α-amylase since early tests suggested that synthetics contained a high incidence of this defect.

Polyphenol oxidase (PPO). More than 30% of the primary synthetics surveyed were ranked as very low or near zero, significantly lower than the observed range for Australian bread wheat cultivars some of which are already regarded as low. Grain of these genotypes showed little or no discoloration of the seed coat even when incubated in the PPO substrate for 24 hours. By comparison, 60% of local and CIMMYT durums also were very low. A random selection of 50 *Ae. tauschii* from the Australian Winter Cereals Collection (AWCC) ranged between near zero and low with approximately 50% being equivalent to the near zero synthetics and durums. As with the very low PPO synthetic lines, the grains of very low PPO *Ae. tauschii* did not discolor even after prolonged incubation in substrate. Interestingly, parallel research and routine surveys of germ plasm from wheat-breeding programs identified two breeding lines from the wheat-breeding program at Australian Grain Technology in South Australia and an EMS-mutant that had PPO phenotypes substantially lower than the current benchmark cultivars. This material ranked midway between the lowest commercial cultivars such as Sunco, Lang, and Krichauff and zero.

Lipoxygenase (LOX). Compared with PPO, there were few primary synthetics with very low LOX. Several lines, however, were significantly lower than conventional bread wheats, in particular lines where the durum parent in the pedigree was 'Gaza/Boy'. LOX activity varied from 0.07U/g to 1.6U/g, with a mean for the collection of 0.8U/g. Very low LOX activity was more common among Australian and CIMMYT durums with 15% being less than 0.1. Interestingly, a random sample of cultivated durums from the AWCC that included many European and African cultivars gave a bimodal distribution with approximately one half similar to the Australian and CIMMYT durums and the other half in the range 0.6 to 1.1U/g. Bread wheats ranged from 0.2 to 1.5 U/g, similar to the primary synthetics with a mean of 0.8U/g. In addition to the germ plasm collections, a population derived by crossing a very low LOX durum, Kamilaroi, and the low LOX bread wheat, Sunco, was screened. A small number of lines with a bread wheat phenotype combined with the very low LOX typical of Kamilaroi were identified.

Flavonoid content. For this trait, the aim is to identify germ plasm with high flavonoid content, because these compounds turn yellow in the presence of alkali and make a significant contribution to the yellow color of alkaline noodles (Asenstorfer et al. 2006). Frequency distributions were compared with a collection of durums and wild tetraploids. The means for the primary synthetics, durums, and *Ae. tauschii* lines were all significantly less than the mean for current bread wheats. Despite this, there were a small number of tetraploid and *Ae. tauschii* lines whose grain flavonoid contents were greater than the highest bread wheat and there may be some value creating new synthetics using this material as parents.

Late maturity α-amylase (LMA). More than 90% of the primary synthetics developed LMA during grain ripening and of these about half had extreme levels of α-amylase normally only seen in wheats lacking semi-dwarfing genes *Rht1* or *Rht2*. Most of the primary synthetics were tall to very tall in height, despite the presence of *Rht1* from the durum parent, and when a subset was compared with and without the cool temperature shock treatment normally required for good expression of LMA there was no significant difference in grain α-amylase activity at ripeness. Secondary or derived synthetics showed a similar frequency distribution to primary synthetics but in this group proportion of individuals with a low to zero LMA ranking (around 65%) was a much higher. Approximately 30% were ranked as high-LMA similar to tall LMA-prone wheat cultivars. Some Australian durum cultivars were also found to be prone to LMA.

Selection of very low PPO recombinants from a locally adapted bread wheat / primary synthetic cross that lacks LMA. Ripe grain from 1600 BC_1F_2 plants were screened for PPO activity and 12 lines identified with PPO phenotype equal to the synthetic parent. The segregation ration approximated to 1 in 128. Three of these lines were further selected for plant type, plant height (semidwarf), and free-threshing habit. All of these lines appeared to be free of LMA following the standard cool temperature shock treatment.

Preharvest sprouting tolerance in white-grained wheats. A severe drought over most of the Australian wheat belt in 2006 ensured that neither preharvest sprouting nor black point were significant problems. We noted in sprouting screening trials, however, that material harvested at harvest-ripeness was more dormant (tolerant to sprouting) than expected. Ranking of cultivars was not affected and the dormancy in genotypes normally considered to be sprouting susceptible disappeared rapidly during after-ripening.

A highly significant QTL on chromosome 4A was associated with dormancy in three wheat genotypes, AUS1408, SW95-50213, and a dormant single gene red genotype, AUS1490, of diverse origin. Flanking SSR markers, gwm269 and barc170, located near the center of the QTL have been validated to two additional populations and should provide near-diagnostic tools for MAS. As previously reported, the phenotype of lines containing the 4A alleles from the dormant parent varied from dormant to intermediate dormant with both the range and absolute values dependent on temperature during grain ripening. As temperature during ripening increased, dormancy decreased, and the range for lines containing the 4A dormancy alleles increased. A DH population, dormant / intermediate dormant, that is fixed for the 4A dormancy allele but varies with respect to putative additional dormancy genes has now been phenotyped in four environments. A new QTL located on chromosome 3B appeared to explain a significant proportion of the variation.

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ITEMS FROM BRAZIL

NATIONAL WHEAT RESEARCH CENTRE — EMBRAPA TRIGO
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BRS Guamirim, a bread wheat cultivar with an early cycle and short stature.

P.L. Scheeren, E. Caierão, M. Sóe Silva, L.J.A. Del Duca, A. Nascimento Junior, A. Linhares, L. Eichelberger, M.Z. Miranda, E.M. Guarienti, L.M. Costamilan, M.I.P.M. Lima, M.S. Chaves, S.P. Brammer, A.L.V. Bonato, E.J. Iorczeski, J.R. Salvadori, and A.C.S. Albuquerque.

The wheat cultivar **BRS Guamirim** was developed by Embrapa and released in 2006 for southern Brazil. BRS Guamirim resulted from a cross between 'Embrapa 27/Buck Nandu' and PF 93159. BRS Guamirim has an early cycle, short stature, and high tillering. This cultivar has similar behavior to many wheat diseases and a resistant reaction to *P. triticina* races B_{27}, B_{29}, B_{32}, B_{33}, B_{35}, B_{38}, B_{39}, B_{40}, B_{41}, B_{43}, B_{44}, B_{45}, B_{48}, B_{49}, B_{51}, and B_{52}. BRS Guamirim belongs to the bread class and is adapted to different wheat regions, showing production stability. The grain yield potential is higher than 5 t/ha.

New wheat cultivar BRS Camboatá.

E. Caierão, P.L. Scheeren, M. Sóe Silva, L.J.A. Del Duca, A. Nascimento Junior, A. Linhares, L. Eichelberger, M.Z. Miranda, E.M. Guarienti, L.M. Costamilan, M.I.P.M. Lima, M.S. Chaves, S.P. Brammer, A.L.V. Bonato, E.J. Iorczeski, J.R. Salvadori, and A.C.S. Albuquerque.

According grain yield, **BRS Camboatá** performed best in colder and higher regions, independent of the state in which it was grown. The vegetative cycle of BRS Camboatá lasts 83 days; a total of 137 days to maturity. The plant type is medium short, with a mean of 85 cm, and has good lodging resistance, which is a fundamental trait for raising yield potential. BRS Camboatá was classified as moderately resistant to shattering and moderately susceptible to preharvest sprouting. Frosts during the vegetative phase did little harm to the cultivar. The reaction of BRS Camboatá to the main wheat diseases includes resistance to powdery mildew and WSMV, moderate resistance to leaf rust, and moderate susceptibility to Fusarium head blight and to other blotch diseases (*D. tritici repentis, St. nodorum*, and *B. sorokiniana*). BRS Camboatá had burnt leaf tips, a trait which is directly associated to adult plant resistance to leaf rust. However, new evaluations are needed to confirm this fact. BRS Camboatá has erect leaves, predominantly colorless auricles, fusiform spikes, and long, red grains. Preliminarily, the cultivar is classified as a soft wheat cultivar in Rio Grande do Sul, with a mean gluten strength of 192 x 10^{-4} J and, in Paraná, as a bread wheat cultivar, with mean of W value of 222 x 10^{-4} J. According to the glutenin content, BRS Camboatá has the subunits n, 2+12, and 7+8. The grain is hard. Experimental data obtained from Brabender Mill showed a flow extraction of 41 to 54%. The mean of falling number was 367 seconds, with a variation from 218 to 514.

New wheat cultivar BRS Timbaúva.

E. Caierão, P.L. Scheeren, M. Só e Silva, L.J.A. Del Duca, A. Nascimento Junior, A. Linhares, L. Eichelberger, M.Z. Miranda, E.M. Guarienti, L.M. Costamilan, M.I.P.M. Lima, M.S. Chaves, S.P. Brammer, A.L.V. Bonato, E.J. Iorczeski, J.R. Salvadori, and A.C.S. Albuquerque.

BRS Timbaúva belongs to the bioclimatic group of spring wheat. With a mean plant height of approximately 97 cm, BRS Timbaúva is classified as a tall cultivar by the current standards; nevertheless, it is moderately resistant to lodging. The use of growth reducers is an interesting practice in the management of this genotype, mainly nitrogen in higher quantities in a topdressing, if there is an interest in a greater investment. The mean vegetative cycle (from emergence until ripening) is approximately 87 days; days-to-maturation vary from 141–146, according to the region of cultivation and climatic conditions. The cultivar is moderately resistant to shattering, moderately susceptible to preharvest sprouting and frost during the vegetative phase of crop development. BRS Timbaúva is tolerant to acid soil toxicity. BRS Timbaúva is moderately resistant to *Stagonospora nodorum* glume blotch, Fusarium head blight, and WSMV; moder-

Table 1. Wheat production in Brazil according to growing area (1,000 ha), production (1,000 t), and grain yield (GY (kg/ha)) in the main wheat production states of Rio Grande do Sul and Paraná between 1976–77 and 2006–07.

	Brazil			Rio Grande do Sul			Paraná		
Crop year	Area	Production	GY	Area	Production	GY	Area	Production	GY
1976–1977	3,153	2,066	655	1,398	1,257	899	1,524	690	453
1977–1978	2,811	2,680	953	1,345	1,042	775	1,244	1,510	1,214
1978–1979	3,898	2,861	734	1,577	1,615	1,024	1,980	965	487
1979–1980	3,105	2,729	879	1,456	1,380	948	1,335	1,050	787
1980–1981	2,114	2,217	1,049	945	915	968	906	1,075	1,187
1981–1982	2,879	1,876	652	1,220	1,049	860	1,313	552	420
1982–1983	1,932	2,191	1,134	903	1,056	1,169	722	752	1,042
1983–1984	2,013	2,029	1,008	920	1,144	1,243	766	634	828
1984–1985	2,614	4,324	1,654	1,280	2,679	2,093	950	982	1,034
1985–1986	3,909	5,633	1,441	1,945	2,898	1,490	1,188	1,801	1,516
1986–1987	3,430	6,127	1,786	1,710	3,297	1,928	983	1,750	1,780
1987–1988	3,490	5,847	1,675	1,800	3,177	1,765	1,030	1,627	1,580
1988–1989	3,307	5,478	1,657	1,900	3,100	1,632	750	1,425	1,900
1989–1990	3,283	3,304	1,006	1,805	1,462	810	959	1,304	1,360
1990–1991	2,146	3,078	1,434	1,191	1,847	1,550	659	811	1,230
1991–1992	1,998	2,739	1,371	1,253	1,454	1,160	461	945	2,050
1992–1993	1,642	2,052	1,250	930	967	1,040	531	844	1,590
1993–1994	1,446	2,138	1,478	730	1,088	1,490	543	826	1,520
1994–1995	1,034	1,524	1,474	635	1,048	1,650	300	330	1,100
1995–1996	1,833	3,198	1,745	1,111	1,956	1,760	570	992	1,740
1996–1997	1,501	2,407	1,604	922	1,651	1,790	485	611	1,260
1997–1998	1,373	2,188	1,593	900	1,494	1,660	392	555	1,415
1998–1999	1,252	2,403	1,919	765	1,522	1,990	387	696	1,800
1999–2000	1,468	1,658	1,130	780	575	737	557	891	1,600
2000–2001	1,710	3,194	1,868	964	1,913	1,985	602	1,023	1,700
2001–2002	2,052	2,914	1,420	1,055	1,509	1,430	790	1,106	1,400
2002–2003	2,464	5,851	2,375	1,182	2,954	2,500	1,043	2,346	2,250
2003–2004	2,464	5,851	2,375	1,182	2,954	2,500	1,043	2,346	2,250
2004–2005	2,756	5,846	2,121	1,351	3,039	2,250	1,098	2,130	1,940
2005–2006[1]	2,362	4,873	2,063	1,276	2,802	2,195	846	1,564	1,850
2006–2007[2]	1,758	2,234	1,271	881	1,127	1,280	693	728	1,050

[1] Preliminary data; [2] Estimate data. (CONAB, 2007).

ately susceptible to leaf rust; and susceptible to leaf spot caused by *D. tritici repentis* and *B. sorokiniana*. We do not have consistent information about resistance to stem rust, Magnaporthe head blast, or BYDV. BRS Timbaúva was preliminarily classified as soft wheat. In alveograph tests, it had a mean value of 157 x 10^{-4} J, with a variation between 91 and 249 10^{-4} J. High-molecular-weight glutenin subunits 1, 2+12, and 7+9 are present. The tenacity/extensibility of gluten (P/L ratio) is a mean of 1.25. BRS Timbaúva is useful for the manufacture of crackers, cookies, doughs of the homemade type, and, in blends with bread wheat, can be used for bread baking and domestic use.

An historical look at growing area, production, and grain yield in Brazil and the main wheat-producing states of Rio Grande do Sul and Paraná.

E. Caierão, P.L. Scheeren, M. Sóe Silva, L.J.A. Del Duca, A. Nascimento Junior, A. Linhares, L. Eichelberger, M.Z. Miranda, E.M. Guarienti, L.M. Costamilan, M.I.P.M. Lima, M.S. Chaves, S.P. Brammer, A.L.V. Bonato, E.J. Iorczeski, J.R. Salvadori, and A.C.S. Albuquerque.

Brazilian wheat consumption is about 10 x 10^6 t/year and, according to forecast of the Ministry of Agriculture, Animal Husbandry and Supply (Ministério da Agricultura, Pecuária e Abastecimento – MAPA, 2006), will increase 20–30% by the year 2016. The variability in wheat-growing area, production, and grain yield across years is a result of the unstable climate of southern Brazil and variable support policies (Table 1, p, 16).

Brazilian wheat production and grain yield – 2006 crop and perspectives

Leo Del Duca (Former Embrapa Trigo wheat breeder) and Eliana M. Guarienti (Embrapa Trigo researcher).

CONAB (Companhia Nacional de Abastecimento: National Company of Provisioning) has projected the Brazilian wheat production for the 2006–07 growing season to be 2.2 x 10^6 tons (Table 2). The cultivated area was of 1.76 x 10^6 hectares, 25.6% lower than the 2005–06 growing season. Such a reduction was stimulated by lower wheat prices. Adverse climatic conditions prevailed at the time of the sowing (drought) and flowering (frosts) in Paraná and Rio Grande do Sul, the two main Brazilian wheat-producing states. As a result, grain yield dropped to 1,271 kg/ha, lower than that of the 2005–06 crop at 54.2% (2.64 x 10^6 tons) (http://www.conab.gov.br/conabweb/download/indicadores/pubindicadores.pdf).

Recently, a significant increase in the domestic price of important agricultural product such as wheat has been observed. The frustration observed in Australia, combined with the 2006 Brazilian crop, resulted in increased domestic prices. Therefore, a significant increase in the wheat-production area should be expected in the next agricultural year

Table 2. Wheat production and grain yield for the 2005–06 and 2006–07 growing seasons in Brazil (Source of data: CONAB, February 2007).

	Production (1,000 t)		Grain yield (kg/ha)	
State	2005–06	2006–07	2005–06	2006–07
Paraná	2,801.5	1,127.2	2,195	1,280
Santa Catarina	114.9	126.8	1,915	2,100
Rio Grande do Sul	1,564.2	728.0	1,850	1,050
Total for southern Brazil	**4,480.6**	**1,982.0**	**2,054**	**1,213**
Minas Gerais	63.7	56.3	4,360	4,500
São Paulo	132.1	81.1	2,350	1,658
Total for southeast Brazil	**195.8**	**137.4**	**2,766**	**2,238**
Mato Grosso	1.7	—	3,300	—
Mato Grosso do Sul	135.2	62.1	1,420	1,230
Goiás	51.2	46.2	4,300	4,576
Distrito Federal	6.1	6.0	5,500	5,000
Total for westcentral Brazil	**194.2**	**114.3**	**1,787**	**1,850**
Bahia	2.5	—	5,000	—
Total for northeast Brazil	**2.5**	**—**	**5,000**	**—**
Total for all Brazil	**4,873.1**	**2,233.7**	**2,063**	**1,271**

(beginning in April), due to the recovery of prices. Another factor that should act positively for increase the wheat area is the cost (http://www.ipea.gov.br/sites/000/2/boletim_conjuntura/boletim75/Bc75j_conj_Agrícola.pdf).

Main Brazilian wheat cultivars sown in the 2004–05 season.

Leo Del Duca (Former Embrapa Trigo wheat breeder) and Eliana M. Guarienti (Embrapa Trigo researcher).

The wheat-producing area in Brazil covers a large number of growing conditions the different states, such as rainfed or irrigated fields, presence or absence of aluminum toxicity in the soil, and high or low soil fertility level. The states of Paraná (PR) and Rio Grande do Sul (RS) are responsible for most Brazilian wheat production. The ten most important wheat cultivars of these two states are listed in Table 3. Additional information regarding the cross that originated the genotype and its industrial quality classification also is presented.

Considering the sum of the two states, the cultivars Ônix, CD 104, BRS 194, BRS 179, and BRS 208 were the five most widely seeded Brazilian wheat cultivars in the 2004–05 season.

Table 3. Seed availability of the most widely grown wheat cultivars in the two most important Brazilian wheat-producing states (Rio Grande do Sul (RS) and Paraná (PR)) in 2004–05. Wheat industrial quality values are (W) from the alveograph method and the deformation energy of the dough, where soft (W ≥ 50 < 180), bread (W ≥ 180 < 300), and strong (W ≥ 300). Seed availability is expressed as tons available for the 2004–05 season. Percentage for each state is for the most used cultivars ranked by that state.

State	Cultivar	Cross	Quality	Available seed	% for state
RS	ÔNIX	CEP 24/RUBI SIB	bread	25,503.74	20.72
	BRS 194	CEP 14/BR 23//CEP 17	bread	13,033.50	10.59
	BRS 179	BR 35/PF 8596/3/PF 772003*2/PF 813//PF 83899	soft	10,966.60	8.91
	FUNDACEP 30	BR 32/CEP 21//CIANO 79	soft	8,327.27	6.76
	BRS ANGICO	PF 87107/2*IAC 13	soft	6,841.96	5.56
	PAMPEANO	ORL 91274/ORL 93807//ORL 95711 SIB	soft	6,611.52	5.37
	CD 105	PFAU SIB/2*OCEPAR 14//IAPAR 41	soft	4,172.62	3.39
	JASPE	ORL 91308/ RUBI SIB	bread	3,826.68	3.11
	ALCOVER	OCEPAR 16/EMBRAPA 27//OCEPAR 16	bread	3,577.32	2.91
	BRS LOURO	PF 86911/BR 23	soft	3,382.06	2.75
PR	CD 104	PFAU SIB/IAPAR 17	strong	27,470.60	36.56
	BRS 208	CPAC 89118/3/BR 23//CEP 19/PF 85490	bread	8,878.52	11.82
	IPR 85	IAPAR 30/BR 18	strong	7,227.10	9.62
	ÔNIX	CEP 24/RUBI SIB	bread	4,207.11	5.60
	IAPAR 78	VEERY SIB/BOBWHITE SIB	bread	4,111.73	5.47
	CD 105	PFAU SIB/2*OCEPAR 14//IAPAR 41	soft	3,936.47	5.24
	BRS 210	CPAC 89118/3/BR 23//CEP 19/PF 85490	strong	3,038.68	4.04
	BRS 220	EMBRAPA 16/TB 108	bread	2,377.06	3.16
	ALCOVER	OCEPAR 16/EMBRAPA 27//OCEPAR 16	bread	2,016.97	2.68
	OR 1	EMBRAPA 27/BAGULA SIB	bread	1,345.17	1.79

Sources of seed availability data include Indicações Técnicas da Comissão Sul-Brasileira de Pesquisa de Trigo, Trigo e Triticale – 2005 e 2006 and Informações Técnicas da Comissão Centro-Sul Brasileira de Pesquisa de Trigo e Triticale para a safra de 2005 (Sistemas de Produção/Embrapa Soja, ISSN 1677-8499; n.7).

ITEMS FROM CROATIA

BC INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS
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S. Tomasovic, R. Mlinar, B. Palaveraic, I. Ikic, K. Puakaric, M. Potoanac, and S. Halagic.

Breeding winter wheat for yield and resistance to Fusarium head blight.

Breeding of Bc wheat cultivars for resistance to Fusarium head blight is aimed at reducing the negative effects of the disease on grain yield and quality and developing our own material with the highest resistance and yield ability. Wheat lines were tested for resistance to Fusarium head blight and grain yield in field trials at Botinec in 2004 and 2005 under artificial and natural infection. In 2004, the highest level of resistance and grain yield was in the line Bc 310/01 (line 22 (Fig. 1), 14.7, 8,108 kg/ha) and line Bc 5073/00 (12 (Fig. 1), 14.7, 8,052 kg/ha). In 2005, the highest level of resistance was in the line Bc 9362/99 (9 (Fig. 2), 7.6, 8,972 kg/ha). A high level of resistance also was expressed in lines Bc 5325/02 (34 (Fig. 2), 10.3, 8,511 kg/ha) and Bc 18/91 (24 (Fig. 2), 6.1, 8,124 kg/ha). Three lines had good levels of resistance, Poncheau (7 (Fig. 2), 5.0) and D48x42x6$_2$ (5 (Fig. 2), 10.3). Roazon (6) expressed a lower level of resistance (20.7). Breeding for resistance to Fusarium head blight has proven to be successful because of a very effective method of artificial inoculation. Good levels of resistance also have been achieved because a good selection of sources of resistance, such as Beauchamp, SO-1065, 434 K-4CM, Mold 1304-83, FD-91147, and the local source Bc 87/87.

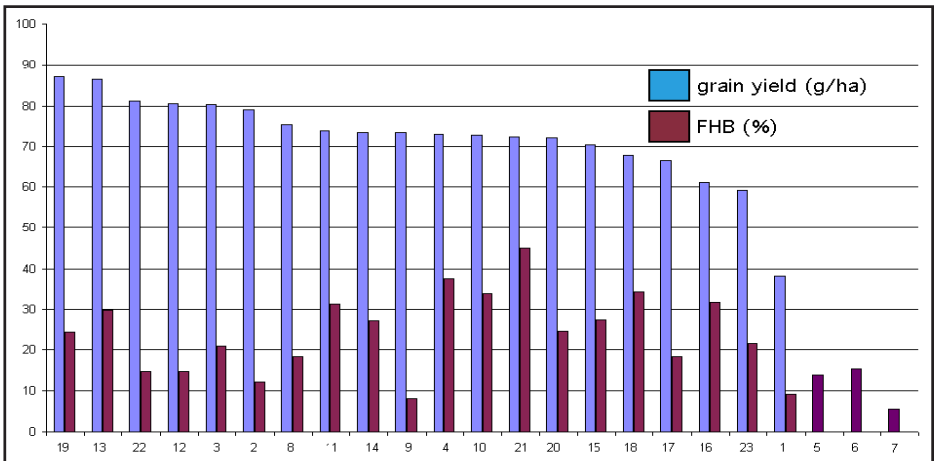

Fig. 1. Results of testing 23 wheat lines for yield and resistance to Fusarium head blight, in Botinec, Croatia, in 2004.

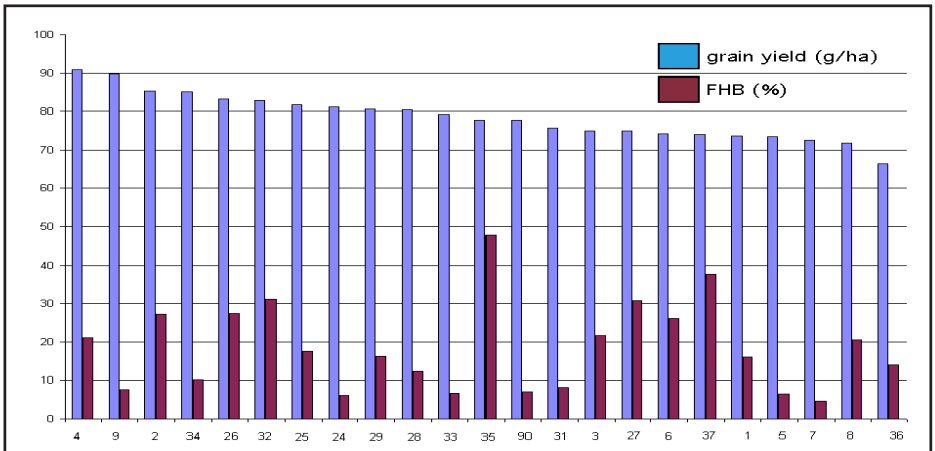

Fig. 2. Results of testing 23 wheat lines for yield and resistance to Fusarium head blight, in Botinec, Croatia, in 2005.

Achievements in breeding durum wheat at the Zagreb Bc Institute with special reference to the cultivar Crodur.

Croatia, with advantages for durum wheat production, puts great importance on producing high quality pasta. From year to year, a growing consumption has been observed. Recognizing the importance of this cereal crop, the first durum wheat breeding program in Croatia was initiated in the Bc Institute prior to 1985. The aim was to develop Croatian durum wheat cultivars with high yield potential and excellent grain quality, especially vitreous and hard grains, and semolina with a high level of yellow pigment and protein content. Twenty years of breeding has resulted in three registered cultivars with good agronomic characters. Primadur, the first cultivar, is a standard of the Board for Registration, Approbation and Protection of Varieties. The newly registered cultivar Crodur, with a positive DUS test and better VCU results relative to the standard, was registered in 2003. Crodur belongs to a group of mid-to-early cultivars. The average plant height is 94.1 cm (Primadur, 97.8 cm) and has very good resistance to lodging. In official trials of the Board for Registration, Crodur produced an average grain yield of 4,543 kg/ha (Primadur, 4,136 kg/ha). The cultivar has good resistance to low temperatures. Test weight, 1,000-kernel weight, and wet gluten also are in the good range. Crodur has good levels of resistance to the major wheat diseases. This cultivar deserves to be accepted widely by the wheat production community.

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ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK
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A. Börner, N. Iqbal, E.K. Khlestkina, S. Landjeva, U. Lohwasser, S. Navakode, K. Neumann, E.G. Pestsova, M.S. Röder, M.R. Simon, A. Weidner, and K. Zaynali Nezhad.

Rht dwarfing genes specific markers.

PCR assays specific for the GA-insensitive dwarfing genes (alleles) *Rht-B1b* and *Rht-D1b* were used to study a series of additional alleles of *Rht-B1* and *Rht-D1*. The amplification profiles of *Rht-B1b* and *Rht-B1d* were not distinguishable from one another, whereas lines carrying *Rht-B1c*, *Rht-B1e*, and *Rht-B1f* amplified a product similar to that of the wild

type. At the 4D locus, no discrimination was possible between *Rht-D1b*, *Rht-D1c*, and *Rht-D1d*. As a result, the utilization of these PCR assays is limited and additional sequencing activities are necessary.

Stripe rust adult-plant resistance.

Recently, a major gene determining nonspecific, adult-plant disease resistance to stripe rust designated *Yrns-B1* was mapped in wheat using a cross between 'Lgst. 79-74' (resistant) and 'Winzi' (susceptible). Linkage to five Gatersleben wheat microsatellite (GWM) markers was discovered, previously mapped on chromosome arm 3BS. This map was improved by the incorporation of four additional GWM markers. QTL analysis revealed high LOD values for the resistance at all nine loci, whereas the largest LOD (20.76) was found for the newly mapped marker *Xgwm1329*.

Microsatellite analysis and resistance tests of a collection of old German/UK wheat cultivars, including probable ancestors of Lgst.79-74 were made. A high coincidence of nonspecific, adult-plant disease resistance to stripe rust and the presence of an Lgst.79-74 allele (117 bp) of the marker *Xgwm533* was observed among the cultivars tested. Linkage during the inheritance of both the resistance and the 117-bp allele of *Xgwm533* was demonstrated. Carriers of this resistance gene have been grown in Germany on large areas for more than 100 years.

To estimate the capability of *Xgwm533* as a diagnostic marker for nonspecific adult-plant disease resistance to stripe rust, microsatellite analysis and resistance tests on a collection of Russian spring wheat cultivars were made. The 117-bp allele of *Xgwm533* was found in about 35% of the Russian cultivars analyzed, however, none possessed the expected disease resistance. Thus, the utilization of *Xgwm533* as diagnostic marker seems to be restricted to certain gene pools.

Leaf rust resistance originated form Ae. markgrafii.

Bread wheat/*Ae. markgrafii* introgression lines expressing leaf rust resistance were developed from a cross between a leaf rust-resistant *Ae. markgrafii* accession and the susceptible bread wheat cultivar Alcedo. The content of the introgressed segments present in five sister introgression lines was assessed with the help of chromosome-specific SSRs. One of the lines was used as a parent of a 140-line, individual F_2 mapping population by crossing with the leaf rust-susceptible bread wheat cultivar Borenos. The population was tested for susceptibility or resistance to leaf rust, and linkage analysis indicated the presence of a QTL (*QLr.ipk-2A*), originating from the *Ae. markgrafii* parent, mapping to the distal segment of chromosome arm 2AS.

Detection of Septoria tritici blotch resistance genes employing wheat/Ae. tauschii introgressions.

At the IPK Gatersleben, a series of 84 bread wheat/goatgrass (*Ae. tauschii*) introgression lines was developed recently. Based on the knowledge that chromosome 7D of this particular *Ae. tauschii* is a donor of resistance to Septoria tritici blotch, a subset of 13, chromosome-7D introgression lines was investigated along with the susceptible recipient cultivar Chinese Spring and the resistant donor line CS (Syn 7D). The material was inoculated with two Argentinian isolates of the pathogen (IPO 92067 and IPO 93014) at both the seedling (two leaf) and adult (tillering) stages at two locations over two years (2003 and 2004). The resistance was effective against both isolates and at both developmental stages, and the resistance locus maps to the centromeric region of chromosome arm 7DS. On the basis of its relationship with the microsatellite marker *Xgwm44,* it is likely that the gene involved is *Stb5*. *Stb5* is, therefore, apparently effective against *M. graminicola* isolates originating from both Europe and South America.

The set of 84 wheat/*Ae. tauschii* introgressions lines is available on request.

Osmotic stress response in wheat seedlings.

A QTL approach was applied to dissect the complex genetic control of plant growth response to osmotic stress in common wheat. A set of 114 RILs of the wheat International Triticeae Mapping Initiative (ITMI) mapping population were subjected to osmotic stress, induced by 12% polyethylene glycol (PEG 6000) from the onset of germination to day

8 of seedling development. Root, coleoptile, and shoot length, and root/shoot length ratio were compared under stress and control conditions. A total of 35 regions on 10 chromosomes contributed effects on seedling growth traits. Almost half of the QTL (16) were detected in controls, 17 under osmotic stress conditions, and two QTL corresponded to tolerance index. In regions on five chromosome arms (1AS, 1BL, 2DS, 5BL, and 6BL) the QTL detected under stress co-mapped with QTL for the same trait under control conditions, so they were classified as QTL affecting seed vigor *per se*. A wide chromosome region on chromosome 1AL, comprising five QTL with major impact of markers *Glu1A* (LOD 3.93) and *Xksuh9d* (LOD 2.91), positively affected root length under stress and the tolerance index for root length, respectively. A major QTL (LOD 3.60), associated with marker *Xcdo456a* in the distal part of chromosome arm 2DS, was detected for tolerance index for shoot length. Three minor QTL (LOD <3.0) for root length and root/shoot length ratio under osmotic stress were identified in the distal part of chromosome arms 6DL (marker *Xksud27a*) and 7DL (marker *Xksue3b*). Selecting for the favorable alleles at marker loci associated with the detected QTL for growth traits may be an efficient approach for increasing the ability of plants to maintain growth of roots, coleoptile, and shoots under water deficit stress at critical early developmental stages.

Salt tolerance.

A set of 20 high-yielding wheat cultivars was compared with a set of preselected Genebank accessions varying in their response to salt stress, the salt-tolerant Indian landrace Kharchia, and the derived tolerant cultivar Kharchia 65. The high-yielding wheat cultivars were released in Germany before 1950 and between 1950 and 1969, 1970 and 1989, and 1990 and 2005.

Experiments were performed at the germination stage (climate chamber) and seedling stage (hydroponics, greenhouse); both with two replications. A germination test was made on filter paper (0, 1, 1.5, and 2 % NaCl; 20˚C; 12-hour light/dark photoperiod; 10 days; score 0–9). For the greenhouse experiment, plant material was pregerminated in a climate chamber on moistened filter paper in the dark at 22˚C for 4 days. Fifteen young, healthy plants/cultivar accession with normal growth habit were selected for hydroponics (greenhouse, 20˚C, 12-hour light/dark photoperiod, 50 % Hoagland's solution). Plant boxes were covered with perforated aluminium foil, which allowed the plants to hang the roots into the solution for nutrient uptake. After a 1-week adaptation time, the nutrient solution was increased to full concentration (100% Hoagland's solution) and the stress variant was subjected to additional 100 mM NaCl. Ten days after stress initiation, shoot and root length and the fresh weight of the biomass were measured.

Germination tests clearly showed a higher tolerance of the wheat cultivars released before 1950. High-yielding cultivars released during the last 15 years were more sensitive. The comparison of the material at the seedling stage was based on the tolerance index (character under stress condition / character in control * 100). The index of the shoot length decreased from cultivars released before 1950 to modern cultivars of present time, which agrees with findings of the germination test. No clear differences were noted within the cultivars with respect to the shoot fresh weight. Most of the cultivars reacted more tolerant than Kharchia 65.

Aluminum tolerance.

Aluminum toxicity is a major problem for cereal production worldwide, especially in the tropics. A nutrient solution culture approach was used to classify the wheat aluminium tolerance, based on the root growth of the seedlings. We investigated cytogenetic stocks of *T. aestivum* subsp. *aestivum* cultivar Chinese Spring, single-chromosome substitution lines available at IPK Gatersleben. As a result, a set of DH lines derived from the cross between 'Chinese Spring / Synthetic 3B' was used to dissect the QTL involved in aluminum tolerance. In order to construct a genetic map for chromosome 3B, the parents were screened for polymorphism using Gatersleben Wheat Microsatellite markers followed by genotyping of the DH lines, linkage analysis, and QTL detection.

Preharvest sprouting / dormancy.

A set of 114 RILs of the ITMI mapping population was evaluated for the domestication traits preharvest sprouting and dormancy. Under field conditions, major QTL could be localized for preharvest sprouting on chromosome 4AL and for dormancy on chromosome 3AL. Under greenhouse conditions, a main QTL on chromosome 4AL was found for both

traits. But the major QTL on chromosome 3AL could not be detected again. In order to find the cereal genome regions responsible in general, two barley mapping populations were evaluated for both traits as well. Ninety-four DH lines of the OWB-population (Oregon Wolfe Barley) and 150 DH lines of the 'Steptoe/Morex' mapping population were grown under field and greenhouse conditions in Gatersleben. QTL for preharvest sprouting and dormancy were detected on chromosome 5H and 7H in the centromeric region. When the data were compared, there is no correlation between wheat and barley.

Gene and genome mapping group – A novel gene for grain weight gw1 and a novel Rht locus on chromosome arm 7DS.

M.S. Röder and X.Q. Huang.

The previously described QTL for grain weight *QTgw.ipk-7D* associated with microsatellite marker *Xgwm1002-7D* was originally detected in a BC_2F_3 advanced backcross population of the German winter wheat cultivar Prinz and the synthetic wheat line W-7984 (lab designation: M6) (Huang et al. 2003). We developed NILs with introgressions of M6 in the genetic background of Prinz with varying sizes on chromosome 7D. The BC_4F_3 NILs had a 10% increased 1,000-kernel weight compared to the control group and the recurrent parent Prinz, and 84.7% of the phenotypic variance could be explained by the segregation of marker *Xgwm1002-7D*. The trait increased grain weight and was strongly correlated with increased grain length and increased plant height, whereas the trait grain number/ear was stable between the NILs and the control group. The QTL *QTgw.ipk-7D* was delimited to the interval *Xgwm295–Xgwm1002*, which is located in the most telomeric bin 7DS4-0.61-1.00 in the physical map of wheat chromosome arm 7DS (Röder et al. 2007). We propose the presence of a gene modulating grain weight with the preliminary designation *gw1*, which has a recessive or intermediate mode of inheritance for the large grain phenotype. Furthermore, our data suggest the presence of a novel, plant-height reducing locus *Rht* on chromosome arm 7DS of Prinz. The two phenotypes, large grain and increased plant height, may reflect the pleiotropic action of one gene or may be caused by two linked genes. In general, our data support the concept of using nearly isogenic introgression lines for validating and dissecting QTL into single Mendelian genes, opening the way for map-based cloning of a grain-weight QTL in wheat.

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ITEMS FROM HUNGARY

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Wheat season. The weather for the 2005–06 crop season was basically favorable for winter wheat. The winter was milder than usual at first, but January 2006 temperatures were below average. However, the snow cover prevented any great damage to the crops. Spring came late and there was standing water in many fields, although there was less rainfall than usual. The warm weather in May helped the crops catch up, and the heading date was similar to the average. The weather was ideal for grain filling until the second half of June, after which the accumulation of assimilates was halted by two heat-waves. Ten to 14 extremely hot days caused forced ripening and shrivelled grains especially in late-maturing cultivars.

Among the biotic stress factors, considerable spontaneous infection with powdery mildew was observed in spring. The level of natural infection with leaf rust was lower than the previous year, but Fusarium head blight was reported in some areas. Harvest began relatively late, in mid-July, but the weather was dry and favorable. The yield average was moderate (4.06 t/ha) and a total of 4.3 x 10^6 tons of good quality wheat was produced in Hungary.

Breeding.

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The winter wheat cultivar Mv Kolo was registered in Hungary and Mv Vekni in Slovakia this year. Several cultivars already registered in Hungary were granted registration in foreign countries; Mv Suba in Serbia, Mv Süveges in Croatia, and Mv Marsall in Romania.

Mv Kolo (Mv 417-03) is a medium, early maturing, top quality cultivar with good abiotic stress resistance, selected from the cross 'Mironovskaya-Ostistaya/Atay-85//Alföld'. Yield level in official trials varied between 6 and 7.5 t/ha. The frost resistance level determined in phytotron tests is good, and it has above-average yield stability in dry years. Mv Kolo has 14.3–16.3% protein content and 33–36% wet-gluten content, with excellent gluten quality. The HWM-glutenin composition is 2*, 7+9, 5+10. Mv Kolo does not carry the T1B·1R translocation. Dough quality is outstanding, whether determined by Farinograph or Alveograph. Mv Kolo is characterized by a reliably high falling number. The cultivar is moderately resistant to powdery mildew, has good field resistance to leaf rust, and is resistant to the stem rust population used in the local artificially inoculated nursery.

Mv Vekni is a mid-late, hard red cultivar with a high gluten content. Good adaptability is proven by the ability to give high yields in production zones with widely differing climates. Mv Vekni has good winter hardiness and lodging resistance, allowing it to be reliably grown. Flour with a high water uptake can be ground from the grain. With a high gluten content (34–38%) and moderate falling number stability, bread-making quality is on par with that of Mv Magdaléna and Mv Csárdás, the cultivars used most widely for conventional bread-making purposes in Hungary. Mv Vekni has the T1B·1R translocation. The cultivar is moderately susceptible to powdery mildew and resistant to leaf rust and stem rust.

Wheat transformation. Experiments in wheat transformation were done with the biolistic method (gene gun) and *Agrobacterium tumefaciens* inoculation using the spring wheat cultivar Cadenza and the winter wheat cultivar Mv Emese, which have good adaptability, as the model plants.

A storage-protein gene from *Amaranthus hypochondriacus* (*AMA1*) and the *1Ax2*B* storage-protein gene, isolated from the wheat cultivar Bánkúti 1201, were used as target genes in the biolistic transformation. Twenty experiments with the *AMA1* gene, using ppt (herbicide) selection, involved a total of 720 embryos from Mv Emese and 1,500 from Cadenza. After the bombardment of the isolated embryos, nine surviving plants of Mv Emese and 37 of Cadenza were planted out into peat cubes. Seven of the Cadenza plants and four of the Mv Emese plants that survived selection were proved to be transgenic using PCR. For the *1Ax2*B* gene, 270 embryos of each genotype were transformed, after which six herbicide-resistant plants of Cadenza and 11 of Mv Emese were grown. The DNA of these plants is currently being analyzed by PCR.

The presence of the transgene (*bar* or *AMA1*) also was detected in genomic DNA extracted from the leaves of T_1 plants raised from T_1 seeds produced on T_0 transgenic plants transformed in 2005. The expression of the mRNA extracted from immature seeds of these plants was confirmed using rtPCR. The expression of the protein coded by the *AMA1* gene is now being investigated using Western blotting. Herbicide spraying was used to examine the expression of the herbicide-resistance gene. The expression of the protein coding for resistance was confirmed in plants from 12 independent transgenic lines.

Work has begun on the genetic transformation of immature embryos freshly isolated from the winter wheat Mv Emese and the spring wheat Cadenza using the hypervirulent *A. tumefaciens* strain AGL1 (pAL154/156). The T-DNA of the pGreen-based pAL156 plasmid contains the *bar* selection marker gene and a modified *uidA* (GUS) reporter gene, which includes an intron inhibiting gene expression in *Agrobacterium*. Gene transfer was detected using the histochemical reaction of GUS. In order to improve the efficiency of callus induction and plant regeneration, several hormone concentration combinations were tested. The *in vitro* selection of the first candidate transformants is now in progress. After selection, the presence of the *GUS* and *bar* genes incorporated into the plants will be detected with the help of specific primers.

Molecular markers. Molecular markers have been used to identify the *Lr37* gene responsible for leaf rust resistance in a number of wheat genotypes . Among the wheat lines bred in Martonvásár, the gene complex *Lr37-Yr17-Sr38* originating from source VPM-1 is carried by the registered cultivar Mv Vekni and the advanced lines Mv17-04 and Mv21-2000. The presence of the *Lr19* gene has been demonstrated in genotypes Mv12-04, Mv35-06, Mv06-07, MVM28-04, and Mv14-06, whereas the *Lr24* gene is in Mv Hombár, Mv08-03, and Mv15-06.

In order to discover molecular markers linked with the yellow index, which is closely correlated with the yellow pigment content of durum wheat, a bulk segregant analysis was made on 98 advanced lines from a progeny population developed using parents exhibiting large deviation for the yellow index and on the DNA of the parents. Five primers were used to identify nine polymorphic RAPD markers, and linkage between these markers and 2-year means of the yellow index was tested by means of correlation analysis. The coefficient of determination had values between 0 and

17%; the closest linkage being found for marker $OPA16_{800}$. Multiple regression gave a coefficient of multiple determination of $R^2 = 0.421$ for all nine markers, and $R^2 = 0.377$ when only the four significant markers were considered. Discriminant analysis was used to check whether the marker data confirmed groupings made on the basis of the yellow index. When all nine markers were used, 80% of the lines were grouped correctly. Using only four markers, this value dropped to 77%, but the analysis confirmed 93.47% of the groupings of lines with low yellow index, indicating that lines with poor technological quality could be reliably identified using these markers.

Wheat quality. Genotypes over-expressing 1Bx7 HMW glutenin are bred in order to develop wheat with strong, elastic dough. Adaptable lines are selected from populations developed by crossing Glenlea, N93-326, and sublines of Bánkúti 1201, which carry the gene responsible for Bx7 over-expression. On the basis of agronomic traits and farinograph curve stability, line Mv08-07 appears to be competitive.

Based on previous analyses that indicated the starch properties of normal winter wheat cultivar populations was unexpectedly variable and on the interest exhibited by the processing industry, tests were made to determine the starch content and amylose/amylopectin ratios of wheat genotypes, the viscosity of the starch suspension, and the level of starch damage. The starch content of the tested cultivars ranged from 60–88% and the amylose content from 18–34%. Values of 10.5–20.5 UCDc were found for the level of starch damage from wheat. When measuring RVA viscosity, greater differences were recorded when testing starch samples (4,706–6,310 cP final viscosity) than for flour samples (3,019–3,775 cP).

Disease-resistance studies. Powdery mildew isolates collected in the neighborhood of Martonvásár were used to determine the race composition of the pathogen population, the degree of virulence, and the effectiveness of known resistance genes. The following wheat powdery mildew races were dominant in 2006 (frequency in parentheses): 51 (26.7%), 72 and 76 (15.1%), and 77 (10.9%). The number of virulence genes in the pathogen population averaged 5.89. Almost complete protection against the wheat powdery mildew isolates tested was provided by the *Pm4a+* resistance gene.

Fusarium head blight resistance of lines developed from populations of old Hungarian cultivars together with foreign sources of resistance was investigated in an artificially inoculated field nursery. The level of head blight severity for nine of the lines developed from populations of old Hungarian cultivars was less than 10%. Among the Martonvásár genotypes, a low level of FHB severity was recorded for Mv Emese, Mv Palotás, Mv Táltos, Mv Kolo, and line Mv08-05.

A survey was made of the virus composition of winter wheat, winter barley, durum wheat, winter oat and triticale crops. The wheat dwarf virus (WDV) was identified on almost 100% of plants exhibiting symptoms.

Abiotic stress resistance studies. As part of the research on abiotic stress resistance, changes in the antioxidant enzyme activity of six wheat cultivars grown in phytotron climatic chambers were studied spectrophotometrically in the course of 15-day heat stress treatment at the beginning of shooting and from the 12th day after heading. High temperature induced substantial differences in the activities of five antioxidant enzymes over the course of plant development. In response to heat stress, a decrease in the antioxidant enzyme activity was observed as the plants aged. High temperature had a degrading effect on the enzymes, manifested as a reduction in the level of activity. The greatest stability was observed for glutathione-S-transferase, catalase, and ascorbate peroxidase. The least change as the result of heat treatment was observed for glutathione reductase, whereas the most instable enzyme proved to be guaiacol peroxidase.

The effect of climatic components on the biomass and yield of cereals and on the quality of the grain yield was investigated in long-term experiments. The appearance and course of diseases was monitored, together with their effect on agronomic traits. For most of the cultivars tested, |the protein content of the grain was significantly lower in plants infected with leaf diseases than in those protected by spraying. The gluten quality (gluten index and gluten extension) suggested, in general, that in the case of natural infection the dough is firmer and less elastic than that of sprayed plants.

In a series of model experiments in the phytotron, the effects, interactions, and correlations of increases in mean temperature and atmospheric CO_2 concentration on the biomass production and yields of various cereal species and cultivars were investigated. High temperature generally accelerated plant development, leading to earlier heading and maturity, sometimes by as much as 5–13 days. Because of the shortening of the vegetation period, there was less biomass accumulation, with a consequent reduction in the grain number/plant and the yield quantity. In general, CO_2 fertilization had a positive influence on biomass accumulation and on quantitative yield parameters. The grain protein

content of plants grown at higher atmospheric CO_2 concentration changed in some cultivars and remained constant in others.

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Molecular cytogenetics and flowering biology.

B. Barnabás, M. Molnár-Láng, G. Linc, É. Szakács, K. Jäger, I. Molnár, F. Bakos, H. Ambrus, A. Schneider, A. Sepsi, and A. Fábián.

Induction of chromosome rearrangements in a 4H(4D) wheat-barley substitution using a wheat line containing a *ph* suppressor gene. Translocation lines were developed by inducing homoeologous chromosome pairing in a 4H(4D) wheat–barley substitution line previously developed in Martonvásár. We hoped to incorporate various segments of the barley 4H chromosome from the 4H(4D) substitution into wheat. Observations were made on the frequency with which wheat–barley translocations appeared in the F_2 progeny from a cross between the line CO4-1, which carries the *Ph* suppressor gene from *Ae. speltoides* and, thus, induces a high level of homoeologous chromosome pairing, and the 4H(4D) wheat–barley substitution line. Translocations were identified by means of genomic *in situ* hybridization. Of the 117 plants examined, three (2.4%) did not contain translocations. A total of four translocations were observed; one plant contained two different translocations. The translocations consisted of one centric fusion, two dicentric translocations, and one acrocentric chromosome. Plants with translocations were grown in the phytotron and selection of homozygous translocation lines was made in the F_3 progeny.

Characterization of chromosome-specific S-SAP markers and their use to study genetic diversity in *Aegilops* species. The short, interspersed nuclear element (SINE), Au, was used to develop sequence-specific amplified polymorphism (S-SAP) markers for the U- and M-genome chromosomes. The markers were localized using wheat–*Ae. geniculata* and wheat–*Ae. biuncialis* disomic chromosome addition lines. Thirty-seven markers distributed over six U- and six M-genome chromosomes were produced. Genetic diversity studies on 37 accessions of *Ae. biuncialis*, *Ae. comosa*, *Ae. geniculata*, and *Ae. umbellulata* suggested that *Ae. biuncialis* arose from its diploid ancestors more recently than *Ae. geniculata*. Several earlier studies indicated that the M genomes in polyploid *Aegilops* species had accumulated substantial rearrangements, whereas the U genomes remained essentially unmodified. However, this cannot be attributed to the preferential insertion of retroelements into the M-genome chromosomes. Fourteen markers from a total of eight chromosomes were sequenced. Three markers were similar to known plant genes. One marker was derived from an LTR-retrotransposon. Ten markers did not match to any known DNA sequences, suggesting that they were located in the highly variable intergenic regions.

Development and molecular cytogenetic identification of new winter wheat/winter barley (Martonvásári 9 kr1/ Igri) disomic addition lines. A series of winter wheat/winter barley disomic addition lines were developed from hybrids between winter wheat line Martonvásári 9 kr1 and the German two-rowed winter barley cultivar Igri. The barley chromosomes in a wheat background were identified from the fluorescent *in situ* hybridization patterns obtained with various combinations of repetitive DNA probes GAA-HvT01 and pTa71-HvT01. The disomic addition lines 2H, 3H, and 4H, and the 1HS isochromosome were identified on the basis of a two-color FISH with the DNA probe pairs GAA-pAs1, GAA-HvT01 and pTa71-HvT01. Genomic *in situ* hybridization was used to confirm the presence of the barley chromosomes in the wheat genome. The identification of the barley chromosomes in the addition lines was further confirmed with SSR markers. The addition lines also were characterized morphologically.

Effect of heat stress and water deficit on reproductive development in wheat. The combined effect of elevated temperature and water deficit on the meiosis, flowering, and early seed development of the drought resistant wheat genotype Plainsman and sensitive Cappelle Desprez were studied. These processes lead to the development of the male and female gametes and those ensuring that the fusion of the gametes and the development of the embryo and endosperm should take place undisturbed. The effects of various kinds of abiotic stress on these processes are different, but in all cases negative, and their influence always results in a decline in the yield quantity. In maize, the effects of these stressors on reproductive development have been studied extensively, but a lack of information exists on their effect on some stages in the gametophytic development in wheat. High temperature and drought applied at the stage of gametogenesis resulted in the production of dysfunctional male and female gametophytes. At the time of flowering and early seed development, stressors negatively affected the fertility rates. The duration of dry matter accumulation decreased, so a dramatic reduction in 1,000-kernel weight was observed in both genotypes. The treatment did not affect the germination ability of seeds treated during the early grain-filling period, but the number of seminal roots markedly decreased in seedlings of the sensitive genotype.

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Genetic and physiological studies.

G. Galiba, G. Kocsy, A. Vágújfalvi, A. Bálint, F. Szira, A.Soltész, and T. Kellös.

Effect of low temperature on gene expression. The frost tolerance locus *Fr-A^{m}2* was recently discovered in *T. monococcum* subsp. *monococcum*. Mapping data showed that 11 *TmCbf* genes are clustered at this locus in a 0.8 cM region. A novel mapping population is being developed to identify which of the *Cbf* genes are responsible for the differences in frost tolerance between the einkorn parental lines at the *Fr-A^{m}2* locus. The changes induced by cold or by chromosome 5A in the expression of wheat candidate genes selected by transcript profiling were confirmed by Northern analysis and RT-PCR.

Physiological changes induced by low temperature. The mechanism of the contribution of light during the development of freezing tolerance was investigated in winter wheat plants. Light induced the activity of certain antioxidant enzymes and altered the lipid composition and the metabolism of salicylic acid. Low-temperature hardening in the light caused a downshift in the far-red-induced AG thermoluminescence band. The faster dark re-reduction of P700$^+$, monitored by 820-nm absorbance, could also be observed in these plants. These results suggest that the induction of cyclic photosynthetic electron flow may also contribute to the advantage of frost hardening under light conditions in wheat plants.

Drought tolerance studies. In order to determine QTL involved in osmotic and drought tolerance in barley, the Oregon Wolfe Barley (OWB) mapping population was examined at germination, as seedlings, and at maturity. Water stress was induced in young plants by adding polyethylene-glycol (PEG) to the growing solution. Limited watering was used at the mature stage. The most effective QTL for drought tolerance were found to be different in each developmental stage. The QTL influencing the yield parameters of mature plants under drought stress were different from those affecting osmotic adjustment in barley.

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Cereal Genebank.

G. Kovács.

Characterization of cereal genetic resources. Last year, the agronomic performance and flowering of 120 new einkorn lines were tested, and an einkorn core collection established. Several new emmer genotypes and landraces were obtained via germ plasm exchange with other cereal genebanks and via collection from French farmers, who still cultivate them. Growth habit and winter hardiness were determined in these emmer wheats, and the frost-tolerant winter types were used in crosses to transfer their quality traits and frost tolerance to advanced winter durum lines. A new interspecific crossing program was started in order to transfer the biotic resistance of einkorn to other cultivated *Triticum* species. Einkorn lines with good crossability were identified in durum/einkorn crosses, and artificial primary hexaploid plants were produced with an ABA-genome structure. These fertile lines will be used for crossing with other hexaploid wheat species such as bread wheat, spelt wheat, and *T. zhukovskyi*.

Organic breeding. Some years ago, organic breeding programs were initiated for einkorn and emmer under certified organic conditions. During this period, several new crosses were produced, resulting in relatively high-yielding lines with good abiotic tolerance. Two of the best-performing lines are currently being tested for VCU, prior to being introduced into cultivation. These lines have very good agronomic performance under organic growth conditions. The einkorn genotype Mv Alkor has excellent wet gluten content, with good bread-making quality, but is an extremely soft-

grained type. By contrast, the emmer line is a very hard-grained type with excellent pasta-making quality. The new advanced einkorn lines include several gluten-free variants, the lutein content of which is now being improved.

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ITEMS FROM INDIA

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Genetic improvement of wheat quality and rust resistance in Indian wheat.

B.K. Das[1], A. Saini[2], N. Jawali [2], and S.G. Bhagwat[1].
[1]Nuclear Agriculture & Biotechnology Division and [2] Molecular Biology Division.

We are using HMW-glutenin subunits as a selection criterion for the genetic improvement of wheat for quality in Indian wheat background. Rust-resistance genes such as *Sr31*/*Lr26*/*Yr9*, *Sr26*, and *Sr24*/*Lr24* are being combined with high-yielding ability and protein subunits for quality traits. A number of intervarietal crosses were made and selections are being carried out. Marker-assisted selection with SCAR markers is being used to select for rust resistance genes *Sr31* and *Sr24* and HMW-glutenin subunits 5+10 (coded by *Glu-D1d*).

Genetic diversity among Indian wheat cultivars as revealed by AP-PCR markers.

B.K.Das[1], A. Saini[2], S.G. Bhagwat[1], and N. Jawali[2] .
[1]Nuclear Agriculture & Biotechnology Division and [2] Molecular Biology Division.

Genetic diversity among 44 Indian wheat genotypes was assessed using arbitrary primed polymerase chain reaction (AP-PCR). Long primers (16–24 bases) were used, and the PCR conditions standardized. At an annealing temperature of 55˚C, the primers worked well. Of the 20 long primers, eight gave consistent results. Using those eight primers, 61 amplified bands were obtained. Twenty-five of the bands were polymorphic, with an average of 3.3 polymorphic bands/primer. Similarity coefficient values were in the range of 0.14 to 1.0. Based on these values, a cluster analysis was done using the UPGAM method, and a dendrogram with three clusters was drawn. One of the clusters consisted of wheat cultivars with the T1BL·1RS translocation. Based upon the pedigrees, similar cultivars were grouped together in the clusters. With the exception of four cultivar pairs, the cultivars could be distinguished from each other. Although only a few primers were studied, our results show that AP-PCR markers can be used to identify cultivars or make DNA finger-prints of wheat genotypes. Based on the similarity coefficient values, we observed that the genotypes have narrow genetic diversity.

Identification of two DNA markers linked to stem rust-resistance gene Sr26 in bread wheat.

Ruchi Rai, B.K. Das, and S.G. Bhagwat (Nuclear Agriculture and Biotechnology Division).

Sr26 is an effective gene not yet used in Indian wheat-breeding programs. Marker-assisted selection and pyramiding with other *Sr* genes will help to achieve durable resistance. A population consisting of 140 individual plants was developed from cross between Kalyansona and Kite (+*Sr26*). The population segregated for a single rust-resistance gene and fit a 3:1 ratio. A total of 100 random decamer primers and 24 AP-PCR primers were analyzed. Two markers were polymorphic in both parents and the resistant and susceptible bulks. Linkage analysis using MAPMAKER detected two markers $SS30R_{480bp}$ and $OPAE\text{-}07_{620bp}$ linked to *Sr26*. One AP-PCR and one RAPD-based marker linked to *Sr26* were cloned and sequenced, and SCAR primers have been designed. Two of the three SCAR markers amplified monomorphic fragments, whereas a third primer detected polymorphism associated with *Sr26* and will be used for screening and validation.

Genetic linkage map of bread wheat and a QTL map for spike-related traits.

Nalini Eswaran[1], Suresh Gopal Bhagwat[2], and Narendra Jawali[1].
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A genetic linkage map was constructed using an F_2 population derived from a cross between two Indian bread wheats Sonalika and Kalyansona. The map consisted of 236 markers and spanned a distance of 3,639 cM with 1,211.2 cM for the A genome, 1,669.2 cM for the B genome, 192.4 cM for the D genome, and 566.2 cM for unassigned groups. The average density was one marker/15.4 cM. The map included 37 linkage groups of which 24 were assigned to 17 chromosomes by making use of anchor markers such as STMS and AFLP markers that were physically mapped using nullitetrasomic lines.

The two spike-related quantitative traits, spike length (SL) and number of spikelets/spike (NSS), are related to yield. The spike of Sonalika is thinner, longer, and has fewer spikelets compared to that of Kalyansona, which has a thicker, shorter spike with more spikelets. The data for SL and NSS were collected on an F_2 population grown in Trombay. QTL were detected by CIM and MCIM with an LOD threshold >2.0. Two QTL were detected for NSS. The QTL on chromosome 5B showed higher phenotypic variation (21.7%) than that on chromosome 1B (6.9%). One marker, ITS-*Hae*III, likely to be from the *Nor-B1* locus of chromosome 1BS, was found to be closest to a QTL for NSS. Four QTL for SL, with phenotypic variation ranging from 8.6 to 36.6 %, were on chromosomes 1B, 2B, 5A, and 6B. The QTL for SL on chromosome 1B was same as that for NSS with the closest marker being ITS-*Hae*III.

Analysis of the data from the F_2 population showed that SL and NSS are significantly correlated (correlation coefficient (r) = 0.58). Seven QTL were detected by joint MCIM for the two traits in combination and of these, two also were detected by CIM, three were detected by individual MCIM, and the remaining two were detected by CIM and individual MCIM. The two QTL on chromosomes 2B and 6B, which were detected by CIM and MCIM, can be considered as QTL that influence both NSS and SL.

Allelic variation at the Rht8 locus in Indian wheat cultivars.

Suman Sud and S.G. Bhagwat (Nuclear Agricultural and Biotechnology Division).

Reduced height in wheat has been used as yield-enhancing option in wheat-growing regions of India. The Norin 10 dwarfing genes were used widely and resulted in a significant yield advantage. The search for an alternative source of dwarfing genes identified another reduced height gene *Rht8* in the Japanese cultivar Akakomughi. The *Rht8* gene also is reported to provide an advantage in warm environments. A wheat microsatellite marker, GWM-261, on the short arm of chromosome 2D cosegregated with the *Rht8* gene in hexaploid wheat. This microsatellite primer is known to give different allelic variants at *Rht8* locus, and an 192-bp allele is associated with the presence of *Rht8*. Therefore, we wanted to find allelic variants at the *Rht8* locus and study the adaptive advantage of this locus in Indian wheats. Ninety-five cultivars were screened for polymorphism at the *Xwms-261* locus. Allelic variants of 165 bp and 192 bp were more

common compared to 174 bp among the analyzed cultivars. Ten cultivars had bands greater than 200 bp, which need to be sequenced and further studied for their advantage over the 192-bp allele.

Characterization of a GA_3-insensitive, reduced height mutant of emmer wheat NP200 (T. turgidum subsp. dicoccum).

Suman Sud, K.A. Nayeem, and S.G. Bhagwat (Nuclear Agricultural and Biotechnology Division).

A γ-ray-induced, reduced height mutant was obtained in the emmer wheat NP200. The mutant was insensitive to externally applied gibberellic acid. An allele-specific marker for the major dwarfing gene *RhtB1b* was used to check the status of the dwarfing gene in the mutant, semidwarf, and tall emmer and semidwarf durum wheat cultivars. The primer showed amplification of the *RhtB1b* gene in the semidwarf durum and emmer cultivars. The NP200 parent had the wild-type allele (*RhtB1a*) with the primer pair BF-WR1. All semidwarf emmer cultivars had a band of 237 bp with primer pair BF-MR1. However, the mutant (HW1095) lacked amplification for both *RhtB1a* and *RhtB1b* alleles with the respective primer pairs. The results indicated that the reduced-height mutant carried a mutation different than from the existing allele *RhtB1b*.

Computer-based image analysis for class and cultivar identification in wheat.

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Computer-based image analysis is being applied for wheat class identification and cultivar identification. Fifteen wheat samples belonging to bread wheat, durum wheat, and emmer wheat were used. Images were taken in transparency or reflectance mode. Shape, size, and color parameters were derived from the images. Correct class identification was indicated for 13 of the 15 samples. Four samples were reused as unknown but could be correctly identified on the basis of minimum Euclidean Distance.

Studies on the sphaerococcum locus in bread wheat.

A.Saini[1], S.G. Bhagwat[2], and N. Jawali[1].
[1]Molecular Biology Division and [2]Nuclear Agriculture & Biotechnology Division.

The sphaerococcum locus is an unused/unexplained locus in breeding that has a pleiotropic effect on many morphological characters, such as reduced height, erect leaves, and round grain. The locus was introduced into *T. aestivum* subsp. *aestivum* from *T. aestivum* subsp. *sphaerococcum*, and NILs were generated after several backcrosses and selection (for the trait) using the cultivar Kalyansona as the recurrent parent.

An F_2 population of 91 NILs and the parentals were scored for several morphological traits such as plant height, spike length, culm length, and seed morphology. Spike and culm length are traits are governed by single, recessive loci. Leaf material from individual plants was collected and DNA isolated. Two bulks, for carrier and noncarrier of sphaerococcum traits, were prepared. The analysis of the bulks and NILs by AP-PCR, RAPD, and AFLP is in progress to identify markers linked or associated with the trait.

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Hybrid chlorosis in some Indian varieties of Triticum turgidum subsp. dicoccum.

S. Premalatha and V.R.K. Reddy.

Introduction. Inter- and intraspecific hybrids of wheat often show various types of hybrid weakness, among which chlorosis is the most frequent. Chlorosis starts at the same time in nearly all leaves and in all parts, and the whole plant becomes greenish-yellow (Tsunewaki 1966). The hybrids in these cases are lethal or semilethal and often unproductive. The likely occurrence of chlorosis not only interferes with the choice of parental material but also restricts the productivity of the cross. Chlorosis is caused by two complementary genes, *Ch1* and *Ch2*. *Ch1* is located on 2A (Tsunewaki 1960; Hermsen and Waninge 1972) and *Ch*2 is located on chromosome 3D (Tsunewaki and Kihara 1961). The distribution of *Ch1* and *Ch2* was studied extensively in polyploid wheat and *Ae. tauschii,* the D-genome donor to common wheat (Sachs 1954; Tsunewaki and Kihara 1962; Tsunewaki and Hori 1967). The gene *Ch2* is widely distributed in all hexaploid wheats except *T. aestivum* subsp. *macha,* which unlike other 6x wheats has the *Ch1* gene. The *Ch1* gene is commonly found in the tetraploid wheats *T. turgidum* subsps. *dicoccum* and *dicoccoides* (Tsunewaki and Nakai 1973; Kochumadhavan et al. 1984). The present study seeks to identify genotypes with respect to hybrid chlorosis in 18 varieties of *T. turgidum* subsp. *dicoccum* by crossing them with the appropriate testers. The tested Thatcher is a noncarrier of necrosis.

Materials and methods. Eighteen lines of *T. turgidum* subsp. *dicoccum* were crossed to a Thatcher tester line (*ne1ne2ch1Ch2*). The F_1 hybrids and plants were raised in the greenhouse under optimum conditions. The F_1 hybrids were observed for the occurrence of hybrid chlorosis and genotype of the parents with respect to the gene for chlorosis, which was determined form the phenotype of the F_1 hybrids.

Results and discussion. The results obtained are presented in Table 1 (p. 35). All the *T. turgidum* subsp. *dicoccum* lines produced strong chlorotic F_1 hybrids when crossed to Thatcher (*ne1ne2ch1Ch2*-carrier), indicating that they carry the *ch1* gene. Because hybrid chlorosis results from the complementation of the *ch1* and *ch2*, the *T. turgidum* subsp. *dicoccum* accessions have the *Ch1* gene. The *Ch1* gene is located on chromosome 2A (Hermson and Waninge 1972),

Table 1. Genotypes of *Triticum turdgidum* subsp. *dicoccum* lines tested for hybrid chlorosis**.** The tester line Thatcher was *ne1ne2Ch1Ch2*.

Line	Tester	Genotype of F_1 hybrid	Genotype of *dicoccum* line tested
Mexican dwarf	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Mexican dicoccum-1	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Mexican dwarf dicoccum-2	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW – 3	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 25	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 38	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 58	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 64	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 69	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Khapli Yellow	Chlorotic	*Ch1Ch2*	*Ch1ch2*
SWAN	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Madamapally local-2	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Madamapally local-7	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Ketti local	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Pink Khapli	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 1016	Chlorotic	*Ch1Ch2*	*Ch1ch2*
HW 1017	Chlorotic	*Ch1Ch2*	*Ch1ch2*
Sangli 2-1	Chlorotic	*Ch1Ch2*	*Ch1ch2*

whereas *Ch2* is on chromosome 3D (Tsunewaki and Kihara 1961). Nisikawa (1967) reported that the Indian, *T. turgidum* subsp. *dicoccum* cultivar Khapli has the *Ch1* gene. Tsunewaki and Nakai (1973) have reported on a *Ch1*-carrier in *T. turgidum* subsps. *dicoccum*, *dicoccoides,* and *durum* of Ethiopian origin. The *Ch2* gene is extremely widespread in hexaploid species (97%) except in subsp. *macha* (Tsunewaki 1971). Tsunewaki and Nakai (1973) reported a high frequency (85%) of *Ch1*-carriers in *T. aestivum* subsp. *macha*. A wide prevalence of the *Ch1* gene in *T. turgidum* subsp. *dicoccum* from India has been reported (Kochumadhavan et al. 1984).

A high level of chlorosis was observed in all F_1 hybrids from crosses between all *T. turgidum* subsp. *dicoccum* lines and Thatcher. The F_1 hybrid plants did not survive beyond the one-leaf stage (severe chlorosis), indicating a very strong interaction between the alleles of *Ch1* and *Ch*2. McIntosh (1973) reported allelic variation at the *Ch2* locus. Lines of *T. turgidum* subsp. *dicoccum,* like other tetrraploid species of wheat, are either *Ne1*-carriers or noncarriers (Nishikawa 1967; Tsunewaki 1969). Because hybrid chlorosis results from complementation of the *Ch1* and *Ch2* genes, the Thatcher tester used in this study has *Ch2*. *Ch2* is distributed widely among the hexaploid wheats, except in *T. aestivum* subsp. *macha,* which has the *Ch1* gene.

The *Ch1* gene also is widely prevalent in *T. turgidum* subsp. *dicoccum* (Table 1), and it is presumed that a *Ch1*-carrying *T. turgidum* subsp. *dicoccum* was involved in the origin of *T. aestivum* subsp. *macha*. Our results show a high frequency of *Ch1*-carriers in *T. turgidum* subsp. *dicoccum* lines of Indian origin, because the *Ch1* gene was present in all *T. turgidum* subsp. *dicoccum* lines tested.

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A biochemical investigation of rust-resistant, near-isogenic wheat lines.

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Through a backcross breeding program, 28 NILs in the BC_2F_5 and BC_5F_5 involving four Indian wheat cultivars (HW 517, HD 2135, HD 2204, and UP 301) and seven donor wheat stocks with four leaf rust-resistance genes (*Lr19, Lr28, Lr32*, and *Lr37)*, six stem rust resistance genes (*Sr25, Sr26, Sr27, Sr34, Sr36*, and *Sr38*), and two stripe rust resistance gene (*Yr8* and *Yr17*) present either singly or in combination (linked condition) were produced. Immune to moderately resistant reaction at the seedling stage and highly resistant reaction at adult-plant stage from the aforementioned genes strongly advocate the use of specific rust-resistance genes for durable resistance. Specific rust-resistance genes such as *Lr19, Lr28, Lr32*, *Lr37, Sr25, Sr26, Sr27, Sr34, Sr36*, and *Sr38* provided single-gene resistance, whereas the stripe rust-resistance genes *Yr8* and *Yr17* provide their resistance in combination with other resistance genes already present in the genetic background of recurrent parents. The benefit from well-characterized traits or resistance based on resistance genes will come only from a detailed investigation of the biochemical pathways involved in host-plant resistance. The NILs were evaluated for various biochemical parameters including peroxidase, polyphenol oxidase, catalase, chitinase, lipoxygenase, ribonuclease, lipid, soluble protein, free amino acids, proline, phenols, and tannin content. In addition, chlorophyll content, nuclear DNA, and respiration rate also was studied to differentiate susceptible wheat parents and their rust-resistant NILs. Changes in biochemical parameters often are used indirectly to confirm gene transfers.

Peroxidase and polyphenol oxidase activity increased in all NILs 2 to 7 days after inoculation but declined in susceptible wheat plants. Catalase and lipoxygenase activity increased more in susceptible wheat parents than resistant NILs. The specific activity of soluble protein, proline, total free amino acids, and chitinase increased more rapidly in the resistant plants than in the susceptible wheat parents. The total lipid content of the leaves showed an increase in both susceptible and rust resistant NILs 2 days after inoculation but subsequently decreased with an increase in postinoculation time.

The specific activity of both ribonuclease-I and combined ribonuclease-II and nuclease-I was high at the 15-day stage as compared to the 10-day stage in both susceptible parents and the NILs. The increase was more pronounced in the resistant lines than in the susceptible parents. Resistant NILs retained a relatively steady level of chlorophyll content, which reduced at a faster rate in the susceptible wheat parents. Respiration rate had a greater increase in the resistant NILs compared to susceptible wheat parents the third day after inoculation. The reduction in respiration rate was drastic in susceptible parents, whereas it was more or less constant in the resistant NILs. A significant increase in total free phenols, tannins, and nuclear DNA content was observed in the NILs over the recurrent parents.

The effect of sodium stearoyl-2-lactylate on rheological properties, baking, and pasting quality in three Indian bread wheats.

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Three hexaploid bread wheat cultivars, HS 240, HUW 549, and VL 852, were used to study the effect of the additive sodium stearoyl-2-lactylate (SSL) on rheological characteristics and baking (bread and biscuit quality) and pasting (chapatti quality) characteristics. Cleaned grain samples (10 kg) from each cultivar were milled in a Naga Research Institute Laboratory Mill, Dindigul, Tamil Nadu, India. The additive SSL is a surfactant that is light tan and does not

effect the quality of bread and other products. We studied the effect of SSL in wheat dough at different concentrations (0.1, 0.2, 0.3, 0.4, 0.5, and 0.6%). Rheologic characteristics used farinographs and extensographs according to the procedures of the American Association of Cereal Chemists**.**

The addition of SSL up to 0.4 % improved the strength and quality of the dough in all the three wheat cultivars (Table 2). The addition of SSL to the dough increased water absorption, dough stability, and the area of the extensograph curve. On the other hand, the mixing tolerance index value of the dough decreased considerably. The effect of SSL on baking and pasting quality increased the overall quality and softness of the baking (bread and biscuit) and pasta (chapatti) products. Bread score, crispness of the biscuits, and hand feel of chapattis also increased with the addition of SSL.

Table 2. Effect of sodium stearoyl-2-lactylate at different levels on the rheological properties on wheat dough of low, medium, and high quality. NA = not applicable, BU = Brabender unit.

		Level of supplementation (%)						
Characteristic	Cultivar	0.0	0.1	0.2	0.3	0.4	0.5	0.6
Farinograph water absorption (%)	HS 240	60.8	61.5	62.0	63.0	63.3	64.0	64.5
	HUW 549	58.0	58.6	58.9	59.4	59.6	59.8	60.0
	VL 852	54.2	54.8	55.1	55.3	55.8	56.0	56.3
Dough development time (min)	HS 240	4.2	4.2	4.2	4.2	4.2	4.3	4.4
	HUW 549	4.0	4.0	4.0	4.0	4.0	4.2	4.2
	VL 852	3.2	3.2	3.2	3.2	3.2	3.3	3.4
Stability (min)	HS 240	8.3	8.5	8.5	8.7	8.9	8.2	8.2
	HUW 549	6.7	6.9	7.0	7.2	7.5	6.5	6.4
	VL 852	5.6	5.7	5.8	5.8	6.0	5.5	5.4
Mixing tolerance index (BU)	HS 240	49	48	47	45	44	50	51
	HUW 549	75	75	74	72	70	76	76
	VL 852	100	97	98	97	96	101	102
Resistance to extension (BU)	HS 240	720	740	760	760	780	900	>1,000
	HUW 549	580	600	610	620	630	780	>1,000
	VL 852	430	450	470	490	510	600	>1,000
Extensibility (mm)	HS 240	78	80	88	89	90	97	99
	HUW 549	135	138	140	145	150	160	180
	VL 852	177	179	180	186	188	195	204
Ratio (R/E)	HS 240	4.1	4.1	4.2	4.1	4.1	4.6	NA
	HUW 549	4.3	4.3	4.4	4.3	4.2	4.9	NA
	VL 852	5.5	5.6	5.3	5.5	5.7	6.2	NA
Area (cm^2)	HS 240	155	158	160	163	165	180	NA
	HUW 549	99	100	115	120	130	160	NA
	VL 852	77	79	79	82	85	89	NA

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Improvised and effective technology of wheat seed storage in farmers' fields in eastern India.

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Introduction. Wheat is an excellent cereal crop for India that serves as a staple food for more than 65 percent of the population of India. The current level of wheat production in India is around 72 x 10^6 tons, whereas the demand for wheat is expected to be around 109 x 10^6 tons by 2020. To achieve this target yield, raising productivity per unit area by adopting modern technologies such as high yielding cultivars, improved cultural practices, and proper management of seed production and storage is needed. The seed of wheat cultivars is stored for both short (from harvest until sowing) and long (1–2 years) periods in storage houses. The inaccessibility of an organized market and imperfect pricing in local and rural markets have made it necessity for growers to store agricultural produce, giving rise to innovative indigenous and low-cost methods of seed storage. Being a cereal crop, the maintenance of wheat seed vigor and viability during storage poses several problems, especially in eastern India and warmer areas, where more than 10 x 10^6 ha of wheat have inadequate or uncontrolled environmental storage facilities.

Aspects of seed storage. The storage life of seed varies with species and cultivar. During storage, viability also is affected by various factors such as the preharvest climatic conditions, temperature, relative humidity, seed moisture content, and packing material. During storage, biotic (insects, fungi, and rodents) and abiotic (temperature, humidity, and light) factors affect the quality and viability of the seed. Roughly 10 percent of total food grains produced in the country is lost due to improper storage alone, whereas waste by insects is as much as 3 % higher than losses inflicted by other debilitating agents. Storage pests that cause significant loss include *Trogoderma granarium, Rhyzopertha dominica, Tribolium castaneum, Sitotroga cerealella*, and *Sitophilus oryzae*.

Methodology and approach. The study was part of a study on seed production and storage conducted in eastern India under the National Agricultural Technology Project. Five different sites were selected, with consideration of their typical, highly humid conditions with respect to seed storage and source of seeds. The respondents comprising 170 farmers were taken randomly from previously selected sites. A comprehensive questionnaire, schedule was prepared incorporating all related variables to be studied. The respondents were contacted personally for collecting the relevant data.

Results and trends. The survey conducted on 170 farmers in eastern India has shown that only 35 percent of the farmers use their own seed, 15 percent purchase seed from neighbors, 30 percent purchase from nongovernmental agencies, and nearly 20 percent purchase seed from governmental seed agencies (Table 1). The results indicated the need for popularizing obtaining quality seed through state agricultural universities (SAUs), government organizations, and NGOs in this large wheat-growing area.

Table 1. Source of wheat seed purchased by farmers in eastern India.

Source	Number of farmers	Percent of farmers
Own seed	60	35
Private agency	51	30
Government organization	33	20
Neighboring farmer	26	15

Methods of seed storage. Our survey, conducted on wheat seed production and storage by the farmers in eastern India, revealed that one percent of the farmers use polybags and five percent farmers use metal bins (Table 2). The survey also highlighted the need for more scientific methods of seed storage at the farmer's own field, which also will help in providing high quality seed for wheat crop cultivation at an affordable cost. The highest percentage (88%) of the farmers packed the seed in gunny bags after drying and kept them in wheat straw, the traditional method of seed storage.

Table 2. Methods of seed storage of wheat used by farmers in eastern India.

Method of storage	Number of farmers	Percent of farmers
Traditional method	150	88
Metal bin	8	5
Like to know scientific method	6	4
No knowledge	4	2
Polybags	2	1

In eastern India, preharvest sprouting is forcing farmers to purchase the fresh seed every year, which they can not afford due to lack of resources. Grain deterioration in storage can be minimized or prevented by keeping the grain dry (less than 12.5 % moisture), cool (less than 10°C), and free from insects. A small number of resident insects in the bin or introduced with the grain when it is warm or if the grain remains in storage for a long time are some possible sources of insect infestation in stored wheat seed. A brief, high-temperature treatment of grain was found to disinfest all stages of *Sitophilus granaries* in wheat (20 minutes at 70°C) and other storage insects (2 minutes at 55°C). In eastern India, the big problem in stored wheat grain is high humidity, which causes a loss of viability. Therefore, the storage pits, bins, or go downs should be moisture proof and fumigated.

On-farm seed storage and quality. The traditional method of seed storage has certain problems and, as a result, the quality of seed produced and utilized by the farmers is very poor. The Participatory Varietal Selection (PVS) program in this region of India was initiated to emphasize the issue of quality seed production and storage. An on-farm seed production and storage system will not only enhance production, but also will help to make this vast wheat-growing region self-sufficient.

Under this program, freshly harvested seed of five wheat cultivars, NW 1014, HD 2643, K 9107, HW 2045, and HD 2733, were stored at selected locations in poly-lined gunny bags to demonstrate a low cost and safe storage system.

At the time of next sowing the bags were opened up and germination percent was tested. In all five cultivars at all sites, germination percentage was very good, ranging between 90 and 98 %, even after storing the seed for one year (Table 3).

Table 3. Seed quality as determined by germination percentage of wheat seed stored in poly-lined gunny bags at selected sites in eastern India.

	Seed storage sites		
Cultivar	I	II	III
NW 1014	96	90	98
HD 2643	94	92	96
K 9107	95	91	95
HW 2045	93	94	97
HD 2733	94	92	96

The above described and demonstrated system of wheat seed storage is much better and more cost effective than the traditional system, being an improved version of the local seed-storage system that still has good scope and potential for quality seed production. This method will help to improve the local availability of quality seed and also the horizontal spread of new technology.

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Diversifying the genetic base for resistance in Indian bread wheat cultivars through introgression and pyramiding of newer, effective stem rust-resistance genes to combat the threat from the Ug99 pathotype virulent on Sr31.

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Introduction. In India, wheat is cultivated on approximately 26 x 10^6 ha with a present day production level of 72 x 10^6 tons. Wheat production has stagnated at around 72 x 10^6 tons for the past 5 years, and we are resorting to imports to meet the requirement of a targeted, public distribution system. To meet the ever increasing demand for wheat grain resulting from population growth, a reduction in area under wheat due to crop diversification, and other biotic and abiotic stresses, we need to reorient our research priorities. The wheat crop in India is grown under various micro- and macroclimatic zones and varied production conditions. The entire region is under the constant threat from stem and leaf rust epidemics. Because of limited use, diverse gene sources for rust resistance are needed for the release of cultivars for commercial cultivation.

The need to diversify the genetic base. Most of our present day cultivars have the gene complex *Sr31, Lr26* (not effective in India), *Yr9* (a new virulent pathotype reported), and *Pm8*, because of the significant yield advantage associated with it in addition to resistance to rust diseases in spring wheat. With the occurrence of the new, virulent stem rust pathotype Ug99, a threat to wheat production worldwide is possible. Ironically, in a Ug99 epidemic, no wheat-producing country in the world is safe, although each zone is protected by micro- and macroenvironmental conditions and the

dispersal mechanism of rust pathogens. In India, avoiding such a rust epidemic will be by deploying new cultivars with new, diverse gene sources in a mosaic pattern to curtail evolution and spread of new rust pathotypes.

Nagaranjan and Singh (1990) reported that the Indian subcontinent, though at a less risk, needs to diversify gene sources to tackle such threats. As the global environmental changes, frequent human travel across the globe can incidentally cause damage, although it could be insignificant. A certain level of genetic diversity in currently grown wheat cultivars in India may not offer a high level of protection against the Ug99 or the likely emergence of future races of all three rusts. Incidentally, a few genes, such as *Sr24* (a virulent pathotype 40-1 for *Sr24* has been reported from India) and *Sr25* have been effective against Ug99 and fully exploited. The gene sources evaluated at Kenya (Njoro) indicated that a number of stem rust-resistance genes, *Sr14*, *Sr24*, *sr25*, *Sr26*, *Sr27*, *Sr29*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr39*, *Sr40*, and *Sr44*, conferred resistance against the race Ug99 (Singh et al. 2006).

Work already done in India. A number of NILs carrying *Sr24*, *Sr25*, *Sr27* (*Ag. elongatum*), and *Sr26* (*S. cereale* cv. Imperial) have been developed in India in the background of the popular Indian wheats C 306, Kalyansona, Lok-1, WH147, and HUW 234 (Tomar and Menon 2000, 2001). The transfer these genes has been confirmed by molecular studies (Kumar et al. 2006). However, considering any stem rust epidemic due to pathotype Ug99, which can spell doom for wheat production in India, front now we need to formulate our new strategy to combat this threat. Although some Indian commercial wheat cultivars do confer resistance against Ug99, we should not remain complacent on this very serious issue. Thus, a well-planned, scientific and systematic crop improvement approach to tackle this issue is needed.

Scientists worldwide are advocating a durable resistance mechanism by exploiting vertical resistance sources. The targeted of effective stem rust genes in a cultivar background already carrying specific leaf and stripe rust genes can effectively combat this new stem rust pathotype.

Strategies and approaches. The present situation demands strategic preparedness to tackle the perceived threat from stem rust epidemics, particularly from one like Ug99 that is virulent on *Sr31*. Our first priority is to utilize resistance sources already available in the background of popular Indian bread wheat cultivars. The long-term strategy is to diversify gene sources for resistance to stem rust with newer genes such as *Sr24*, *Sr26*, *Sr27*, *Sr29*, *Sr32*, *Sr33*, *Sr33*, *Sr36*, *Sr39*, *Sr40*, and *Sr44*, which confer effective resistance against Ug99 (Singh et al. 2006*).* These genes should be pyramided in the background of a targeted cultivar(s) already carrying resistance genes for leaf and stripe rusts to combat stem rust in more scientific and efficient way. Many popular Indian bread wheat cultivars developed at the IARI Regional Station in Wellington carry *Lr19+Sr25*, *Lr24+Sr24*, *Lr28*, *Lr32*, and *Lr37* and can effectively be utilized for further incorporating effective new stem rust genes.

Marker-assisted backcross selection offers a more efficient way of selecting material carrying the targeted genes, although there is an inherent risk of producing a low-yielding phenotype. We need to slightly modify our approach, effectively using backcross selection to introgress targeted genes in a particular cultivar background. The simultaneous validation of markers and seedling evaluation for host-pathogen interaction to confirm the presence of these genes in more than one elite, high-yielding phenotype in each cultivar background will offer useful material, and these lines will be used for for multilocation testing and further selection.

Work already initiated at IARI, RS, Wellington to develop rust resistant wheat lines with effective genes against the Ug99 stem rust pathotype. Newer genes for stem rust resistance and their source, chromosomal location, which were used for the backcross program, are in Table 1 (p. 42).

Popular Indian bread wheat cultivars used in this program. C 306, HD 2285, HD2402, HD2687, HS240, HUW234, K9107, Lok1, Lok bold, Lok-45, PBW226, PBW 343, PBW 502, HD2733, NIAW34, UP262, HI 977, RAJ3077, KRL99, HD 2833, and WH147.

Backcross selection at IARI, Regional Station, in Wellington, which is a hot spot for wheat rust, can take three generations of wheat in a single year. Simultaneous selection using MAS is at IARI, New Delhi, and the Directorate for Wheat Research (DWR), Karnal, for the targeted genes. The entire lot will be shuttled between the centers for selection of best yielding phenotype with specific genes with wider adaptability. Segregating material will be regularly screened at DWR, Regional Station, Shimla, for host-pathogen interaction and confirmation of the resistance offered by each targeted gene(s).

Our objectives are to

1. develop elite diverse genetic base for resistance to stem rust in select popular India wheat cultivars using modified simultaneous/ stepwise transfer of genes,
2. effectively combat stem rust disease resulting due to emergence of new rust pathotypes,
3. pyramid the effective genes in the elite wheat lines constituted through modified background selection and molecular-assisted selection,
4. develop newer isogenic lines of popular Indian bread wheat cultivars for use as donors in breeding program and use in gene tagging and if need be as new cultivars,
5. evaluate the constituted stem rust resistant lines under field conditions for yield parameters,
6. study the effect of newer genes on quantitative and qualitative traits in the popular Indian wheat background,
7. validate molecular markers for the targeted genes, and
8. study the host-pathogen interaction for the lines carrying newer rust resistance genes.

Table 1. Newer genes for rust resistance used in a backcross program at the IARI Regional Station, Wellington, India, and their source and chromosomal location. An * indicates a gene source already available at IARI Wellington.

	Genes	Source	Chromosomal location
Leaf rust genes already transferred into several cultivars	*Lr19+Sr25*	*Ag. elongatum*	7DL
	Lr24+Sr24	*Ag. elongatum*	3DL
	Lr28	*Ae. speltoides*	4AL
	Lr32	*Ae. tauschii*	3D
	Lr37+Sr38+Yr17	*Ae. ventricosa*	2AS
Stem rust genes taken for pyramiding along with the leaf rust-resistance genes	*Sr24**	*Ag. elongatum*	3DL
	*Sr25**	*Ag. elongatum*	7DL
	*Sr26**	*Ag. elongatum*	6AL
	*Sr27**	*S. cereale* Imperial	3A
	*Sr36**	*T. timopheevii*	3AL
	*Sr39**	subsp. *timopheevii*	2AS
	*Sr40**	*Ae. venticosa*	2BS
	*Sr44**	*T. timopheevii* subsp. *armeniacum*	

Expected outcomes of our approach will be to

1. effectively combat rust diseases including the present threat from Ug99 pathotype for stem rust and avoid frequent evolution of new virulent pathotypes,
2. develop elite wheat lines carrying specific stem rust resistance genes (NILs),
3. develop high-yielding and rust resistant wheat lines carrying confirmed pyramided genes for durable resistance,
4. make available diverse, genetic base material for stem rust resistance for use in the national wheat improvement program,
5. produce mapping populations for effectively targeting gene tagging, and
6. validate molecular markers linked to each targeted gene.

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ITEMS FROM JAPAN

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Nobuyoshi Watanabe.

Cytological and microsatellite mapping of the gene for brittle rachis in a Triticum aestivum–Aegilops tauschii introgression line.

Aegilops tauschii, a wild relative of wheat, has been considered to be a valuable source of variation for the improvement of cultivated wheat. However, undesirable genes can be incorporated into the cultivars from wild relatives. The spontaneous spike shattering caused by the brittle rachis character is of adaptive value in wild grass species, but not in cultivars. The rachis of R-61, which was derived from the cross of *T. aestivum* subsp. *aestivum* cultivar Bet Hashita with an accession of *Ae. tauschii*, was brittle. Using telosomic stocks, the brittle rachis gene *Br61* (tentatively designated) of R-61 was located on the short arm of chromosome 3D. The distance between *Br61* and the centromere was 31.9 cM. The distance of *Br61* from the centromeric marker *Xgdm72* was 25.3 cM on the short arm of chromosome 3D. The location of *Br61* was similar to that of *Br1*, whose location was determined by telosomic mapping and microsatellite mapping. A discrepancy of disarticulation type was found between R-61 and *Ae. tauschii*, suggesting that recombination around the regions of the *Br1* locus and *Brt* locus created the wedge-type disarticulation of R-61.

Genetic mapping of the gene affecting polyphenol oxidase activity in durum wheat.

The quality of durum wheat is influenced by polyphenol oxidase (PPO) activity and its corresponding substrates. A saturated, molecular-marker linkage map was constructed previously using a set of RILs derived from a cross between the durum wheat cultivars Jennah Khetifa and Cham 1. Quantitative trait loci for PPO activity in seeds were mapped in this population. PPO activity in seeds of the parents and 110 RILs was measured spectrophotometrically. The PPO activity of Cham 1 was significantly lower than that of Jennah Khetifa. QTL analysis of these data indicated that most of PPO activity was associated with major loci on the long arm of chromosome 2A. The trait was found to be strongly associated with the SSR marker *Xgwm312*@2A. With this knowledge, marker-assisted selection can be used to select genotypes with lower PPO activity in durum wheat populations.

Microsatellite mapping of the genes for brittle rachis on homoeologous group-3 chromosomes in tetraploid and hexaploid wheats.

The brittle rachis character, which causes spontaneous shattering of spikelets, has an adaptive value in wild grass species. The loci *Br1* and *Br2* in durum wheat and *Br3* in hexaploid wheat determine disarticulation of the rachis above the junction of the rachilla with the rachis such that a fragment of the rachis is attached below each spikelet. Using microsatellite markers, the loci *Br1*, *Br2*, and *Br3* were mapped on the homoeologous group-3 chromosomes. The *Br2* locus was located on the short arm of chromosome 3A and linked with the centromeric marker *Xgwm*32 at a distance of 13.3 cM. The *Br3* locus was located on the short arm of chromosome 3B and linked with the centromeric marker *Xgwm72* (at a distance of 14.2 cM). The *Br1* locus was located on the short arm of chromosome 3D. The distance of *Br1* from the centromeric marker *Xgdm72* was 25.3 cM. Mapping the *Br1*, *Br2*, and *Br3* loci of the brittle rachis suggests the homoeologous origin of these three loci for brittle rachis. Because the genes for brittle rachis have been retained in the gene pool of durum wheat, the more closely linked markers with the brittle rachis locus are required to select against brittle rachis genotypes and then to avoid yield loss in improved cultivars.

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ITEMS FROM MEXICO

INIFAP, CAMPO EXPERIMENTAL CENTRO-ALTOS DE JALISCO
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Evaluation of head selections from 14 elite bread wheat lines for resistance to Karnal bunt.

Guillermo Fuentes-Dávila and Miguel Alfonso Camacho-Casas.

Introduction. Karnal bunt of wheat affects bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). Generally, kernels are partially bunted (Mitra 1935; Bedi et al. 1949; Chona et al. 1961). 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 susceptibility of bread wheat has been documented (Fuentes-Dávila et al. 1992, 1993) reaching infection levels above 50% under artificial inoculations; however, there also are reports of bread wheats which consistently have shown low infection levels (Fuentes-Dávila and Rajaram 1994). Maintaing an evaluation program of new lines that have reached an advanced stage of homocygosis and which are suitable for commercial release as a measure to avoid economic problems for farmers due to Karnal bunt is important. Our objective was to evaluate individual head selections of elite bread wheat lines for resistance to Karnal bunt.

Materials and methods. Head selections from 14 elite bread wheat lines (Table 1, p. 45) were evaluated for resistance to Karnal bunt during the crop cycle autumn–winter 2003–04 in the Yaqui valley, Sonora, Mexico. Planting date was 10 December, 2003, using a 1-m bed with two rows. Inoculations were by injecting 1 mL of an allantoid sporidial suspension (10,000/mL) during the boot stage on two spikes from each of 106 head selections per line, with the exception of lines 6, 8, and 12, where 95, 94, and 103 spikes were inoculated, respectively. Harvest was manual, 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 CIMMYT and INIFAP.

Results and discussion. The range of mean infection of head selections was 1.02 to 14.7% (Fig. 1, p. 45). Sixty-five percent of the head selections had infection levels between 0 and 2.5%, 5.2% between 2.6–5%, 12.2% between 5.1–10%, 16.2% between 10.1–30%, and 1.3% had infection levels greater than 30% (Fig. 2, p. 45). Lines with less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). Although the range of mean infection was rather low, there was quite of variation among head selections within single lines. The range of infection of head selections

Table 1. Elite bread wheat lines from which head selections were obtained and evaluated under artificial inoculation with Karnal bunt (*Tilletia indica*) in the field in one planting date, during the crop cycle autumn–winter 2003–04, in the Yaqui Valley, Sonora, Mexico.

Line	Pedigree
1	RABE/6/WRM/4/FN/3*TH//K58/2*N/3/AUS-6869/5/PelotaS-Arthur/7/2*RABE/8/Irena CMSS95Y01330S-0100Y-51-1DH-0Y-05B-0Y
2	Milan/KAUZ//BABAX/3/Babax CMSS96Y03253T-050M-2Y-010M-10SY-010M-2SY-0M-0SY
3	Attila/Pastor CMSS97Y04045S-040Y-050M-040SY-030M-14SY -010M-0Y
4	Pastor//HXL7573/2*BAU CMSS97M00306S-0P5M-0P5Y-66M-010Y
5	Weebill_(35Y)
6	RDWG/Milan CMSS92Y02949S-129Y-05M-010Y-010Y-5M-0Y-5KBY-0KBY-0M
7	SITE/MO/3/Vorona/BAU//BAU CMSS93B00566S-2Y-010M-010Y-010M-4Y-0M-2KBY-0KBY-0M
8	CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii* (TAUS)/4/Weaver/5/2*Pastor CMSS93B01830M-040Y-10Y-010M-010Y-010M-10Y-0M-0KBY-0KBY-0M
9	CROC_1/*Ae.tauschii* (205)//BORL95/3/2*Milan CMSS93B01879M-040Y-1Y-010M-010Y-010M-6Y-0M-3KBY-0KBY-0M
10	Fiscal (11Y) CMSS95Y01596S-4Y-010M-010Y-010M-11Y-0Y-1M-0Y
11	Fiscal (27Y) CMSS95Y01596S-4Y-010M-010Y-010M-27Y-0Y-1M-0Y
12	Soroca CMSS96Y02567S-040Y-020M-050SY-020SY-6M-0Y
13	Irena/Babax//Pastor CMSS96M05638T-040Y-26M-010SY-010M-010SY-4M-0Y
14	CNO79//PF70354/MUS/3/Pastor/4/Babax CMSS97M02936T-040Y-030M-040SY-030M-040SY-21M-0Y-0SY

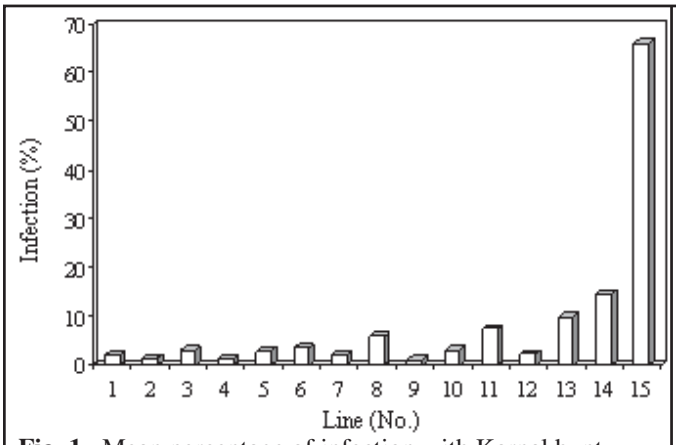

Fig. 1. Mean percentage of infection with Karnal bunt (*Tilletia indica*) of head selections derived from 14 elite bread wheats after artificial field inoculation at one planting date during the crop cycle autumn–winter 2003–04 in the Yaqui Valley, Sonora, Mexico. Line 15 = WL711, the susceptible check.

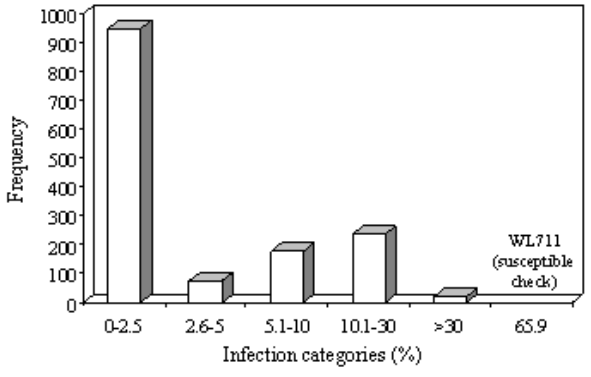

Fig. 2. Results of artificial field inoculations with Karnal bunt (*Tilletia indica*) of 1,458 head selections derived from 14 elite bread wheats after artificial field inoculation at one planting date during the crop cycle autumn–winter 2003–04 in the Yaqui Valley, Sonora, Mexico. The level of infection of the check WL711 is the average of the three highest levels.

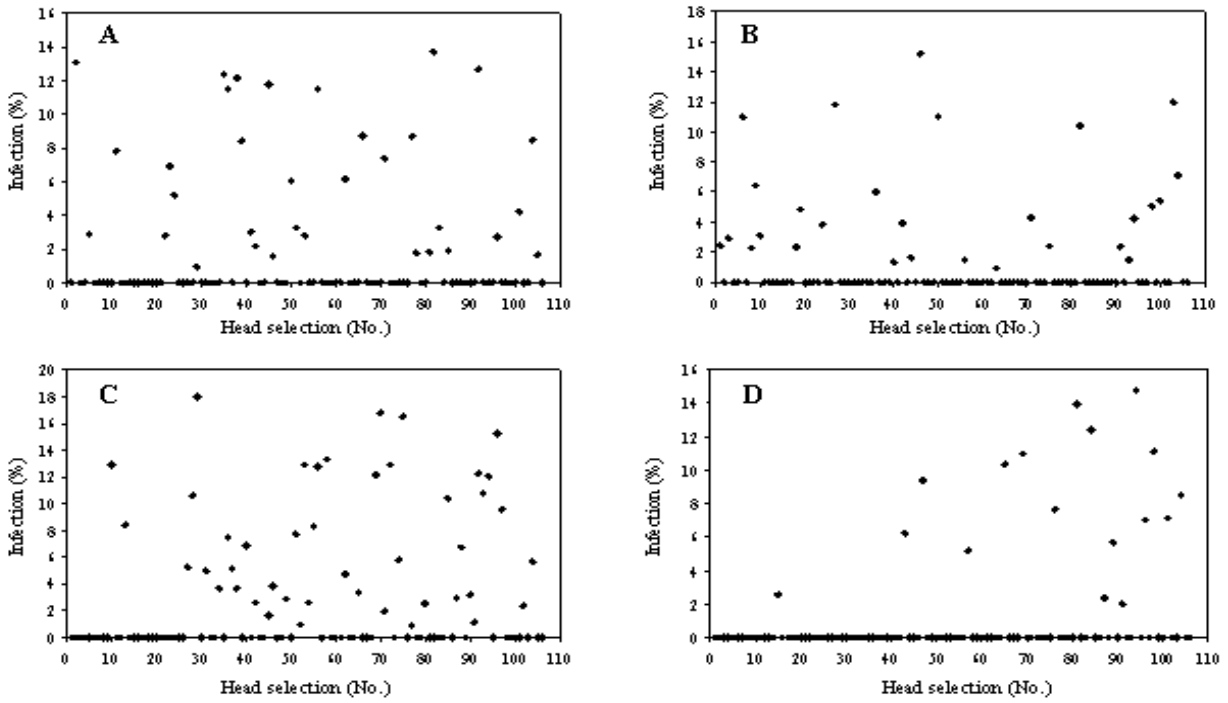

Fig. 3. Percent infection with Karnal bunt on 106 head selections derived from the elite bread wheats RABE/6/WRM/4/FN/3*TH//K58/2*N/3/AUS-6869/5/Pelota S-Arthur/7/2*RABE/8/Irena (A), Milan/KAUZ//Babax/3/Babax (B), Attila/Pastor (C), and Pastor//HXL7573/2*BAU (D), after artificial field inoculation at one planting date during the crop cycle autumn–winter 2003–04 in the Yaqui Vallye, Sonora, Mexico.

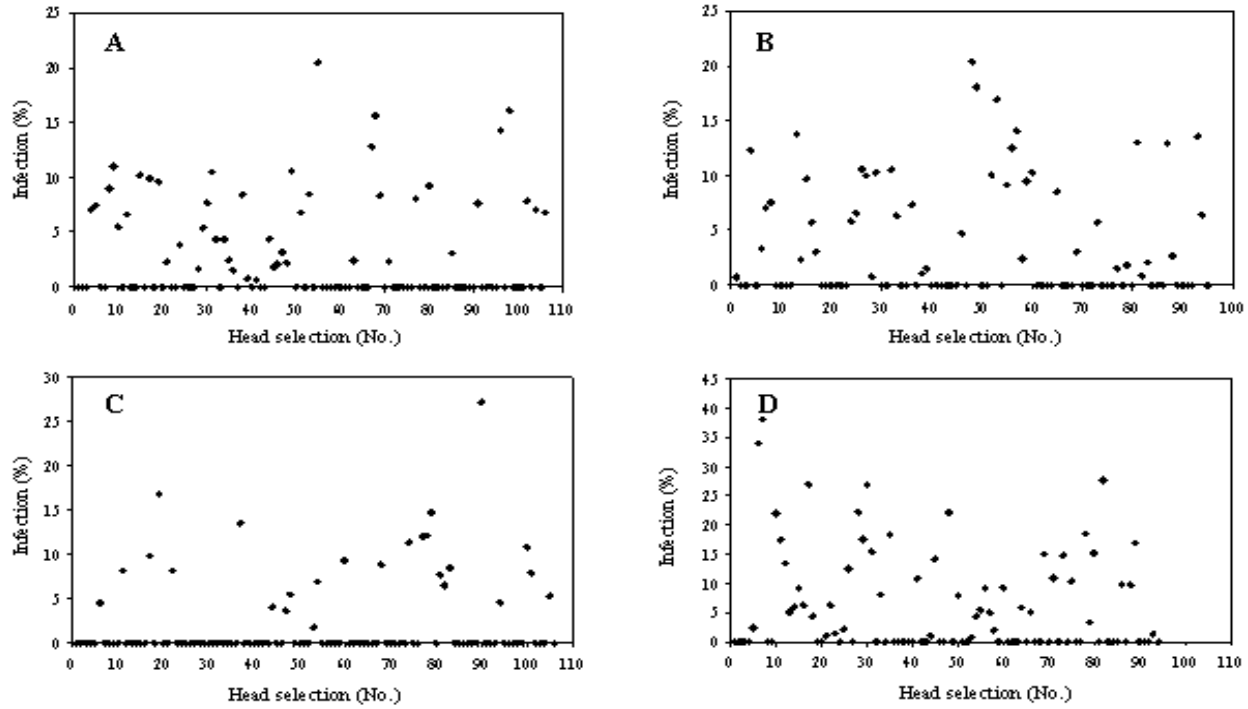

Fig. 4. Percent infection with Karnal bunt on 106 head selections derived from the elite breat wheats Weebill_(35Y) (A), RDWG/Milan (95 head selections, B), SITE/MO/3/Vorona/BAU//BAU (C), and CNDO/R143//ENTE/MEXI_2/3/*Ae. tauschii*/4/Weaver/5/2*Pastor (94 head selections, D), after artificial field inoculation at one planting date during the crop cycle autumn–winter 2003–04 in the Yaqui Valley, Sonora, Mexico.

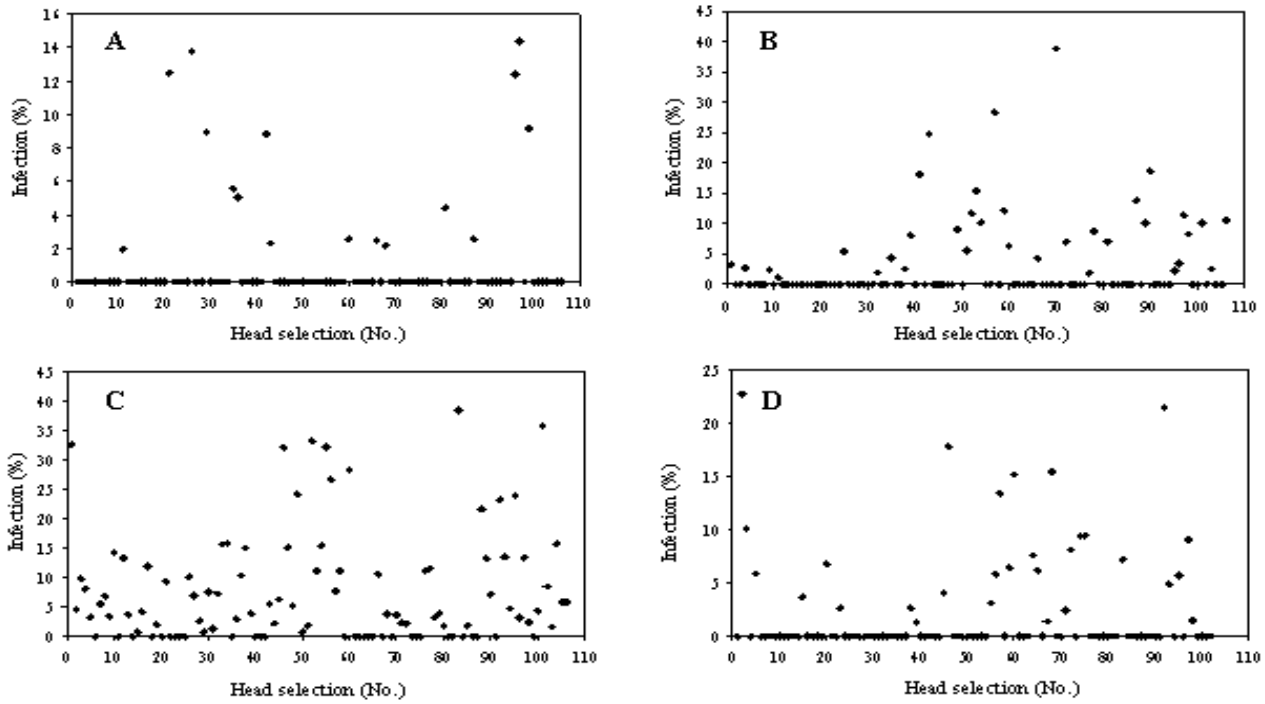

Fig. 5. Percent infection with Karnal bunt on 106 head selections derived from the elite bread wheats CROC_1/*Ae. tauschii* (205)//BORL95/3/2*Milan (A), Fiscal (11Y) (B),Fiscal (27Y) (C), and Soroca (103 head selections, D), after artificial field inoculation at one planting date during the crop cycle autumn–winter 2003–04 in the Yaqui Volley, Sonora, Mexico.

derived from lines 1 to 14 were 0–13.7, 0–15.2, 0–17.9, 0–13.9, 0–20.5, 0–18, 0–27.1, 0–38.1, 0–14.3, 0–38.9, 0–38.5, 0–22.8, 0–30.1, and 0–41, respectively (Figs. 3–6, pp. 46-47). Head selections with the highest levels of infection derived from the following lines: IRENA/BABAX//PASTOR, CNDO/R143//ENTE/MEXI_2/3/AEGILOPSSQUARROSA (TAUS)/4/WEAVER/5/2*PASTOR, FISCAL (27Y), FISCAL (11Y), and CNO79//PF70354/MUS/3/PASTOR/4/BABAX, with 30.1, 38.1, 38.5, 38.9, and 41%, respectively. These results indicate that a) escapes are more possible when inoculating a low number of spikes, and in only one planting date, as this was the case and b) segregation might be responsible in part for the variation in levels of infection within lines, because elite lines are bulked in F_6 and F_7. However, additional testing of greater number of spikes in more planting dates would be necessary to confirm the resistance shown by the group of head selections with infection levels between 0 and 5%.

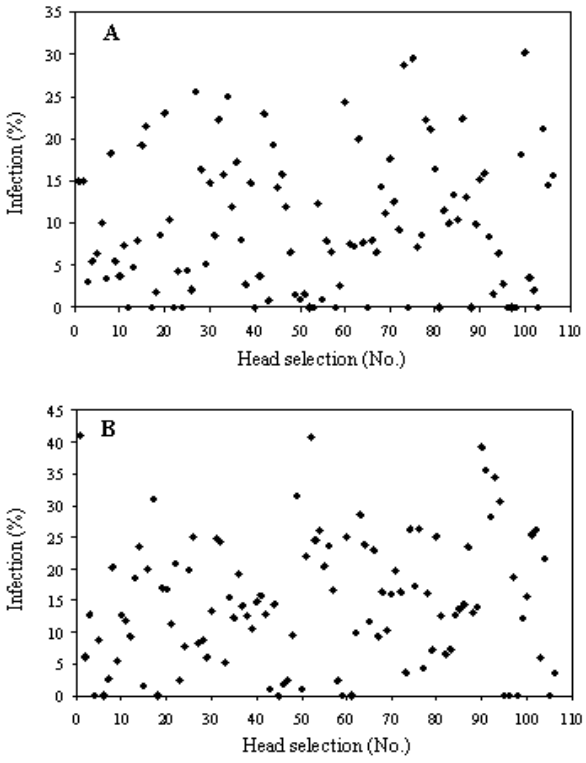

Fig. 6. Percent infection with Karnal bunt on 106 head selections derived from the elite bread wheats Irena/Babax//Pastor (A) and CNO79//PF70354/MUS/3/Pastor/4/Babax (B) after artificial field inoculation at one planting date during the crop cycle autumn–winter 2003–04 in the Yaqui Valley, Sonora, Mexico.

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Reaction of wheat cultivars WL-711 (Triticum aestivum) and Altar C84 (T. turgidum subsp. turgidum) to inoculation with Tilletia indica cultures obtained from infected wheat cultivars Baviacora M92 (T. aestivum) and Altar C84 under natural conditions in the Yaqui valley, Sonora, Mexico.

Irazema Fuentes-Bueno (Instituto Technológico de Sonora) and Guillermo Fuentes-Dávila.

Introduction. Since the early 1980s, a project on breeding for resistance to Karnal bunt in the Yaqui Valley was initiated by the wheat program of CIMMYT (Metzger 1986). The project contemplated three main objectives: a) identification of sources of resistance, b) hybridization to incorporate resistance genes into suitable genotypes, and c) evaluation of advanced lines (Fuentes-Dávila 1997). During the course of the project, artificial inoculations in the field have been an essential component (Fuentes-Davila et al. 2001), because disease incidence is quite erratic in the Yaqui Valley (Lira-Ibarra 1992). The inoculum used has been a mixture of fungal cultures obtained from teliospores produced in wheat commercially grown and naturally infected in the Yaqui Valley (Fuentes-Dávila and Rajaram 1994). Our objective was perform preliminary testing of fungal cultures of *T. indica* for physiologic specialization.

Inoculum preparation. Infected grains from cultivars Baviacora M92 and Altar C84 were obtained from commercial fields in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2002–03. Teliospores were scraped off infected grains with a dissecting needle and kept in a water–Tween 20 solution for 24 h, then the suspension was filtered through a 60 µm nylon sieve and centrifuged at 3,000 rpm. After discarding the supernatant, sodium hypochlorite (0.5% a.i.) was used to disinfect teliospores for 2 min while centrifuging again. Teliospores were then rinsed twice with sterile distilled water while centrifuging. Teliospores were resuspended in sterile distilled water in the centrifuge tube, and one mL of the teliospore suspension was spread on Petri plates with 2% water-agar (AA), which were incubated at 20°C in the dark. After 6 to 9 days, teliospore germination was evaluated using a compound microscope at 10X. Pieces of AA with germinated teliospores were removed and placed upside down on the lid of Petri plates containing potato-dextrose-agar (PDA). After 10 to 14 days, 2 to 3 mL of sterile distilled water were added to the plates and the colonies were scraped gently using a sterile spatula. Hyphae and sporidia were inoculated onto other plates with PDA using a sterile syringe, and the plates were incubated at 20°C in the dark for about nine days. After incubation, pieces of PDA with the

different fungal propagules were transferred and placed upside down on the lids of sterile glass Petri plates, in order to induce production of allantoid secondary sporidia (Dhaliwal and Singh 1989; Fuentes-Dávila et al. 1993). Three mL of sterile distilled water were added to the bottom of the plates. Plates with fungal propagules derived from teliospores produced on Altar C84 and Baviacora M92 were kept separately. Water from the plates was collected every 24 h, secondary allantoid sporidia were collected and counted using a hemocytometer; then, the concentration was adjusted to 10,000/mL.

Artificial inoculation in the field. Twenty heads of the cultivars WL-711 (susceptible) and Altar C84 (resistant) were inoculated by injecting 1 mL of the allantoid sporidial suspension during the boot stage (stage 49, Zadoks et al. 1974), in five planting dates (10, 21, 22, 23, and 24 February). Harvest was done manually, and the counting of healthy and infected grains was done by visual inspection to calculate the percentage of infection (infected grains).

Results. The reaction of WL-711 and Altar C-84 to fungal cultures used in this study showed some consistency. In general, the percentage of infection was low in WL-711, perhaps due to high temperatures that predominated at the end of February (average 26.6˚C during the last four planting dates), and the low relative humidity. The culture obtained from *T. turgidum* subsp. *turgidum* caused the greatest infection level on WL-711 with 27.5% in the first planting date; however, the range of infection in the following dates was 0.14 to 3.31% (Fig. 7A). The number of infected heads varied considerably among dates; in 10 February there were 16 infected heads, while in Feb. 21, 22, 23, and 24 there were 1, 1, 8, and 3, respectively (Fig. 8, p. 50). The highest percent infection in individual heads was 90% for 10 February, and 1.89, 6.8, 22, and 10.3% for the rest of the dates, respectively. This culture also caused infection in Altar C84, but the levels of infection were low, which might be expected, because this cultivar is resistant to Karnal bunt (range of infection 0 to 1.47%) (Fig. 7B). The number of infected heads was lower than in WL-711, with 0, 7, 0, 1, and 8 for the different dates. The highest infection levels in individual heads were 2.8, 5.5, and 13.3 for 21, 23, and 24 February, respectively (Fig. 9, p. 51).

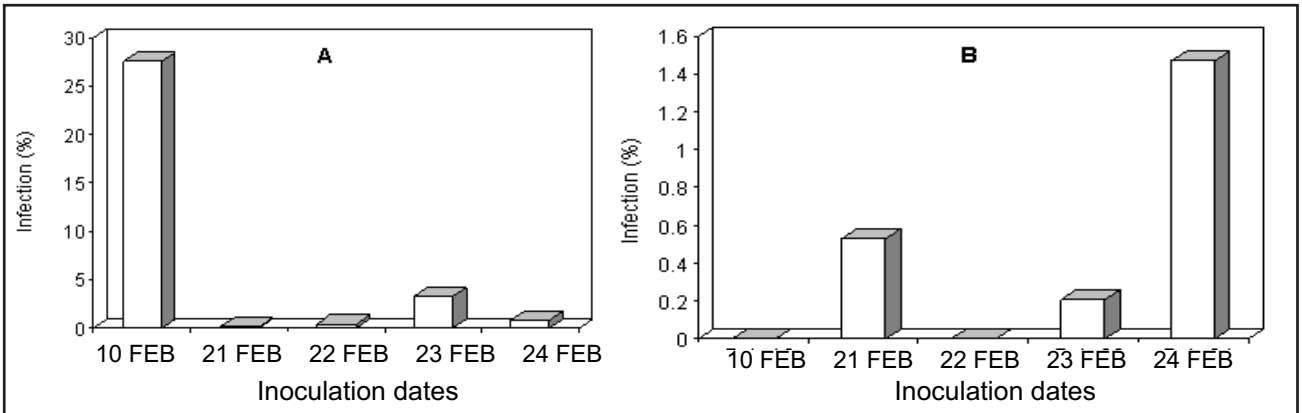

Fig. 7. Mean percent infection obtained in five dates, from inoculum originated from *Tilletia indica* teliospores produced in the cultivar Altar C84 under natural conditions and inoculated on cultivar WL-711 (susceptible bread wheat) (A) and on Altar C84 (resistant durum wheat) (B).

The fungal culture obtained from *T. aestivum* caused the greatest level of infection on WL-711 on the third planting date with 14.12% (Fig. 10A, p. 51). This culture showed more consistency in the infection level of WL-711 than the previous culture, with a range of 2.82 to 14.12%. Also, this culture showed more consistency in relation to a greater number of infected heads, with 15, 10, 17, 6, and 13 for 10, 21, 22, 23, and 24 February, respectively (Fig. 11, p. 52). The highest levels of infection in individual heads were 37, 32, 45, 24, and 10.3 for the different dates. Altar C84 showed a resistant reaction to this fungal culture with a range of infection of 0 to 0.95% (Fig. 10B, p. 51). The number of infected heads was 2, 0, 3, 3, and 2 for 10, 21, 24, 23, and 24 February, respectively (Fig. 12, p. 53). The highest levels of infection in individual heads were 7.9, 14.3, 15.6, and 4.3 for 10, 22, 23, and 24 February, respectively.

Although differences were found in levels of infection and in number of infected heads of WL-711 and Altar C84, after artificial inoculation with individual fungal cultures obtained from naturally infected durum and bread wheat, the results do not indicate physiologic specialization. Further studies should be conducted, including molecular characterization of fungal cultures.

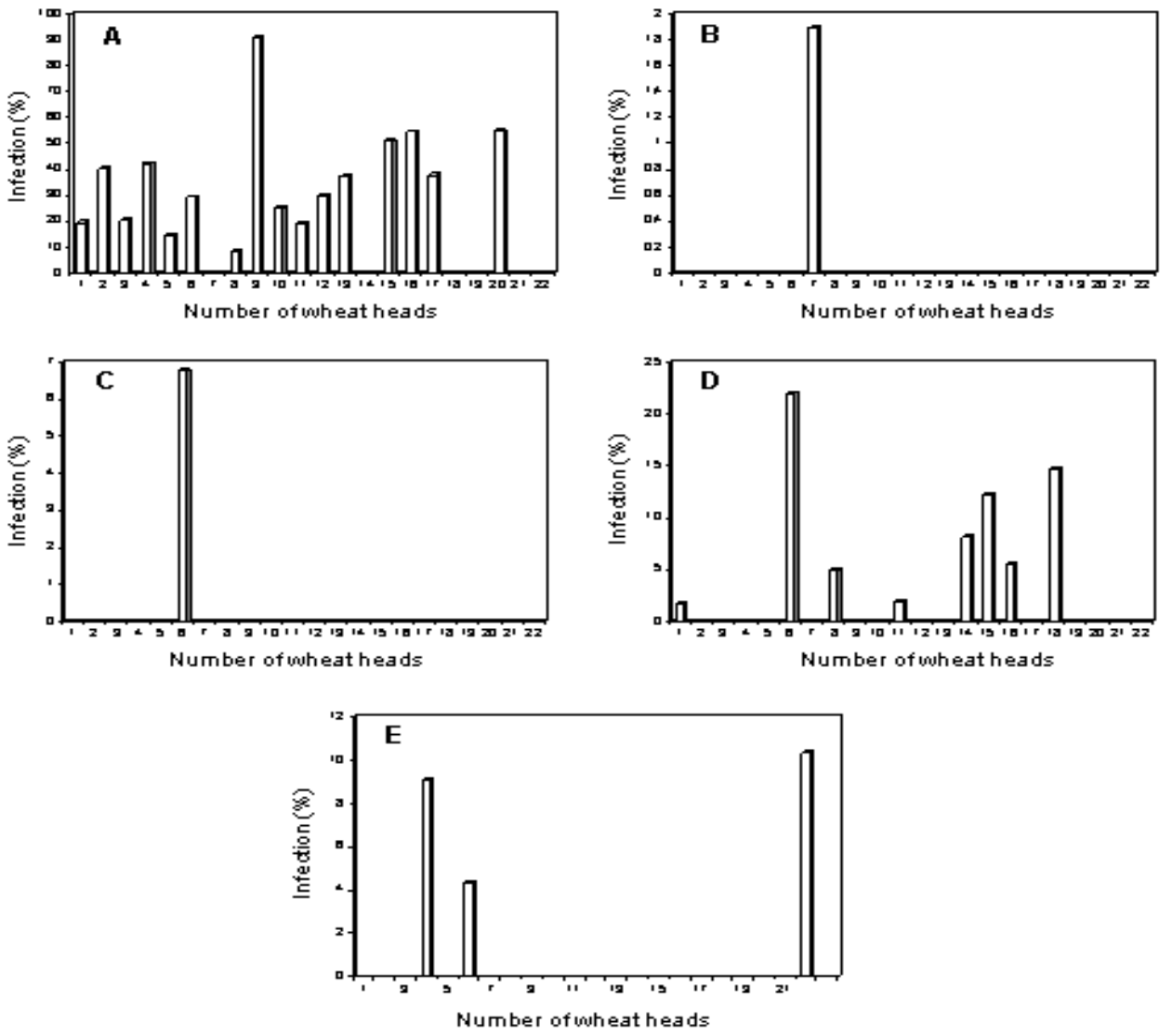

Fig. 8. Percent infection and number of infected heads in five planting dates (10 FEB (A), 21 FEB (B), 22 FEB (C), 23 FEB (D), and 24 FEB (D)) by inoculum originated from *Tilletia indica* teliospores produced in the cultivar Altar C84 under natural conditions and inoculated on cultivar WL-711 (susceptible bread wheat).

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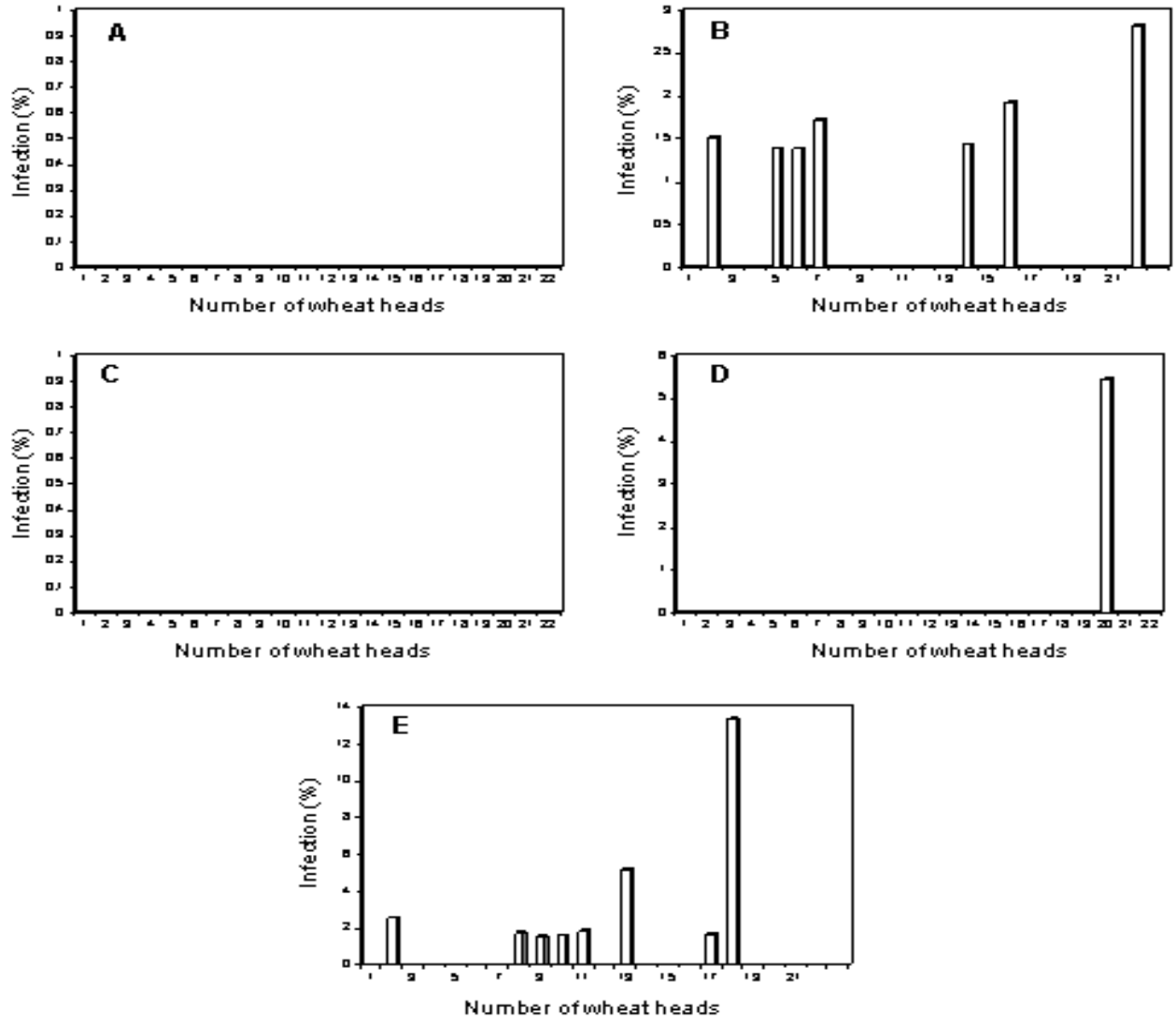

Fig. 9. Percent infection and number of infected heads in five planting dates (10 FEB (A), 21 FEB (B), 22 FEB (C), 23 FEB (D), and 24 FEB (D)) by inoculum originated from *Tilletia indica* teliospores produced in the cultivar Altar C84 under natural conditions and inoculated on the same cultivar (resistant durum wheat).

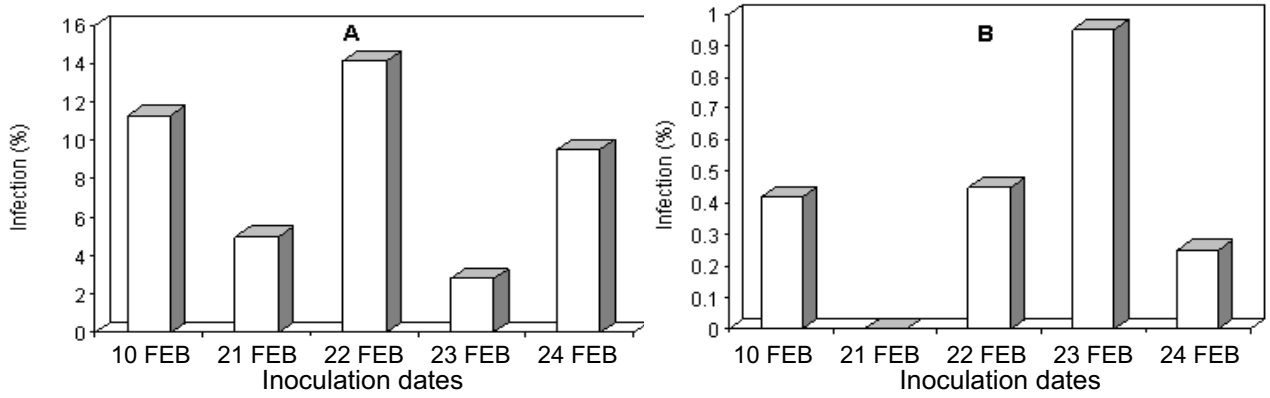

Fig. 10. Mean percent infection obtained in five dates, from inoculum originated from *Tilletia indica* teliospores produced in the cultivar Baviacora M92 under natural conditions and inoculated on cultivar WL-711 (susceptible bread wheat) (A) and on Altar C84 (resistant durum wheat) (B).

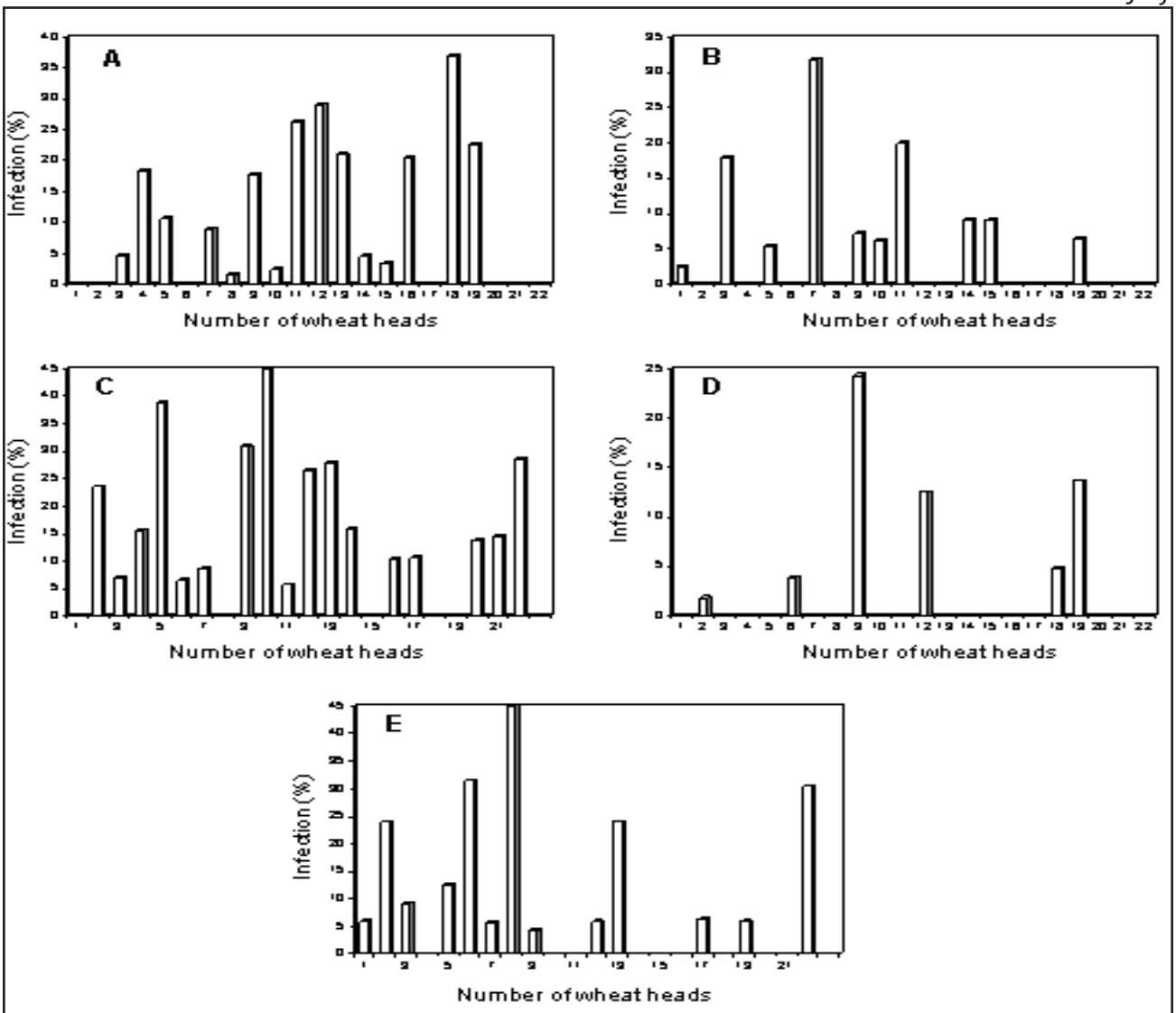

Fig. 11. Percent infection and number of infected heads in five planting dates (10 FEB (A), 21 FEB (B), 22 FEB (C), 23 FEB (D), and 24 FEB (D)) by inoculum originated from *Tilletia indica* teliospores produced in the cultivar Baviacora M92 under natural conditions and inoculated on cultivar WL-711 (susceptible bread wheat).

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Reaction of advanced lines and cultivars of wheat to Karnal bunt artificial inoculation.

Guillermo Fuentes-Dávila, Héctor Eduardo Villaseñor-Mir (Campo Experimental **Altos de Jalisco**), and Pedro Figueroa-López.

Introduction. Karnal bunt is caused by the fungus *Tilletia indica*. This disease occurs in bread wheat (Mitra 1931), durum wheat, and triticale (Agarwal et al. 1977). In general, infected kernels are partially affected (Mitra 1935, Bedi et al. 1949, Chona et al. 1961). The susceptibility of bread wheat has been documented (Fuentes-Dávila et al. 1992, 1993) reaching infection levels above 50% under artificial inoculations, therefore, it is important to have in place a program of evaluation of wheat germplasm, in order to provide to farmers wheat cultivars which are tolerant to this disease. The

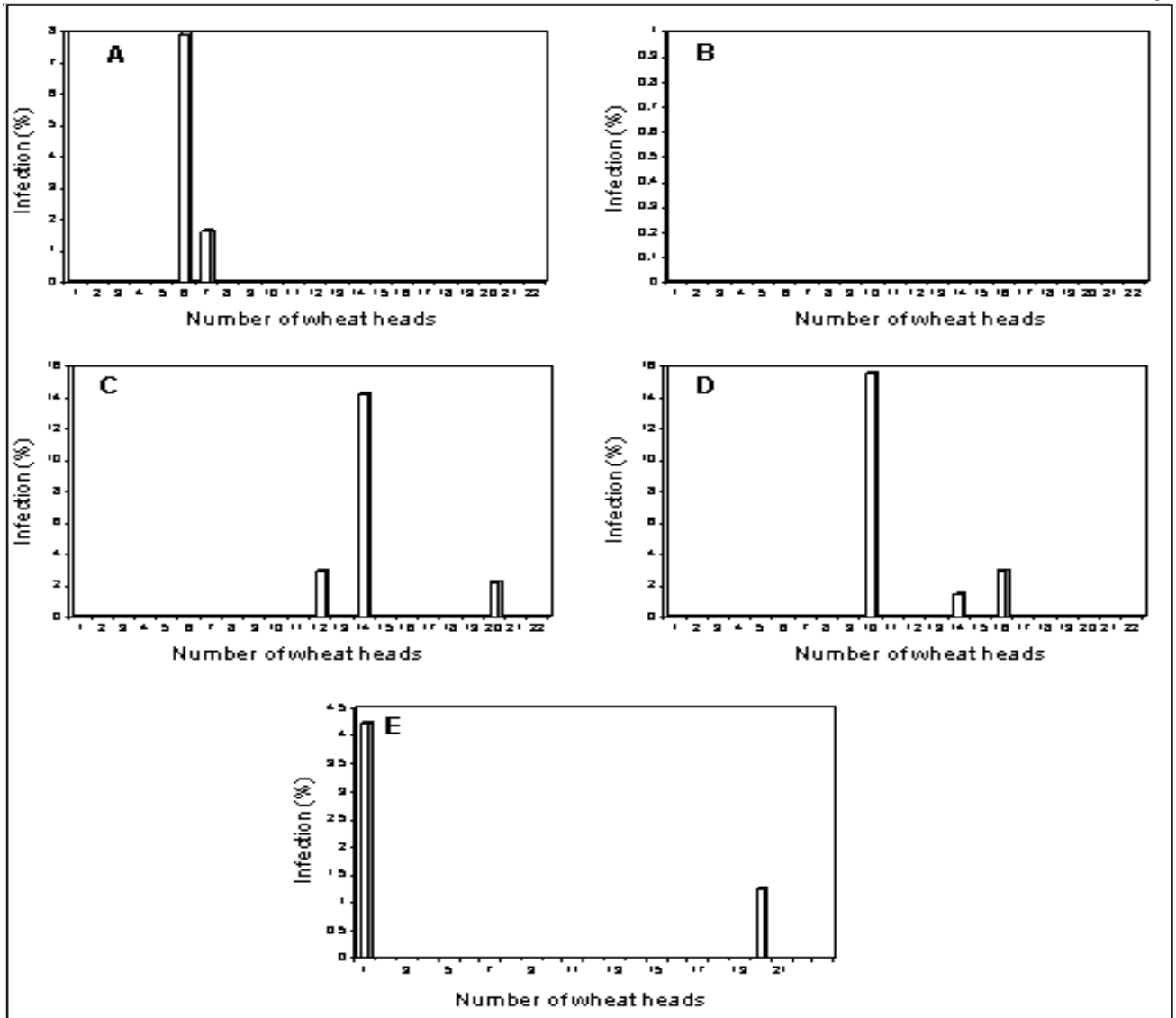

Fig. 12. Percent infection and number of infected heads in five planting dates (10 FEB (A), 21 FEB (B), 22 FEB (C), 23 FEB (D), and 24 FEB (D)) by inoculum originated from *Tilletia indica* teliospores produced in the cultivar Baviacora M92 under natural conditions and inoculated on the same cultivar (resistant durum wheat).

objective of this work was to evaluate the reaction of new wheat advanced lines and cultivars to artificial inoculation with Karnal bunt.

Materials and methods. Thirty-nine advanced bread wheat lines and eleven cultivars produced in the collaborative project CIMMYT–INIFAP, were evaluated for resistance to Karnal bunt during the crop cycle autumn–winter 2005–06 in the Yaqui Valley, Sonora, Mexico. Planting dates were 28 November and 19 December, 2005, using approximately 10 g of seed in 1-m beds with two rows. A mist irrigation system was used 3 to 5 times each day for 15 min each time, to provide high relative humidity in the experimental area. Inoculations were by injecting 1 ml of an allantoid sporidial suspension (10,000/mL) during the boot stage on 10 heads/line. Harvest was done manually, and the counting of healthy and infected grains was done by visual inspection to calculate the percentage of infection (infected grains).

Results. The range of infection for the first planting date was 0 to 13.9%, with a mean of 4.31. In this date, 34 genotypes had infection levels below 5% (Fig. 13, p. 54). The range of infection for the second planting date was 0 to 23.9%, with a mean of 5.6; 29 genotypes had infection levels below 5% (Fig. 14, p. 54). Considering the highest levels of infection obtained in each genotype, the distribution was the following: 9 genotypes were in the 0.1-2.5 infection category, 17 in 2.6-5.0, 11 in 5.1-10.0, and 13 in 10.1-30 (Fig. 15, p. 54). The mean of the three highest infection scores

in the check was 78.6%. Lines that have less than 5% infection are considered resistant (Fuentes-Dávila and Rajaram 1994). Genotypes with the lowest mean infection level were: WBLL1*2/TUKURU, SNTURK M183.84375/NIGRIS.5//TANTLO1/3/CAMON5, BANAMICHI C2004, CROC_1/AE. SQUARROSA(213)//PGO/3/BABAX, and CROC_1/AE. SQUARROSA(224)//OPATA /3/PASTOR/4/JARU, with 0.30, 0.32, 0.41, 0.43, and 0.84%, respectively. Results of this work show that in general, the genotypes evaluated had a reaction of moderate susceptibility to Karnal bunt. Repeating evaluation of genotypes that are being considered for commercial release would be important. A combination of quality, yield, and resistance to leaf rust and to Karnal bunt is difficult in bread wheat, therefore, efforts by CIMMYT and INIFAP will continue to assure acceptable resistance levels in the new and promising materials of bread wheat, in order to produce a commercial viable crop, especially for the wheat-producing states of Mexico that will suit the industry requirements.

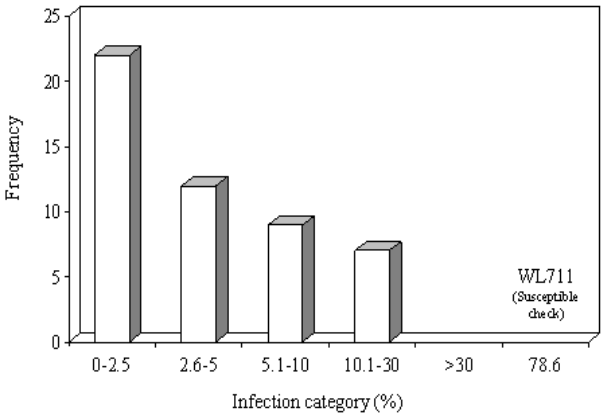

Fig. 13. Results of artificial inoculations in the field with Karnal bunt (*Tilletia indica*) in the first planting date of 50 genotypes of bread wheat in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2005–06. The level of infection of WL-711 is the mean of the three highest infection scores.

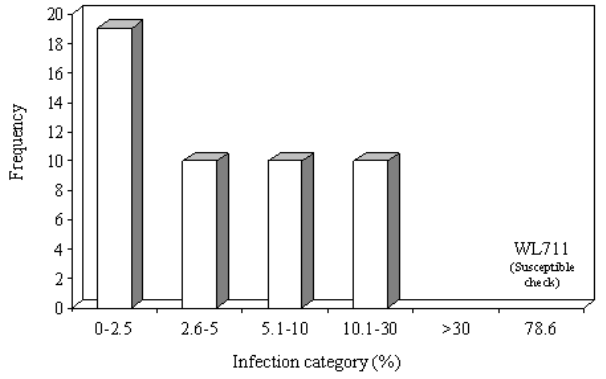

Fig. 14. Results of artificial inoculations in the field with Karnal bunt (*Tilletia indica*) in the second planting date of 50 genotypes of bread wheat in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2005–06. The level of infection of WL-711 is the mean of the three highest infection scores.

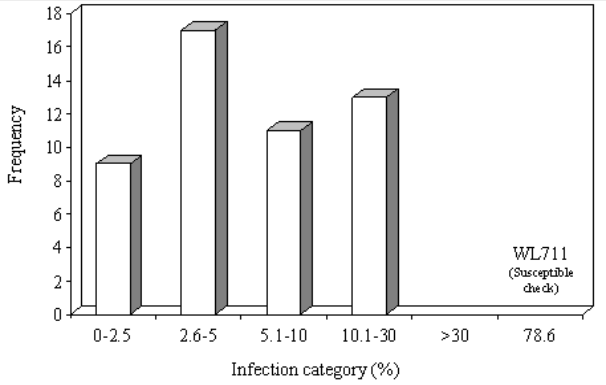

Fig. 15. Results of artificial inoculations in the field with Karnal bunt (*Tilletia indica*) in two planting dates of 50 genotypes of bread wheat in the Yaqui Valley, Sonora, Mexico, during the crop cycle autumn–winter 2005–06. The level of infection of WL-711 is the mean of the three highest infection scores.

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Tillage methods for wheat cultivation in Southern Sonora, Mexico.

Juan Manuel Cortés-Jiménez and Guillermo Fuentes-Dávila.

Introduction. Farmers in the Yaqui Valley, Sonora, Mexico, practice at least four tillage methods for wheat cultivation: conventional tillage, reduced tillage, minimum tillage, and conservation tillage (Cortés 1997). In the first method, subsoiling and plowing are considered the primary tillage operations. In the second method, both operations are eliminated, and the soil is prepared only with disking. In the third method, beds are used for several seasons; after each harvest beds are reformed and residues generally are burned. For conservation tillage, crops are established on a variable amount of harvest residues, which generally cover about 30% or more of the soil surface.

As a definition, Jasa et al. (2000) indicate that conventional tillage is the sequence of operations commonly used in a given geographic area in order to prepare the planting bed to be able to produce a specific crop. Because such activities vary under different conditions, the definition of conventional tillage varies from region to region and even within a region. Conventional tillage operations leave much less than 30% of residues after planting.

In the case of reduced tillage, the same authors indicate that this term refers to any system which is less intensive than conventional tillage. The number of operations is lower or the tillage implements require less energy by unit area than those commonly used in the conventional system. In the case of minimum tillage, they indicate that it is not a useful term, because in most cases it refers to reduced tillage (Jasa et al. 2000). In conservation tillage, most researchers coincide in pointing out that the objective is to provide a proper environment for crop development, while minimizing soil erosion caused by wind and water. Basically, this can be achieved leaving a residue cover on the soil or establishing a cover crop (Jasa et al. 2000).

Although emphasis has been given to soil conservation, water and energy conservation, as well as less depreciation of equipment and agricultural machinery, represent some additional benefits of using this technology.

An economic analysis about the most used tillage systems is in Table 2 and describes the cost of each operation involved in soil preparation. The sequence of operations for each one of the tillage methods and the total cost of soil preparation varies from one farmer to the next.

As general criteria, in the case of conventional tillage, after harvest a disking operation followed by plowing or subsoiling, then one or two diskings, planking, and bed formation is common. The cost of the most used tillage methods is described in Table 3.

In reduced tillage, preparing the soil with one or two disking operations is possible if harvest residues are burned; otherwise, 2–3 diskings are necessary to properly incorporate residues. The cost of this method with and without residue burning is $81.87 and $106.71/ha, respectively.

In minimum tillage, the bed from the previous crop is used, and the cost of preparation is equivalent to ridge-till, that is $18.39/ha. This operation should be performed once or twice to properly make the bed for the following crop. However, with the machinery available in the valley, this can only be possible after burning residues, because the amount left after the wheat harvest is proportional to the yield obtained, which fluctuates from 1.1 to 1.4 ton of residue

Table 2. Cost of tillage operations for wheat cultivation. Exchange rate in April 2007, $1 USD = 10.87 Mexican pesos.

Operation	Cost/ha ($ USD)
Plowing	53.36
Subsoiling	41.39
Disking	24.83
Planking	16.10
Bed formation	16.10
Ridge-till	16.10
Ground application	16.10

Table 3. Cost of different tillage systems for wheat cultivation, wheat season 2006–07. Exchange rate in April 2007, $1 USD = 10.87 Mexican pesos. Source: DDR-148 Cajeme.

Sequence of operations	Cost/ha ($ USD)
Disking, plowing, disking, plowing, bed formation	135.23
3 diskings, planking, bed formation (without burning residues)	106.71
2 diskings, planking, bed formation (burning residues)	81.87
2 herbicide applications	54.27
2 ridge-tills	36.79

per ton of grain produced. Nevertheless, results of research and validation of technology indicate that with minor adaptations it is possible to reuse the bed with all the residue present.

Progress. From 1996 to the present, several evaluations were made on tillage methods. In the first evaluation, plowing did not affect wheat production since yield in the check (without plowing) yielded only 35 kg less than the treatment with plowing (Table 4).

Subsoiling is considered a component of the conventional tillage method. The evaluation indicated that this operation did not have any effect on yield, which makes the relationship between benefit/cost more favorable for the treatment without the use of this implement (Table 4).

Table 4. The effect of different tillage methods on wheat yield in the Yaqui Valley, Sonora, Mexico.

Tillage method	Yield (ton/ha)
With plowing	6.998
Without plowing	6.963
With subsoiling	5.710
Without subsoiling	5.730
3 diskings, plowing, bed formation	6.670
Ridge-till	6.560
Ridge-till with residues	6.605
Ridge-till with burned residues	6.365
2 diskings, bed formation	6.855
Conservation tillage	6.835

After analyzing the effects of primary tillage, the following evaluations consisted in testing secondary or reduced tillage schemes: disking, planking, and bed formation. We observed during the evaluation, a greater economic benefit upon using the minimum tillage scheme which consisted in burning residues of previous crop and reforming the bed (Table 4).

However, burning residues is considered an unacceptable practice because of its effects on the environment. Therefore, methods for reforming the bed with residues were evaluated, and it was observed in the short term that burning residues decreased wheat yield (Table 4).

This intermediate technology consists in bed tillage, which implies using the same bed for several years, and it is only reformed after each harvest, or after the rains when there is weed infestation. With this system, it is possible to reach the planting time with a residue cover of about 30%, which does not limit the use of conventional planters.

Results of using conventional tillage in wheat, indicated that disking operations did not have any effect on yield and it only contributed to increase production costs (Table 4). Results also indicated that the cost of disking was $115.45 while conservation tillage $43.23. We observed that conservation tillage increased in $60.25 the economic return per ha, in relation to the disking treatment. According to the results, the use of tillage implements did not have any impact of economic importance on wheat production. Therefore, we concluded that the minimum number of operations should only be made in order to establish the crop. These results agree with reports by other researchers on conservation tillage under drip irrigation (Félix et al. 2003).

Even when efforts by national or international institutions to promote the use ot conservation technologies have been important, this has not been reflected in a significant increase of area planted under this system.

To reform the bed with all residues, it is necessary to adapt to the traditional implements a corrugated disk which cuts the straw before the pass of a moldboard which reforms the bed; this is done with the objective that the straw does not agglutinate or makes balls. The straw must be dry for a more efficient work. This system, similarly to conservation tillage, should be visualized as a system for which one should be prepared from the previous crop, leveling the land, controlling perennial weeds, using adequate seeding methods, and harvesting with the necessary adjustments in the combine.

Conclusions. The use of tillage implements did not have any impact of economic importance on wheat yield; therefore we can conclude that a minimum number of operations should be carried out in order to establish the crop; it is possible to implement tillage methods that are not so aggressive to the environment that allow to reduce production costs and increase the profitability of wheat in the Yaqui valley; and aside from the technical and economical aspects, information should be generated in order to determine the environmental impact that burning crop residues has on soil, air, and human health.

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ITEMS FROM PAKISTAN

NUCLEAR INSTITUTE OF AGRICULTURE (NIA)
Tando Jam, Pakistan.

Karim Dino Jamali, Saima Arain, and M.A. Arain.

Wheat breeding for semidwarf plant height and high grain yield.

The production of wheat has always been the main occupation of the farmers in the diversified agroclimatic conditions of Sindh, because wheat is an important source of human nutrition and deserves special attention. The evolution of cultivars with high yield potential and a desirable combination of traits has always been the major objective of our wheat-breeding programs. In 2005–06, an overall production of 21.7 x 10^6 tons was achieved from an area of 8.307 x 10^6 hectares, which is an improvement of 0.4% in production over last year's harvest of 21.6 10^6 tons (Table 1).

Table 1. Area, production, and average yield (2005–06) of wheat in Pakistan (Source: Ministry of Food, Agriculture and Livestock, Islamabad Pakistan).

Province	Area (x 10^6 ha)	Production (x 10^6 tons)	Yield (kg/ha)
Punjab	6.322	16.811	2,660
Sindh	0.933	2.897	3,104
NWFP	0.743	1.294	1,742
Balochistan	0.309	0.706	2,284
Pakistan	8.307	21.708	2,615

Wheat breeding at NIA Tando Jam.

Wheat breeding at NIA is being pursued with the objective of developing high-yielding, good-quality cultivars with tolerance to biotic and abiotic stresses. The institute has released nine cultivars of wheat for the province of Sindh, Pakistan, which have contributed significantly to the national economy. Currently, our breeding material is at different stages of evaluation and is summarized below.

Work done during the year 2004–05.

National Trials. The candidate line 7-03 completed 2 years of evaluation in National Uniform Wheat Yield Trials (NUWYT). This line produced comparatively higher yields than other lines, especially that in the Sindh province, and also is resistant to yellow rust with an RRI value of 6.

Advance Station Trials. Advanced lines developed at NIA were evaluated in different yield trials and the results are summarized here.

Sowing Date Trials. Wheat sowing in the Sindh province begins the 1st week of November and continues until the end of December; however, the ideal sowing period is during the first 3 weeks of November. We evaluated 15 lines at three different sowing dates (11 November, 25 November, and 22 December) with three replicates in a 9-m^2 plot for each genotype.

Sowing date 1 (11-11-2005). In this comparison, line 7-03 had the highest grain yield (1,358g)/plot. Other lines that had high grain yield/plot were 15-10 (1,258 g), 54-03 (1,250 g), 6-12 (1,233 g), 51-02 (1,200 g), 17-11 (1,200 g), 3-02 (1,183g), 14-06 (1,175 g), and 8-14 (1,175 g). The higher grain yield in line 7-03 could be due to its medium number of days-to-heading and bolder grains and line 15-10 due to its maximum number of spikelets/spike and highest main spike grain yield. Similarly, line 54-03, with a dwarf plant height, long spike (12.97cm), and greater number of grains/spikelet, and line 6-12, due to a medium heading date and higher number of spikelets/spike, also gave good yields.

Sowing date 2 (25-11-2004). In this yield comparison, line 7-03 again had the highest grain yield (1,217 g/plot). Other lines that had high grain yields were 15-10 (1,192 g/plot) and 54-03 (1,175 g/plot). The higher grain yield

in line 7-03 could be due to its higher grain weight (33.42 g); line 15-10 has a longer vegetative period resulting in delayed heading, longer spikes, a greater number of spikelets/spike, grains/spike, a higher main spike grain yield, and an increased 1,000-kernel weight (32.90 g); and line 54-03 has a tall plant height, long spikes, increased number of grains/spike and grains/spikelet, and an increased main spike grain yield.

Sowing Date-3 (22-12-2004). In this yield comparison, the highest grain yield was in line 15-10. Other lines having high grain yields were 54-03, 7-03, 6-12, and 4-03.

Mean performance over the sowing dates. In this comparison, line 7-03 (1150 g/plot) a candidate cultivar had the highest grain yield. However, line 7-03 was not significantly different from 15-10 (1,128 g/plot) and 54-03 (1,108 g/plot). Other lines with high grain yields were 6-12 (1,064 g/plot) and 14-06 (1,000 g/plot). These results show that line 7-03 has stability to perform better in different agro-ecological environments. A significant difference between the sowing dates was observed. The early sowing date had a 1,162 g/plot, the middle sowing date 1,049 g, and the late sowing date 756 g grain yield. Lines 7-03 and 15-10 had the highest mean grain yields over the three sowing dates.

Breeding material. Five F_7 trials were conducted. Each trial consisted 13 genotypes including two check cultivars. Each trial had six 3-m rows with three replicates. Agronomic and yield data were recorded for these trials.

Line 05 (817 g/plot) had the highest grain yield, followed by lines 06 (800 g/plot), 03 (767 g/plot), and 04 (758 g/plot). The high grain yield in line 05 could be due to an early heading date and increased number of spikelets/spike; in line 06 to early heading date, a high grain yield of main spike, and an increased 1,000-kernel weight; and in line 03 to the 'tall dwarf' plant height and increased number of grains/spike.

Isoline studies. Thirty isogenic lines varying for plant height (47.53 to 111.5) were selected from four different cross combinations. Line, 07 had the highest grain yield (371.7 g) followed by lines 23 (356.7 g) and 20 (338.3 g). The high grain yield in lines 07 and 23 could be due to their early heading date and semidwarf plant height. Line 20 also was high yielding, early in heading, and had a double dwarf plant height. Of the 30 lines, eight (03 semidwarf and 05 double dwarf) yielded comparatively higher than the best check cultivar Sarsabz. These studies will be continued for further selection.

Introduction of Rht8. Mara, which has *Rht*8, a new semidwarfing gene, was introduced into existing candidate lines for further studies in combination with *Rht1* and *Rht2*. *Rht*8 is GA3-sensitive, less temperature sensitive, and may not reduce coleoptile length unlike the Norin-10 genes, which tend to restrict coleoptile elongation that results in poor stand establishment.

New cultivars and germ plasm releases.

The following wheat cultivars were released for general cultivation in Sindh province of Pakistan during the year 2006:

Khirman. This cultivar was released in 2006. Khirman is a medium-duration cultivar with a high grain yield that is particularly suitable for areas where water availability is a limiting factor. The average yield of Khirman is 4,619 kg/ha with a potential yield of 7,667 kg/ha.

Sassui. The variety evolved in the year 2006, having high grain yield, bold amber grain, drought tolerant, good quality and resistant to leaf and yellow rust. Its average yield is 4700 kg/ha and potential yield is 7800 kg/ha.

Special events.

A wheat 'Field Day' and a '/Farmers' Day' are the regular activities of the institute that provide opportunities for sharing knowledge with progressive growers. Wheat 'Field Day' was held on 17 February and 'Farmers Day' on 9 March, 2006. In these events, eminent growers from the Sindh province visited the wheat fields and shared their views. These events provide a means for farmer-participatory research and technological transfer.

Publications.

Arain S, Jamali SD, Naqvi MH, Soomro AM, Arain MA, and Ali SA. 2006. Impact of molecular markers in wheat **In:** Proc Natl Symp on Biotechnology for Economic Prosperity, 24-26 July, 2006, Nathiagali, Pakistan (Abstract).

Arain S, Jamali KD, Naqvi MH, Soomro AM, Arain MA, and Ali SA. 2006. Evaluation of semi-dwarf wheat (*Triticum aestivum* L.) genotypes for yield and yield components. **In:** Proc 9th Natl Bot Conf, 13-15 February, 2006, Univ Sindh Jamshoro, Pakistan (Abstract).

Arain S, Jamali KD, Naqvi MH, Soomro AM, Arain MA, and Ali SA. 2006. Genetic diversity for agronomic characters and their association with grain yield components in durum wheat. **In:** Proc Internat Wheat Sem, 20-22 February 2006, Wheat Res Inst, Faisalabad, Pakistan (Abstract).

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ITEMS FROM THE RUSSIAN FEDERATION

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Inheritance of caryopsis pigmentation in F_1 and F_2 hybrids from 'pistilloid spring soft wheat / xenia colored-caryopsis lines'.

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In previous investigations (Kyzlasov 2001, 2003), we determined that the the segregation observed in F_1 plants from the cross combination light-colored line with bisexual flowers (female) / colored xenia caryopsis line (male) gives a dihybrid ratio of 9 dark : 7 light (Table 1). Pigmented caryopses are those F_0 caryopses set on light-colored maternal plants after hybridization.

A blue-green pigment is formed in the caryopses as a result of the complementary interaction of hypostatic genes of xenia caryopsis coloration *a* and *b*. In succeeding generations, the light-colored progeny remain unchanged, whereas progeny of the dark-colored genotype *aabb*

Table 1. Segregation pattern of a *AaBb* dihybrid for caryopsis coloration in F_1 plants from the cross 'light / xenia colored-caryopsis' (L = light-colored progeny, D = dark-colored progeny).

Paternal gametes	Maternal gametes *AB*	*Ab*	*aB*	*ab*
AB	L	L	L	D
Ab	L	L	D	D
aB	L	D	L	D
ab	D	D	D	D

also are unchanged. The *AaBb* genotypes segregate in the F_2 according to the pattern in Table 1 (p. 61). The *Aabb* and *aaBb* genotypes segregate according to a monohybrid ratio, 3 pigmented : 1 light-colored caryopsis. Therefore, the heterozygous progeny of the F_2 generation (4 *AaBb* + 2 *Aabb* + 2 *aaBb*) are expected to have a ratio of pigmented caryopses to light-colored caryopses of 9 : 7 + 12 : 4 = 1.91. The actual, observed ratio was similar; 3,831 pigmented : 1,998 light-colored = 1.92 : 1.

In our experiment, dark-colored F_0 hybrid caryopses were obtained from the cross 'pistilloid light-colored plants / xenia colored-caryopsis line'. In the F_1 plants, as expected, the ratio of pigmented : uncolored caryopses was 3,739 : 2,946 = 1.27 : 1 ≈ 1.29 : 1 (9 : 7). A deviation from the expected was observed in the F_2 hybrid population (Table 2). The ratio of pigmented caryopses (9,151) to light-colored (6,876) grains was 1.33 : 1. The expected ratio is 1.91 : 1 = 10,520 : 5,507. The calculated X^2 (518.47) greatly exceeded the limit (3.84), a significant deviation of the observed hybrid progeny segregation pattern from the expected values.

Table 2. The ratio of pigmented caryopses to light-colored grains in a hybrid F_2 population 'pistilloid light-colored plants / colored xenia caryopsis line'.

Grain rate (%)	Ratio					
	<1.28	1.28	3.00	4.72	6.44	>6.44
Actual	5.59	71.11	14.60	2.18	0.93	5.59
Expected	—	50.00	50.00	—	—	—

The deviation revealed in the segregation pattern of caryopsis pigmentation in the F_2 hybrids of 'pistilloid plants / xenia colored-caryopsis line' (1.33 : 1) differs from that observed when crossing bisexual lines with the xenia trait (1.91 : 1). A deficiency was discovered in genotypes that segregated in a monohybrid pattern. In the maternal plants of the hybrid studied, the stamenless flower phenotype is a result of transformation of stamens to pistils (Kyzlasov 1998). In such a case, the absence of stamens in the flowers results from the functioning of three recessive pistilloidy genes in the homozygous state (*aabbcc*). The inheritance of grain coloration by F_2 hybrids of 'pistilloid plants / xenia colored-caryopsis line' can depend on the homology of chromosomes, where pistilloidy and caryopsis coloration genes are located.

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Haploproduction in primary triticales using anther culture.

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Primary hexaploid and octoploid triticale with genomic compositions AABBRR and AABBDDRR, respectively, were developed using Saratov cultivars of winter bread wheat and rye with embryo rescue followed by colchicine treatment of the plants.

Doubled haploid plants were obtained from primary hexaploid and octoploid triticales by anther culture. We found that cold pretreatment of the donor spikes at 2–5°C is unnecessary for induction of sporophytic microspore development. Embryogenic structures were obtained without shock temperatures. In two genotypes (Amphidiploid 1 and the cultivar Student), microspores developed at 1.7 and 7.8 %, respectively, only in freshly harvested anthers that were not subject to cold.

The results of this research are similar to those for anther culture in bread wheat (Tkachenko 2001; Dyatchouk 2003) and did not confirm the role of shock temperatures as a trigger of microspore development (Kruglova et al. 2005). Cold storage of the anthers, however, is a necessary component of the anther culture method, because it preserves the 'embryogenic window' and prolongs the suitable period for anther inoculation.

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Inheritance of productivity in soft wheat hybrids under the conditions of the Far East of the Russian Federation.

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The main goal of any selection program is creating cultivars with high genetic productivity. Cultivar productivity in spring wheat is determined from productive tillering, spike size, the number of spikelets and grains/spike, grains/spikelet, and 1,000-kernel weight. Thus, knowing the inheritance of plant productivity components is very important. Similar research is being done in the Russian Federation and other countries. Inheritance is determined by the genetics of the crossing material and the specific natural and climatic conditions, which is why results obtained in some conditions and populations can not be used in others.

The Far East of the Russian Federation does not have a climatic equal at the same latitude anywhere on earth. The specific features of the region are drought in spring and early-summer, high precipitation in summer, excessive humidity (95–100 %), sharp drops from excessive moisture to drought, and high insolation.

Here we summarize our research on the inheritance of plant height on productivity in soft spring wheat hybrids and the process of natural hybrid populations. This knowledge is very important, because it is a basis of selection.

Materials and methods. Genetic resources included 2,500 cultivars from the world collection of the Russian Research Institute of Plant Growing. Before hybridization, samples were studied for 3–5 years in the fields of the Far Eastern Breeding Center in Khabarovsk. The 720 hybrid combinations in the F_1–F_2, which were selected from the crosses of the best cultivars, were used for the analysis. Experimental data were processed by common methods.

Results and discussion. The general picture shows complicated inheritance (Table 1). Plant height is the main form of lodging resistance. Height was inherited in 33.4% of the hybrids from their tall parents; 22 % of the hybrids inherited this feature through heterosis. Heterosis was between 1.5–19.4 % and the coefficient of dominance (h_p) was 1.09–4.28. The greatest number of short, nonlodging forms were selected from combinations with intermediate inheritance and from short parents (38.9 % of the hybrids). These combinations included Monakinka/Nainari 60, Monakinka/Siete Cerros, and Acadia/Sonora 64. High coefficients for plant height heritability in the F_2 (h^2 = 0.51-0.83) were used to select short forms. However, not all

Table 1. Hybrid distribution according to inheritance feature in the F_1 (% of total number of hybrids). D = depression or superdominance of low indicator; D^- and D^+ = dominance of low ($^-$) and high indicator ($^+$), respectively; I I = intermediate inheritance; H = heterosis or superdoinance of high indicator.

Feature	D	D^-	I I	D^+	H
Plant height	5.0	11.1	27.8	33.4	22.2
Productive tillers	27.8	5.5	22.2	27.7	16.8
Spike length	11.0	11.0	33.4	16.8	27.8
Spikelets/spike	27.8	22.2	11.1	11.1	27.8
Grains/spikelet	16.8	27.7	5.5	22.2	44.5
1.000-kernel weight	5.5	22.3	5.5	27.8	38.9
Grains/spike weight	5.5	27.7	11.0	16.5	39.3
Productivity of one plant	22.2	11.0	5.5	22.2	39.1

hybrids with high inheritance have high productivity, traits that are mostly from heterosis and dominance. Selecting positive transgressions in hybrid populations is greatly lowered after productivity from dominance and superdominance in the F_1. Culling such hybrids in the F_1 is needed.

Analyzing the F_1 hybrids and F_2 populations showed that most do not have a connection with plant height and productivity, which indicates independence in inheritance (Table 2). A positive correlation with the number of spikelets/spike, which was noticed in 44% of the F_2 hybrids, was the exception. The selection of short forms may cause a decline in the number of spikelets/spike in hybrids with such a connection. Because the selection of spring wheat for shorter plant height (maximum 65–70 cm) does not lead to a decrease in productivity, selection of productive cultivars with different heights is possible in our conditions. The optimum height should be 80–90 cm.

Table 2. Plant height as related to productivity features in F_2 hybrid populations.

Indicator	Plant productivity	Productive tillering	Spike length	Spikelets /spike	Grains /spikelet	Grains /spike
Variation of correlation coefficient (r)	–0.05±0.45	–0.50±0.40	–0.27±0.71	–0.33±0.60	–0.35±0.40	–0.28±0.62
Average r in all hybrids	0.28	0.13	0.22	0.23	0.04	0.17
% of hybrids with certain connection	16.0	8.0	28.0	44.0	4.2	17.4

Depression (in 27.8% of the hybrids) is the main feature of productive tillering inheritance. In 16.8% of the hybrids, high heterosis (18–50%) was caused by nonadditive effects of genes (dominance or epistasis). Inheritance in the F_2 is insufficient (h^2 = 0.03-0.16), proving weak genetic control of the trait and strong environmental dependence (for successful selection capacity, the h^2 should be not less than 0.4–0.5). Therefore, despite the fact that productive tillering plays a big role in yield capacity (r = 0.73–0.89, it is difficult to study because of low inheritance and high phenotypic variability (V = 43–54%). Thus, selection should be done in later generations (F_4–F_5).

Not only is it possible, but it is necessary, to breed cultivars with high tillering (1.6–2 productive stems) especially those that are used in the intensive agriculture in the Russian Far East. A survey of the world collection showed that short cultivars (< 65 cm) are the most productive (three or more stems) but did not have other productive elements when compared to tall cultivars. These facts are important for breeding short-stem cultivars that have high yielding capacity and productive tillering.

Spike length is the least variable feature with V = 9.4–15%, more often than other inherited intermediately (in 33.4% of hybrids), which indicates that this feature is controlled by additive gene action. However, another type of inheritance was observed; 6.8% of hybrids had a high index and 27.5% of hybrids had heterosis. Heterosis was not high (2.2–7.6%) with the exception of the 'Acadia / Jaral 66' hybrid, where heterosis was 15.6%. Spikes in these hybrids were large when a long-spike cultivar (r = 0.62) was the female. This fact should be taken into account in crossing. A connection with plant productivity (r = 0.42–0.68) was noted in 48% of hybrids. The inheritance coefficient ranged from 0.19 to 0.55 depending on the cross combination. Thus, the effectiveness of the selection depends on cross combinations.

The number of spikelets/spike is important and has a certain connection with plant productivity (r = 0.42–0.60). This connection was found in 56% of the hybrids and has small variability (V = 9–14%). Depression and dominance of a low index (27.8 and 22.2%, respectively) were noted in 50% of the hybrids. Heterosis was observed in 27.8% of the hybrids. However, heterosis was not large (2.1–10.1%). Philipchenko (1934) and Phedin (1974) indicate that low dominance and correlated pleiotropism with the spike length. According to our data, the correlation coefficient between these factors is 0.50–0.88 (average 0.65%). However, this explanation is not right for all the combinations, because a decrease in spike length and the number of spikelets/spike and heterosis were observed.

The low 1,000-kernel weight (27–32 g, 23–25 g in bad years) is the main shortcoming of spring wheat cultivars of the Far East. Increasing the 1,000-kernel weight to 35–38 g, keeping some other productivity elements equal, raises the yield by 20–25%, which is why we pay great attention to this feature despite the lack of correlation between plant productivity and 1,000-kernel weight (r = 0.02). Our research showed 1,000-kernel weight was inherited according to

the type of heterosis (in 38.9% of the hybrids) and dominance of high index (in 27.8% of the hybrids). The rate of heterosis is 4.2–18.1 %. Inheritance coefficients in F_2 populations are high (> 0.4), which proves the possibility of effective selection. The connection between 1,000-kernel weight and other productivity elements, with the exception of the number of grains/spike, is weak and uncertain (r = –0.49). The 1,000-kernel weight is genetically independent and during hybridization and selection different forms can be created. Dalnevostochnaya 10, Khabarovchanka, Zaryanka, and Lira 98 are examples, where 1,000-kernel weight is 35–40 g. This way of cultivar development is suitable to the conditions of the Russian Far East. Cultivars with a large 1,000-kernel weight suffer from drought (form weak kernels and have low quality) and monsoons (have phusarios, low seed quality, and are not resistant to enzyme and mycosis seed depletion).

All types of inheritance, from depression to heterosis, were noted in grain weight/spike and the number of grains/spike, giving the opportunity to select for valuable productivity features. However, grain weight/spike was often inherited according to the type of heterosis (39.3% of the hybrids) and dominance of low indicator (in 27.7% of the hybrids). Heterosis is large (110–120 %). For example, valuable lines were selected from the hybrids 'Dalnevostochnaya/World Seeds 1616', 'Acadia/Sonora 64', 'Acadia/Noroeste 66', and 'Monakinka/Akadia'. The latter was an ancestor of Dalnevostochnaya 10. Grain weight/spike in lighter seedlings (150–200 grains/m^2) is weakly correlated with plant productivity (r = 0.35), because of the influence of tillering on yield. A certain connection between these traits (r = 0.50–0.71) was noted in 65 % of F_2 population. Thus, selection for this trait in populations with close plant stands (400–450 spikes/m^2) is better.

Plant productivity is the result of all elements. Cultivar productivity is defined is a combination of plant productivity and a close plant stand. Analyzing hybrid populations showed that the correlation coefficient between plant productivity and its components, with the exception of 1,000-kernel weight, varied from low to high positive values in different hybrids (Table 3).

Table 3. Plant productivity related with components in an F_2 hybrid population (* and** significant at P = 0.95 and 0.99, respectively).

Indicators	Productive tillering	Spike length	Spikelets /spike	Grains /spike	Grains /spike weight	1,000-kernel weight
Variation of correlation coefficient (r)	0.45±0.89	0.03±0.68	0.01±0.75	0.22±0.73	0.07±0.71	–0.12±0.15
Average r in all hybrids	0.67**	0.37*	0.36*	0.46*	0.48*	0.02
% of hybrids with certain connection	100	48	56	80	65	0

Productive tillering, grain weight/spike, and number of grains/spike (r = 0.67, 0.48, and 0.46, respectively) are the most important elements of productivity. Spike length and the number of spikelets/spike (r = 0.37 and 0.36, respectively), are less important elements of productivity. A connection was noted with productive tillering in 100% of the hybrids, with the number of grains/spike in 80% of the hybrids, and with other features in 48–65% of the hybrids.

A different character of inheritance of the same features in F_1 hybrids and a large difference in correlation coefficients of these features with plant productivity in F_2 populations is evidence of developing spring wheat cultivars with a different correlation of its components in the structure of

Table 4. Yield structure of new spring wheat cultivars Dalnevostochnaya 10 (D10), Khabarovchanka (K), and Lira 98 (L98) in comparison to Monakinka (check cultivar).

Feature	Monakinka	New cultivars		
		D10	K	L98
Potential productivity (t/ha)	3.5	4.0	5.0	5.5
Productive tillering	1.35	1.10	1.60	1.60
Spikelets/spike	13.0	11.0	12.7	13.5
Grains/spike	23.5	22.0	28.2	32.5
Grains/spikelet	1.8	2.0	2.2	2.4
1.000-kernel weight	27.4	36.0	37.3	35.0
Grains/spike weight	0.68	0.79	0.98	1.10
First plant productivity (g)	0.85	0.92	1.21	1.35

yield. The cultivars Dalnevostochnaya 10, Khabarovchanka, and Lira 98 prove this. Plant productivity and yield in Dalnevostochnaya 10 are mostly due to a high 1,000-kernel weight when compared to Monakinka. Khabarovchanka and Lira 98 have plant productivity due to all elements with the exception of the number of spikelets/spike (Table 4, p. 64).

We have developed the optimum model for soft spring wheat cultivar until 2010. About 30 parameters, both qualitative and quantitative characteristics estimating productivity, were put into this model. Inheritance, the climate of Far East Russia, technological requirements of the cultivar, the level of agrotechnics are important. In our model, the productivity is supposed to increase owing to even development of several features but not owing to maximum development of one or two features. In the Russian Far East, many factors are limiting. First is the unstable hydrothermal regime during all growth and development stages. The level of productivity of a new cultivar in optimal soil fertility should be the following: productive tillering, 1.8–2 spikes/plant; grain weight/spike, 1.5–1.6 g; number of grains/spike, 38–40; number of spikelets/spike, 14–15; number of grains/spikelet, 2.5–2.8; 1,000-kernel weight, 38–40 g; and grains, 400–420 grains/m^2. The task is to select genotypes balanced with the complex of features that provide productivity of new cultivars up to 6.0–6.5 t/ha. Far Eastern breeders have been developing this kind of cultivar.

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Races of Puccinia graminis f.sp. tritici in Russian Federation in 2001–05.

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The wheat stem rust pathogen *P. graminis* f.sp. *tritici* was found in 2001–05 in various regions of the Russian Federation on barberry, wheat, barley, and wild Graminaceous species; wheatgrass (*Elytrigia repens*), sheep-fescue (*Festuca* sp.); lyme grass (*Elymus* sp.); perennial ryegrass (*Lolium perenne*); timothy (*Phleum pratense*); and cocksfoot (*Dactylis glomerata*). Aecia on barberry were collected in collections of Botanical Garden of the Moscow University, the Main Botanical Garden of the Russian Academy of Sciences, and various districts of the Moscow Region at the end of May–June. A massive appearance of wheat stem rust on wild species was observed at the end of vegetative season, from the end of August into September. Rust developed on crops of wheat and barley in July and early August, usually at the start of harvest, as separate spots consisting of a few plants. The years 2001 and 2002 were most favorable for development of the fungus.

Plant samples infected with wheat stem rust pathogen were collected in central Russia (Moscow region), the Northern Caucasus (Rostovskaya region), and western Siberia (Tomskaya region). We isolated 354 monouredinial clones from the collected samples and multiplied on wheat cultivar Khakasskaya, which is sensitive to pathogen infection. Races were determined with the Pgt system according to reaction of 16 isogenic wheat lines (Roelfs and Martens 1998). The Shannon diversity index (Shannon's index, Magurran 1983) was used for evaluation of diversity of race composition in populations in different seasons, various host plants, and different geographical zones.

The race composition of *P. graminis* f.sp. *tritici* was highly diversity in 2001–05. We identified 43 pathogen races during this period. Two to three fungal races dominated annually. The frequency of other races was less than 8%. We classified these races as rare. The percentage of rare races varied from season to season. In 2001, rare races comprised more than 50%; in 2002 about 36% (Table 1, p. 66).

The highest diversity of fungal races was observed in 2001–02, a season relatively favorable for development of wheat stem rust. We identified 23 races in 2001 and 11 in 2002. Rare races comprised 50.68 in 2001 and 35.91% in 2002 (Table 1). The dominance of highly virulent races TTNT (virulence formula 5, 21, 9e, 7b, 11, 6, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp), TKNT (5, 21, 9e, 7b, 6, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp), and TKST (5, 21, 9e, 7b, 6, 8a, 9g, 36, 30, 9a, 9d, 10) was observed in 2003–05, years relatively unfavorable for development of wheat stem rust pathogen.

Table 1. Races of *P. graminis* f.sp. *tritici* identified in the Russian Federation in 2001–05.

Year	Dominate races (%)	Rare races (%)	Number of clones	Number of races
2001	TKNT (32), TKNS (9, 32), MRBT (8)	50.68	75	23
2002	MKLT (25, 64), MKBT (23, 07), PKLT (15, 38)	35.91	39	11
2003	TTNT (61, 9), MKNS (19, 06)	19.04	42	7
2004	TKNT (75, 36), TKST (14, 49)	10.10	69	4
2005	TKNT (52, 38), TTNT (32, 15)	15.47	84	13

Statistical evaluation of the race composition in 2001 to 2005 using the Shannon coefficient indicated the highest race diversity in 2001 and 2002 (Table 2). The race composition was relatively diverse in 2003 and 2005. Low diversity was observed in 2004 when race TKNT comprised 75.36% (Tables 1 and 2). Evaluation of race composition on various host plants in central Russia (Moscow region) revealed the highest diversity among clones obtained from barberry (Table 3).

Table 2. Diversity in the race composition of *P. graminis* f.sp. *tritici* collected between 2001 and 2005 in the Moscow, Northern Caucasus, and western Siberian regions of the Russian Federation.

Year	Number of races	Shannon index
2001	24	2,444
2002	10	1,938
2003	7	1,777
2004	5	797
2005	10	1,226

Table 3. Diversity of race composition *P. graminis* f.sp. *tritici* on various plant hosts in central Russia (Moscow region) from 2001 to 2005.

Plant host	Shannon index
Barberry	1,847
Wild grasses	1,513
Wheat	1,238

Our results indicate that sexual recombination leads to the diversity of *P. graminis* f.sp. *tritici* in this region as well as to variability of race composition of wild cereals. The race composition of wheat becomes poor because highly virulent races dominate.

Evaluation of resistance in isogenic wheat lines (*Sr*) by estimating the frequency of virulence genes (pp) on different host plants in 2001–05 indicated that *Sr9b* and *Sr13–Sr17* were efficient for selection of plants resistance to wheat stem rust pathogen in Russia (Table 4).

An increase in the number of clones of pathogen virulent towards gene *Sr11*, relatively resistant to wheat stem rust pathogen in Russia has discovered (Lekomtseva et. al 2004). The stem rust pathogen showed high virulence during the studied period (Table 4). The mean number of pp-genes/ pathogen clone of different hosts was equal to 11-12 and greater. The highest level of virulence was found on wheat and barberry.

Table 4. *P. graminis* f.sp. *tritici* virulence genes on various plant hosts collected in 2001–05 (%) in the Russian Federation.

Virulence gene	Plant host			
	Wheat	Barberry	Wild grasses	Barley
5	98.7	100.0	100.0	100.0
6	99.6	100.0	100.0	100.0
7b	100.0	100.0	100.0	100.0
8a	56.2	100.0	94.7	60.0
9b	5.1	22.0	7.9	0.0
9c	88.4	64.7	41.1	60.0
9d	92.3	98.5	92.1	100.0
9e	90.1	98.5	92.1	100.0
9g	100.0	100.0	97.4	100.0
10	97.4	95.6	100.0	100.0
11	34.8	29.4	39.5	73.3
13-17	6.9	0.0	0.0	0.0
21	91.0	58.8	18.4	60.0
30	96.3	89.7	78.9	60.0
36	89.7	92.6	89.5	60.0
Tmp	77.2	77.9	42.1	100.0
Number of genes/clone	12.2	12.3	10.9	11.2

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Molecular variability of Puccinia graminis f.sp. tritici on various plant hosts in some regions of the Russian Federation in 2003 and 2004.

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Stem rust, *P. graminis* f.sp. *tritici*, is a dangerous pathogen of wheat and some wild grasses that develops worldwide including in the Russian Federation. The great genetic variability in the pathogen has been established using different molecular markers (McCallum et. al. 1999; Kim et. al. 1992; Maleeva et. al. 2003). However, incomplete information is known about the intraspecies structure that is formed by these molecular phenotypes. To further understand microevolution of this pathogen, it is essential to find the current population structure in nature. A RAPD analysis of DNA polymorphism in *P. graminis* f.sp. *tritici* from some wheat lines showed a relative geographic separation of the tested isolates (Skolotneva et. al. 2005).

A complex analysis of *P. graminis* f. sp. *secalis* isolates from various grasses also was performed by several molecular methods. Some evidence exists for host specialization of the tested isolates, which were grouped according to their response to the source of inoculum (unpublished data). This study focuses on molecular variation of *P. graminis* f.sp. *tritici* on various plants in separate regions of the Russian Federation, Central Russia, the Moscow area, and the Northern Caucasus, the Ruston area, in 2003 and 2004 (Table 1). Monouredinial isolates were examined using isozyme and RAPD markers. Protein extracts of homogenized urediniospores

Table 1. Isolates of *Puccinia graminis* f.sp. *tritici* in different regions of the Russian Federation in 2003 and 2004.

Isolate No.	Region	Host plant
2003 spore collection		
1.	Central Russia, Moscow area, Semhoz	*Berberis vulgaris*
2.1/2.2	Central Russia, Moscow area, Semhoz	*Elytrigia repens*
3.	Central Russia, Moscow	*Berberis vulgaris*
4.	Central Russia, Moscow	*Berberis vulgaris v. purpurea*
5.	Moscow area, Nemchinovka	*Elytrigia repens*
6.	Moscow area, Nemchinovka	*Hordeum distichum*
7.	Moscow area, Nemchinovka	*Elytrigia repens*
2004 spore collection		
1.1/1.2	Central Russia, Moscow area, Semhoz	*Berberis vulgaris*
3.1/3.2	Central Russia, Moscow-1	*Berberis vulgaris*
4.1/4.2	Central Russia, Moscow-2	*Berberis vulgaris*
5.1/5.2	Central Russia, Moscow-3	*Berberis vulgaris*
6.1/6.2	Central Russia, Moscow-4	*Berberis vulgaris*
7.1/7.2	Moscow area, Pushkino	*Berberis vulgaris*
9.1/9.2	Moscow area, Krukovo	*Berberis vulgaris*
10.1/10.2/10.3	Moscow area, Nemchinovka	*Hordeum distichum*
11.1/11.2	Moscow area, Nemchinovka	*Elytrigia repens*
12.1/12.2	Central Russia, Moscow-1	*Elytrigia repens*
13.1/13.2	Central Russia, Moscow -2	*Elytrigia repens*
14.1/14.2/14.3	Central Russia, Moscow	*Dactylis glomerata*
15.1/15.2	Northern Caucasus	*Elytrigia repens*
16.1/16.2/16.3	Northern Caucasus	*Hordeum distichus*
17.1/17.2	Northern Caucasus	*Triticum aestivum*
18.1/18.2	Northern Caucasus	Wheat cultivar Annushka

were subjected to vertical PAGE as described in Maleeva et al. (2003). The gel was stained for detection of malate dehydrogenase (MDH) (Korochkin et al. 1977), which earlier was used successfully to estimate genetic variation in *P. graminis* f.sp. *tritici* (McCallum et al. 1999; Maleeva et al. 2003).

To assess DNA polymorphism in *P. graminis* f.sp. *tritici* collections, DNA was extracted by the CTAB-method (Griffith and Shaw 1998) and RAPD-fragments were generated for all isolates using the primers Core (5'–GAGGGTGGXGGXTCT–3') and PR3 (5'–(GTG)5–3') separately and in combination (Maleeva et. al. 2003). Isozyme analysis and RAPD profiles revealed polymorphisms among the *P. graminis* f.sp. *tritici* isolates of both collections and were measured by the UPGMA clustering (Treecon for Windows version 1.3b) and calculation of genetic distance (after Link et al. 1995) for the dendrogram construction.

Puccinia graminis f.sp. *tritici* isolates from the 2003 spore collection clearly segregated into three groups; one from barberry, and of *Triticale* (*Elytrigia* and *Hordeum*), which were confirmed by the isozyme analysis and the RAPD data (Fig. 1A and B). Among the spore collection of 2004 there were isolates from *Triticum* (the Northern Caucasus). Their RAPD- and MDH-phenotypes were grouped together on the dendrograms (Fig. 2A and B). The both of the markers also formed the cluster, which contained isolates from *Elytrigia* (the Central Russia) like in previous case.

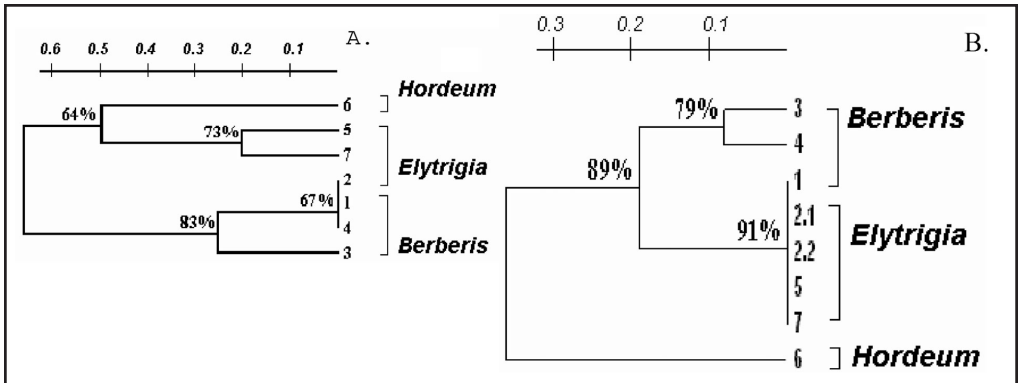

Fig. 1. Dendrograms of *Puccinia graminis* f.sp. *tritici* isolates from the spore collection of 2003 based on (A) isozyme analysis of MDH polymorphism and (B) RAPD analysis with three primer combinations, Core, PR3, and Core+PR3.

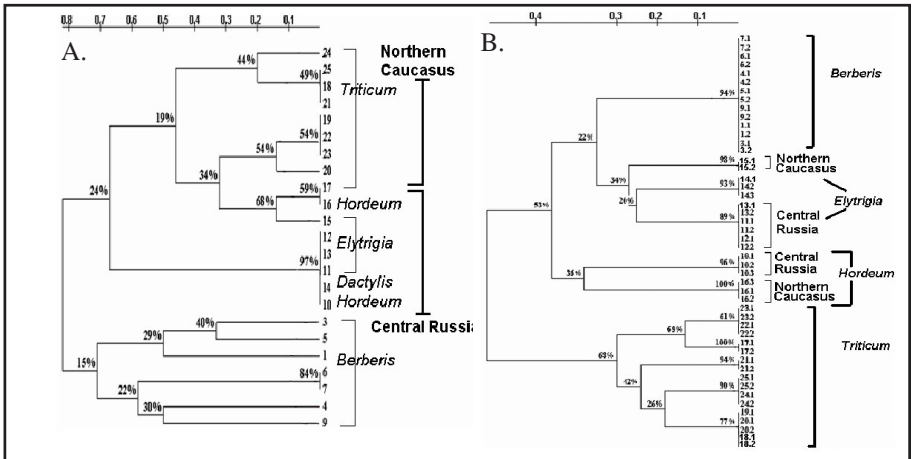

Fig. 2. Dendrograms of *Puccinia graminis* f.sp. *tritici* isolates from the spore collection of 2004 based on (A) isozyme analysis of MDH polymorphism and (B) RAPD analysis with three primer combinations, Core, PR3, and Core+PR3.

The sexual process *P. graminis* takes place on alternative host *Berberis* and contributes significantly to the intraspecies variation. It could be demonstrated by both of the markers we used. The genotypes of isolates from barberry (the Central Russia) were constantly clustered into the distinguished stable (by index bootstrap up to 94%) group (Figs. 1 and 2). However, to contrast with the RAPD-data, the clusters of the MDG-phenotypes of the "barberry" isolates were more strictly opposed to the groups of isolates from grasses, probably due to the function differences between these markers.

The isozyme and RAPD analysis only suggested the existence of some distinct groups of isolates, but showed different relationships between them. Following to the MDH-polymorphism there was a geographic variation among the isolates from different grasses of the spore collection of 2004. These phenotypes were clustered into two major groups: one of them combined the Central Russia isolates from *Elytrigia, Hordeum* and *Dactylis*, and another was comprised of the Northern Caucasus isolates from *Elytrigia, Hordeum* and *Triticum*. However, there was other interrelation between the

RAPD-profiles. The grouping of isolates was independent of their geographic origin. The host plants determined the structure of RAPD-diversity as the dendrogram indicated.

The genomes of the parasitic fungi are characterized by highly flexibility. It is necessary to keep up to the changeable environment, which is comprised of the natural conditions as much as the specific biochemistry and resistant system of the host plant. These results could suggest there are several trends of *P. graminis* f.sp. *tritici* alteration on the molecular level.

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The effects in bread wheat of some dwarfing genes in vitro androgenesis.

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Many crops use biotechnological methods for plant breeding. *In vitro* androgenesis is a very significant technology for the mass production of doubled haploids in any genotype. Information on the genetic control of the induction of haploids and their regeneration is difficult, limited, and unusual.

We conducted research on the influence of the *Rht* gene system on *in vitro* androgenesis in bread wheat (Djatchouk et al. 2001) using the semidwarf NILs for *Rht-1b*, *Rht-1A*, *Rht-14*, *s1*, and *Q* in the background of the spring bread wheat Saratovskaya 29. We analyzed the rate of callus induction, embryoid formation, and normal and albino plant regeneration from anthers.

Lines with *Rht-B1c* and *Q* had the highest percentage of plant regenerates from anthers. A positive influence was found in lines with *Rht14*, but not all genes were statistically significant.

A low level of morphogenic anthers and regenerations was found in lines with *s1*, however, these results were from a single experiment. This gene does not influence plant regeneration. The line with *Rht-B1b* was not distinct from the sib.

This data may be useful for predicting the efficiency of haploid production *in vitro* and for establishing methods using this technology.

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Possible paths of the impact of low-intensity laser radiation on membrane structures in plant cells (exemplified by wheat cultivar callus).

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The impact of laser radiation on living organisms, including plants, has been raising an intense interest from researchers since the moment the laser was invented in the mid 1960s. Nevertheless, up to now, not a single theory can explain all the effects that lasers make on living things because of the relative complexity of biological systems and the difficulty of analyzing the regularities of energy transformation in living tissues.

Of particular interest is the impact of low-intensity laser radiation on biological objects. This impact does not normally cause damage. Vice versa, the stimulating influence of laser radiation on many physiological processes, in humans, animals, and plants, is regarded as proven fact. Few studies have investigated any possible paths of the stimulating influence of low-intensity laser radiation on plants. However, from an evolutionary viewpoint, plants are well suited to the perception of light energy and its physiological use. The impact of light on plants is not only restricted to photosynthesis, and many other photobiological processes, such as photoregulation, should be noted. The physiological status of a plant depends, to a large extent, on light intensity, its spectral composition, radiation dose, and the period of illumination. Apart from the chloroplasts, plant tissues are rich in pigments that perform various, but primarily signaling, functions in plant cells. The study of the biological impact of low-intensity laser radiation on the plants may be aimed not only at the identification of optimal conditions for its practical application, but for the study of fundamental regularities of light impact on plant organisms.

The literature and our data prove that low-intensity laser radiation may produce a stimulating influence on various physiological processes, including those that do not show a pronounced interconnection. For example, the lack of an interaction between the degree of plant regeneration and callus formation in individual genotypes confirms a lack of connection between the genetic factors that determine these two characteristics (Yurkova 1989).

We have established that the primary response of plant tissue to radiation is an increase in the content of secondary products of peroxide oxidation. Our data demonstrate that laser light stimulates morphogenetic processes in plant tissues at later stages as well (Salyaev et al. 2001). We believe that this stimulation may be conditioned metabolic changes caused by the change of content of a number of compounds formed as a result of the primary photoreactions. Such compounds might also include products of peroxide oxidation, with an increase in their amount in response to the impact of laser radiation. This increase, in turn, affects membrane properties and changes its functional state. The impact of PLO on the phospholipid stratum of membranes is well studied and may be reduced to several principal effects (Vladimirov 1999); a selective increase in membrane permeability and a reduction of their electrical stability. One of the major results is an increase in the Ca^{2+} concentration inside the cells. The sequence of events following laser radiation exposure may be as follows:

1. photon adsorption by endogenous photosensitizers and further peroxidation of lipids (photoperoxidation); followed by
2. calcium ion introduction into the cell.

Activation of intracellular processes. PLO-products accumulation may act as a signal not only for the start-up of relevant protection mechanisms, but, probably, for some secondary responses, perhaps, at the transcription level (0°C, 2001). This probability is indirectly confirmed by the stimulating effect of laser light on morphogenetic processes in

wheat and wild crops tissue cultivar. When exposing plants to laser radiation, it is important to remember that is is possible to dose the stress impact strictly.

Based on data from the stimulation of morphogenetic processes in wheat tissue culture by low-intensity laser radiation (Salyaev et al. 2001), we suggest that the changes observed should be accompanied by molecular shifts and structural reconstruction in the tissues subjected to radiation. Chirkova (2000) indicated that such reconstructions should take place primarily in cell and organellar membranes. These reconstructions produce a profound impact on all forms of functional activity in the membrane, with lipids to a considerable extent. In lipids, fatty acids are the primary subject influenced by both genetic control and environmental conditions. Stress may cause shifts in the proportion between various groups of fatty acids, and the degree of their nonsaturation may change. The length of fatty acids chains, positional situation of double bonds, or the number of polar groups also may change. If we are able to show a difference in the structure of the lipid matrix in control tissues and tissues subjected to radiation, we could confirm the biological impact of laser light on plants via its influence on membrane structure. Thus, part of our work studied qualitative changes in lipid structure caused by the impact of low-intensity, laser radiation by infrared spectroscopy.

Callus tissue from the wheat cultivar Skala, a Siberian selection, were subjected to irradiation on the second day after the first transfer. The radiation dose (4.5 J/cm^2) was identical to that in experiments investigating the impact of laser radiation on morphogenetic processes in wheat callus. Extracts from unradiated calli were used as control. Calli were taken for analysis 72 hours (3 days) after irradiation. The molecular spectra obtained found that coherent radiation caused significant changes in the structure of lipids (Table 1).

Table 1. Changes caused in wheat calli after the impact of a low-intensity laser irradiation of 4.5 J/cm^2.

Spectrum region (per cm)	Control callus	Test callus
3,300		Significant reduction of OH^{-2} and NH^{-} groups
1,730–1,690	Carbonyl (C=O) fluctuations intense bands	Indistinct bands
1,620–1,630	Aromatic groups, most likely phenols	Absence of bands
1,230–1,050	Phosphate groups, symmetrical and asymmetrical PO^{-2} fluctuations, weakly expressed	Considerable enhancement of band intensity
721	No band	Emergence of a band, characterizes pendulum CH^{-2} fluctuations in long-chain aliphatic structures

In the test, the stripe 3,300/Am, which confirms the presence of NH groups, was significantly shorter than in control. In the lipid spectra of the calli subjected to radiation, we found considerable weakening of the stripes in the regions between 1,730–1,690 cm and 700–900/cm proving the presence of heteroaromatic structures. Stripes with the maximum levels of 1,220/cm and 1,050/cm increased considerably in intensity. The presence of these stripes favors the availability of phosphate and ether groups. Of particular interest is emergence of pendulum CH_2 fluctuations in the spectra of stripe 721/A< samples subjected to radiation; confirming the presence of long-chain aliphatic structures in transplanar configurations.

On the other hand, the presence of this stripe shows that radiation brought about changes in geometry of lipid matrix, as absorption in this zone means unfolding of heteroaromatic (cyclic) structures into long chains. Therefore,

1. the biological response of callus tissue from the impact of low-intensity laser radiation was prolonged in time; 72 hours after irradiation, we observed a distinct difference in the molecular structure of lipids between test and control calli, and
2. infrared spectroscopy showed a response of callus tissue to laser light that manifested itself in structural reconstruction of the cell membrane, such as intensifying the membrane formation processes.

We conclude that exposure to helium-neon laser light causes remarkable structural changes in membrane lipids. In particular, in IK spectrum of absorption of lipids extracted from irradiated calli registered a stripe of 721/cm, which indicated intensification of the membrane formation processes in the tissues subjected to radiation.

We believe that the reaction of tissue after exposure to laser light has two responses. The first is a primary stress impact, which shows an increase in the number of peroxide oxidation products and a change in membrane-associated enzyme activity. Second are longer secondary reactions connected with adaptive changes in metabolism manifested in structural reconstruction in the membranes, intensification of membrane formation processes, and the stimulation of morphogenetic processes, including regenerative. In both cases, we observed a significant impact of low-intensity laser radiation on membrane structures of plant cells.

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The influence of linoleic and linolenic acids on the swelling of winter wheat mitochondria.

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Free fatty acids (FFA) have a number of effects on membranes in general and on mitochondria in particular, where they can significantly affect energy coupling. They increase proton conductance causing dissipation of electrochemical proton gradient. Oxidative phosphorylation uncoupling by free fatty acids in plant mitochondria depends on the function of FFA as protonophores and their interaction with such specific mitochondrial proteins from the family of mitochondrial anion carriers as ADP/ATP-antiporter, plant uncoupling mitochondrial protein (PUMP), and others (Jezek 1999). Fatty acid-dependent uncoupling of oxidative phosphorylation plays an adaptive role during hypothermia and oxidative stress in the plant mitochondria (Casolo et al. 2000; Pastore et al. 2000).

We have shown that such unsaturated (linoleic, oleic, petrozelinic, and erucic) and saturated (lauric, palmitic, stearic, and begenic) fatty acids cause uncoupling of oxidative phosphorylation in winter wheat mitochondria (Grabelnych et al. 2003, 2004, 2005). Using FFA as mitochondrial oxidation substrate was discovered only at early stages of germination of oil-contained seeds such as sunflower and lettuce (Raymond et al. 1992). In our previous work, we found that unsaturated FFA can be used as the sole oxidation substrate for winter wheat mitochondria (Grabelnych et al. 2003, 2004). Data on the influence of FFA on the swelling of animal mitochondria has been published (Schonfeld et al. 2004; Di Paola and Lorusso 2006). At the same time, there is not much data about the influence of fatty acids on plant mitochondria swelling.

This investigation studied the influence of such unsaturated fatty acids as linoleic and linolenic on the winter wheat mitochondria swelling and to determine the role of ADP/ATP-antiporter and plant UCP in this process.

Materials and methods. Three-day-old etiolated shoots of winter wheat (*T. aestivum* cv. Zalarinka) were germinated on moist paper at 26^0C. Mitochondria were extracted from winter wheat shoots by differential centrifugation as describes previously (Pobezhimova et al. 2001). The isolated mitochondria were resuspended in the following medium: 40 mM MOPS-KOH buffer (pH 7.4), 300 mM sucrose, 10 mM KCl, 5 mM EDTA, 1 mM $MgCl_2$. Mitochondrial swelling was followed spectrophotometrically by the decrease in optical density (OD) of the mitochondrial suspension (0.25 mg/ml) under deënergized conditions at 26^0C at 540 nm. We used the incubation medium as for mitochondrial respiration activity measurement including 125 mM KCl, 18 mM KH_2PO_4, 1 mM $MgCl_2$, and 5 mM EDTA, pH 7.4. Mitochondrial swelling was initiated by FFA addition. FFA concentrations were from 10 mkM to 500 mkM. The concentrations of ADP/ATP-antiporter and uncoupling UCP-like proteins inhibitors were 1 mkM carboxyatractyloside (Catr) and 2 mM GDP, respectively. The concentration of artificial uncoupler carbonyl cyanide *m*-chlorophenyl-hydrazone (CCCP) was 0.5 mkM. The concentration of mitochondrial protein was analyzed by Lowry method (Lowry et al. 1951). All the

experiments were performed on 3–6 separate mitochondrial preparations. The data were analyzed statistically and arithmetic means and standard deviations are presented.

Results and discussion. Previously, we found that among studied unsaturated fatty acids the most uncoupling activity had C18 FFA, especially linoleic (18:2, n-9, 12) and α-linolenic (18:3, n-3) acids, the addition of which caused a 4- and 7-fold stimulation of nonphosphorylative respiration, respectively. In the present work, we showed that all studied concentrations (10, 50, 100, and 500 mkM) of linoleic and linolenic acids caused effective swelling of winter wheat mitochondria (Fig. 1).

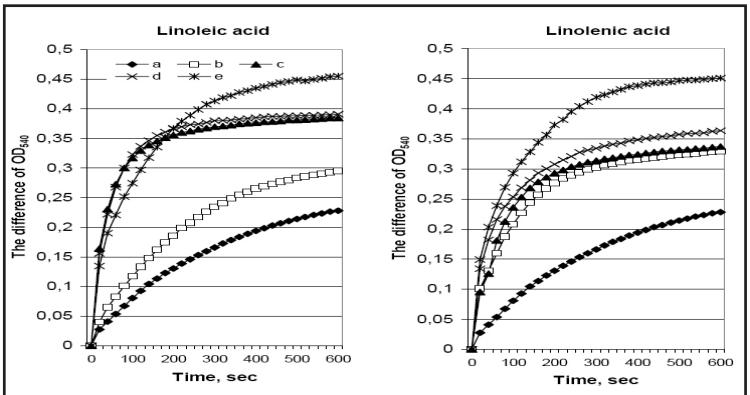

Fig. 1. Influence of different linoleic and linolenic concentrations on the swelling of winter wheat mitochondria. Winter wheat mitochondria (0.25 mg/ml) were suspended in a reaction medium and swelling was initiated by FFA addition. The difference in optical density was calculated by the formula: $dOD = (OD_{t0} - OD_{t1})$, where OD_{t0} = initial optical density and OD_{t1} = optical density after given time of incubation. Traces: mitochondria without the addition of any FFA (a) and after the addition of 10 mkM FFA (b), 50 mkM FFA (c), 100 mkM FFA (c) and 500 mkM FFA (e). Results are represented as the mean of at least three determinations/experiment.

Addition of linoleic acid in the incubation medium led to decrease in the optical density (or increase difference between the initial optical density and optical density after given time of incubation) that depended on the fatty acid concentration. Addition of 10 mkM linoleic acid caused an approximately 41% decrease of optical density in 5 min of incubation. The higher concentrations of this acid (50 and 100 mkM) caused more significant decrease of optical density (123 and 129%, respectively) in 5 min of incubation. The maximum decrease in optical density (148%) was observed in experiments with using of 500 mkM linoleic acid and 5 min of incubation. However, the most significant decrease in optical density was observed 20 sec after the addition of linoleic acid. The increase in the optical density difference was 1.5-fold for 10 mkM, 5-fold for 500 mkM, and 6-fold for concentrations 50 and 100 mkM of linoleic acid compared with mitochondria incubated without FFA.

The swelling of winter wheat mitochondria induced by the addition of linolenic acid depended on concentration to a lesser extent (Fig. 1). The smallest decrease of optical density in 5 min of incubation was caused by 10 mkM and 50 mkM linolenic acid addition (82% and 89%, respectively). The addition of 100 mkM linolenic acid led to approximately a 101% decrease of optical density in 5 min of incubation. The maximum decrease in optical density in 5 min of incubation was caused by 500 mkM linolenic acid (152%) but with a 10-min incubation, changes in the optical density between control and linolenate-incubated mitochondria decreased. The most significant decrease in optical density was observed in 20 sec after the addition of linolenic acid, similar to experiments with linoleic acid. After 20 sec of incubation of mitochondrial suspension in 10 and 50 mkM linoleic acid, we observed a 3.6-fold and a 3.4-fold increase in the difference of optical densities. Concentrations of 100 and 500 mkM linolenic acid caused approximately 5-fold and 5.4-fold increases, respectively, in the difference of optical densities after 20 sec of incubation of the mitochondrial suspension.

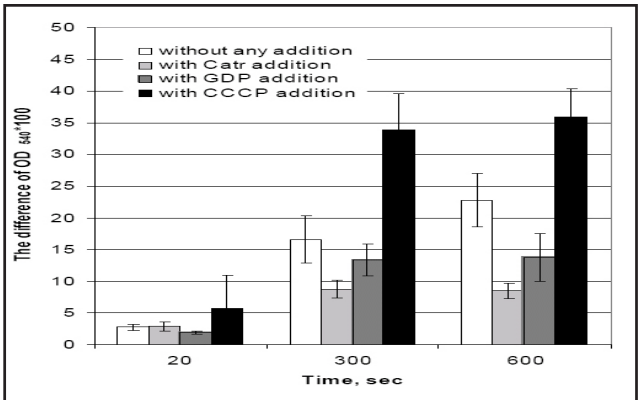

Fig. 2. Swelling of winter wheat mitochondria in the presence of ADP/ATP-antiporter and uncoupling UCP-like protein inhibitors. The concentrations were 1 mkM Catr, 2 mM GDP, and 0.5 mkM CCCP. Difference of optical density was calculated by the formula $dOD=(OD_{t0} - OD_{t1})*100$, where OD_{t0} is the initial optical density and OD_{t1} is the optical density after 20, 300, and 600 sec of incubation (M+SD, n=3–6).

We observed increase of mitochondrial swelling extent in the presence of CCCP that was 2-fold in 20 sec

and 5 min incubation (Fig. 2, p. 73). Mitochondria swelling induced by studied FFA were higher than swelling induced by this artificial uncoupler. We suppose that different mechanisms like FFA interaction with ADP/ATP-antiporter and uncoupling UCP-like proteins can participate in FFA-caused winter wheat mitochondria swelling.

To determine the participation of the ADP/ATP-antiporter and plant uncoupling protein in mitochondria swelling induced by C18 fatty acids, we studied the sensitivity of this swelling to inhibitors of the ADP/ATP-antiporter and uncoupling UCP-like proteins. In our experiments, we used FFA concentrations that had the maximum action on winter wheat mitochondria swelling (500 mkM linoleic and 500 mkM linolenic). In experiments with incubating control winter wheat mitochondria with Catr and GDP, we detected a decrease in the optical density of a mitochondrial suspension at 47% and 19%, respectively, after 5 min of incubation (63% and 40% after 10 min of incubation) (Fig. 2, p. 74). Linoleate-induced mitochondria swelling was sensitive to the addition of Catr and GDP. After a 5-min incubation, we observed a 64% and 58% decrease after the addition of Catr and GTP, respectively (Fig. 3). Mitochondrial swelling induced by linolenic acid was less sensitive to Catr and GDP addition (Fig. 3). We observed a 49% decrease of linolenate-induced mitochondria swelling by Catr after 5 and 10 min. At the same time, GDP addition inhibited this swelling significantly only after the first 20 sec of incubation (46%). The effect of GDP decreased after 10 min of incubation and was about 14%. Sensitivity of mitochondria swelling induced by linoleic and linolenic acids to inhibitors of the ADP/ATP-antiporter and uncoupling UCP-like proteins indicated their participation in fatty acid-induced swelling.

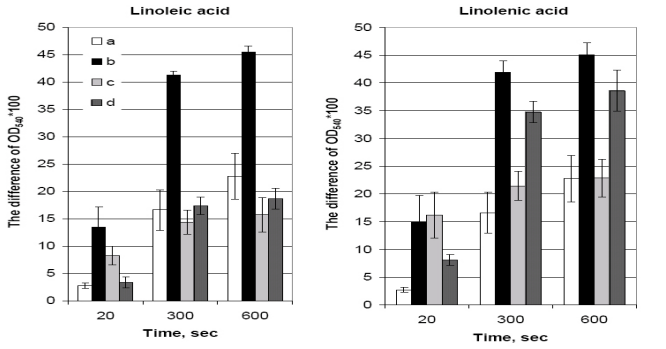

Fig. 3. Influence of ADP/ATP-antiporter and uncoupling UCP-like protein inhibitors on the swelling of winter wheat mitochondria induced by linoleic and linolenic acids. The difference in optical density was calculated by the formula $dOD = (ODt0 – OD_{t1})*100$, where OD_{t0} is the initial optical density and OD_{t1} is the optical density after 20, 300, and 600 sec of incubation. a – mitochondria without any addition; b – mitochondria after 500 mkM FFA addition; c – mitochondria after 500 mkM FFA + 1 mkM Catr addition; d – mitochondria after 500 mkM FFA + 2 mM GDP addition. M+SD, n=3-6.

From the data, we concluded that the uncoupling activity of FFA depends on the chain length and number of double bounds in their molecules. The oxidative phosphorylation uncoupling and mitochondria swelling in presence of FFA are relative processes (Di Paola and Lorusso 2006). Mechanisms of FFA-induced swelling in plant mitochondria deal with the interaction of such specific mitochondrial proteins from the family of mitochondrial anion carriers such as ADP/ATP-antiporter and UCP-like plant proteins.

Acknowledgments. This work was performed in part with the support of President Russian Federation grant for state support of leading scientific schools of the Russian Federation (SS-4812.2006.4), an interdisciplinary integration project of the Russian Academy of Sciences N47, the Russian Science Support Foundation, and the Siberian Division of Russian Academy of Sciences Youth Grant (project 115).

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Mitochondrial respiration and swelling in the presence of cyclosporin A, Ca^{2+} ions, and palmitic acid of cold-stressed and cold-hardened winter wheat shoots after subsequent oxidative stress.

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The uncoupling of oxidative phosphorylation and swelling are events that precede the opening of the permeability transition pore (PTP) in mitochondria, the release of cytochrome *c*, and the induction of programmed cell death (Crompton 1999; He and Lemasters 2002; Tsujimoto et al. 2006). Recent evidence suggests that mitochondrial volume seems to affect mitochondrial electron transport, reactive oxygen species production, cytochrome *c* release in the process of apoptosis, and participates in mechanical signaling pathways (Kaasik et al. 2007). Lim et al. (2002) showed that an increase in the matrix volume correlates well with an increase in respiration rate. The induction mechanism of PTP is poorly understood. In plants, PTP is both sensitive to CsA (Arpagaus et al. 2002; Tiwari et al. 2002) and insensitive (Fortes et al. 2001; Curtis and Wolpert 2002; Virolainen et al. 2002). Data about influence of stress factors for opening of PTP in plant mitochondria are lacking.

Our previous study showed that CsA causes a decrease in state-4 respiration in winter wheat mitochondria, and its influence is substrate-specific (Grabelnych et al. 2004). We detected the most pronounced effect of this treatment in mitochondria in the presence of Ca^{2+} ions. Furthermore, we detected the stimulation of swelling in winter wheat mitochondria from nonstressed seedlings shoots by Ca^{2+} ions and palmitic acid and the inhibitory effect of CsA (Pavlovskaya et al. 2006). Pavlovskaya et al. (2006) found that CsA inhibits the Ca^{2+}-induced swelling of mitochondria from non-stressed shoots but did not inhibit the Ca^{2+}-induced swelling of mitochondria from cold-stressed and cold-hardened shoots. The data allowed us to suggest the existence of a CsA-insensitive, mitochondrial pore function in winter wheat shoots in conditions of cold stress and hardening. The involvement of the mitochondrial cyclosporin A-insensitive pore induced by palmitic acid and Ca^{2+} ions complexes in the apoptotic process of animal cells was shown (Belosludtsev et al. 2006).

Our aim was to study respiration and swelling in the presence of inductors (Ca^{2+} ions and palmitic acid) and an inhibitor (cyclosporin A) of PTP in mitochondria from cold-stressed and cold-hardened shoots of cold-resistant winter wheat after subsequent oxidative stress.

Materials and methods. Three-day-old etiolated seedlings of cold-resistant winter wheat (*T. aestivum* subsp. *aestivum* cv. Zalarinka) were germinated on moist paper at 26°C. Seedlings were subjected to short-term (-4°C, 1 h) cold stress with subsequent oxidative stress or cold hardening for 7 days at 4°C with subsequent oxidative stress. Oxidative stress was induced by immersing root tips of intact 3-day-old etiolated seedlings in 0.5 mM solution of H_2O_2 in the dark at 26°C for 4 h. The mitochondria were isolated from seedling shoots by differential centrifugation (Pobezhimova et al. 2001), and their energetic activity and swelling were studied. The isolated mitochondria were resuspended in the following medium: 40 mM MOPS–KOH buffer (pH 7.4), 300 mM sucrose, 10 mM KCl, 5 mM EDTA, and 1 mM $MgCl_2$. Mitochondria activity was recorded polarographically at 26°C using a closed-type platinum electrode in a 1.4 ml cell volume. The reaction mixture contained 125 mM KCl, 18 mM KH_2PO_4 (pH 7.4), 5 mM EDTA, and 1 mM $MgCl_2$. Oxidation substrates were 10 mM malate in the presence of 10 mM glutamate, 8 mM succinate in the presence of 5 mM glutamate, and 1 mM NADH. During succinate and NADH oxidation, 3 mkM rotenone was added to the incubation medium. Polarograms were used to calculate the rates of phosphorylative respiration (state 3), nonphosphorylative

respiration (state 4), respiratory control by Chance-Williams, and the ADP:O ratio (Estabrook 1967). Mitochondrial swelling was followed spectrophotometrically by the decrease in optical density (OD) of the mitochondrial suspension (0.25 mg/ml) under deënergized conditions at 26°C at 540 nm. We used an incubation medium containing 200 mM KCl and 20 mM MOPS (pH 7.4). The following concentrations of test reagents were used: 1 mkM cyclosporin A, 1.75 mM Ca^{2+}, and 50 mkM palmitic acid. In the experiments using CsA and Ca^{2+}, the preincubation time was 5 min at 0°C. The concentration of mitochondrial protein was analyzed according to Lowry et al. (1951). Results are represented as the mean of at least three determinations/experiment.

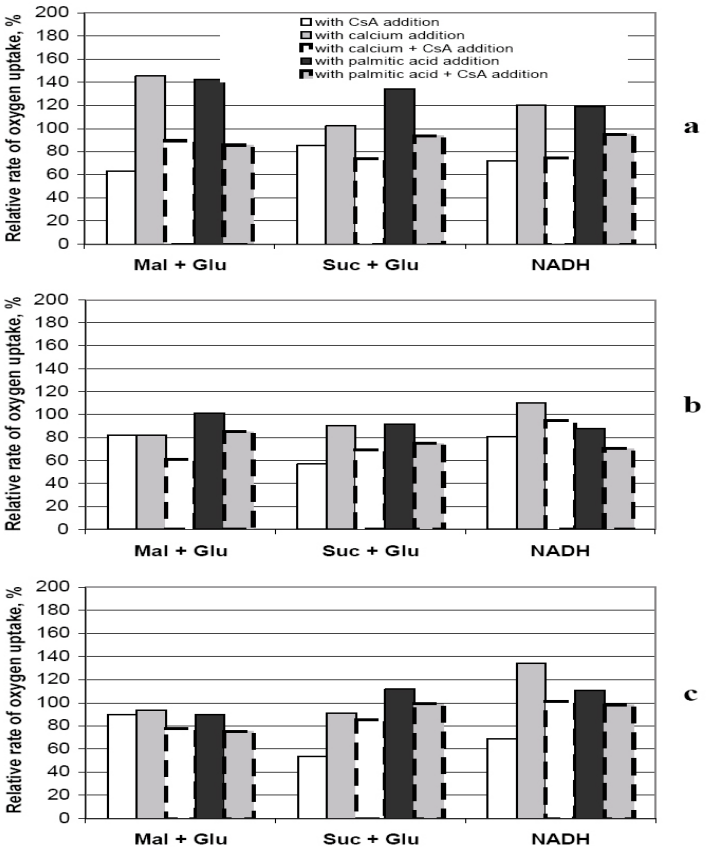

Fig. 4. The influence of cyclosporin A (CsA), Ca^{2+} ions, and palmitic acid on the oxygen uptake in state-4 (nonphosphorylative) respiration of mitochondria from control (a), cold stressed (-4°C, 1 h) with subsequent oxidative stress (0.5 mM H_2O_2, 4 h) (b), and cold hardened (4°C, 7 days) with subsequent oxidative stress (0.5 mM H_2O_2, 4 h) winter wheat shoots. Results are represented as the mean of at least three determinations/experiment. Oxygen uptake at state-4 respiration of mitochondria without any addition is 100%.

Results and discussion. The study of respiration in the mitochondria isolated from control (non-stressed), cold-stressed with subsequent oxidative stress, and cold-hardened with subsequent oxidative stress in winter wheat shoots showed that it was sensitive to CsA (Fig. 4). Ions of Ca^{2+} stimulated nonphosphorylative respiration (state 4) in mitochondria except for mitochondria of cold-stressed with subsequent oxidative stress seedlings (Fig. 4). The Ca^{2+}-induced increase in respiration rate was CsA sensitive (Fig. 4). The addition of palmitic acid did not cause a significant increase of respiration in mitochondria both cold-stressed with subsequent oxidative stress and cold-hardened with subsequent oxidative one winter wheat shoots (Fig. 4b and 4c). Palmitate-induced respiration of the control mitochondria was CsA sensitive (Fig. 4). The results also indicated substrate dependence with respect to action of inhibitor and inductors of the mitochondrial pore. Mitochondria of the control seedling shoots were the most sensitive to the addition of CsA, Ca^{2+} ions, and palmitic acid during oxidation of malate (Fig. 4a). At the same time, sensitivity to the addition of these reagents in mitochondria isolated from cold-stressed with subsequent oxidative stress and cold-hardened with subsequent oxidative stress in winter wheat shoots was the most during succinate or NADH oxidation (Fig. 4b and 4c).

In experiments with incubated mitochondria isolated from control winter wheat shoots with CsA, we detected the decrease in the optical density of the mitochondrial suspension after 5 min of incubation (34%, Fig. 5, p. 77). The influence of Ca^{2+} ions on the swelling of winter wheat mitochondria was studied on mitochondria that were preliminarily incubated with and without CsA. The presence of Ca^{2+} in the incubation medium stimulated the extent of swelling (3 fold) in control winter wheat mitochondria compared to swelling of mitochondria incubated without Ca^{2+} (Fig. 5, p. 77). The Ca^{2+}-induced swelling was fully inhibited after a preliminarily incubating mitochondria with CsA (Fig. 5, p. 77). We observed an increase in the swelling extent of the control winter wheat mitochondria in the presence of palmitic acid, the effect of that was similarly to Ca^{2+} action. Palmitic acid caused a 4-fold increase of swelling after 5 min of incubation, which was sensitive to CsA addition (Fig. 5, p. 77).

Cold stress with subsequent oxidative stress and cold hardening with subsequent oxidative stress of winter wheat seedling shoots increased the extent of mitochondrial swelling compared with control (Fig. 5, p. 77). This swelling is fully inhibited by CsA. Ions of Ca^{2+} and palmitic acid did not influence on swelling of mitochondria isolated

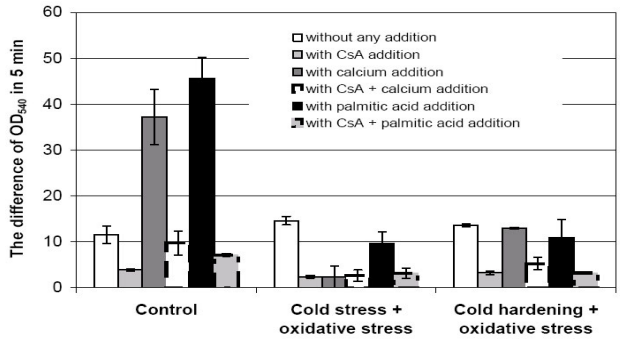

Fig. 5. The influence of cyclosporin A (CsA), Ca^{2+} ions, and palmitic acid on the swelling under deënergized conditions of mitochondria from control (a), cold stressed (-4°C, 1 h) with subsequent oxidative stress (0.5 mM H_2O_2, 4 h) (b), and cold hardened (4°C, 7 days) with subsequent oxidative stress (0.5 mM H_2O_2, 4 h) winter wheat shoots. Experiments were run at 26°C in isotonic KCl-based swelling buffer, pH 7.4. The difference in optical density (OD) was calculated by formula: dOD = $(OD_{t0} – OD_{t1})*100$, where OD_{t0} is the initial optical density and OD_{t1} is the optical density after 5 min of incubation (M±SD, n=3–4).

from cold-stressed plants with subsequent oxidative stress and cold-hardened plants with subsequent oxidative stress (Fig. 5). For mitochondria isolated from cold-hardened winter wheat shoots with subsequent oxidative stress, the ions of Ca^{2+} even inhibited the swelling (Fig. 5).

Based on our previous work, short-term cold stress and cold hardening decrease the sensitivity of mitochondrial swelling to CsA both in the absence and presence of Ca^{2+} ions (Pavlovskaya et al. 2006) and the present work regarding oxidative stress followed by short-term cold stress and cold hardening causes the appearance of mitochondria sensitive to the action that the mitochondrial pore inhibitor, we can propose a function of the CsA-sensitive mitochondrial pore in winter wheat shoots in normal conditions and under oxidative stress. Different mechanisms seem to be responsible for the PTP function. Accordingly, studying the influence of a single oxidative stress on mitochondria function in winter wheat shoots and its effect on the sensitivity of respiration and swelling to inductors and inhibitors of mitochondrial pore is necessary.

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Defensins of Triticum kiharae and diploid Triticum and Aegilops species.

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All living organisms have evolved mechanisms to defend themselves against pathogen attack. Although plants do not have an immune system, they synthesize a variety of defense molecules including low-molecular-weight compounds, proteins, and peptides with antifungal and antimicrobial activity. These proteins and peptides are involved in either constitutive or induced resistance to fungal or bacterial attack. Hundreds of antifungal/antibacterial peptides and proteins are known and, among them, antimicrobial peptides play an important role.

Defensins are small basic cysteine-rich peptides (45–47 amino acid residues long) that form an amphiphilic structure (Thomma et al. 2002). They play diverse roles in nature, showing antibacterial and/or antifungal activity (Lay and Anderson, 2005) and the capability to inhibit insect α-amylases and proteinases (Melo et al. 2002). Defensins are encoded by multigene families. In recent studies, more than 300 defensin-like genes have been identified in the *Arabidopsis* genome (Silverstein et al. 2005). Defensins are attractive candidates for the control of pathogenic microorganisms and pests by genetic engineering of crops.

In our previous studies, we showed that *Triticum kiharae*, a synthetic allopolyploid produced by crossing *T. timopheevii* subsp. *timopheevii* with *Ae. tauschii* contains a variety of antimicrobial peptides, 24 of which were new (Egorov et al. 2005). We showed that defensins of this species comprised at least 13 components that differed in their N-terminal sequences. Three subgroups of defensins were discriminated. In this work, we completely sequenced the so-called D defensins, which belong to a new previously unknown group, and isolated defensins in seeds of the presumable of A-, B-, and D-genome donors to polyploid wheat.

Materials and methods. Seeds of several species were used in this study: *Triticum kiharae* Dorof. et Migush., *T. monococcum* subsp. *monococcum* (AA), *Ae. speltoides* (BB), and *Ae. tauschii* (DD). Wheat flour was defatted with petroleum ether (1:10) and extracted with an acid solution (1 M HCl and 5% HCOOH) for 1 h at room temperature and desalted on a 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 l/min and monitored by absorbance at 214 nm. The peptide fraction was further separated by RP-HPLC on a Reprosil

C18 column (4.6 x 250 mm, particle size 5 m) 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 MALDI-TOF mass spectrometer (Micromass, UK). Amino acid sequencing was performed by automated Edman degradation on a model 492 Procise sequencer (Applied Biosystems).

Results and discussion. From seeds of *T. kiharae* and related species, eight new defensins were isolated from the 100-mM fraction and completely sequenced (Table 1).

Table 1. Amino acid sequences of *T. kiharae* D defensins. Manual alignment of sequenced defensins. Gaps have been introduced to maximize sequence similarity. Amino acid residues that differ in all or some sequences are shaded in grey and dark grey, respectively. Molecular masses are given for unreduced peptides.

Peptide	Amino acid sequence	Molecular mass (Da)
Tk-AMP-D1	RTCQSQSHKFKGACFSDTNCDSVCRTENFPRGQCNQHHVERKCYCERDC^{49}	5,736
Tk-AMP-D2	RTCESQSHKFKGPCFSDSNCATVCRTENFPRGQCNQHHVERKCYCERSC^{49}	5,691
Tk-AMP-D1.1	RDCESDSHKFHGACFSDTNCANVCQTEGFTAGKCVG--VQRHCHCTKDC^{47}	5,130
Tk-AMP-D5	RECRSESKKFVGLCVSDTNCASVCLTERFPGGKCDG--Y-RRCFCTKDC^{46}	5,152
Tk-AMP-D6	RDCRSQSKTFVGLCVSDTNCASVCLTEHFPGGKCDG--Y-RRCFCTKDC^{46}	5,091
Tk-AMP-D6.1	RECRSQSKQFVGLCVSDTNCASVCLTEHFPGGKCDG--Y-RRCFCTKDC^{46}	5,132
Tk-AMP-D3	RDCKSDSHKFHGACFSDTNCANVCQTEGFTRGKCDG--I--HCHCIKDC^{45}	4,971
Tk-AMP-D4	RDCTSQSHKFVGLCLSDRNCASVCLTEYFTGGKCD-H---RRCVCTKGC^{45}	4,982

Sequence alignment of wheat D defensins with those of other cereals with a CLUSTAL W program showed the highest homology with TAD1, a defensin specifically induced in wheat during cold acclimation (Koeke et al. 2002). D defensins share sequence similarity with defensins from other Poaceae species, but differ considerably from those of other plant families. Analysis of defensins from diploid species, the putative donors of A, B, and D genomes to polyploid wheat, showed that all of them possess D defensins. The number of defensins identified in each diploid species and expressed in seeds suggests the existence of at least three defensin-encoding genes in each genome. Sequence data and mass analysis showed that the structure of D defensins is highly conserved during at least 10,000 years of separate evolution of diploid and polyploid forms. Most defensins are genome-specific, namely present in a single genome type (A, B, or D genome), allowing us to locate most D-defensin-encoding genes: D1-group defensins, as well as D4 and D5, are A-genome encoded; D3 and D6 are D-genome encoded; and D6.1 and D3.1 (D3 homologue) are B-genome encoded. The origin of D2 defensin remains unclear, because it was found both in B and D genome. We speculate that this defensin type emerged in the evolution before the divergence of *Aegilops* species and was preserved in hexaploid forms.

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Distribution of hybrid necrosis genes in 32 cultivars of winter common wheat in Serbia.

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Introduction. The distribution of hybrid necrosis genes in winter wheat cultivars of the former Yugoslavia was first published in the works of Hermsen (1963) and Tsunewaki and Nakai (1976). All the genotypes studied were noncarriers of hybrid necrosis genes (*ne1ne1ne2ne2* genotype). In subsequent studies, the data on necrotic genotypes of the recognized cultivars of the former Yugoslavia and of the selection lines produced in different years appeared (Zeven 1969, 1971, 1973, 1976, 1981; Shoran et al. 1983; Dimitrijevic 1988; Kochumadhavan et al. 1988; Jost et al. 1989). Following Hermsen (1963) and Tsunewaki and Nakai (1976), the necrotic genotypes of 53 cultivars and lines of winter wheat were described. Thirty-eight varieties (71.1%) had the *ne1ne1ne2ne2* genotype, nine cultivars (17.0%) possessed the *Ne1Ne1ne2ne2* genotype, and six cultivars (11.3%) had the *ne1ne1Ne2Ne2* genotype. The cultivars studied were developed in different years beginning from 1919 (the cultivar Non plus ultra) to the beginning of the 1980s (the cultivars Sava, Zitnica, and Sutjeska). The studies of changes in necrotic genotype frequencies in modern populations of this region caused by breeding strategy are of particular interest.

Materials and methods. We studied the distribution of necrotic genotypes in 32 cultivars of winter wheat produced in two breeding centers in Serbia, the Institute of Cereal and Vegetable Crops (Novi Sad) and the Cereal Center (Kragujevac). Winter wheat cultivars Co 725872 (*Ne1Ne1ne2ne2* genotype) and Mironovskaya 808 (*ne1ne1Ne2Ne2* genotype) were used as testers. Crossing was in the field by conventional procedures including emasculating and isolating spikes. Plants of the first hybrid generation were examined for the symptoms of hybrid necrosis. The strength of hybrid necrosis alleles was evaluated according to Hermsen (1963).

Results and discussion. Of the 31 cultivars studied, (Table 1, p. 81), five had the genotype *ne1ne1Ne2Ne2* (Licanka ($Ne2^w$), Senica ($Ne2^w$), Selecta ($Ne2^w$), Ibarka ($Ne2^w$), and Orasanka ($Ne2^m$). The first four cultivars were bred in Novi Sad and have a weak allele *w* of the *Ne2* gene, whereas Oransanka is from the Cereal Center and has the moderate allele *m*. This difference is most likely due to the specific original selection material used in these breeding centers. The data shown in Fig. 1 demonstrate different approach to the selection of the original material. In both centers, noncarriers of hybrid necrosis genes were selected (*ne1ne1ne2ne2* genotype). In all probability, such forms have selective advantages over the carriers of hybrid necrosis genes in this region, which follows from the fact that during selection the presence or absence of hybrid necrosis genes was not taken into account. The *Ne1Ne1ne2ne2* genotype was not found among the cultivars studied.

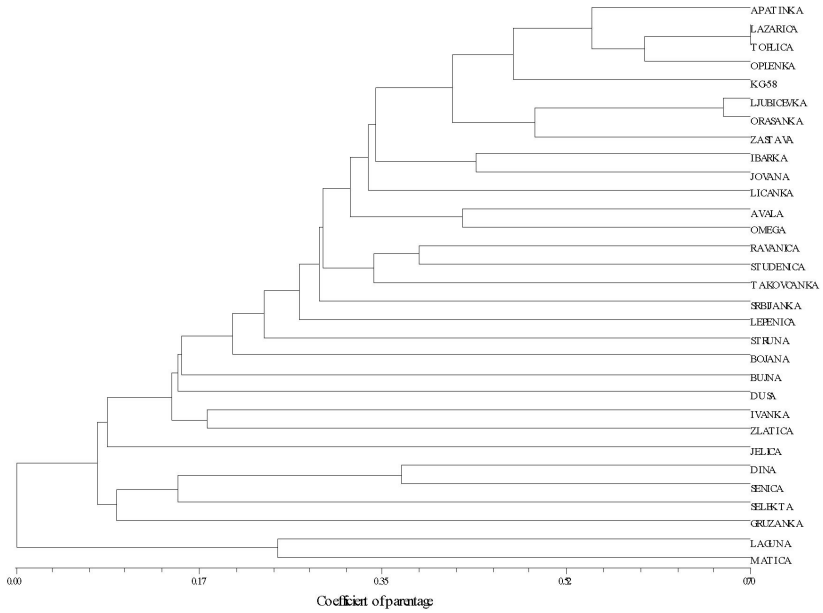

Fig. 1. A dendrogram based on cluster analysis of the relatedness coefficient matrix for Serbian winter wheat cultivars using the Information and Analytical System of Wheat Genetic Resources GRIS 3.0 (Martynov and Dobrotvorskaya 1993). In summary, breeding of winter common wheat in Serbia is oriented towards the production of noncarriers of hybrid necrosis genes, however, a certain increase in frequencies of the *ne1ne1Ne2Ne2* genotype is observed. This tendency is characteristic of many breeding centers in the world, although it is still difficult to explain.

Acknowledgment. This work was supported in part by the Program of the Russian Academy of Sciences 'Gene pool dynamics'.

Table 1. Necrosis genotypes of winter wheat cultivars in Serbia (*Ne2*^{w} and *Ne2*^{m} are weak and moderate alleles, respectively).

Cultivar	Pedigree	Year of registration	Origin	Genotype
Apatinka	NS-646 / Bezostaya1 // *2 Avrora	1989	Novi Sad	*ne1ne2*
Avala	NS-7001 / Bezostaya1 / NS-116 / Mironovskaya 808 / NS-413-4 // Kavkas/Dunav / HeineVII / Genus129	1986	Novi Sad	*ne1ne2*
Bojana	Sremica / NS-2767-4	1992	Novi Sad	*ne1ne2*
Bujana	Partizanka / ZG-3497	1999	Novi Sad	*ne1ne2*
Gruzanka	Argento / Leonardo	1972	Novi Sad	*ne1ne2*
Dina	Drava / Zitnica	1994	Novi Sad	*ne1ne2*
Dusa	Posarka 2 / NS-52-53	1991	Novi Sad	*ne1ne2*
Ibarka	Sava / NS-2795-6	1988	Novi Sad	*ne1Ne2*^{w}
Jelica	NS-7000 / NS-7001 / NS-7002	1989	Novi Sad	*ne1ne2*
Zlatica	Novosadska Rana 2 / Mutant 48 // Sutjeska	1992	Novi Sad	*ne1ne2*
Iovana	Nova Banatka / Macunka 1	1992	Novi Sad	*ne1ne2*
Ivanka	Duga /Sutjeska // Novosadska 6001	1996	Novi Sad	*ne1ne2*
Kragujevcanka 58	Bezostaya 1 / Halle Stamm // Bezostaya 1	1977	Kragujevac	*ne1ne2*
Laguna	NS-2879-5-1 / Nova Posauka	1995	Novi Sad	*ne1ne2*
Lazarica	Yugoslavia / NG-56	1995	Kragujevac	*ne1ne2*
Lepenica	Bezostaya 1 / 1W-66	1980	Novi Sad	*ne1ne2*
Ljubisevka	?	1985	Kragujevac	*ne1ne2*
Matica	KG-V-3 / Nova Posavka	1999	Kragujevac	*ne1ne2*
Novosadska Rana 6	Talent / Novosadska Rana 2	1991	Novi Sad	*ne1ne2*
Oplenka	Kavkas / Kragujevcanka 56	1982	Kragujevac	*ne1ne2*
Omega	?	1995	Novi Sad	*ne1ne2*
Orasanka	Bezostaya1 / Halle Stamm // Bezostaya 1	1976	Kragujevac	*ne1Ne2*^{m}
Ravanica	Kavkas / L-5393 // Tena	1990	Kragujevac	*ne1ne2*
Selecta	?	1996	Novi Sad	*ne1Ne2*^{w}
Senica	Dwarf A / Zitnica // Zitnica	1996	Novi Sad	*ne1Ne2*^{w}
Srbijanka	Kavkas / Line-29-60	1986	Kragujevac	*ne1ne2*
Studenica	Kavkas /L-5393 // Tena	1989	Kragujevac	*ne1ne2*
Zastava	Bezostaya 1 / Abbondanza	1973	Kragujevac	*ne1ne2*
Licanka	Avrora / NS-845	1982	Novi Sad	*ne1Ne2*^{w}
Struna	NS-2785 /Partizanka // Tena	1994	Novi Sad	*ne1ne2*
Toplica	Yugoslavia / Kragujevcanka 56	1997	Novi Sad	*ne1ne2*
Takovcanka	Kavkas /L-5993	1990	Novi Sad	*ne1ne2*

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Zeven AC. 1981. Eighth supplementary list of wheat varieties classified according to their genotype for hybrid necrosis. Euphytica 30:521-539.

Hybrid necrosis genes in modern cultivars of winter common wheat of the Czech Republic.

V.A. Pukhalskiy, E.N. Bilinskaya, S.P. Martynov, and L.A. Obolenkova.

Introduction. Modern breeding contributes considerably to the distribution of hybrid necrosis genes in wheat populations in different countries (Altukhov et al. 2005). The genetic erosion is clearly seen that dictates the necessity to develop a new strategy of breeding and formation of gene bank collections. Therefore, the study the microevolution of the wheat genome using different genetic markers including hybrid necrosis genes is interesting. Here, we present data on the analysis of necrotic genotypes in the former Czechoslovakia and modern Czech Republic.

Materials and methods. Thirty cultivars of winter wheat released in different breeding centers of the former Czechoslovakia and the Czech Republic were studied. Mironovskaya 808 (*ne1ne1Ne2Ne2* genotype) and Co725082 (*Ne1Ne1ne2ne2* genotype) were used as testers. Crosses were made in the field by conventional procedures with isolation of spikes. F_1 hybrids were grown in the field, and the symptoms of hybrid necrosis were evaluated at different ontogeny stages.

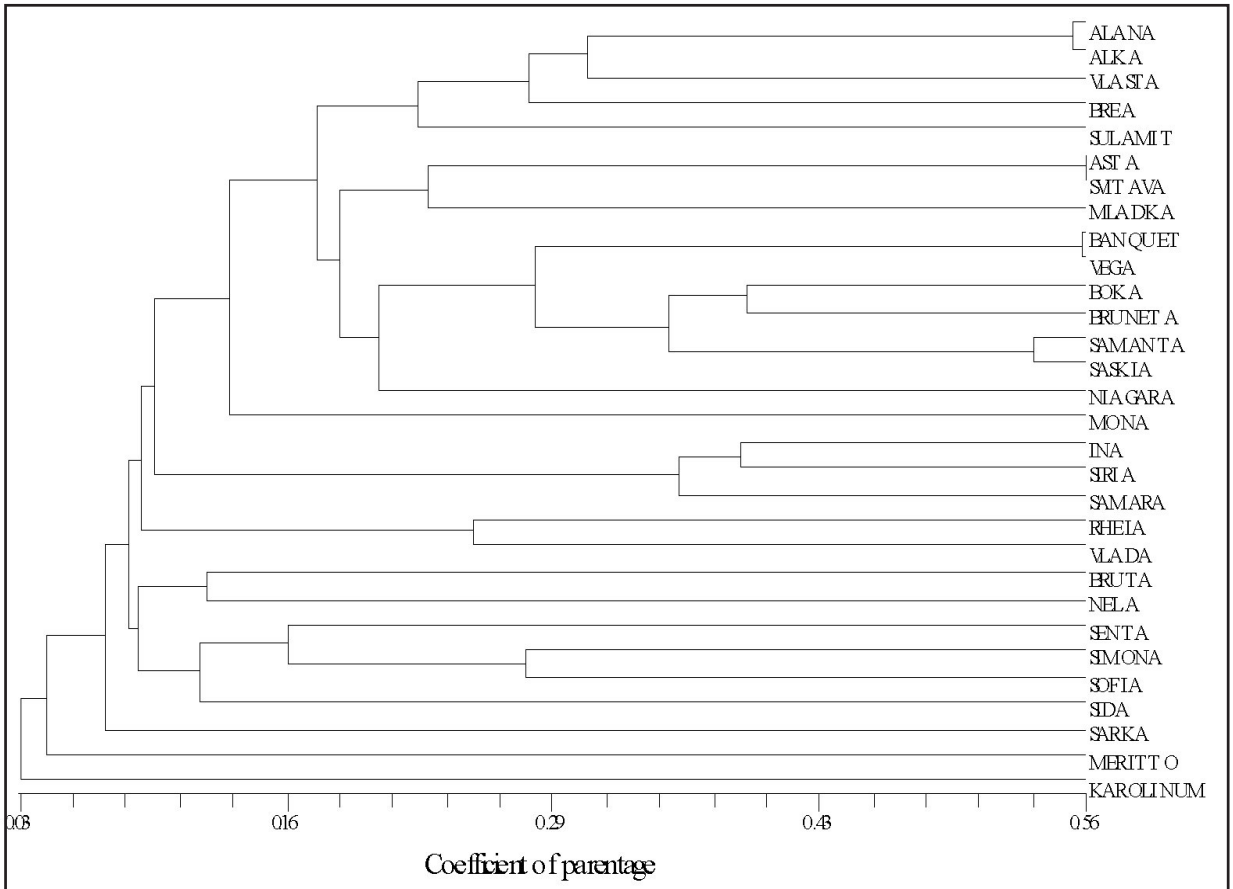

Fig. 2. A dendrogram based on cluster analysis of the coefficient relatedness matrix of the Czech cutivars using the Informational-Analytical System of Genetic Resources GRIS 3.0 (Martynov and Dobrotvorskaya 1993).

Table 2. Necrosis genotypes of winter wheat cultivars in the Czech Republic (CSK – former Czechoslovakia; CZE – Czech Republic, and NLD – the Netherlands; *Ne2^{w}, Ne2^{mw}, Ne2^{m}, Ne2^{ms}, and Ne2^{s}* are weak, moderately weak, moderate, moderately strong, and strong alleles, respectively).

Cultivar	Pedigree	Year of registration	Origin	Genotype
Vlada	Mironovskaya 808 / BR-682	1990	CSK	*ne1ne2*
Sofia	ST 933-74 / ST-39-76	1990	CSK	*ne1Ne2^{s}*
Vega	Hana / Selenta	1992	CSK	*ne1Ne2^{s}*
Simona	ST 39-76 / Zdar	1991	CSK	*ne1ne2*
Senta	Benno / Sava // ST 933-74	1991	CSK	*ne1Ne2^{s}*
Bruta	BR-693 / Mara	1994	CSK	*ne1ne2*
Sida	ST 39-76 / Alcecdo // ST-104-78	1993	CSK	*ne1ne2*
Siria	Arminda / Maris-Marusman // Regina	1994	CSK	*ne1ne2*
Samanta	Nana / Uiginta	1993	CSK	*ne1Ne2^{m}*
Asta	Akhtyrchanka / Maris-Marusman	1994	CSK	*ne1Ne2^{m}*
Mona	Il'ichevka / Line 5608-74	1994	CSK	*ne1Ne2^{mw}*
Boka	Viginta / Selecta	1995	CSK	*ne1Ne2^{s}*
Ina	HE-2789 / Regina(CSK)	1995	CSK	*ne1Ne2^{ms}*
Samara	Regina / CWW-WN-156	1995	CSK	*ne1Ne2 ^{ms}*
Alka	Hana / Mercia	1995	CSK	*ne1ne2*
Brea	BR 918 / Hana	1996	CSK	*ne1Ne2^{s}*
Bruneta	Viginta // Viginta / BR 918	1996	CSK	*ne1Ne2^{s}*
Alana	Hana / Mercia	1997	CSK	*ne1Ne2^{ms}*
Saskia	Hana / Viginta	1996	CSK	*ne1Ne2^{s}*
Nela	HE-2394 / Selecta	1998	CSK	*ne1ne2*
Sarka	UN / Mironovskaya nizkoroslaya // Avalon / Mironovskaya nizkoroslaya	1997	CZE	*ne1Ne2^{m}*
Niagara	BU-LSA -89 / Jlona	1999	CZE	*ne1Ne2^{ms}*
Vlasta	Hana / Brimstone / S-13	1999	CZE	*ne1Ne2^{mw}*
Banquet	Vega / Blava	2001	CZE	*ne1Ne2^{S}*
Sulamit	Hana / Zdar*2 // Alidos	2000	CZE	*ne1ne2*
Svitava	Asta // (ST 950-89) Hana / Viginta	2001	CZE	*ne1ne2*
Mladka	ST-467 / Contra	2002	CZE	*ne1Ne2^{w}*
Rheia	Hubertas / SG-U-153-A /3/ SG-U-153A / BR-1193 // US-74-709	2002	CZE	*ne1ne2*
Meritto	?	2003	CZE	*ne1Ne2^{s}*
Karolinum	?	2003	NLD	*ne1Ne2^{w}*

Results and discussion. Our results on the presence of hybrid necrosis genes in wheat cultivars are given in Table 2. In the cultivars studied, the *Ne1* gene was absent, whereas 66.7% of the cultivars had the *ne1ne1Ne2Ne2* genotype. The *ne1n51n52ne2* genotype was identified in 33.3% of the wheats. Because we investigated wheat cultivars produced between 1990 and 2003, we compared our data with the results obtained earlier (Apltauerova 1983; Zeven 1969, 1973, 1976, 1981; Sarkisyan 1972; Sarkisyan and Petrosyan 1972; Pukhalskiy et al. 1997). In the literature, the necrotic genotypes of 30 cultivars of winter wheat of the former Czechoslovakia have been described. Two of these cutivars (6.7%) have *Ne1*, whereas 14 (46.7%) were *Ne2*-carriers, and 14 (46.7%) were noncarriers of hybrid necrosis genes. The *Ne1* gene was identified in the cultivar Iva released in 1962 and in the selection line ST-46-78 (Apltauerova 1983).

Cultivars produced in the former Czechoslovakia between 1915 and 1930 were noncarriers of hybrid necrosis genes and included Diosecka (1915), Chemecka 12 (1919), Dobrovicka (?), Valtcka osinata (1936), and Diosecka Nova (1930) (Zeven 1981). Hybrid necrosis genes probably appeared in the breeding centers of the former Czechoslovakia after the 1950s.

Our data, together with the findings of other researchers, indicate a dramatic increase in the *ne1ne1Ne2Ne2* genotype frequencies among winter common wheat cultivars of the former Chech Republic. Similar processes occur in other wheat-growing regions of the world (Altukhov et al. 2005; Pukhalskiy and Bilinskaya, 2006). This tendency is still difficult to explain. Another interesting peculiarity is the high frequency of strong alleles *s* (45%) and *ms* (20%), although the frequency of the *m* allele was 15%, of the *mw* allele 10%, and of the *w* allele 10%. This is a rare case of a relatively small population, especially if we take into consideration that according to Zeven (1976), the former Czechoslovakia belonged to a region where noncarriers of hybrid necrosis genes were predominantly cultivated (*ne1ne1 ne2ne2* genotype). Cluster analysis of the relatedness coefficients showed rather low variation among the cultivars with the strong allele of the *Ne2* gene (Fig. 2, p. 82). In 9 out of 10 instances, the Mironovskaya 808 ($Ne2^{ms}$) gene was the donor of strong alleles. This cultivar is in the pedigree of Vega, Ina, Boka, Brea, Bruneta, Saskia, Banquet, Senta, and Sofia. Together with Mironovskaya 808, this allele could have been from Noe via Maris Huntsman (Sofia) and Turkey via Benno (Senta). Mironovskaya 808 is absent only from the pedigree of Meritto. In this case, the donor of the $Ne2^{s}$ allele could be Noe through Maris Huntsman and Heines VII or Turkey through Carstens VIII. We cannot exclude that in this case, together with certain alleles of the *Ne2* gene, some other genes located on the D genome that function as catalyzers or minor promoters were involved in breeding (Jha et al. 1980).

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ITEMS FROM THE REPUBLIC OF SOUTH AFRICA

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Triticale breeding.

In 2004, one of our top yielding cultivars (Tobie) became susceptible to a new leaf rust race and, in 2005, to a new stem rust race. In 2006, more than 90% of our germ plasm were susceptible to one or both races. The best combined resistance comes from a local cross of which the parentage includes both local cultivars/lines and CIMMYT germ plasm. The line is being multiplied for release in 2008 and has the pedigree IBIS/7/HARE 212/3/Champlain/Aronde 68//VPM/Moisson/4/Juanillo 100/5/Andas "S"/6/Durum wheat/Balbo//BOK"S"/3/Andas "S"//TJ/BGL "S".

Wheat recurrent mass selection.

Recurrent mass selection based on the *Ms3* gene for dominant male sterility and hydroponic culture of cut wheat spikes was continued. In this breeding scheme, female and male plants are handled differently. Each year F_1 seedlings are screened for resistance to a mixture of leaf and stem rust pathotypes. Selected female (male sterile) plants are used directly in crosses and the male component is field planted and selected. Superior F_6 populations are then used as male parents in the crossing block. Single-seed descent steps have been integrated into the program, making it possible to rapidly (two seasons) advance from the F_1 to the F_5. In 2006, approximately 10,500 F_1 were tested for seedling resistance to an inoculum mix of eight leaf rust and six stem rust pathotypes. About 3,200 (50% female and 50% male) resistant F_1 plants were planted for crosses and single-seed descent. The female group was randomly pollinated with 100 field selected (2005) F_6 lines to produce about 50,000 F_1 seeds. A total of 959 F_4 and 1,401 F_6 lines were planted. An additional 110 senior trial selections (1–3 localities) and 34 elite trial entries (five localities) were tested. Following selection of the 2005 F_6 population for agrotype, rust resistance and mixograph properties, 100 lines were used to compile an F_7 nursery that was distributed to local breeding organizations in 2006. The same material was sent to Uganda to be evaluated for resistance to the new UG99 stem rust virulence.

To continue enriching the base population with resistance genes, recurrent backcrosses with the *Lr19*, *Sr31*/*Lr26*/*Yr9*/*Pm8*, and *Lr21* genes were continued.

Genetic studies.

Homoeologous pairing induction experiments to remodel the alien translocation in four species-derived resistance sources were continued; these include (a) the *Lr56*/*Yr38* translocation (6A; from *Ae. sharonensis*), (b) the *Lr54*/*Yr37* translocation (2DL; from *Ae. kotschyi*), (c) the *LrS15* translocation (1BL, *Ae. peregrina*), and (d) the *LrS13*/*YrS13*/*SrS13* translocation (3AS, from *Ae. speltoides*). Test cross populations are being screened for recombinants making use of mapped microsatellite loci. Attempts to map (using the Inia 66 monosomics) leaf and stripe rust resistance genes (*LrS20*/*YrS20*) from *Ae. neglecta* and leaf rust resistance (*Lrmac*) from *Ae. biuncialis* were continued.

Disomic addition lines of *Th. distichum* chromosomes that appear to be involved in salt tolerance were produced in triticale and subsequently were used to develop two or more SCAR markers for each of the *Thinopyrum* target chromosomes. The markers could be employed to derive a panel of secondary *Thinopyrum*/triticale hybrids with different combinations of the critical chromosomes that were evaluated in tolerance tests. Results showed that single chromosomes had only minor effects on salt tolerance. Chromosomes $2J_1^d$ & $3J_1^d$ was the only combination of two

chromosomes at a time to produce a notable effect whereas combinations $2J_1^d$, $3J_1^d$ & $5J_1^d$ and $3J_1^d$, $4J_1^d$, and $5J_1^d$ resulted in high levels of tolerance comparable to that of the primary amphiploid.

Broad strategies to utilize the tolerance in cereals include (i) systematic production of Robertsonian translocations of the target J_1^d chromosomes to triticale /wheat homoeologues, (ii) production of plants with genomes 2n = 42 = $AABBJ_{1/2}^dJ_{1/2}^d$ that include the *Thinopyrum* target chromosomes, and (iii) production of octoploids with genomes 2n = 56=$AABBRRJ_{1/2}^dJ_{1/2}^d$. To facilitate the latter attempts, pivotal genotypes were produced that are being used in molecular marker assisted backcrosses to produce the desired plants. An attempt also is being made to saturate the target chromosomes with anonymous markers that can be employed in attempts to further dissect the chromosomes and determine the locations of the genes involved.

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ITEMS FROM SPAIN

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Characterization of the Hessian fly biotype present in southwestern Spain.

Hessian fly is a major pest of wheat worldwide and also an endemic pest in southwestern Spain. Two generations per year occur in infested fields in this area (Delibes et al. 1997). The most practical way of Hessian fly control remains the development of resistant cultivars. The biological interaction between *Triticum spp*. and Hessian fly is highly specific, with a gene-for-gene relationship between resistance genes in wheat and avirulence genes in the insect (Hatchett and Gallum 1970). Wheat resistance to *M. destructor* attack is conditioned mostly by dominant alleles at single loci (*H* genes). Virulence against each resistance wheat allele is determined by recessive alleles at a single locus in *M. destructor* (*vH*^{a} genes). To date, 33 resistance genes have been identified (*H1–H32* and *Hdic*) (Liu et al. 2005). In the U.S., 16 biotypes (designated Great Plains and biotypes A–O) have been isolated from field populations. Biotypes were defined by their response (virulence or avirulence) to four common wheat cultivars carrying the *H3, H5, H6*, or *H7H8* resistance genes (Gallum 1977). Insect biotypes occur in nature as a result of selection from the population in response to exposure to resistant cultivars. However, Hessian fly virulence has been confirmed to some resistance genes that have not been deployed in wheat cultivars in the U.S. (Ratcliffe et al. 1994). Therefore, testing the available genes against as many biotypes and current populations of Hessian fly as possible is necessary, which would prevent the release of wheat cultivars with ineffective sources of resistance. The main objective of this research was to determine the biotype of Hessian fly prevalent in southwestern Spain and to test the effectiveness of resistant wheat cultivar carrying different *H* genes (*H*3, *H5* to *H15, H18*, *H21*, and *H24*) against this population.

Material and methods. In order to determine the biotype of Hessian fly, four differential cultivars (Monon (*H3*), Abe (*H5*), Caldwell (*H6*), and Seneca (*H7H8*)) were evaluated for resistance four consecutive years at Azuaga (38°15' N; 5°40' W) and, in the last season also at La Granjuela (38°22'N; 5°21'W). Additionally, they were evaluated for two consecutive years in greenhouse under controlled conditions. We also tested a series of wheat cultivars carrying *H* genes from the Uniform Hessian fly Nursery (UHFN) under the same conditions. Dr. H.E. Bockelman and F. Maas from the National Small Grains Collection of USDA-ARS supplied this collection. The wheat cultivars Newton and Astral were used as susceptible controls.

Each experiment was completely randomized with three replications, and 30 seeds were sown per cultivar and test. In the greenhouse, plants were infested with a fly population collected on the susceptible cultivar Astral during the

previous season at Azuaga and stored in the 'flaxseed' stage at 5°C. Infestation was according to Cartwright and La Hue (1944). Plants were examined for presence of puparia as described by Martín-Sánchez et al. (2003) and scores were expressed as the number of puparia per tiller.

Results and conclusions. The response of wheat cultivars with different *H* genes and the susceptible control (Astral) to the population of Hessian fly from southwestern Spain is summarized in Fig. 1. The four differential cultivars Monon (*H3*), Abe (*H5*), Caldwell (*H6*), and Seneca (*H7H8*) were resistant to Hessian fly population in all the conditions evaluated, but there was some variability in infestation across years. These results suggest that biotype GP, nonvirulent to any resistance gene, is the prevalent biotype in southwestern Spain, but we cannot discard the presence of other biotypes. In the state of Washington, U.S., where Hessian fly resistance genes are not yet deployed, biotype GP also is the most prevalent, but it coexists with other biotypes (Ratcliffe et al. 1996). Thereby, populations of flies are heterogeneous in biotype composition, but a single virulent biotype usually is prevalent and corresponds with the predominant resistance genes deployed in the region (Ratcliffe et al. 1996, 2000; Naber et al. 2003; Bouktila et al. 2005).

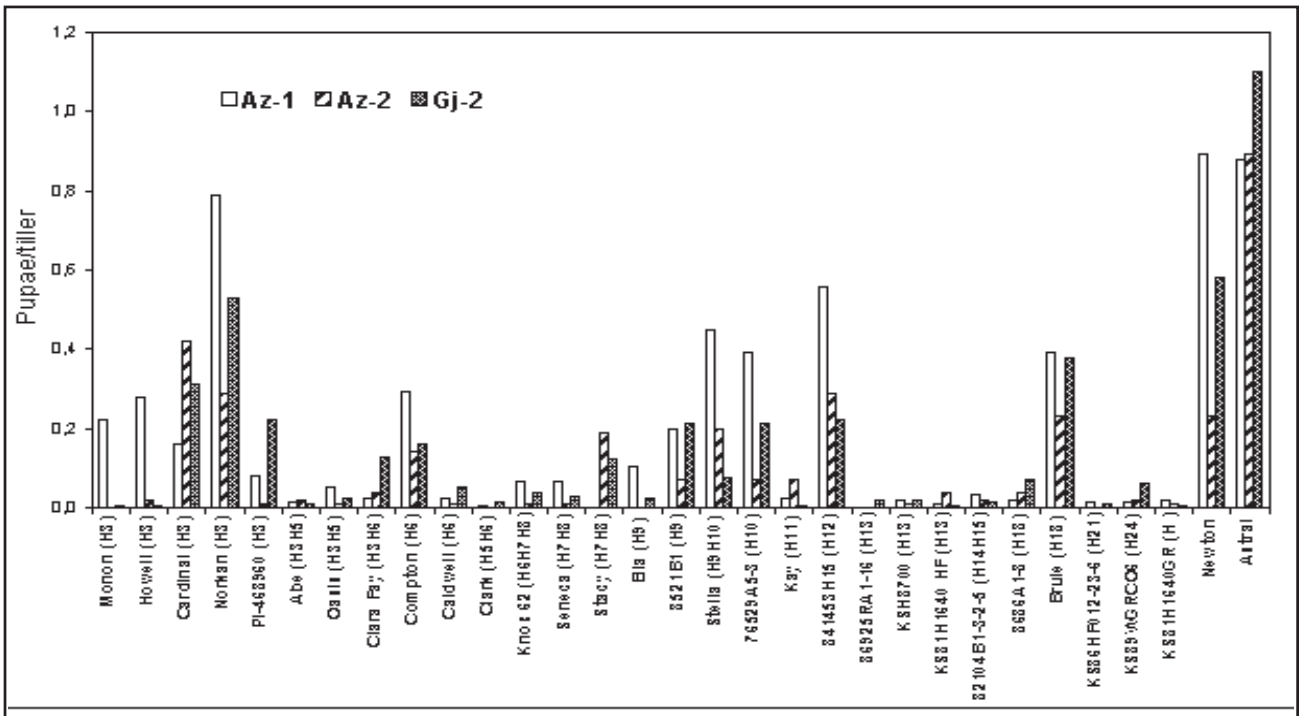

Fig. 1. Response of wheat lines and cultivars from the Unified Hessian fly Nursery to a Hessian fly population from southwestern Spain. *T. aestivum* cultivar Astral was used as the susceptible control. Each bar represents the average of a minimum 100 tillers/stock. Data are from 2 years for the Azuaga (1, Az) and Granjuela (2, Gj) locations.

The level of virulence to *H5*, *H11*, *H13*, *H14*, *H15*, *H21*, and *H24* genes was low at all conditions. Most of the wheat with *H9, H10* , or *H12* had high infestation levels. Genes *H3*, *H6, H7H8*, and *H18* genes showed different resistance levels depending on the genetic background. Cultivar response was similar in both greenhouse and field conditions but was higher in the greenhouse tests, especially among cultivars with *H9* and *H10* resistance (data not shown).

Most of these genes (*H9* to *H24*) had previously been tested against biotypes A, B, C, D, E, L, and GP. All were effective, with the exception of *H9*, *H10*, and *H12*, which are susceptible or weakly resistant to biotype C; *H12* also has weak resistance to biotype E, and *H11* and *H15* to biotype L. The expression of several of these genes is affected by high temperatures (Amri et al. 1992; El Bouhssini et al. 1999). Our results, according to studies of Hessian fly populations in North Africa where the genes *H5*, *H7H8*, *H11*, and *H14H15* and those from *S. cereale* and *Ae. tauschii* were effective against Hessian fly populations (El Bouhssini et al. 1992 a,b; 1996; Naber et al. 2003; Bouktila et al. 2005). In the U.S. populations, *H9*, *H10*, and *H12* genes showed weak resistance to fly populations in which biotype C was not present (Ratcliffe et al. 1996).

In this study, we demonstrated the importance of the wheat genetic background in the expression of Hessian fly resistance genes and, thereby, the necessity of not separating H genes from wheat genetic background. Virulence to *H3*, *H6*, *H9*, *H10*, and *H12* was present in Hessian fly population from Azuaga, thus the use of these resistance genes in wheat cultivars adapted to southwestern Spain may be limited. Resistant genes from wild relatives are effective but, because of potential rapid change in Hessian fly populations, it is important to continue studying virulence in the field, which would help to develop appropriate gene deployment strategy for Hessian fly in Spain.

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New releases.

Victorino is a spring bread wheat cultivar released in 2006. Developed from the backcross 'H-93-8/4*Rinconada' under the designation ID-2150, Victorino has the *Cre*2 gene, transferred from *Ae. ventricosa*, for resistance to the cereal cyst nematode *H. avenae* (Delibes et al. 1993). Victorino is a high-yielding, medium maturing, semidwarf cultivar with moderate resistance to powdery mildew and leaf rust. This cultivar is best adapted to the southern and northeastern wheat-growing regions of Spain and has good quality properties suitable for the baking industry.

T-2003, developed from the backcross 'TR-353/3*Osona//4*Cartaya' with the *Cre*7 resistance gene to *H. avenae,* transferred from *Ae. triuncialis* (Romero et al. 1998), was one of the top yielding lines in the National Variety Trial Testing of Spain (OEVV). T-2003 is an early maturing, semidwarf cultivar moderately resistant to powdery mildew and resistant to leaf rust. This cultivar is better adapted to the southern and northeastern wheat-growing regions of Spain. Because the dough strength (W) values have been below average, T-2003 appears to have regular baking quality.

The induction of several defense responses during early infection by juveniles of *H. avenae* (pathotype Ha71) in both resistant cultivars (Victorino and T-2003) was studied. Isoelectricfocusing isozyme analysis revealed that peroxidase activity increased in roots of resistant cultivars after nematode infection compared with the susceptible parent cultivar Almatense H-10-15. This result agrees with previous observations on resistance conferred by the *Cre*2 and *Cre*7 resistance genes (Andrés et al. 2001; Montes et al. 2004). The *H. avenae* pathotype Ha71 was unable to overcome their resistance mechanisms in introgression lines with *Cre* genes, and peroxidase activity increased in roots of these lines after nematode infection.

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New release.

Catedral, a spring bread wheat cultivar released in 2006 in Spain, was developed at the Institut de Recerca i Tecnologia Agroalimentaries (IRTA) from the cross 'Chil "S"/Recital'. Catedral was tested as ID-2163. This cultivar has better adaptation to the southern and northeastern wheat-growing regions of Spain. Catedral is a high-yielding, medium maturing, semidwarf cultivar, moderately resistant to powdery mildew and leaf rust and has good quality properties suitable for the baking industry.

ITEMS FROM THE UKRAINE

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Morphological traits of polyploid wheat forms of the subgenus Boeoticum E.Migusch.Et Dorof.

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The use of synthetic wheats with the G genome seems to be a fruitful way for genetic improvement of cultivated wheat because of genes controlling a number of valuable traits including disease and pests resistance, high protein content in the grain, high groat quality, specific starch quality (waxy), and tolerance to soil acidity.

According Dorofeev et al. (1979), species and forms with the G genome constitute a separate branch of evolution of the genus *Triticum* and are included in subgenus *Boeoticum* E.Migusch.et Dorof., which consists of the sections *Monococcon* Dum., *Timopheevii* A. Filat. et Dorof., *Kiharae* Dorof. et E.Migusch. Species with the G genome are found in the last two sections.

Section *Timopheevii* (genomes A^bG) includes wild emmer *T. araraticum* Jakubz., cultivated emmer *T. timopheevii* Zhuk., and also a naked analogue of *T. timopheevii* named *T. militinae* Zhuk. et E.Migusch. The free threshing ability of the last species is caused by the *Q* gene.

Section *Kiharae* (A^bGD) includes artificially obtained synthetic forms. *Triticum kiharae* Dorof. et E.Migusch. (A^bGD) is an amphidiploid (*T. timopheevii*/*Ae. tauschii*) synthesized in Japan and named in honor of the Japanese geneticist H. Kihara. This species is homologue of *T. spelta* and has all the genes for resistance that are in *T. timopheevii*.

Triticum miguschovae (A^bGD) is the first homologue of bread wheat and was synthesized by E.G. Zhirov (1980) in the Krasnodar Institute of Agriculture n.a. P.P.Luk'yanenko, Russian Federation, from cross of *T. militinae* and *Ae. tauschii subsp. strangulata*. This species is named in honor of E.F. Migushova.

In 1940, Bulgarian geneticist D. Kostov obtained a hexaploid amphidiploid by crossing *T. monococcum* and *T. timopheevii*, naming it *T. timococcum* Kost (genome A^bA^bG). At the Kihara Institute, Japan, by crossing *T. timopheevii* and *Ae. umbellulata*, Amphidiploid 217 was created (genome A^bGU).

Natural octoploid (2n = 56) wheat species do not exist. One of the first a such forms, obtained by P.M. Zhukovskyi in 1944 and named *T. fungicidum* Zhuk. (A^bA^uBG), was from the cross '*T. persicum*/*T. timopheevii*' followed by a colchicine treatment. In 1959, the French botanist H. Heslot obtained and described with R. Ferrari the octoploid form *T. timonovum* Heslot et Ferrari as an autopolyploid of *T. timopheevii* (genome A^bA^bGG). In 1981, N. Navruzbekov of the Daghestan Experimental Station of the N.I. Vavilov Institute of Plant Industry, Russia, obtained an octoploid wheat by crossing two naked tetraploid (2n = 28) species, *T. militinae* and *T. persicum*, and named the resulting amphidiploid *T. flaksbergeri* Navr. (genome A^bA^uBG) in honor of K.A. Flaksberger.

We studied the morphological traits connected with plant productivity in 10 polyploid species and forms of subgenus *Boeoticum*. The material was obtained from the N.I.Vavilov Institute of Plant Industry. The base species are *T. timopheevii* and *T. militinae*, both 2n = 28 and A^bG genomes. However, as Navruzbekov found in 1979, *T. militinae* seems to be created by hybridization of *T. timopheevii* with *T. persicum* and may have a modified genome.

The addition of the D genome from *Ae. tauschii* to genomes of both species resulted in *T. kiharae* and *T. miguschovae* and lead to lengthening of spike internodes and a decrease in the number of spikelets and, consequently, grains/spike.

The addition of the U genome from *Ae. umbellulata* to *T. timopheevii* resulted in AD 217 (2n = 42, genomes A^bGU), decreased plant height, spike length, grain weight/spike, and the length and width of the flag and penultimate leaf blades. The addition of subgenome A^{bl} from *T. monococcum*, resulting in *T. timococcum* (2n = 42, genomes $A^bA^{bl}G$), decreased tiller number but increased spike length, spikelets/spike, amd also the length and width of the flag and penultimate leaf blades.

Chromosome doubling of the *T. timopheevii* genome resulted in *T. timonovum* (2n = 56, genomes A^bA^bGG) increased spike length and grains/spike, and length and width of the flag and penultimate leaf blades but decreased plant height, which may explain the reaction on of this species to drought during the development of the upper internode.

The specific influence of the different genomes added those of *T. timopheevii* and *T. militinae* should be understood when they and their derivatives are used in breeding and experiments.

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Phytosanitary state of winter wheat with different sowing dates at spring tillering stage.

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Winter wheat is one of the staple cereal crops in Ukraine and a general level of production is ensured. To date, harmful organisms are one of the limiting factors. At the first growth stages, insect pests of the stalk and root roots are most injurious, controlled most by sowing date. At present, global climate changes are causing an urgent need to adapt sowing dates for winter wheat, thus the search for optimal sowing dates for wheat are quite topical.

The investigations were conducted in a nine-course rotation stationary field at the Laboratory for Plant Production and Cultivar Investigations of the Yurjev Plant Production Institute of UAAS (Eastern-Steppe of Ukraine). During 2001–05, we studied the degree of damage in winter wheat plants with flies and the intensity of root rot development depending on sowing dates. Winter wheat was sown on 10, 20, and 30 September in 2001–04 and 1, 10, and 20 September in 2004–05.

Our results showed that during 2001–05 in winter wheat field at during autumn tillering, the dominant flies were *Oscinella spp.* (55–70%) and *Phorbia securis* Tiens. (11–32%). During spring tillering, crop damage also was caused by *Opomyza florum* F. (37.5–45.5%). *Mayetiola destructor* and *Leptochylemyia coarctata* Fll. were observed but were fewer in number. Among the root roots, Helminthosporium rot (*B. sorokiniana*) dominated in dry years and Fusarium rot in humid years.

Table 1. Hessian fly and root rot damage on winter wheat at spring tillering three different sowing dates. The forecrop was black fallow and an organic mineral fertilizer was used.

	2001–04			2004–05		
	10/09	20/09	30/09	01/09	10/09	20/09
Plants/m^2	491	495	455	313	383	373
Tillers number/m^2	2,040	1,834	1,450	1,282	1,482	1,445
Hessian fly						
larvae/m^2	83	57	35	276	190	102
damage (%) by fly larvae						
plants	14.2	13.0	8.9	44.8	34.9	21.4
tillers	5.0	4.2	2.5	22.0	13.1	7.3
biological effectiveness (%)	—	16.0	50.0	—	40.5	66.8
undamaged tillers/m^2	1,953	1,773	1,415	1,013	1,288	1,342
Root rots						
% infection	31.9	32.0	27.5	38.0	21.0	29.6
development	13.5	14.2	12.8	18.4	8.3	12.3
biological effectiveness (%)	—	—	5.2	—	54.9	33.2
undamaged plants/m^2	294	314	346	196	300	258
grain yield (t/ha)	6.26	6.51	6.39	5.45	6.73	6.88

The average number of plants/m^2 at spring tillering of winter wheat for sowing dates from 10–30 September was nearly similar between 2001–04, 455–495 (Table 1). However, wheat sown on the first date had more tillers compared to the second and third dates, 10 and 29% less, respectively. On the 10 September sowing date, there was a higher density of fly larvae than the later sowing dates 20 (1.5% less) and 30 (2.4% less) September. For winter wheat sown on the first date, we observed a higher degree of pest damage of plants and tillers compared with plants sown on the last date. When sowing on 20 September, plants and tiller damage were insignificantly less than for those sown on 10 September. The damage index at the first sowing date was 14.2%, 13.0% at the second, and 8.9% at the third. TIller damage was 5.0, 4.2, and 2.5% for the first, second, and third sowing dates, respectively. Thus, plant damage was 1.6 times greater for plant sown on the first sowing date compared to those sown on 30 September. Tiller damage was twice as high for plants sown on 10 September. The biological effectiveness of the second sowing date was 16.0% and 50.0% for the third sowing date. Correlation analysis revealed a strong positive correlation (r = 0.9) between the total number of tillers/m^2 and the number of tillers that were undamaged by fly larvae; 1,953 healthy tillers at the 1st sowing date, 1,773 at the 2nd sowing date, and 1,415 at the third date. The occurrence and development of root rots in the spring tillering stage were the least for plants sown on 30 September compared to the first and second dates. The biological effectiveness of the second sowing date was 16.0% and 50.0% for the third compared to plants sown on the first date.

The incidence of root rots at the 30 September sowing date was 27.5%, whereas at the earlier date former dates it was 31.9 (10 September) and 32.0% (20 September). Disease intensity, as indicated by the number of plants undamaged by root rots/m^2, was 12.8% greater at the second sowing date and 15% greater at the first sowing date when compared to the last sowing date.

We concluded that the influence of these different factors depends on tiller number/m^2 as well as on the occurrence and intensity of root rot development (positive correlation r = 0.3–0.4). Shifting the sowing date for winter wheat can increase grain yield from 6.26 t/ha (first sowing date), to 6.51 (second sowing date), and 6.93 t/ha (third sowing date); a difference in grain yield between the first and third dates of 0.67 t/ha.

In 2004–05, a considerably larger number of harmful flies was noted at spring tillering compared to previous years. Shifting the first sowing date to 1 September, the fly density was 27.6 larvae/m^2. At 10 September, the number was 31% lower and 63% lower by 20 September. The maximum damage on plants and tillers was observed at the first sowing date, 44.8% (plants) and 22.0% (tillers) and the minimum at the third date, 21.4% (plants) and 7.3% (tillers). The biological effectiveness of the second sowing date was 40.5% and for the third was 66.8% compared to the first date. A larger number of healthy plants/m^2 (24.5% more) was noted for the third sowing date compared with the first.

The highest values for the spread and intensity of root rots were for the 1 September sowing date (38.0% spread, 18.4% intensity); the lowest values were for 10 September (29.6 spread, 18.4% intensity). Biological effective-

ness for the reduction in disease intensity for plants sown on 10 September was 54.9% greater than those sown on 1 September and 33.2% greater for those sown on 20 September. Shifting the first sowing date from 1 September to 10 September increased the number of undamaged plants/m^2 to 300.

Winter wheat sown between 10 and 20 September out yielded that sown on 1 September by 1.28 and 1.45 t/ha, respectively. Taking into account the phytosanitary state of winter wheat being cultivated for the Forest-Steppe zone of the Eastern part of Ukraine, we found that the optimal sowing date for winter wheat was 10–20 September.

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Associative nitrogen fixation in the rhizosphere of near-isogenic VRN lines of soft winter wheat.

V.V. Zhmurko, O.A. Avksentyeva, and A.M. Samoilov.

Introduction. Associative nitrogen fixation is the process of fixing atmospheric N_2 by microorganisms of the rhizosphere. Today, N_2-fixing bacteria are thought to provide plants with some nitrogen compounds (Bashan et al. 2004), synthesize growth stimulating substances (Cassanet al. 2001; Zakharova et al. 1999), increase nitrate assimilation by bacterial nitratereductase (Patyka et al. 2002), influence on root cell membrane penetration (Katupitiya et al. 1995), and prevent plants from pathogens (Patyka et al. 2002). Plants provide the bacteria with essential nutritive substances in the form of the root exudates that contains different carbohydrates, amino and organic acids, vitamins, and other bioactive substances used by bacteria for their metabolism. Genetic and physiological investigations of associative nitrogen fixation are not numerous and need supplementation with experimental data.

Our research studied associative nitrogen fixation in the rhizosphere of soft winter wheat NILs with *Vrn1–Vrn3* genes for determining the type and rates of development. This paper presents the results of the total number of diazotrophic bacteria and *Azospirillum brasilense* measurement, a study of nitrogenase activity, and the species structure of the rhizosphere.

Materials and methods. The NILs of the soft winter wheat cultivar Mironovskaya 808 (one dominant *Vrn* gene), a spring type with the genotype *Vrn112233* , and a winter wheat with the genotype *vrn112233* were used. Plants were grown in the field after a spring sowing in 2005–06. Nitrogen-fixing bacteria were cultured from the plant roots during flowering and/or spike maturation. Monolayer and multilayer agar plates; liquid culture; and Federov-Kalininskaya, Rotter, Dobereiner, modified media with Congo-red (CR), and a simple synthetic media not containing a source of nitrogen but with different sources of carbohydrates were used. Colonies of each type were streaked onto nutrient agar to check for purity and were identified according to the standard biochemical, cultural, and cytological methods (Bergy 1994). The total number of the rhizosphere diazotrophic bacteria was counted using the Federov-Kalininskaya medium in liquid culture by means of MacCredy's tables. The number of the specific diazotrophic bacteria of wheat–*Azospirillum brasilense* was counted and identified using Dobereiner's, CR, and BMS media. Nitrogenase activity was measured by acetylene reduction. The data tables present averages and standard errors.

Results and discussion. Studying the time of transition of the Mironovskaya 808 NILs demonstrated that spring wheat lines with *Vrn112233* come into the tillering phase 27–29 days earlier than the line *vrn112233*. Two of the lines flowered 31–33 days earlier than the other. The winter-type line with *vrn112233* after a spring sowing only tillered (Table 1). These results confirmed our earlier results

Table 1. Time of transition of NILs of the cultivar Mironovskaya 808 with *Vrn* genes.

		Days to		
Genotype	Type	tillering	booting	flowering
Vrn112233	spring	22 ± 1	31 ± 1	56 ± 3
Vrn112233	spring	29 ± 1	58 ± 2	87 ± 3
Vrn112233	spring	20 ± 1	29 ± 1	54 ± 2
vrn112233	winter	25 ± 2	did not flower	

(Zhmurko et al. 2004) and those of Zakharova et al. (1999) about the effect of *Vrn* genes on the rate of plant development.

Associative nitrogen fixation activity may correlate with the general physiological status of a plant and determine productivity (Zakharova et al. 1999). We studied two characteristics of productivity, the number and weight of grains/ear. Two of the NILs greater than the third (Table 2). We believe that the *Vrn* genes determine both the rate of development and productivity.

Table 2. Productivity of the NILs of the cultivar Mironovskaya 808 with *Vrn* genes.

Genotype	Type	Grain/ spike	Grain weight (mg) /spike	/seed
Vrn112233	spring	17 ± 1	283 ± 25	17.0 ± 2.6
Vrn112233	spring	14 ± 1	229 ± 32	16.4 ± 3.0
Vrn112233	spring	17 ± 1	402 ± 26	23.1 ± 3.3
vrn112233	winter		did not flower	

The main characteristics of associative nitrogen fixation show that the total number of diazotrophic bacteria, the number of *Azospirillum brasilense* and nitrogenase activity (NA) in the rhizosphere of two of the *Vrn112233* lines were higher than those of the other *Vrn112233* line and the winter wheat *vrn112233* (Table 3). We do not believe that associative N_2-fixation activity is determined by *Vrn1–Vrn3* genes.

Table 3. The number of diazotrophic bacteria and nitrogenase activity (NA) in the rhizosphere of the NILs of cultivar Mironovskaya 808 with *Vrn* genes.

Genotype	Type	Diazotrophic bacteria (x 10^6) Total number cells/g soil	*A. brasilense* cells/g roots	Nitrogenase activity, ng of N_2/ g soil/hour
Vrn112233	spring	3.1 ± 0.11	0.71 ± 0.04	17 ± 0.5
Vrn112233	spring	2.7 ± 0.09	0.56 ± 0.02	13 ± 0.2
Vrn112233	spring	3.6 ± 0.12	0.80 ± 0.03	26 ± 0.6
vrn112233	winter	2.8 ± 0.07	0.60 ± 0.03	14 ± 0.2

Within the species f diazotrophic bacteria of the rhizosphere, we did not find any correlation between the species structure and the genotype. The species structure (microcenosis) may be typical for *T. aestivum* and not determined by *Vrn* genes. The results show the high diversity of associative N_2-fixing bacteria (Table 4). We isolated 15 species belonging to seven families, six orders, four classes, and two phyla. The majority of the nitrogen-fixing bacteria isolated from wheat rhizosphere belong to the Pseudomonadaceae, Bacillaceae (four species), Bradyrhizobiaceae (two species) and Rhodospirillaceae. Population diversity of the rhizosphere is higher than that of the rhizoplane (a small zone around the roots). We identified and classified the following species of diazotrophic bacteria in the rhizosphere of the NILs: *Azospirillum brasilense*,

Table 4. The diazotrophic bacteria species structure of the rhizosphere of the NILs of cultivar Mironovskaya 808 with *Vrn* genes.

Class	Order	Family	Species
Phylum Proteobacteria			
Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	*Azospirillum brasilense*
	Rhizobiales	Rhizobiaceae	*Agrobacterium sp.*
		Bradyrhizobiaceae	*Agromonas oligotrophica*
			Xantobacter autotrophicus
Betaproteobacteria	Burkholderiaceae	Oxalobacteraceae	*Herbaspirillum seropedicae*
Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	*Pseudomonas sp.*
			Pseudomonas fluorescens
			Azomonas agilis
			Azotobacter vinelandii
	Enterobacteriales	Entetrobacteriaceae	*Enterobacter aerogenes*
Phylum Firmacutes			
	Bacillales	Bacillaceae	*Bacillus subtilis*
			Bacillus macerans
			Bacillus polymyxa
			Bacillus mesentericus
Others			*Arthrobacter sp.*

Azotobacter vinelandii, Agrobacterium sp., Agromonas oligotrophica, *Azomonas agilis*, *Arthrobacter sp*., *Bacillus subtilis, Bacillus mesentericus, Bacillus macerans, Bacillus polymyxa*, *Enterobacter aerogenes*, *Herbaspirillum seropedicae*, *Pseudomonas sp*., *Pseudomonas fluorescens*, and *Xanthobacter autotrophicus*. We identified only three species in the rhizoplane, *Bacillus subtilis*, *Azospirillum brasilense*, and *Agrobacterium sp*.

Thus, the NILs with *Vrn* genes are characterized with different nitrogenase activity and number of associative N_2-fixing bacteria. According to their level, the NILs with *Vrn* genes may be arranged: *Vrn112233* > *Vrn112233* > *vrn112233* ≥ *Vrn112233*. We have reason to believe that *Vrn* genes determine the type of development and the process of associative nitrogen fixation.

One of the possible mechanisms of the determination may be the following: in accordance with our previous results (Zhmurko et al. 2004) these lines are differed in an intensity of a carbohydrates metabolism. Two of the *Vrn112233* lines have a more intensive reflux of carbohydrates and other organic substances from leaves to the acceptor zones than *vrn112233* and the other *Vrn112233* lines have. Consequently, carbohydrates are transported faster to the roots influencing growth and development of associative N_2-fixing microflora (bacteria) and, therefore, the total number of diazotrophic bacteria and nitrogenase activity increase.

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ITEMS FROM UNITED KINGDOM

JOHN INNES CENTRE
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Genetic biodiversity for yellow rust resistance in UK wheat cultivars.

Lesley A. Boyd, Clare Lewis, James Melichar, Luke Jagger, and Nicola Powell.

A number of programs are continuing to characterize the genes/QTL responsible for yellow rust resistance in UK wheat cultivars, including the UK cultivars Claire, Guardian, and Brigadier. Genetic mapping is utilizing SSR, AFLP, and NBS-based PCR marker systems to identify partial, adult-plant expressed resistance towards the fungus *P. striiformis*, the causal agent of yellow rust. Yellow rust resistance genes/QTL identified will be located across a diverse range of UK wheat cultivars, both current and historic, that are representative of the current winter wheat germ plasm pool utilized by UK wheat breeders.

Genetic biodiversity studies also have been extended to include an assessment of Turkish wheat cultivars (durum and bread) as part of a collaboration with Prof. M. Sayar, Bogazici University, Istanbul (EU–Marie Curie Fellow) and CIMMYT in Ankara, Turkey, and Mexico. NBS-profiling has been used to characterize the genetic diversity associated with NBS (R-gene) sequences within the wheat genome. The Turkish cultivars are being compared to a selection of 30 wheats from across Europe.

Novel sources of resistance to biotrophic fungal pathogens in wheat.

James Melichar and Lesley A. Boyd.

A number of mutants, generated by γ-radiation in the UK wheat cultivar Guardian, were selected originally in the field for enhanced resistance to yellow rust. This enhanced resistance was shown not to express in seedlings but to be developmentally regulated, expressing at adult-plant growth stages.

In addition to the enhancement of resistance to yellow rust, a number of the mutants also exhibit enhanced resistance to leaf rust and/or powdery mildew. Doubled-haploid populations have been developed in Guardian and two of the mutants. Having identified the QTL for the partial, APR to yellow rust in Guardian, the mutations responsible for the enhancement of yellow rust resistance will be mapped. These populations now form part of a European Union-funded program BioExploit.

Factors affecting yellow rust infection efficiency in wheat.

Ruth MacCormack and Lesley A. Boyd.

A Defra-funded program examined the early stages of *P. striiformis* infection to determine what environmental factors influenced infection efficiency of this fungal pathogen. The quanta of light received by wheat seedlings and preinoculation by the pathogen, influenced the ability of *P. striiformis* to find and enter stomata. A preliminary screen of a small number of wheat cultivars showed genetic variation between wheat genotypes for the ability of preinoculation light quanta to effect *P. striiformis* infection efficiency.

Nonhost resistance in wheat and rice.

Hale Tufan and Lesley A. Boyd.

The CGIAR Generation Challenge Program project 'Cereal Immnity' consists of a collaboration between seven research groups around the world and is lead by AGROPOLIS, Montpelliar, France. The program uses the Affymetrix wheat micro array to study gene expression in wheat in host and nonhost pathogen interactions and links in with similar studies in rice being carried out by Prof. P. Ronald, UC Davis, USA, and Prof. S. Kikuchi, NIAS, Japan. Initial microarray screens have identified a number of common transcripts that are up-regulated in wheat and rice in the nonhost-pathogen interactions.

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ITEMS FROM THE UNITED STATES OF AMERICA

COLORADO

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Wheat breeding and genetics.

S. Haley, J. Stromberger, J. Butler, E. Heaton, H. Miller, B. Beyer, and J. Roth.

Production conditions, test sites, and cultivar distribution. Total winter wheat production in 2006 was estimated at 39.9 x 10^6 bushels, a 24% decrease from the 2005 crop and 41% lower than the 10-year average. Average grain yield, at 21.0 bushels/acre, was 13% lower than in 2005, 31% lower than the 10-year average, and the lowest grain yield since 1968. The area harvested for grain was estimated at 1.9 x 10^6 acres, down from 2.2 x 10^6 acres in 2005.

In 2005–06, the breeding program conducted field trials at six main locations in eastern Colorado (Akron, Burlington, Dailey, Julesburg, Sheridan Lake, and Walsh) in addition to the main location at the ARDEC research facility near Fort Collins. Overall, environmental conditions experienced at these locations where characterized by severe drought and high temperature stress that adversely affected both yield and quality. The following descriptions highlight the conditions experienced at our main testing locations. Akron – good autumn emergence and growth, very dry winter, warm spring with very limited moisture, severe drought stress from late spring through grain filling. All breeding trials were harvested. Burlington – good planting conditions, crusting from rain after planting caused very uneven emergence. Adequate spring rains allowed stands to fill in some, though some trials remained problematic. Some trials with very poor emergence were abandoned. Dailey – marginal planting conditions (no-till), spotty emergence, excellent autumn precipitation, adequate spring rains though stands remained spotty and drought stress was evident by early June. Some minor freeze damage noted. All breeding trials were harvested. Julesburg – very dry planting conditions, excellent fall emergence and autumn growth following heavy October rains, dry winter and spring, very severe drought stress with wheat only 6" tall in places. Variety trial was harvested by all other trials were abandoned. Sheridan Lake – marginal planting moisture (no-till), spotty emergence, good autumn rains, dry and warm winter, adequate spring rains. All breeding trials were harvested. Walsh – very dry planting conditions, good October rains immediately following planting, adequate emergence and autumn growth, some minor crusting, very warm and dry winter, significant drought stress developed by early spring. Most yield trials were harvested, although some had multiple missing plots due to non-uniformity of drought stress and Tordon spots. Fort Collins (irrigated) – excellent autumn stands and growth, significant drought stress from due to dry and warm winter and spring and inadequate and late irrigation. No significant disease or insect pressure. High temperature throughout grain filling also was a significant factor reducing yields and quality. Little significant lodging observed. All breeding trials were harvested.

Under the direction of CSU Extension Agronomist Dr. Jerry Johnson, the CSU Variety Testing Program evaluated check cultivars and experimental lines at seven other dryland trial locations (UVPT – Bennett, Cheyenne Wells, Genoa, Lamar, Orchard, Sheridan Lake, and Yuma) and two other irrigated trial locations (IVPT – Haxtun and Rocky Ford). Overall, the various UVPT trial locations experienced significant high temperature and drought stress throughout the crop season. In spite of the low grain yields of the trials, all 11 UVPT locations were successfully harvested and incorporated into the statewide data summary. In addition to the Fort Collins IVPT, both Haxtun and Rocky Ford were successfully harvested though yields at Fort Collins and Rocky Ford were reduced due to high temperatures.

No significant disease or insect problems were found in the trials in 2006. Although not a problem in the trials, wheat streak mosaic virus was a significant problem in some areas of the state because of the mild conditions experienced in late summer and autumn 2005 that provided ideal conditions for the wheat curl mite that transmits WSMV. Stripe rust, which had been so severe in 2005, was absent in 2006, significantly complicating selection to improve

resistance to this disease. Aside from RWA that were observed at several locations, no other significant insect (bird cherry-oat aphid, greenbug) problems were noted.

Planted acreage estimates for the 2006 crop were as follows: Akron – 13.6%; TAM 107 – 9.8%; Prairie Red – 9.3%; Jagalene – 8.6%; Jagger – 7.2%; Above and Prowers/Prowers 99 – 6.1%; TAM 111 – 5.1%; Ankor – 4.8%; Trego – 4.3%; Yumar – 4.1%; Yuma – 2.6%; Lamar – 2.3%; Halt – 1.4%; Weston – 1.3%; Other – 13.4%.

New cultivar releases.

One new winter wheat cultivar was released in autumn 2006. The new cultivar, named **Ripper** (denoting 'something of uncommon worth'), is a hard red winter wheat with very high dryland yields, excellent drought and high temperature tolerance, and excellent milling and baking quality characteristics. In 4 years of statewide testing in the dryland Colorado Uniform Variety Performance Trial (UVPT), Ripper was the top yielding entry in the trials; about 7% (1.8 bu/acre) higher than the next closest entry and 13% (3.2 bu/a) higher than Prairie Red. Ripper will be an excellent replacement for other stress tolerant, early-maturing cultivars in Colorado, particularly TAM 107 and Prairie Red, which tend to perform better in dry years yet have a marketing penalty due to their poor milling and baking quality.

Ripper was selected from the cross 'CO940606 / TAM107-R2'. CO940606 is an unreleased sib-selection of KS94WGRC29, a germ plasm release from Kansas State University with the pedigree 'PI 220127 / P5 // TAM-200 / KS87H66'. TAM107R-2 is an unreleased sib-selection of Prairie Red. Ripper is a bearded (awned), white-chaffed, early maturing, semidwarf with heading date about one day later than that of Prairie Red and three days earlier than that of Hatcher. Plant height of Ripper is about one inch taller than those of both Prairie Red and Hatcher with most of this difference occurring in 2005 and 2006 when drought stress was most severe (i.e., suggesting that Ripper may maintain plant height better under drought stress conditions). Ripper has a medium-long coleoptile (similar to Prairie Red, slightly longer than Hatcher), good shattering tolerance (similar to Prairie Red and Hatcher), and good straw strength (similar to Prairie Red, slightly better than Hatcher). The test weight of Ripper is slightly below average (similar to those of Jagger and Yuma) and grain protein content is slightly below average (similar to those of Prairie Red and Hatcher). Ripper is moderately resistant to prevalent races of stem rust, resistant to the virulent *Ug-99* race of stem rust identified in Africa, susceptible to both stripe and leaf rust, moderately susceptible to WSMV, resistant to biotype 1 Russian wheat aphid (RWA), and susceptible to biotype 2 RWA. Comprehensive milling and baking quality evaluations (using Above, Ankor, and Hatcher as check entries) have shown that Ripper has superior values for both milling-related and baking-related variables compared to the check entries.

Detailed data on Ripper and other recently released cultivars may be found at the home page of the CSU Wheat Breeding and Genetics Program (http://wheat.colostate.edu).

New foundation seed increases.

One new experimental line, designated as **CO01385-A1**, was advanced for Foundation Seed increase in autumn 2006. Pending further yield and quality evaluations in 2006-2007, CO01385-A1 is targeted for release as a new cultivar in autumn 2007. CO01385-A1 is a medium height, medium maturing, hard red winter wheat with very high dryland and irrigated yields, high test weight, good resistance to both leaf and stripe rust, and above-average milling and baking quality characteristics. CO01385-A1 was derived from the cross 'Yumar / Arlin' made in 1997, with initial line selection (CO01385) done in 2001 and a pure-line reselection done in Yuma, AZ, in 2003. CO01385-A1 has been the highest yielding entry averaged across two years of testing in the UVPT (21 location-years), with its yield 0.8 bu/acre greater than Ripper, 1.7 bu/acre greater than Bond CL, 2.9 bu/acre greater than Hatcher, 3.7 bu/acre greater than Keota, and 4.4 bu/acre greater than Avalanche (the next five highest yielding lines in the UVPT on a 2-year average). Test weight of CO01385-A1 was the third highest in the UVPT, about 1 lb/bu greater than the average of all entries, 0.3 lb/bu less than Danby and Trego, 0.2 lb/bu less than Avalanche, and 0.5 lb/bu greater than Prowers 99. In the irrigated IVPT, CO01385-A1 also was the highest yielding entry averaged across two years of testing (six location-years). Yield has been 3.1 bu/acre greater than TAM 111, 4.9 bu/acre greater than Bond CL, and 9.2 bu/acre greater than Hatcher (these are the next three highest yielding lines in the IVPT on a two-year average). Test weight of CO01385-A1 was the third highest in the IVPT, about 1 lb/bu above the average of all entries, 0.2 lb/bu less than Jagalene and NuGrain, 0.1 lb/bu greater than TAM 111, and 0.3 lb/bu greater than NuFrontier.

Personnel changes.

In July 2006, two new Research Associates joined our program as a result of the departure of Sally Clayshulte in December 2005 and Bruce Clifford in May 2006. Emily Heaton came to us from the soybean breeding program at South Dakota State University. Prior to this, Emily completed a B.S. degree at CSU (while working in Dr. Pat Byrne's laboratory) and then her M.S. degree at North Carolina State University. Emily will be coördinating our molecular marker-assisted selection and mapping activities. Hayley Miller came to us from the field crops entomology program at CSU. Hayley completed both her B.S. and M.S. degrees at CSU. Hayley will be managing our wheat quality testing efforts. Emily and Hayley enjoy both field and laboratory work, and we are very excited about these new changes for our program.

New Russian wheat aphid biotype research.

With the identification of a new, virulent biotype of RWA in Colorado in 2003, and additional virulent biotypes in 2004, we continue to be actively involved in several different research areas to address this problem. These activities have focused on continued germ plasm screening, molecular marker identification for key resistance genes, and breeding line and population development. The following are the highlights of these activities.

—We completed the screening of 1,700 selections from the NPGS for resistance to RWA biotype 2. These selections had previously shown susceptibility to RWA biotype 1 in screenings done by the USDA–ARS lab at Stillwater, OK. We have identified many germ plasm accessions with resistance to the new biotypes and do not plan any new germ plasm evaluations in the near future.

—In autumn 2006, we planted a coöperative RWA biotype-2 resistance nursery at five of our breeding sites (Akron, Dailey, Walsh, Sheridan Lake, Fort Collins). This trial includes eight resistant lines from the ARS program in Stillwater and 13 lines from our own program. All of these lines appear to carry the *Dn7* gene from the 2414-11 and Altus-034 accessions that we obtained from ARS–Stillwater in 2003. Based on yield and quality evaluations, we would hope to advance a subset of these lines for testing in autumn 2007 and being seed increase of the most promising lines.

—We completed backcrossing of the *Dn7* gene in 2414-11 into two elite HRWW backgrounds from our program (CO00739 and CO00554). Both of these wheats were high-yielding lines in 2003 but neither were released as Hatcher showed slightly superior performance. Backcross derivatives from these two groups were increased in our greenhouse in autumn 2006. Seed samples from heads harvested separately were split, part of the sample was retained at CSU for RWA biotype 2 testing and part was sent to Yuma, AZ, for seed increase. We would hope to advance a group of these line selections to multiple location testing in autumn 2007, but it is too early to project when a cultivar release might be made from these materials.

—Many new crosses and backcross populations have been developed using resistance sources identified. We have begun top-crossing several backcross-derived resistance sources with other susceptible wheats in our breeding program. Many of these populations are now going to the field.

Preharvest-sprouting tolerance evaluation.

Many hard white wheats have a predisposition to sprout in the head if wet conditions persist at harvest maturity. In 2005–06, we continued to increase the number of samples evaluated in our sprout testing systems. For our kernel germination protocol, we implemented a 'germination index' calculation, which weights the kernels germinated according the day that they sprout (i.e., kernels sprouting after 1 day in the chamber are weighted greater in the calculation than those sprouting on the sixth day in the chamber). With the intact head sprouting test, we continue to perform reselection within Preliminary and Advanced lines as a means to selectively identify sprout-tolerant segregates within heterogeneous lines. In this test, line reselections showing better sprout tolerance than the checks are dried, threshed, and planted in the headrow nursery in the autumn. We are optimistic that this scheme will yield positive results with regard to improved sprouting tolerance in our breeding program. We also have been working to optimize several molecular markers reportedly associated with sprouting tolerance using the data from our own sprout tests to determine if the markers are predictive in our own germ plasm.

USDA–CAPS grant.

Working cooperatively with Drs. Pat Byrne and Nora Lapitan, we continue to work on the USDA–CAPS grant secured by Dr. Jorge Dubcovsky at UC-Davis. We are nearing completion of our mapping population and planted a subset of this population at Fort Collins for phenotypic evaluation in 2006–07. Marker mapping in the population is progressing well. As part of the grant, we will also be increasing our use of molecular MAS through collaboration with the USDA–ARS Genotyping Center in Manhattan, KS. We are initially focusing on topcross populations segregating for various glutenin alleles, stripe rust resistance (*Yr5* and *Yr15*), leaf and stem rust resistance (*Lr19*/*Sr25*, *Sr2*, *Sr24* sources), and the high grain protein content gene from tetraploid wheat. We continue to screen all parents entering our crossing block with molecular markers and over the coming year we are planning to implement routine marker screening in both F_1-topcross and single seed descent populations derived from F_2 populations.

Colorado Wheat Variety Database.

In August 2006, we launched a revised version of the Colorado Wheat Variety Database. The database had been available over the web since 2000, but it had become increasingly difficult to maintain over the web and internet security concerns had also become an issue. To alleviate these concerns, we modified the database such that users can now download a stand-alone version of the database over the Internet and install this on their own computer. Once installed, all functions of the database system are available from the user's computer without accessing the Internet/web. The new Colorado Wheat Variety Database maintains the same functions as the previous version while providing several enhancements. The database allows users to search for wheat cultivar information, display trial results from all Colorado trial locations since 1990, create yield and test weight summaries averaged over years and trial locations specified by the user, and create head-to-head yield and test weight comparisons between two varieties of interest. Users interested in obtaining the database may download the database from the following link: http://wheat.colostate.edu/vpt.html.

Graduate student research.

Three graduate student research projects are currently underway in our breeding program. Although we expect that these research projects will contribute vital information to help direct and focus breeding efforts, both the breeding project and the students benefit in many other ways though direct student involvement in the overall breeding program. Briefly, these include the following areas of research.

—Development and validation of near infrared reflectance (NIR) spectroscopy calibrations for whole-grain prediction of end-use quality characteristics (Joshua Butler). Josh began his Ph.D. dissertation studies (and his appointment as a research associate) in autumn 2004 and has been working on development of a variety of whole grain NIR calibrations. Josh currently has a field study underway, planted at four of our field locations, to validate the results of selection based on three different whole grain calibrations. Josh hopes to complete his studies and defend his dissertation in spring 2008.

—Validation of the BYDV resistance and high grain protein content traits introgressed to several elite backgrounds as part of the IFAFS molecular marker grant (Jennifer Roth). Backcross derived near-isogenic lines have been developed following several generations of marker-assisted backcross selection. These lines were increased in Yuma, AZ, during winter 2005–06 to allow us to plant yield trials at several locations in autumn 2006. The objective of Jennifer's thesis study is to determine the direct and indirect effects of transfer of these segments to several elite backgrounds in our program. Jennifer hopes to complete her studies after summer 2007 and defend her thesis in autumn 2007.

—RWA biotype-2 resistance gene mapping and gene transfer from *T. turgidum* subsp. *dicoccoides* (Ben Beyer). Ben has completed the development of a mapping population segregating for resistance to RWA biotype 2. He has screened bulks and the parents with many microsatellite markers and has identified a few that are showing linkage with the gene of interest. Further mapping is underway. Ben also has been working to transfer RWA biotype 2 RWA resistance from a tetraploid wheat (*T. turgidum* subsp. *dicoccoides*) to common wheat. In this study, Ben has developed selfed and backcross-derived lines that apparently carry the resistance from the tetraploid parents. Ben will be completing his studies and defending his thesis in autumn 2007.

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GEORGIA / FLORIDA

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The 2006 Georgia winter wheat crop was grown on about 280,000 planted acres. Yields of wheat grown by top producers were around 6,000 kg/ha on cultivars resistant to stripe rust. Average yield for the state was 3,200 kg/ha. The growing season was characterized by mild weather and very dry conditions during the winter and spring. A lack of vernalization was a problem for late maturing varieties. Only 60% of the average rainfall occurred during the spring. A severe epidemic of stripe rust was observed in Georgia and the lower southeastern U.S.

Breeding.

GA 951395-3A31 (AGS 2031) is a medium-maturing, white-chaffed, medium-height line derived from the cross 'GA 87110 / VA93-52-55 // GA 88151'. With a maturity is similar to that of AGS 2000, it is an average of 1.0 day later in Georgia. GA 951395.3A31 is susceptible to current biotypes of Hessian fly in Georgia and is resistant to races of leaf rust and stripe rust due to adult plant resistance and has adult plant resistance to powdery mildew. The cultivar also is resistant to soilborne mosaic virus.

GA 951395-3E25 (USG 3295) is a medium-maturing, white-chaffed, medium-height line derived from the cross 'GA 87110 / VA93-52-55 // GA 88151'. At maturity, it is similar to AGS 2000 with an average of 2.0 days later in Georgia. GA 951395-3E25 is susceptible to current biotypes of Hessian fly in Georgia and is resistant to races of leaf rust and stripe rust due to adult-plant resistance and has adult-plant resistance to powdery mildew. The cultivar also is resistant to soilborne mosaic virus.

GA 96229-3A41 (SS8641) is a medium-maturing, white-chaffed, medium-tall line derived from the cross 'GA 881130 / 2* GA 881582'. The pedigree of GA 881130 is 'KSH8998 / FR 81-10 // Gore'. KSH8998 was developed from the cross of a hard wheat with *Ae. tauschii* to transfer Hessian fly resistance gene *H13*. FR 81-10 was selected because of its resistance to leaf rust (*Lr37* and *Yr17*) from the cross 'Novisad 138 /4/ (4) *Ae. ventricosa* / *T. persicum* /2/ Marve*3 /3/ Moisson'. GA 96229-3A41 has maturity is similar to that of AGS 2000 with an average of 1 day later in Georgia. The cultivar is resistant to current biotypes (B and E) of Hessian fly in Georgia and is resistant to races of powdery mildew, leaf rust, and stripe rust in Georgia. GA 96229-3A41 also is resistant to wheat soil-borne mosaic virus. GA 96229-3A41 has an excellent combination of resistance to diseases (powdery mildew, stripe rust, leaf rust, and soil-borne mosaic virus).

Scab.

In the southeast region of the U.S., resistance to FHB in local adaptive soft red winter wheat is limited. Introduction of resistant genes from exotic sources with QTL located at 3BS and 5AS could enhance the resistance of local adaptive germ plasm. Thirty-six elite breeding lines from breeding programs in the southeast region including eight from Arkansas, four from North Carolina, six from Virginia, and six from the University of Georgia were evaluated with Ernie and Coker 9835, as resistant and susceptible controls, respectively, under misted conditions at the Griffin Campus, Georgia. Eight lines showed similar level of severity as the resistant control, and 26 lines were significantly more severe than the resistant check, Ernie. A Georgia line, GA991109, from a cross with Ernie showed better resistance than Ernie. A Virginia line, VA05W-500, from a cross 'Roane / PIO 2684 // OH 552' showed the best and consistent resistance among all three replications in 36 lines. VA05W-500 showed a significantly higher level of resistance than other lines, including the resistant control. Many crosses have been made using Sumai 3 or its derivatives as FHB-resistance donors. However, FHB resistance could be enhanced significantly by combining the native resistance in soft red winter wheat and reduced the negative yield dragging associate with crosses including exotic of Sumai 3 or its derivatives. Studies on the native resistance for FHB is needed for more efficient accumulation of native resistance into local adaptive cultivars.

Stripe rust.

Stripe rust was very severe in 2006. We identified the effective genes as *Yr17* (GA96229-3A41) and *Yr18* in combination with other genes (PIO 26R61), adult-plant resistance in GA951395-3A31 and GA951395-3E25). *Yr5*, *Yr15*, and *Yr27* also provided effective resistance.

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INDIANA

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J.M. Anderson, S.E. Cambron, C. Crane, S.B. Goodwin, S. Scofield, B. Schemerhorn, R.H. Shukle, and C.E. Williams (USDA–ARS); H.W. Ohm, M. Deb, L. Kong, and X. Shen (Department of Agronomy); G. Buechley, G. Shaner, and J.R. Xu (Department of Botany and Plant Pathology); and J. Stuart (Department of Entomology).

Wheat production.

According to the USDA National Agricultural Statistics Service, Indiana farmers harvested 182,112 hectares (450,000 acres) of wheat in 2006, up 32% from 2005. Wheat yields in Indiana averaged 4,773 kg/ha (71 bu/a) in 2006, 1 bu less than the record high yield in 2005. Like most winters in Indiana since 1996, temperatures averaged above normal and winterkill due to low temperatures was limited. Similar to 2005, growing conditions for winter wheat in 2006 were excellent: ample soil moisture and cool temperatures continued to late June when much of the wheat crop was physiologically mature. Beginning in late June and through the harvest season to mid July, temperatures were elevated and soil moisture was limiting, providing excellent drying conditions during the harvest season, and resulting in high grain yields and high test weight. Acreage prospects for 2006–07: wet field conditions delayed harvest of corn and soybeans in September–October 2006, delaying wheat seeding, and likely reduced intended wheat area seeded.

Wheat disease summary.

Cool temperatures delayed the onset of symptoms of Fusarium head blight, although warm conditions beginning approximately two weeks after flowering in central to southern Indiana resulted in significant severity of the disease. Crop losses from other diseases, including powdery mildew, leaf rust, stem rust, Stagonospora glume blotch and Septoria leaf blotch were moderate to minor. Hessian fly was found in 2006 near Battleground, just north of Lafayette, IN. Evaluation with markers revealed that the population sample is similar to other populations collected in the upper Midwest and not similar to those from the Southeast.

New cultivar released.

INW0731, tested as P99608C1-1-3-4, was developed cooperatively by Purdue University and USDA–ARS and released in 2007. INW0731is a soft red winter wheat line and is the progeny of an F_4 plant selection. The cultivar was performance tested at multiple locations in Indiana since 2004, in the 5-State regional nursery in 2005, the Uniform Eastern Winter Wheat nursery in 2006, and in the Preliminary Northern Uniform Winter Wheat Scab Nursery in 2005. INW0731has high yield potential, excellent soft wheat milling and baking quality, moderate resistance to Fusarium head blight (having resistance from Freedom and Fundulea 201R), moderate resistance to leaf rust, resistance/tolerance to yellow dwarf virus, powdery mildew, Stagonospora nodorum blotch, Septoria leaf blotch, soilborne mosaic virus, and wheat spindle streak mosaic virus, and is susceptible to Hessian fly, stripe rust and stem rust in Indiana. Adapted to southern Indiana and surrounding regions; INW0731 has survived winters very well in central and northern Indiana, but winters have been mild since 1996. The parentage of INW0731 is 'Sunset / Pioneer 2571 /3/ Clark // Roazon / Caldwell /4/ VPM / Moisson // Clark /3/ Clark*2 / Caldwell /9/ Caldwell*2 / S76 /8/ Beau*2 / Potomac // Auburn / Caldwell*2 /7/ Benhur / Arthur /6/ Laporte / Knox*2 /5/ Hart / Beau /4/Arthur /3/ Monon // Funo / Knox /10/ Freedom / Fundulea 201R'. After the last cross, plant selections were made in F_2, F_3, and F_4, with the pedigree method of selection.

Hessian fly.

Characterization of plant processes manipulated by virulent Hessian fly (Christie Williams, Jill Nemacheck, Subhashree Subramanyam, Marcelo Giovanini, Kurt Saltzmann, and Stephen Baluch).

Oxidative burst. Resistant wheat was assayed for the rapid increase in the levels of active oxygen species, characteristic of an oxidative burst, as an early response to Hessian fly larvae. No correlation was found between Hessian fly larval feeding and accumulation of O_2^- or H_2O_2 in wheat tissues. Loss of resistance was not detected after treatments that inhibit NADPH oxidases and thus interrupt the signal pathway that generates an oxidative burst. In addition, Hessian fly larval feeding did not result in increased mRNA for genes that produce or scavenge active oxygen species. These data suggest that the wheat gene-for-gene recognition of Hessian fly larvae does not activate the oxidative burst component of resistance that is common to many gene-for-gene interactions between plants and other pathogens (Mol Plant Microbe Interact 19:1023-1033, 2006).

Putative feeding deterrent. Quantification of *Hfr-3* mRNA, encoding a novel wheat germ agglutinin-like protein, in the incompatible interaction confirmed a rapid response up to 3,000-fold above the uninfested control. The abundance of mRNA was influenced by the number of larvae/plant, suggesting localized rather than systemic resistance, HFR-3 protein increased in parallel to the mRNA during incompatible interactions and was detected in both virulent and avirulent larvae, indicating ingestion. Antinutritional proteins, such as lectins, may be responsible for the apparent death by starvation of avirulent Hessian fly larvae during the initial few days of incompatible interactions with resistant wheat plants (Mol Plant Pathol 8:69-82, 2007).

Protein analysis. With collaborators, a standardized protein extraction protocol was developed that works for wheat as well as other monocot and dicot plants. This protocol significantly improves solubilization of total proteins. Total protein was first precipitated with trichloroacetic acid/acetone extraction buffer and subsequently solubilized with a modified O'Farrell lysis buffer. The separation of leaf total proteins by two-dimensional gel electrophoresis revealed improved solubilization and increased spot numbers, visualized with Coomassie brilliant blue staining (J Plant Biol 49:413-420, 2006).

Lab members. Subhashree Subramanyam is a Purdue University postdoctoral researcher. Kurt Saltzmann is a USDA-ARS postdoctoral researcher. Jill Nemacheck is a research technician.

Molecular interactions between the larval Hessian fly and wheat (Richard Shukle, Omprakash Mittapalli, Alisha Johnson, and Jacob Shreve).

Response of genes expressed in the larval Hessian fly during interactions with wheat. The focus of this work is to understand the molecular interactions that are induced or suppressed by Hessian fly larvae during their attack of wheat and that trigger host susceptibility or resistance. We have constructed a Hessian fly EST library and gene expression analyses have detected genes differentially expressed in larvae feeding on susceptible wheat compared to resistant wheat. Results have provided insight into the expression of genes involved in detoxification and antioxidant defense responses.

Comparative transcriptomics of larval salivary glands. Salivary gland EST libraries have been constructed for Hessian fly (USDA–ARS, Manhattan, KS), the Asian rice gall midge, and the orange wheat blossom midge (USDA–ARS, West Lafayette, IN). The discovery of transcripts in the larval salivary glands of all three of these gall midges that encode small secreted proteins supports the hypothesis that these secreted proteins are the elicitors that trigger host responses resulting in susceptibility or resistance. Comparative transcriptomics has identified novel genes encoding secreted proteins common to all three gall midges as well as novel genes encoding secreted proteins unique to each species. We speculate the genes in common encode proteins that have a common role in the parasitizing of host plants, while those unique to each species are involved in the adaptation of the gall midges to their respective host plant/tissue feeding site. Among the pools of the unique genes should reside genes for virulence.

RNAi knockdown to test the role of Hessian fly genes in parasitizing wheat. The role of Hessian fly genes identified through differential expression and/or comparative transcriptomics will be tested using small interfering RNAs (siRNAs) targeting specific transcripts. RNAi knockdown will initially be used to examine the role of three genes expressed in Hessian fly salivary gland that have been identified as encoding proteins in common with other gall midges and two genes novel to the Hessian fly.

Virus-induced gene silencing (VIGS). Using virus-induced gene silencing to identify genes required in disease resistance pathways of wheat (Amanda Brandt, Cahid Cakir, Megan Gillespie, and S. Scofield), we have developed a VIGS system, based on barley stripe mosaic virus, for the rapid analysis of gene function in hexaploid wheat. In VIGS, plants are infected with a virus that has been engineered to contain sequences from a plant gene of interest. The dsRNA produced as the virus replicates triggers the plant's sequence-specific RNA degradation mechanism, which targets all RNAs with homology to the viral genome for destruction. As the viral RNA contains transcribed plant sequence, any homologous host mRNAs are also targeted for destruction, resulting in silencing the expression of the plant gene of interest. This VIGS system has proven to be very effective in creating gene knockout phenotypes in hexaploid wheat and our lab is focusing on developing VIGS assays for the functional identification of genes required in the pathways providing resistance to leaf rust and Fusarium head blight.

Lab members. Amanda Brandt is a USDA–ARS research technician and Cahid Cakir is a USDA–ARS postdoctoral researcher.

Yellow dwarf viruses.

Small Grain Cereal Virus detection (M. Deb and J.M. Anderson). In this study, a multiplex reverse transcription polymerase chain reaction (M-RT-PCR) method was developed for the simultaneous detection and discrimination of eight viruses including five strains of B/CYDVs, WSSMV, SBWMV, and WSMV. The protocol uses specific primers sets for each virus producing five B/CYDV distinct fragments for BYDV-PAV, BYDV-MAV, CYDV-RPV, and two unassigned Luteoviridae BYDV-SGV and -RMV, respectively. This system also produces WSSMV-, SBWMV-, and WSMV-specific amplicons, respectively. The eight amplicons produced in this one-tube PCR can be readily separated in a high resolution agarose gel. The amplification specificity of these primers was tested against a range of field samples from different parts of United States. This study has produced a rapid and specific wheat and small grain cereal virus diagnostic tool which will also be very effective in examining the epidemiology of these viral diseases.

Wheat–*Thinopyrum* mosaic chromosomes (K. Card, L. Ayala, N. Thompson, and J.M. Anderson). Previously, marker and virus inoculation analyses indicated that two lines that contained *Thinopyrum*–wheat translocations when crossed to Chinese Spring produced a large number of recombinants in which the translocation chromosomes consist of an array of wheat and *Th. intermedium* chromatin segments. From these recombinants a set of lines were identified that are resistant to B/CYDV and have interstitial *Th. intermedium* translocations. Current efforts are centered on characterizing the length of these translocations.

Identification of wheatgrass-specific molecular markers (E. Buescher and J.M. Anderson). Wheatgrass species such as *Thinopyrum* and *Lophopyrum* are important sources of useful traits particularly disease resistance to barley and cereal yellow dwarf viruses, leaf rust, and Fusarium head blight. Molecular markers derived from wheat typically do not identify wheatgrass-specific polymorphisms and consequently are used as negative (wheat DNA fragment missing) markers. In order to identify polymorphisms that are either codominant for wheatgrass and wheat or are dominant for wheatgrass, wheat oligonucleotide arrays were hybridized with RNA isolated from five wheat–wheatgrass substitution or addition lines each having a wheatgrass 7el1 or 7el2 chromosome and the reference wheat line Chinese Spring. These arrays were analyzed for SNPs and insertion/deletions using a robustified projection pursuit (RPP) algorithm (Cui et al. 2005). This analysis yielded approximately 44 putative 7E polymorphisms in addition to a large set of already known SNPs present in the wheat SNP database search (http://wheat.pw.usda.gov/GG2/blast.shtml). Current efforts are centered on validating the putative 7E polymorphisms through cloning and sequencing, mapping them to the 7E chromosomes for use as markers linked to wheatgrass-derived disease resistance traits.

Septoria tritici blotch.

Sequencing of *Mycosphaerella graminicola* (S.B. Goodwin). A project to sequence the genome of the *Septoria tritici* blotch pathogen, *Mycosphaerella graminicola*, was completed, and the 8.9x draft sequence (version 1) is available on the web pages of the Joint Genome Institute (http://genome.jgi-psf.org/Mycgr1/Mycgr1.home.html). A jamboree for manual annotation of the genome was convened in Walnut Creek, CA, 7–9 June, 2006, and included more than 20 participants. More than 1,200 genes have been annotated manually. The genome of approximately 40 Mb is being finished currently and contains 15 complete chromosome sequences from telomere to telomere and five more large scaffolds, four of which

have a telomere at one end. Thus, the finished genome is expected to contain the 18 chromosomes predicted from the genetic linkage map. The few remaining gaps in the sequence correspond mostly to centromeres.

Research personnel. Don Huber, Department of Botany and Plant Pathology, retired in September 2006. Hari Sharma, Department of Agronomy, retired in December, 2006. Stephen Baluch is a Ph.D. student with co-advisors Christie Williams and Herb Ohm. Elizabeth Buescher is a Ph.D. student with co-advisors Joe Anderson and Herb Ohm. Megan Gillespie is a Ph.D. student with co-advisors Steve Scofield and Herb Ohm. Marcelo Giovanini with co-advisors Herb Ohm and Christie Williams, completed the Ph.D. degree and is in a postdoctoral position in his home country of Brazil. Julie Zwiesler-Vollick completed her postdoctoral position with Stephen Goodwin and accepted an Assistant Professor position at Lawrence Technical Institute in Detroit.

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KANSAS

KANSAS AGRICULTURAL STATISTICS
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Overley captures number one.

Overley became the leading cultivar of wheat seeded in Kansas for the 2007 crop. Jagalene held this position last year. Accounting for 23.3 percent of the state's wheat, Overley increased 8 points from a year ago and was the most popular cultivar in four of the nine districts. Jagalene moved down to second place, with 23.1 percent of the acreage. Jagalene decreased 4.1 points but was the most popular cultivar in four of the nine districts. Jagger came in third at 17.1 percent, down 2.6 points. TAM 111 moved up to fourth place, with 4.0 percent of the acreage. The KSU-maintained cultivar 2137 moved down to fifth place with 2.9 percent of the acreage. Cutter moved up to sixth place with 2.1 percent of the acreage. T81 dropped to seventh place at 2.0 percent and TAM 110 moved down to eighth place at 1.5 percent. Santa Fe moved up to ninth place with 1.3 percent of the state's acreage. Ike rounded up the top ten at 1.2 percent. Acres planted with blended cultivars were not included in the rankings by cutivar. Blends accounted for 10.4 percent of the state's planted acres and were used more extentively in the north central, northeast, and central areas of the state. Out of the total acres planted with blends, 62.1 percent included Jagger in the blend, 51.0 had Jagalene in the blend, and 39.6 percent included Overley. Hard white cultivars accounted for 1.7 percent of the state/s acreage. Danby was the leading hard white cultivar, accounting for 41 percent 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 wheat cultivars grown in the state of Kansas for the 2007 crop and percent of seeded acreage.

1. Overley	23.3	6. Cutter	2.1
2. Jagalene	23.1	7. T81	2.0
3. Jagger	17.1	8. TAM 110	1.5
4. TAM 111	4.0	9. Santa Fe	1.3
5. 2137	2.9	10. Ike	1.2

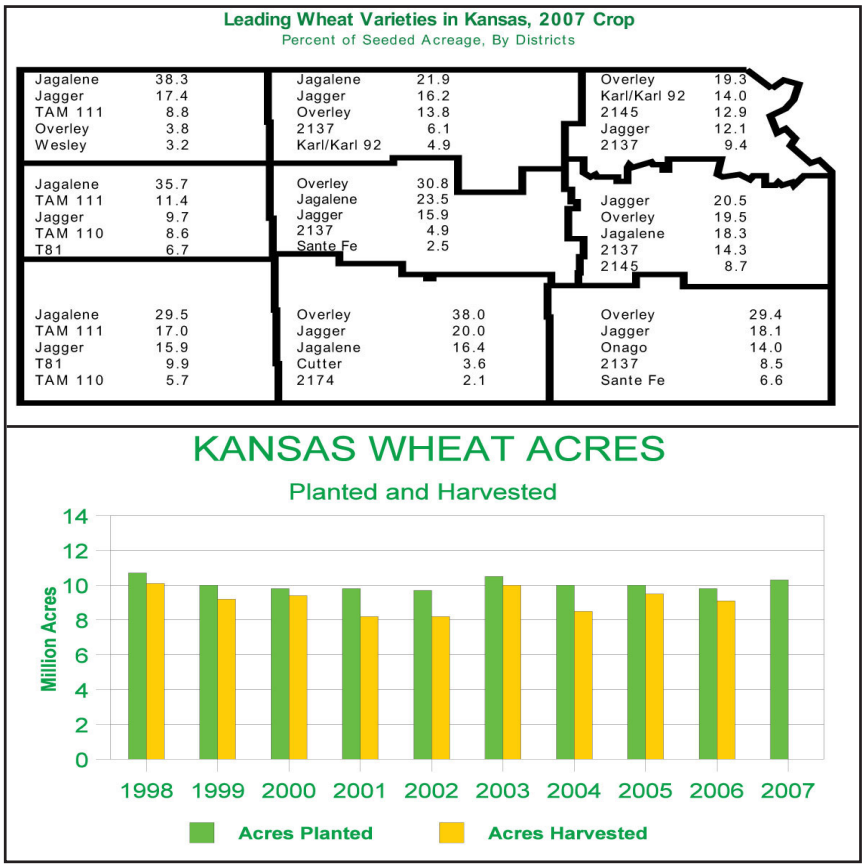

Table 2. Distribution of Kansas winter wheat cultivars, 2007 crop (— = cultivar not reported in this district; 0 = < 1%).

	Agricultural Statistics Districts									
Cultivar	NW	WC	SW	NC	C	SC	NE	EC	SE	State
	percent of seeded acreage									
Overley	3.8	0.8	0.4	13.8	30.8	38.0	19.3	19.5	29.4	23.3
Jagalene	38.3	35.7	29.5	21.9	23.5	16.4	8.8	18.3	5.8	23.1
Jagger	17.4	9.7	15.9	16.2	15.9	20.0	12.1	20.5	18.1	17.1
TAM 111	8.8	11.4	17.0	0.7	0.8	0.2	—	—	—	4.0
2137	2.3	2.1	1.7	6.1	4.9	1.1	9.4	14.3	8.5	2.9
Cutter	0.4	0.4	—	1.9	2.2	3.6	0.1	—	—	2.1
T81	1.3	6.7	9.9	1.1	—	0.1	—	1.0	—	2.0
TAM 110	1.1	8.6	5.7	0.0	0.0	—	—	—	—	1.5
Santa Fe	0.1	—	—	1.9	2.5	1.1	2.2	2.0	6.6	1.3
Ike	1.6	1.3	4.4	0.1	0.3	1.1	—	—	—	1.2
2174	—	0.1	0.0	0.0	0.9	2.1	—	2.9	2.8	1.1
Karl/Karl 92	0.1	—	0.6	4.9	0.8	0.4	14.0	2.0	0.7	1.0
Danby	2.2	0.7	3.7	0.2	—	—	—	—	—	0.7
2145	—	—	—	1.1	0.6	0.5	12.9	8.7	1.0	0.5
Trego–HWWW	0.3	1.1	2.9	0.1	0.1	—	—	—	—	0.5
TAM 112	0.1	5.2	0.1	—	—	—	—	—	—	0.4
Dominator	—	—	—	1.5	1.2	—	1.3	0.5	—	0.4
Wesley	3.2	—	—	1.0	0.0	0.3	—	—	—	0.4
Thunderbolt	2.8	0.9	0.1	0.1	0.1	0.1	—	—	—	0.4
Protection	—	—	0.2	0.1	0.7	0.4	0.0	—	—	0.3
Larned	0.5	0.5	0.2	0.1	0.6	0.2	—	—	—	0.3
Coronado	—	—	—	—	0.1	0.6	—	—	—	0.2
2163	—	—	—	0.2	0.4	0.2	0.5	2.9	2.0	0.2
NuHills–HWWW	0.4	0.5	1.1	—	—	—	—	—	—	0.2
Onaga	—	—	—	—	—	—	—	—	14.0	0.2
T83	0.3	1.7	0.2	—	—	0.1	—	—	—	0.2
NuFrontier–HWWW	1.0	1.5	—	—	—	—	—	—	—	0.2
Stanton	0.5	1.3	0.2	—	—	—	—	—	—	0.2
Blends	7.0	4.8	4.1	24.2	10.6	10.5	14.4	3.4	1.6	10.4
Other HWWW Cultivars	0.1	0.3	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.1
Other HRWW Cultivars	6.4	4.7	2.1	2.8	2.6	3.0	5.0	4.0	5.2	3.5
All Soft Red Cultivars	—	—	—	—	—	—	—	—	4.3	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, 1998–2007.

Cultivar	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
	percent of seeded acreage									
Overley	—	—	—	—	—	—	0.1	2.2	16.3	23.3
Jagalene	—	—	—	—	—	—	3.0	21.2	27.2	23.1
Jagger	20.2	29.2	34.0	35.8	42.8	45.2	40.9	28.2	19.7	17.1
TAM 111	—	—	—	—	—	—	—	1.5	2.2	40.0
2137	13.5	22.0	23.1	22.3	15.5	13.3	8.6	5.7	3.1	2.9
Cutter	—	—	—	—	—	—	0.7	1.7	1.8	2.1
T81	—	—	0.2	0.2	0.8	0.6	1.8	1.6	2.6	2.0
TAM 110	—	0.5	1.3	2.8	3.0	3.8	4.2	3.3	2.2	1.5
Santa Fe	—	—	—	—	—	—	—	—	0.2	1.3
Ike	7.0	5.5	4.1	3.6	2.6	2.1	2.0	1.4	1.1	1.2
2174	—	—	1.1	3.0	3.1	3.1	2.8	3.0	1.2	1.1
Karl/Karl 92	10.8	5.9	3.5	3.3	3.6	3.2	2.3	1.5	1.1	1.0
Danby	—	—	—	—	—	—	—	—	—	0.7
2145	—	—	—	—	—	—	1.5	2.2	0.8	0.5
Trego–HWWW	—	—	—	0.3	0.8	1.8	3.5	2.9	0.4	0.5
TAM 112	—	—	—	—	—	—	—	—	—	0.4
Dominator	0.2	0.8	1.4	1.5	2.0	2.2	1.5	1.1	0.8	0.4
Wesley	—	—	—	—	—	0.1	0.1	0.1	0.3	0.4
Thunderbolt	—	—	—	0.2	0.6	0.8	1.4	1.7	1.1	0.4
Protection	—	—	—	—	—	—	—	—	0.2	0.3
Larned	2.4	1.9	1.2	1.0	0.9	0.8	0.4	0.3	0.2	0.3
Coronado	0.8	1.3	1.0	1.1	0.7	0.8	0.5	0.4	0.4	0.2
2163	10.4	3.4	2.3	2.0	1.3	0.8	0.3	0.2	0.2	0.2
NuHills–HWWW	—	—	—	—	—	—	—	0.3	0.2	0.2
Onaga	—	0.1	0.1	0.2	0.2	0.2	0.1	0.1	0.3	0.2
T83	—	—	0.1	0.2	0.1	0.2	0.1	—	0.1	0.2
NuFrontier–HWWW	—	—	—	—	0.1	0.3	0.6	0.2	0.4	0.2
Stanton	—	—	—	—	0.1	0.6	1.4	1.4	0.8	0.2
Blends	2.6	6.1	7.5	7.0	11.4	12.8	15.2	11.3	10.0	10.4
Other HWWW Cultivars	—	—	0.2	0.8	0.3	0.2	0.1	0.5	0.3	0.1
Other HRWW Cultivars	17.3	13.3	11.3	8.6	5.9	3.9	4.6	5.8	4.5	3.5
All Soft Red Cultivars	0.0	0.0	0.0	0.0	0.1	0.1	0.0	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

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Stomatal resistance of wheat grown horizontally and vertically.

M.B. Kirkham

Crops must grow in space, if astronauts are to have food on long flights. However, plant roots need gravity to grow into soil. The response to gravity developed when plants invaded land. This response is believed to be mediated through statoliths (amyloplasts), which are gravisensors in roots and cause them to grow downward. They are capable of swiftly responding when a root is displaced relative to the gravity vector. In space, roots grow in any direction, including upwards. To keep roots in soil, covers are placed on top of pots in space. Despite the primary function of roots in taking up water for plant growth, essentially no information exists in the published literature on the plant-water relations of roots in space. The objective of this study was to determine the effect of gravity on stomatal resistance of wheat. Response of stomata in leaves is closely linked to the roots. Hormones are produced in the roots, which travel to the guard cells, where they either open stomata or close stomata. Hence, one would assume that stomatal resistance might be affected, if roots are grown in space. In this experiment to simulate gravity-free conditions, plants were grown in columns oriented horizontally. Horizontal columns reduce the effect of gravity, because gravity acts only through the diameter-depth of the column.

Two experiments, each with a different depth of planting, were carried out in a growth room. Four columns (each 7 cm in diameter and 40 cm long) were used in each experiment. Two columns were oriented horizontally (placed on their sides) and two columns were oriented vertically (the control columns which had the normal orientation to the earth's surface). The columns were clear so root growth could be observed. In the first experiment, 15 winter wheat (*Triticum aestivum* subsp. *aestivum* cultivar Jagger) seeds were planted at the 3-cm depth. In the second experiment, seeds were planted at the 3-mm depth. Stomatal resistance was measured with a leaf porometer (Model SC-1, Decagon Devices, Pullman, WA). Experiments ended when the plants in the horizontal columns were dead or dying, which was two weeks after planting in each experiment.

In the first experiment, plants grown in the horizontal columns germinated but emerged poorly. Four plants emerged out of 15 seeds planted in one horizontal column, and one plant emerged out of 15 seeds planted in the other horizontal column. In the vertical columns, 14 out of the 15 seeds planted in each column germinated and emerged. Average stomatal resistances of the control plants and of the plants that emerged in the horizontal columns were 20 s/cm and >50 s/cm, respectively. In the second experiment, because the seeds were planted near the surface, seeds germinated and emerged from the horizontal columns, as well as the control columns. But, in the horizontal columns, roots did not grow down into the columns and stayed where the seed was planted. Because the roots could not grow down, they used up the water where they were planted and stomatal resistance increased until the plants died. During the second experiment, average stomatal resistances for the control plants and for the plants in the horizontal columns were 28 s/cm and 34 s/cm, respectively. At the end of the experiment, the stomatal resistances of plants grown in horizontal columns were >50 s/cm, as they were in the first experiment. Because the roots could not grow down into the horizontal columns to take up water, the stomata closed, the plants stopped growing, and they died due to lack of water. The results showed that, for stomata to remain open in space, the response to gravity is going to have to be bred out of crop plants like wheat or else undifferentiated, primitive forms of plants, like unicellular algae, may have to be used for food. Alternatively, water and nutrients may have to be supplied by foliar application, negating the need for roots to supply them.

News.

Mr. Prasanna Ayyaru Thevar from India is a Master's degree student who arrived in May, 2006, and is working jointly under M.B. Kirkham and R.M. Aiken.

Mr. Intkhab Hazoor Wahla, a Ph.D. student at the University of Agriculture, Faisalabad, Pakistan, is spending six months (February–August 2007) in the laboratory on a research fellowship sponsored by the Pakistani–USA Ph.D. Partial Support Program of the Higher Education Commission in Islamabad, Pakistan.

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Wheat Genetics Resource Center: the first 25 years.

B.S. Gill, B. Friebe, W.J. Raupp, D.L. Wilson, T.S. Cox, R.G. Sears, G.L. Brown-Guedira, A.K. Fritz.

Research from the WGGRC for the last 25 years was summarized for an article in Advances in Agronomy. During this time, over 30,000 samples from the WGGRC collection of wild wheat relatives, cytogenetic stocks, and improved germ plasm have been distributed to scientists in 45 countries and 39 states in the U.S. Karyotypes (chromosome constitution) of 26 wild species and 72 introgression lines with useful agronomic traits have been described. Over 800 new cytogenetic stocks have been developed. These materials are part of the basic tool kit of every wheat geneticist. The WGGRC has released 47 improved germ plasm lines incorporating over 50 new pest-resistance genes that are being exploited in wheat-breeding programs. The K-State cultivar Overley wheat is protected from leaf rust from a gene extracted from a wild wheat strain collected in Iran. The WGGRC hosted over 36 scientists, especially from developing countries, for advanced training. CIMMYT has made extensive use of WGGRC germ plasm, being present in the pedigree of over a quarter of their advanced breeding lines.

Stripe rust and leaf rust resistance from Ae. geniculata.

V. Kuraparthy, P. Chhuneja, H.S. Dhaliwal, S. Kaur, R.L. Bowden, and B.S. Gill.

Previously, leaf and stripe rust-resistant introgression lines were developed through induced homoeologous chromosome pairing between wheat chromosome 5D and 5Mg of *Ae. geniculata*. Genomic in situ hybridization with *Ae. comosa* DNA as a probe showed three different kinds of introgressions. All three types of introgression lines had complete and similar resistance to the most prevalent races of leaf (PRTUS 25, PRTUS 35, PNMQ, MCDL, and PRTUS 6) and stripe rust (03 and 04) in Kansas. One resistant line (TA5602) with a cytologically undetectable introgressed segment was used for molecular characterization of leaf and stripe rust resistance. This line (TA5602), which is agronomically as good as the recipient parent (WL711), was used to transfer the leaf rust and stripe rust resistance to the Kansas winter wheat cultivars Jagger and Overley. The F_1 between Jagger and the rust-resistant introgression line (TA5602) was backcrossed further with Jagger and Overley to produce a BC_3F_1 where the BC_3F_1 plants are being grown in the greenhouse to isolate homozygous, rust-resistant BC_3F_2 progenies in the Jagger and Overley background for further agronomic evaluations in the field and subsequent germ plasm release. Diagnostic polymorphisms between the rust-resistant introgression line and the recipient parents were identified using physically mapped RFLP and EST probes. CAPS (cleaved amplified polymorphic sequences) markers are being developed from the diagnostic ESTs, which will be useful for the marker-assisted breeding for rust resistance in wheat.

Leaf rust resistance from Ae. triuncialis.

V. Kuraparthy, S. Sood, P. Chhuneja, H.S. Dhaliwal, S. Kaur, R.L. Bowden, and B.S. Gill.

Working with the scientists at Punjab Agricultural University, Ludhiana, India (Chhuneja, Dhaliwal, and Kaur), we identified one novel, leaf rust-resistant introgression line (TA5604) from progenies that were developed by directly crossing hexaploid wheat with rust-resistant *Ae. triuncialis*. Bulk segregant analysis was used to identify the chromosome location of the rust-resistant introgression using molecular markers and an F_2 population from the cross 'Jagger/ TA5604'. Further genetic mapping using SSRs and RFLP markers showed that the leaf rust resistance gene (tentatively designated as *LrTri*) mapped on the long arm of chromosome 2B. One SSR marker and one RFLP marker diagnostically identified the rust resistance of *Ae. triuncialis*. The rust resistant line (TA5604), which is agronomically as good as the recipient parent (WL711), was used to transfer the leaf rust resistance to the Kansas winter wheat cultivars Jagger and Overley through a backcross- breeding program. Presently, the BC_3F_1 plants are being grown to isolate homozygous, rust-resistant BC_3F_2 progenies in the Jagger and Overley background for further agronomic evaluations in the field and subsequent germ plasm release. CAPS (cleaved amplified polymorphic sequences) markers are being developed from the diagnostic RFLP marker, which will be useful for the marker-assisted breeding for rust resistance in wheat.

Stripe and leaf rust resistance transfers from T. monococcum subsp. monococcum.

V. Kuraparthy, S. Sood, and B.S. Gill.

With the departure of Gina Brown-Guedira, we inherited rust-resistant breeding materials from interspecific crosses. Two lines from this material with leaf and stripe resistance from *T. monococcum* subsp. *monococcum* (Trit 2R and Trit 3R) were backcrossed to Overley wheat. We screened 333 progeny from 49 BC_2 lines for resistance to leaf and stripe rust. Twelve BC_2F_2 lines resistant to both leaf and stripe rust will be selfed and their progeny screened for isolation of homozygous resistant lines.

Wheat streak mosaic virus resistance.

B. Friebe, L.L. Qi, and B.S. Gill.

Previously, we released the germ plasm line 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·4DL translocation. *Wsm1* confers

immunity to the virus, but germ plasm with the T4Ai#2S·4DL translocation suffers from a yield penalty. For several years, we have been trying chromosome engineering to improve the agronomic performance of this germ plasm. Line WGRC27 was crossed with *ph1b* mutant, and the F_1 was backcrossed with *ph1b*. In the BC_1 of the cross T4Ai·4DL/*ph1b* mutant, we identified 12 plants homozygous for *ph1b* of which four plants were heterozygous for 4D and the translocation chromosome. At meiotic metaphase I, a ring bivalent between 4D and T4Ai#2S·4DL was observed in one out of 57 pollen mother cells analyzed. In 245 plants of the BC_1F_2, we identified five recombinants using molecular markers and confirmed them by GISH. Four lines (45, 64, 87, and 213) had recombinant 4D chromosomes with about 80% of the proximal region of the short arm derived from 4DS and the distal 20% of this arm derived from 4Ai#2S. Line 36 had a recombinant chromosome in which about 80% of the short arm was derived from 4Ai#2S and the distal 20 % from 4DS. Preliminary greenhouse data suggest that at least the recombinant #213 retains the *Wsm1* resistance gene. The recombinants were crossed with the Kansas-adapted wheat cultivar Overley and, after a second backcross with Overley and selfing, we will select homozygous recombinant stocks. In parallel, we selected lines that are homozygous for the recombinant chromosomes, and these lines will be inoculated with WSMV this autumn and the presence of the virus determined by ELISA. The recombinant with the smallest 4Ai#2S segment that still contains the *Wsm1* will be made available for cultivar improvement.

A second source of WSMV resistance was mapped to the long arm of an *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 and such studies have been initiated.

Fusarium head blight resistance.

L.L. Qi, B. Friebe, D.L. Wilson, and B.S. Gill.

Fusarium head blight or wheat head scab can be a significant disease 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 Lr#1S) from this grass specifying resistance to FHB has been transferred to a chromosome arm of wheat (7AL) in the form of a translocation T7AL·7Lr#1S. This translocation stock was crossed twice with *ph1b*, and plants homozygous for *ph1b* and heterozygous for T7AL·7Lr#1S and 7A will be identified this autumn. In these genotypes, homoeologous recombination can occur between the 7Lr#1S and 7A arms, and putative recombinants will be identified by molecular marker analyses and then confirmed by GISH.

Complex genome rearrangements reveal evolutionary dynamics of pericentromeric regions in the Triticeae.

LL Qi, P. Zhang, B. Friebe, and B.S. Gill.

The closely related genomes within hexaploid wheat as well as in the related Triticeae taxa share large, conserved chromosome segments and provide a good model for studying the evolution of pericentromeric regions that are known to be often heterochromatic and among the most rapidly evolving regions of eukaryotic genomes. We initiated a comparative analysis of pericentromeric regions in the Triticeae and confirmed the presence of four pericentric inversions involving chromosomes 2B, 4A, 4B, and 5A in Chinese Spring wheat. In addition, we identified two more pericentric inversions involving chromosomes 3B and 6B of Chinese Spring. Only the 3B inversion pre-existed in chromosomes 3S, $3S^l$, and $3S^s$ of *Aegilops* species belonging to the section Sitopsis, whereas the remaining inversions occurred after wheat polyploidization. The B genome appears to be more prone to chromosomal rearrangements than are the A and D genomes. Five different pericentric inversions were detected in rye chromosomes 3R and 4R, $4S^l$ of *Ae. longissima*, 4H of barley, and 6E of *Ag. elongatum*. The pericentromeric regions in the Triticeae, especially those of group-4 chromosomes, are undergoing rapid and recurrent rearrangements.

Homoeologous recombination, chromosome engineering and crop improvement.

L.L. Qi, B. Friebe, and B.S. Gill.

We recently reviewed the status of chromosome engineering using homoeologous recombination and crop improvement and demonstrated that the integrated use of cytogenetic stocks, molecular marker resources, and molecular cytogenetic techniques can enhance the efficiency of homoeologous recombination based chromosome engineering. In this study, we reported on homoeologous recombination based transfer of virus resistance from and alien chromosome to a wheat chromosome, its characterization, and the prospects for further engineering by a second round of recombination. Previous chromosome engineering has been limited to single chromosomes or chromosome arms. The power of molecular marker analyses now opens the way for a genome wide production of recombinant chromosome stocks. We have proposed a scheme that is based on the fact that homoeologous recombination is limited to one or a few sites in each chromosome arm and that the genes determining most agronomic traits are located in the distal ends of the chromosomes. For each alien chromosome, four recombination events, two per arm, are needed. In addition, a battery of codominant centromeric and telomeric markers are required. We have outlined crossing schemes to obtain plants that are homozygous for *ph1b* and heterozygous for a set of seven wheat and alien chromosomes. Presently, we are verifying this strategy by producing genome wide recombinant chromosome stocks involving D-genome chromosomes of wheat and V-genome chromosomes of the close relative *Haynaldia villosa*.

Structural variation and evolution of a defense-gene cluster in natural populations of Ae. tauschii.

S.A. Brooks, L. Huang, M.N. Herbel, B.S. Gill, G.L. Brown-Guedira, and J.P. Fellers.

It is important to know how genetic variation that we want to tap for crop improvement is organized in natural populations of wild relatives of crop plants. This research produced the surprising result of gene deletion and insertion polymorphism for a defense-gene cluster in a diploid wild wheat species. This paper is adding to the mounting evidence of rapid evolution for genes involved in biotic and abiotic stress response and, thereby, stresses the need for conservation *in situ* so that evolutionary processes can continue in nature in response to the rapidly changing environment. This work was done in collaboration with John Fellers, USDA–ARS Plant Science Unit, Manhattan, KS.

Gene evolution at the ends of wheat chromosomes.

D.R. See, S.A. Brooks, J.C. Nelson, G.L. Brown-Guedira, B. Friebe, and B.S. Gill.

Although wheat and rice separated from a common ancestor 40 million years ago, they share extensive gene synteny, which means that wheat genes can be discovered using the rice genome template that has been sequenced completely. Five percent of the wheat genes were not found in rice. Wheat-specific genes were located in the distal ends of chromosomes where there is, presumably, a high turnover of genes because of high recombination.

Personnel.

Two students received their Ph.D. degrees recently. Kolluru Vijayalakshmi (dissertation topic “Genetic characterization of heat tolerance in wheat”), in December 2006, and Vasu Kuraparthy (“Genomic targeting and mapping of agronomically important genes in wheat”) in May 2007. Li Huang will join the faculty of the Department of Crop Sciences and Plant Pathology at Montana State University, Bozeman, in September 2007.

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M. Tilley, F.E. Dowell, B.W. Seabourn, J.D. Wilson, S.R. Bean, E.B. Maghirang, O.K. Chung, S.H. Park, T.C. Pearson, F. Xie, T.J. Schober, H. Akdogan, G.L. Lookhart, M.S. Caley, S.Z. Xiao, F.H. Arthur, M.E. Casada, D.B. Bechtel, D.L. Brabec, D.R. Tilley, R.K. Lyne, and R.C. Kaufman.

Registration of 'Deliver' wheat.

B. Carver, R. Hunger, A. Klatt, J. Edwards, D.R. Porter, J. Verchot-Lubicz, B. Martin, B.W. Seabourn, and P. Rayas-Duarte.

Deliver (PI 639232) hard red winter wheat was released to certified seed growers with permission of the Oklahoma Agricultural Experiment Station (AES) and the USDA–ARS in 2004. Deliver, an awnletted cultivar, was named for its unique and competitive ability to deliver in grain-only, graze-plus-grain, and forage-plus-hay management systems. The targeted production area extends throughout Oklahoma and the southern Great Plains except in areas limited by soil acidity and aluminum toxicity. Deliver was selected from the single cross 'OK91724 / Karl', in which Karl is a HRWW

cultivar developed by the Kansas AES and the USDA–ARS and released in 1988. OK91724 is an unreleased breeding line developed by the Oklahoma AES from the cross 'Yantar / 2*Chisholm'. Deliver is semidwarf and intermediate in plant stature relative to most HRW wheat cultivars. Mature-plant height (85 cm in Oklahoma) is within 2 cm of Jagger, 2174, and Ok101. Based on field observations under natural infection in Oklahoma and cooperative evaluations in the USDA–ARS regional nursery program, Deliver has adult-plant resistance to wheat leaf rust races currently present in Oklahoma. Based on single-kernel characterization system data recorded from 27 breeder trials from 1999 to 2003, Deliver has above-average kernel size and below-average kernel hardness. Dough strength based on the mixograph is slightly superior to Ok101. Overall milling and baking quality was rated acceptable in the 2003 evaluation program of the Wheat Quality Council.

Registration of 'OK Bullet' wheat.

D.R. Porter, B.W. Seabourn, F.E. Dowell, B.F. Carver, R.M. Hunger, A.R. Klatt, J.T. Edwards, W.D. Worrall, P. Rayas-Duarte, and B.C. Martin.

OK Bullet is a hard red winter wheat cultivar developed coöperatively by the Oklahoma AES, USDA–ARS, and the Texas AES and released by the Oklahoma AES and the USDA–ARS in 2005. OK Bullet is recommended for grain-only and dualpurpose production systems throughout Oklahoma and the southern Great Plains, and dryland and irrigated systems in the southern High Plains. The name was chosen to acknowledge its exceptional ability to satisfy several targets for end-use quality attributes. OK Bullet is an awned, white-chaffed, tall, semidwarf wheat with early arrival to first-hollow-stem stage and moderately early heading date. Flag leaves of OK Bullet at the boot stage are green, recurved, twisted, and nonwaxy. Spikes are white-chaffed, awned, oblong, middense, and inclined at harvest-maturity. Kernels are red, hard-textured, ovate, and they have a mid-wide, mid-deep crease, rounded cheeks, and large germ. Heading date is intermediate to Jagger and 2174, and it exceeds most currently grown hard winter wheat cultivars in plant height, which could be associated with its extended peduncle. OK Bullet shows rapid stand establishment with low sensitivity to high temperature during germination. The plant has erect to semierect vegetative growth habit that may not be conducive to intensive autumn grazing in a dual-purpose (graze-plusgrain) management system. OK Bullet is moderately resistant to WSBMV and WSSMV, but moderately susceptible to BYDV. Based on greenhouse observations, OK Bullet is moderately resistant to tan spot and to septoria leaf blotch, but susceptible to powdery mildew. OK Bullet is susceptible to biotypes C and E of the greenbug and to Hessian fly. Milling and baking quality represent exceptional features of OK Bullet. In head-to-head comparisons in two of the four years, OK Bullet exceeded Jagger by 48% in large-kernel fraction, 21% in kernel weight, and 14% in kernel diameter. Coupled with its large kernel size is high test weight for OK Bullet. From multilocation composite grain samples evaluated in two crop seasons (2003 and 2004), OK Bullet averaged 700 g/kg in flour yield with a flour ash of 3.3 g/kg. Wheat and flour protein (14 g/kg moisture basis) averaged 126 g/kg and 114 g/kg, respectively. Values for farinograph peak time and stability were 11.2 and 17.2 minutes. Straight-dough baking quality of OK Bullet is considered above-average, with 624 g/kg bake absorption, 5.3 min bake mixing time, 870 cc loaf volume, and 4.4 for crumb-grain score on a 0 (poor)-to-6 (outstanding) scale. High-molecular-weight glutenin subunits which are present in OK Bullet at the *Glu-A1*, *Glu-B1*, and *Glu-D1* loci are, respectively, 1, 17+18, and 5+10.

Registration of 'Hatcher' wheat.

S.D. Haley, J.S. Quick, J.J., Johnson, F.B. Peairs, J.A. Stromberger, S.R. Clayshulte, B.L. Clifford, J.B. Rudolf, B.W. Seabourn, O.K. Chung, Y. Jin, and J.A. Kolmer.

Hatcher (Reg. no. CV-971, PI 638512) hard red winter wheat was developed by the Colorado Agricultural Experiment Station and released to seed producers in August 2004. Hatcher was released based on its resistance to the original North American biotype, designated as Biotype 1 (D.R. Porter, personal communication, 2004) of the Russian wheat aphid, and its adaptation to nonirrigated production in eastern Colorado and the west-central Great Plains. Hatcher is susceptible to both WSMV and BYDV, heterogeneous for resistance to the Great Plains biotype of Hessian fly , and susceptible to greenbug. Resistance to Russian wheat aphid Biotype 1 in Hatcher is conditioned by the *Dn4* resistance gene. Russian wheat aphid resistance scores for Hatcher in standard greenhouse seedling screening tests using Biotype 1 are similar to other cultivars that carry *Dn4*. Values for milling-related variables were generally superior to those of both Ankor and Prowers 99. Hatcher had a higher Quadromat Senior flour extraction (685 g/kg sup) than those of Ankor (658 g/kg sup)

and Prowers 99 (4.8 g/kg sup). Values for baking-related variables of Hatcher were generally intermediate between Ankor and Prowers 99. Hatcher (120 g/kg sup) had a similar grain protein content as that of Ankor (120 g/kg sup) and lower than that of Prowers 99 (138 g/kg sup). In mixograph tests optimized for water absorption, Hatcher had higer water absorption (618 g/kg sup) than that of Ankor (615 g/kg sup) and lower than that of Prowers 99 (649 g/kg sup); a higher tolerance score (3.2; 0 = unacceptable to 6 = excellent) than that of Ankor (2.2 score) and lower than that of Prowers 99 (4.0); and longer mixing time (3.2 min) than that of Ankor (2.9 min) and shorter than that of Prowers 99 (4.0 min). In straight-grad pup loaf baking tests, Hatcher had lower bake water absorption (600 g/kg sup) than those of Ankor (605 g/kg sup) and Prowers 99 (633 g/kg sup); a longer bake mixing time (4.2 min) than that of Ankor (3.6 min) and shorter than that of Prowers 99 (5.1 min); a smaller pup loaf volume (0.872 L) than those of Ankor (0.888 L) and Prowers 99 (0.945 L); and a lower loaf crumb grain score (3.8; 0 = unacceptable to 6 = excellent) than Ankor (4.0) and Prowers 99 (4.5).

Predicting wheat quality characteristics and functionality using near-infrared spectroscopy.

F.E. Dowell, E.B. Maghirang, F. Xie, G.L. Lookhart, R. Pierce, B.W. Seabourn, S. R. Bean, J.D. Wilson, and O.K. Chung.

The accuracy of using near-infrared spectroscopy (NIRS) for predicting 190 grain, milling, flour, dough, and breadmaking quality parameters of 100 HRWW and 98 HRSW and flour samples was evaluated. NIRS shows the potential for predicting protein content, moisture content, and flour color b* values with accuracies suitable for process control ($R^2 > 0.97$). Many other parameters were predicted with accuracies suitable for rough screening including test weight, single-kernel diameter and moisture content, SDS sedimentation volume, color a* values, total gluten content, mixograph, farinograph, and alveograph parameters, loaf volume, specific loaf volume, baking water absorption and mix time, gliadin and glutenin content, flour particle size, and dark hard and vitreous kernels. Similar results were seen for HRWW and HRSW, and when predicting quality using spectra from grain or flour. However, many attributes were correlated to protein content. When the influence of protein content was removed from the analyses, the only factors that could be predicted by NIRS with $R^2 > 0.70$ were moisture content, flour color, and dark hard and vitreous kernels. Thus, NIRS can be used to predict many grain quality and functionality traits, but mainly because of the high correlations of these traits to protein content.

Detection of wheat kernels with hidden insect infestations using an electrically conductive roller mill.

T.C. Pearson and D.L. Brabec.

Grain kernels infested by insects may show no indication on their exterior, but often contain hidden larvae. Although grain is always inspected for insect infestations upon shipping and receiving, many infested samples go undetected. Many methods for detecting infested wheat have been developed but none has seen widespread use due to expense or inadequate accuracy, or both. In this study, a laboratory roller mill system was modified to measure and analyze the electrical conductance of wheat as it was crushed. This facilitated detection of wheat kernels with live insects hidden inside of them. Furthermore, the apparatus is low cost (~$1,500 for parts) and can inspect a 1-kg sample in less than two minutes.

Potentials and method improvements of capillary zone electrophoresis for use in spelt breeding programs.

T.J. Schober and S.R. Bean.

Capillary zone electrophoresis (CZE) in acidic buffer systems is capable of separating cereal storage proteins based on similar separation principles as classical acidic polyacrylamide gel electrophoresis. However, it is faster, its resolution is distinctly higher and data evaluation is much simpler. Applying a 100 mM sodium phosphate buffer system, pH 2.5, containing hydroxypropyl methylcellulose (HPMC), and using a 60-cm capillary, CZE was successfully used in a spelt

breeding program. Several examples are given: mislabeled samples could be identified, although the differences in the patterns were very small. Relatedness between different spelt cultivars could be shown. However, it was not possible to clearly differentiate between pure spelts and wheat-spelt crosses. Crossing spelt with modern wheat may be, but is not necessarily, reflected in the gliadin pattern. This latter finding is in agreement with several studies, showing that one single protein class (LMW-glutenin subunits, gliadins) did not always reflect purity of spelt. The acidic phosphate buffer system was compared to an isoelectric buffer system composed of 50 mM iminodiacetic acid (IDA), HPMC and acetonitrile, using a short (27 cm) capillary. We found that the IDA system provided more than 10 times faster separations with almost the same resolution as the sodium phosphate system. We concluded that CZE, especially with the IDA buffer, is a fast and powerful tool in spelt breeding programs to avoid mislabeling, and gain insight into the relatedness of new lines with unknown pedigrees.

Quality of spelt wheat and its starch.

J.D. Wilson, D.B. Bechtel, G.W.T. Wilson, and P.A. Seib.

Flours from five spelt cultivars grown over 3 years were evaluated as to their bread baking quality and isolated starch properties. The starch properties included amylose contents, gelatinization temperatures (differential scanning calorimetry), granule size distributions and pasting properties. Milled flour showed highly variable protein content and was higher than hard winter wheat, with short dough-mix times indicating weak gluten. High protein cultivars gave good crumb scores, some of which surpassed the HRWW baking control. Loaf volume was correlated to protein and all spelt varieties were at least 10–15% lower than the HRWW control. Isolated starch properties revealed an increase in amylose in the spelt starches of between 4–7% over the HRWW control. Negative correlations were observed for the large A-type granules to bread crumb score, amylose level, and final pasting viscosity for cultivars grown in year 1999 and to pasting temperature for samples grown in 1998. Positive correlations were found for the small B- and C-type granules relative to crumb score, loaf volume, amylose, and RVA final pasting viscosity for cultivars grown in year 1999, and to RVA pasting temperature in 1998. The environmental impact on spelt properties seemed to have a greater effect than genetic control.

The environmental impact on starch size distribution in developing hard red winter wheat.

J.D. Wilson, R.C. Kaufman, 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. 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. Our objective was to study starch size distribution in identical varieties of developing HRWW grown in the same location over at least five consecutive years and correlate differences to various environmental factors. The samples were collected from the Kansas State University Agronomy field plots in Manhattan, KS. The heads were tagged as to flowering dates and samples were collected starting at 7 days-after-flowering (DAF) and regularly sampled until harvest. The starch was isolated, then freeze-dried and starch size distribution was analyzed on a laser diffraction particle size analyzer. Trends were observed within varieties 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.

Predicting wheat quality characteristics and functionality using near-infrared spectroscopy.

F.E. Dowell, E. B. Maghirang, F. Xie, G.L. Lookhart, R. Pierce, B.W. Seabourn, S. Bean, J. Wilson, and O.K. Chung.

Rapid tests are needed by the wheat industry to measure grain quality to determine value, and to predict the bread quality that will be produced from that grain. Near-infrared spectroscopy commonly is used to measure characteristics such as

protein and moisture content, and may have potential for measuring other parameters. This rapid technology was examined from measuring 190 grain, milling, flour, dough, and bread-making quality parameters of 100 HRWW and 98 HRSW samples. Protein content, moisture content, and flour color were predicted with very high accuracies. Other parameters that showed some potential for rough screening using NIRS include test weight, dark hard and vitreous kernels, SDS sedimentation volume, gluten content, gliadin and glutenin content, water absorption, and loaf volume. However, many of these characteristics are highly correlated to protein content. When the influence of protein content was removed, the only factors that could be predicted by NIRS were moisture content, flour color, and dark hard and vitreous kernels. Similar results were seen for hard red winter and spring wheat, and when using spectra from grain or flour. This study emphasizes the advantages and limitations of NIR technology, and the need for developing other rapid quality prediction tests.

Rapid determination of dough optimum mixing time for early generation breeding lines using FT–HATR infrared spectroscopy.

B.W. Seabourn, F. Xie, and O.K. Chung.

The traditional method in the U.S. for screening hard winter wheat breeding lines is based upon the optimum mixing time (MT), an important rheological property of a wheat flour-water (dough) system typically obtained from the mixograph. This method is time-consuming and requires some degree of subjective interpretation, especially with regard to mixing tolerance. The purpose of this study was to investigate the potential of FT–HATR spectroscopy to objectively predict optimum MT in doughs from a short-duration mixing cycle (1 min). Hard winter wheat flours with varying protein content and MT were scanned in the amide III region of the mid-infrared by FT–HATR immediately after being mixed 1 min with a mixograph. The ratio of the band areas at 1,336/cm (α-helix) and 1,242/cm (β-sheet) was highly correlated to optimum MT as determined by the mixograph ($R^2 = 0.81$). Results from this study indicate that optimum MT could be predicted early in the mixing process based upon changes in the secondary structure of the dough protein. This method could provide the basis for new technology to rapidly and accurately screen wheat samples in early generation breeding lines, thus saving considerable time and expense in the development of new cultivars.

Correlation between gluten secondary structures and wheat end-use properties for early generation breeding lines using FT–HATR mid-infrared spectroscopy.

B.W. Seabourn, F. Xie, and P.A. Seib.

The relatively recent advent of FT–HATR mid-infrared spectroscopy has provided a unique and simple tool for evaluating gluten protein secondary structures in dough. In a previous study we reported that dough optimum mixing time (MT) was closely related to gluten protein secondary structures that developed early in the mixing cycle. To more fully understand the role of gluten secondary structure in dough rheology, further investigation into the relationship between wheat gluten secondary structure and wheat end-use properties was carried out. A total of 55 hard red winter wheat flours with varying protein contents (8.7–14.2%) and MT (1.63–7.38 min) were scanned with three replicates for each sample by FT–HATR (4,000–700/cm) immediately after being mixed with a mixograph (MIXO) for 1 min. A total of 34 end-use properties of each sample were evaluated including milling, baking, noodle making, PPO, RVA, SKCS, Mixograph, and other analytical tests. The second derivative band areas at 1,339/cm (α-helix), 1,285/cm (β-turn), 1,265/cm (random coil), and 1,242/cm (β-sheet) were highly correlated to MIXO MT, MIXO tolerance, baking MT, and LV potential. The band area at 1,242/cm (β-sheet) and MIXO tolerance had the highest correlation coefficient (r) –0.89. Crumb grain was negatively related to β-sheet and β-turn structures at 1,242/cm and 1,285/cm with r value –0.61, respectively. Multiple regression results showed that approximately 73%, 81%, and 70% of the total variance in MIXO MT, MIXO tolerance, and bake MT could be explained by the relationship between gluten secondary structures and these parameters, respectively.

Comparison of 5% lactic acid solvent retention capacity and SDS-sedimentation tests in predicting loaf volume of hard winter and spring wheat flour.

Z.S. Xiao, S.H. Park, M.S. Caley, R.K. Lyne, M. Tilley, B.W. Seabourn, and O.K. Chung.

The 5% lactic acid solvent retention capacity (SRC) test and SDS-sedimentation test were investigated to find their relationships to loaf volumes (LV) of HWW and HSW flour. A total of 196 flours, 98 HWW and 98 HSW with protein ranges of 8.2–14.2% and 10.4–17.8%, respectively, were used. The 5% lactic acid SRC value was a good indicator for LV, showing high correlations for both HWW and HSW flours ($r = 0.84$, respectively, $P < 0.0001$). On the other hand, SDS-sedimentation volume was highly correlated only with LV of HWW flours ($r = 0.76$, $P < 0.0001$), but not with HSW flour ($r = 0.47$, $P < 0.0001$). Even though this r value is statically significant, the r value is lower than that obtained by 5% lactic acid SRC test. In addition, the 196 samples were divided into low and high protein groups (8.2–13%, $n = 135$ and 13.1–17.8%, $n = 61$, respectively) to find how those two tests correlated to the LV of each group. We found that both 5% lactic acid SRC and SDS sedimentation tests showed strong correlations with the LV of the low protein group ($r = 0.83$ and 0.78, respectively), whereas with the high protein group, only 5% lactic acid SRC test showed a high correlation ($r = 0.81$) and SDS-sedimentation test showed a lower correlation ($r = 0.38$, $P < 0.01$). Similar results were obtained when each HWW and HSW flours were divided into low and high protein groups. Wheat class had little influence on the 5% lactic acid SRC test results, whereas protein content did. The results demonstrate that 5% lactic acid SRC test is a more robust test to predict the LV of both classes of wheat flours over a broad range of protein content.

Solvent retention capacity values in relation to hard winter wheat and flour properties and straight-dough bread-making quality.

S.Z. Xiao, S.H. Park, O.K. Chung, and M.S. Caley.

Solvent retention capacity was investigated in assessing the end-use quality of HWW. The four SRC values of 116 HWW flours were determined using 5% lactic acid, 50% sucrose, 5% sodium carbonate, and distilled water. The SRC values were greatly affected by wheat and flour protein contents, and showed significant linear correlations with 1,000-kernel weight and single kernel weight, size, and hardness. The 5% lactic acid SRC value showed the highest correlation ($r = 0.83$, $P < 0.0001$) with straight-dough bread volume, followed by 50% sucrose, and least by distilled water. We found that the 5% lactic acid SRC value differentiated the quality of protein relating to loaf volume. When we selected a set of flours that had a narrow range of protein content between 12–13% ($n = 37$) from the 116 flours, flour protein content was not significantly correlated with loaf volume. The 5% lactic acid SRC value, however, showed a significant correlation ($r = 0.84$, $P < 0.0001$) with loaf volume. The 5% lactic acid SRC value was significantly correlated with SDS-sedimentation volume ($r = 0.83$, $P < 0.0001$). The SDS-sedimentation test showed a similar capability to 5% lactic acid SRC, correlating significantly with loaf volume for flours with similar protein content ($r = 0.72$, $P < 0.0001$). Prediction models for loaf volume were derived from a series of wheat and flour quality parameters. The inclusion of 5% lactic acid SRC values in the prediction model improved R^2 of 0.778 and root mean square error (RMSE) of 57.2 from R^2 of 0.609 and RMSE of 75.6, respectively, from the prediction model developed with Single Kernel Characterization System and near-infrared reflectance spectroscopy data. The prediction models were tested with three validation sets having different protein ranges, and confirmed that 5% lactic acid SRC test is valuable in predicting the loaf volume of bread from a HWW flour, especially for flours with similar protein contents.

Differentiation of allelic variations of the HMW glutenin subunits of wheat flours by use of mixing parameters and polymeric protein content.

H. Akdogan, M. Tilley, S.R. Bean, and R.A. Graybosch.

The mixing parameters and polymeric proteins (PP) of two different wheat cultivars, Centurk (CK) and OK102, each with four lines differing in HMW-glutenin subunit composition were analyzed using multivariate statistical analysis of mixograph parameters. Stepwise discriminant analysis was used to identify significant mixing parameters at $P < 0.0001$ level. The selected variables, mixing tolerance, peak mixing time, and peak height (torque), were subjected to Principle

Component Analysis. The score plots of the first two principal components (PC 1 and PC 2) indicated a clustering in samples: CK with 7+8 and 7+9 at the *Glu-B1* and 5+10 at the *Glu-D1* loci; CK with 7+8 and 7+9 at the *Glu-B1* and 2+12 at the *Glu-D1* loci; OK102 with 6+8 and 7+9 at the *Glu-B1* and 5+10 at the *Glu-D1* loci; OK102 with 6+8 and 7+9 at the *Glu-B1* and 3+12 at the *Glu-D1* loci. Samples from different cultivars (CK and OK102) were successfully grouped using the same score plots. Polymeric proteins consistently correlated well with mixing tolerance and peak mix time. Insoluble polymeric proteins (IPP) showed a positive relationship with mixing tolerance and peak time, soluble polymeric proteins (SPP) showed a negative correlation with the same parameters. Overall, SPP was a better identifier in terms of grouping *Glu-D1* subunits and contributed to higher correlation coefficients than IPP. This method could be beneficial in developing analysis tools in early selection of lines for quality traits in wheat breeding programs.

Arabic flat bread: A study of mold inhibition and staling as determined by Near-infrared spectroscopy and texture analysis.

M. Abu-Ghoush, T. Herald, F.E. Dowell, F. Xie, F.M. Aramouni, and R. Madl.

Flat bread is the oldest and most popular bread in the world. However, in the Middle East where much of this bread is consumed, many people do not have refrigeration or frozen storage to keep bread fresh and free from mold for more than a few days. In order to extend bread shelf-life, this study evaluated fumaric acid and sodium propionate separately and in combination as mold growth inhibitors. Bread quality was measured by the bread tearing time and tearing strength, and by NIRS. The combination of the two inhibitors inhibited mold growth by 320% when compared to the control. NIRS was shown to be a rapid means of monitoring bread quality. These results will help reduce the estimated one billion dollars lost each year due to bread spoilage and staling.

Effect of antimicrobial agents and dough conditioners on the shelf-life extension and quality of flat bread, as determined by near-infrared spectroscopy.

M. Abu-Ghoush, T. Herald, F.E. Dowell, F. Xie, F.M. Aramouni, and C. Walker.

Middle Eastern Countries are experiencing the emergence of Arabic flat bread high volume production and retail marketing over traditional unit baking and retailing. However, shelf life needs to be increased and bread quality improved to limit economic loss. We examined five improvers for improving shelf-life and bread quality, and the use of near-infrared spectroscopy to evaluate bread quality. The improver treatments included sodium 9 stearoyl-2-lactylate, monoglycerides, hydroxyl propyl methyl cellulose gum, high fructose corn syrup, and a combination of all the aforementioned improvers. The high fructose corn syrup and the improver combination caused the bread to exhibit a significantly longer tearing time to rupture than the other treatments at day zero. The sensory evaluation showed that the improver combination significantly improved the quality attributes. The spectroscopic analysis indicated that after 3 days, the control was less fresh than bread formulated with high fructose corn syrup or improver combinations.

Measurement of wheat tortilla quality.

M. Tilley, H.P. Akdogan, and O.K. Chung.

Once predominantly limited to Mexico and the Southwestern U.S., tortillas have become the most prevalent ethnic bread in the U.S., often replacing white pan bread in many products. As a result, tortillas are the fastest growing segment of the U.S. baking industry with annual sales over $6 billion USD and growth exceeding 10%/year. The majority of tortillas consumed in the U.S. are made from wheat flour, although traditional maize tortillas are also produced. Sustaining this tremendous demand requires sufficient definition and determination of fundamental quality characteristics of wheat flour tortillas. Quality characteristics include visual and textural properties as well as shelf-life. Good quality tortillas should remain flexible without cracking and breaking when folded. One of the major challenges in tortilla quality is the deterioration of texture with time (staling). In instances where tortillas are freshly prepared and consumed, shelf life is not an issue, however, in the U.S. retention of fresh properties is important since tortillas are packaged sealed in plastic bags and consumed over the course of several weeks. Tortilla quality is measured using both objective and

subjective methods and is dependent upon flour properties as well as ingredient formulation. Tortilla quality parameters and current evaluation methods are discussed.

Textural properties of commercial wheat flour tortillas during storage.

H.P. Akdogan, O.K. Chung, H. Singh, and G.L. Lookhart.

The tortilla industry is the fastest growing segment of the baking industry. In the U.S., annual sales of tortillas exceed all other ethnic and specialty bread sales. Consumers' assessment of tortilla quality is highly linked to its texture. The purpose of this study was to evaluate the shelf-life of commercial wheat flour tortillas through their textural parameters. Three types of tortillas (regular, 98% fat-free, and whole wheat) of two different commercial brands (Brand A and Brand B) were studied. All samples were subjected to extensibility and stress relaxation tests by using a TA-XT2 Texture Analyzer at days 0, 2, 6, 9, 12, 15, 19, 23, and 33 of storage. One-way analysis of variance (ANOVA) was used to analyze the data. Fisher's least significant difference (LSD) at 0.05 were used to identify the significant differences in the means of measured and calculated textural parameters. The gradient (modulus of deformation) and work (area under the curve up to maximum force to tear) were not indicative of the textural changes of the studied tortillas. The calculated parameters from the stress relaxation (SR) curve, k1, k2, and % SR, and the distance to tear from the extensibility measurements were able to identify either the first days of storage (day 0 and/or 2) or the last days of storage (day 23 and/or 33). The significant changes came shortly after opening their packages for both brands of regular tortillas. Detectable changes for 98% fat-free tortillas of Brand A and B came after 23 and 2 days of storage, respectively. For whole wheat tortillas most results were not conclusive. The calculated textural parameters, k1, k2, % SR , and distance to tear, identified the significant differences among days of storage. Further research on tortilla formulation and ingredient functionality may provide a better understanding on tortilla staling.

Effect of emulsifiers on textural properties of whole wheat tortillas during storage.

H.P. Akdogan, M. Tilley, and O.K. Chung.

All three emulsifiers tested (SSL, GMS, and de-oiled lecithin) impacted the textural quality of 100% WW tortillas during storage. However, the amount of emulsifier incorporated into the formulation was crucial. SSL was more effective at its lowest usage level (0.125%), unlike the de-oiled lecithin, which was most effective at its highest usage level (2%). The diameters of tortillas with mid (0.25%) and high (0.50%) levels of added SSL were significantly smaller than the rest of the tortillas. Rollability scores and Fr of tortillas were improved with emulsifier addition. Control tortillas consistently resulted in higher Fr values as well as lowest rollability scores at the end of full storage. None of the emulsifiers studied enhanced the stretchability of tortillas, as it abruptly declined during the first two days of storage. Type and level of emulsifier addition to tortillas should be determined carefully as it influences textural properties besides shelf life.

Effects of processing on wheat tortilla quality: benefits of hard white wheat.

M. Tilley, V. Pierucci, K.A. Tilley, and O.K. Chung.

The suitability of Kansas (HWWW milled at a high extraction rate for tortilla production was investigated. Tortillas were made from eight wheat cultivars milled at 80% extraction: four HWWW cultivars included Betty, Heyne, Oro Blanco, and NuWest; three HRWW samples were Jagger and Ike grown at Hutchinson, Kansas (Ike-Hutch) and at Hays, Kansas (Ike-Hays); and one HWSW cultivar, Idaho 377-S. Tortillas made from these flours were compared to tortillas made from one commercial tortilla flour milled to 72% extraction from a blend of HRW wheat. Mixograph parameters, starch pasting properties, dough-handling characteristics and tortilla-making attributes of the Kansas HWWW cultivars, Betty and Heyne, were superior. All of the Kansas HWWW flours, milled to 80% extraction, produced tortillas which were equal to, or superior to, those made from 80%- extraction HRWW flours and 72%-extraction commercial tortilla flour.

Hard winter wheat and flour properties in relation to bread-making quality of straight-dough bread: flour particle size and bread crumb grain.

S.H. Park, O.K. Chung, and P.A. Seib.

Samples of 12 HWW and their flours that produced breads varying in crumb grain scores were studied for 38 quality parameters including wheat physical and chemical characteristics; flour ash and protein contents, starch damage, swelling power, pasting characteristics, and flour particle size distribution; dough properties determined by a mixograph; and bread-making properties for pup loaves. Only two parameters, the protein content of wheat and the granulation of flour, showed significant correlations with crumb grain scores. Protein content of wheat ranging from 12.9–14.5% determined by an NIR method showed a weak inverse relationship ($r = -0.61$, $P < 0.05$) with bread crumb grain score. Flour particle size distribution measured by both Alpine Air Jet Sieve and NIR methods revealed that the weight (wt) % of particles less than 38 um in size and representing 9.6–19.3% of the flour weights was correlated positively ($r = 0.78$, $P < 0.01$) with crumb grain score, whereas wt % of flour particles larger than 125 μm had an inverse relationship ($r = -0.60$, $P < 0.05$) with crumb grain score.

Description of a wheat endosperm peroxidase with potential to catalyze dityrosine formation during dough processing.

M. Tilley, V. Pierucci, and K.A. Tilley.

The water-soluble extract from wheat flour was fractionated using preparative isoelectric focusing and the fractions were tested for the ability to synthesize dityrosine from tyrosine *in vitro*. The fraction that catalyzed dityrosine also possessed a high level of peroxidase activity. The major protein was purified and the N-terminal amino acid sequence was determined. The sequence was similar to barley endosperm peroxidase BP1. An oligonucleotide probe based on this sequence was used to screen cDNA libraries from developing kernels of wheat and the progenitor *Ae. tauschii*. Resulting cDNAs were identical at the amino acid level and had a high similarity to BP1. These findings support data on the nature of endogenous wheat peroxidase and the potential of peroxidase to catalyze dityrosine formation in dough.

The relationship between single wheat kernel particle size distribution and the Perten SKCS 4100 Hardness Index.

T.C. Pearson, J.D. Wilson, J. Gwirtz, E.B. Maghirang, F.E. Dowell, P. McCluskey, and S. Bean.

Grain inspectors have observed that in the U.S. Pacific Northwest region, discriminating soft white wheat from hard white wheat has become increasingly difficult. This poses problems for assigning a proper grade to wheat loads being exported to international customers. Additionally, wheat loads with mixed hard white and soft white wheat may have different baking qualities, and their presence reduces the desirability of U.S.-grown wheat, especially for international customers. The primary instrument for distinguishing hard and soft classes of wheat is called the Single Kernel Characterization System. This research found that, through simple data processing software changes to the SKCS, classification errors between hard white and soft white wheat can be reduced by about 50% over the current configuration of the SKCS. This should help those who use the SKCS to determine wheat class purity, such as wheat inspectors. Also, this should help wheat millers and international customers better understand the quality and properties of incoming wheat loads.

Levels of protein and protein composition in hard winter wheat flours and their relationships to breadmaking.

S.H. Park, S.R. Bean, O.K. Chung, and P.A. Seib.

Protein and protein fractions were measured in 49 hard winter wheat flours to investigate their relationship to bread-making properties, particularly loaf volume which varied from 760 to 1/055cm^3/100 g flour, and crumb grain score of

1.0–5.0. Total soluble protein (SP) in 50% 1-propanol was separated into albumins and globulins (AG), gliadins, and soluble polymeric proteins (SPP) using size exclusion high-performance liquid chromatography (SE-HPLC). Insoluble polymeric protein (IPP) was determined by combustion assay of the residue. Protein composition varied with flour protein content because SP and gliadin levels increased proportionally to increased protein content, but AG, SPP, and IPP levels did not. Flour protein content was positively correlated with loaf volume and bake water absorption ($r = 0.80$, $P < 0.0001$ and $r = 0.45$, $P < 0.01$, respectively). The percent SP based on flour showed the highest correlation with loaf volume ($r = 0.85$) and low but significant correlation with crumb grain core ($r = 0.35$, $P = 0.05$). Percent gliadins based on flour and on protein content were positively correlated to loaf volume ($r = 0.73$, $P < 0.0001$ and $r = 0.46$, $P < 0.001$, respectively). The percent IPP based on flour was the only protein fraction that was highly correlated ($r = 0.62$, $P < 0.0001$) with bake water absorption followed by AG in flour ($r = 0.30$, $P < 0.05$). Bake mix time was correlated positively with percent IPP based on protein ($r = 0.86$) but negatively with percent SPP based on protein ($r = –0.56$, $P < 0.0001$).

Comparison of quality characteristics and breadmaking functionality of hard red winter and hard red spring wheat.

E.B. Maghirang, G.L. Lookhart, S. Bean, R.O. Pierce, F. Xie, M.S. Caley, J.D. Wilson, B.W. Seabourn, O.K. Chung, and F.E. Dowell.

Various whole-kernel, milling, flour, dough, and bread-making quality parameters were compared between HRWW and HRSW. From the 43 quality parameters evaluated, only eight quality characteristics, test weight, moisture content, kernel size, polyphenol oxidase content, average gluten index, % insoluble polymeric protein, loaf volume adjusted for protein content, and mixograph tolerance, were found to be the same. Some of the quality characteristics that had significantly higher levels in HRSW than in HRWW samples included protein content, flour yield, bread crumb grain score, and other proteindependent parameters such as sodium dodecyl sulfate sedimentation volume, average total gluten, baking water absorption, and loaf volume. When HRWW and HRSW samples were grouped to be within the same wheat protein content range (11.4 to 15.8%), the average value of most other grain and bread-making quality characteristics were the same for both wheat classes. Values that were significantly higher for HRW wheat were color b* and farinograph tolerance. Values that were higher for HRS wheat were mg insoluble polymeric proteins, mg gliadins, mixograph time, alveograph configuration ratio, and crumb score. Test of homogeneity of intercepts showed HRS wheat had higher water absorption, loaf volume, and SDS sedimentation volume.

Effect of drying methods on functional properties of precooked wheat flour obtained by extrusion.

H. Gajula, S. Liu, S. Alavi, T. Herald, and S.R. Bean.

Cereal products with high fiber can reduce calorie uptake and provide health benefits linked to chronic disease. However, high fiber content tends to diminish the final product quality and consumer acceptability of cereal products such as baked goods and pasta. Our overall objective is to produce high-fiber, precooked flour using extrusion in order to increase functional properties. Our specific objective of this study was to compare rheological and functional properties of extrusion processed wheat precooked whole wheat flour obtained by oven drying and freeze drying. Precooked flours were produced using lab-scale, twin-screw, co-rotating extruder configuring for low shear, low temperature. Swelling and pasting properties of the precooked flours was characterized using rapid visco-analyser standard methodology. Rheological properties were characterized using mixograph standard methodology. The quality of cookies and tortillas were also characterized by AACC Approved Methods.

The results showed that precooked flour using freezer dryer had a similar swelling and pasting properties with oven dried flour. Water absorption increased in the precooked flours as compared to the commercial available flours. The drying methods had no significant effect on the quality of the cookies using precooked flour and commercial available wheat flours. The diameters of cookies using these flours were 9.3 cm, 9.8 cm, and 10 cm with similar spread factor (118.70, 107.09, and 129.35, respectively). The weight, diameter, height, and specific volume of tortilla using oven dried, freeze dried precooked flour, and controlled wheat flour were 22.34 g, 11.33 cm, 0.20 cm, and 0.947 cm^3/g; 22.65 g, 11.39 cm, 0.215 cm, and 0.964 cm^3/g; and 22.69 g, 12.21 cm, 0.18 cm, and 0.952 cm^3/g, respectively. The

results suggest that extrusion technology can produce precooked wheat flour with same functionality for baked products, and precooked flour obtained by oven-drying have similar rheological and functional properties as freeze dried flour.

Cost and risk analysis of heat and chemical treatments.

D.R. Tilley, M.R. Langemeier, M. Casada, and F.H. Arthur.

Our previous research has shown that heat treatments are effective as a non-chemical method for disinfestation of empty grain storage bins. We developed an empirical economic risk model to compare variable costs for five tested heating systems for disinfestation of empty, 5,000-bu grain storage bins with fitted drying floors. The high-output, 29 kW, propane heating system had the lowest cost and risk level of all heating systems and achieved the target temperature of 50 C within 2 hours at all test locations. Lower power systems requiring complex heat distribution or recirculation were not cost effective and exhibited higher risk levels of insect survival. These results indicate that properly-sized portable propane heat treatment systems are equal to chemical applications for low-cost, low-risk disinfestation of empty bins, but without the concerns that arise with using chemicals.

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Wheat rusts in the United States in 2006.

Wheat stem rust (*Puccinia graminis f. sp. tritici*). The first reports of wheat stem rust were in mid-April in soft red winter wheat plots at Crowley, in south-central Louisiana, with severities of up to 40%. Stem rust was found in 28 of the 102 plots, which were located near rice paddies. The regular dew formation in these plots provided a suitable environment for stem rust infections. On 18 April, wheat stem rust was at low levels in plots at Baton Rouge, Louisiana. By late May, severe stem rust was observed on late-planted wheat nurseries at this same location.

The first report of wheat stem rust in Texas was in late April, where traces were found in a field in Ellis County in north central Texas.

In mid-May, low levels of wheat stem rust were found in southwestern Georgia plots at Plains.

In late May, traces of stem rust were observed on late-maturing lines of wheat at Kinston, North Carolina.

In mid-July, the susceptible spring wheat cultivar Baart in southern and west-central Minnesota and east-central North Dakota plots had trace to 10% severities of stem rust infection. In late July, 5 to 10% stem rust severities were reported in plots of Baart in east central South Dakota and trace levels in northwestern Minnesota. All of the currently grown spring wheat cultivars are resistant to the prevalent U.S. races.

In late July, low levels of wheat stem rust were found in plots at Colfax in Whitman County, Washington.

In early August, light to moderate levels of stem rust were observed in spring wheat plots in Aberdeen, Idaho. The rust appeared to come in late as most infection was on late tillers or late maturing lines.

Virulence of wheat stem rust. From collections made from the above locations, race QFCS was identified as the predominant race (Table 1). This is a common race that has been found in the U.S. in the past several years. This race is relatively avirulent; the majority of the U.S. cultivars are resistant to QFCS. Races MCCD and TTTT, one isolate each, were identified from collections in Louisiana.

Table 1. Races of *Puccinia graminis* f. sp. *tritici* identified from wheat in 2006. Pgt race code after Roelfs and Martens (Phytopathology **78**:526-533).

Race	Collections	State
QFCS	25	LA, TX, GA, MN, SD, ND, ID
MCCD	1	LA
TTTT	1	LA

Stem rust on barberry. In mid-May, aecial development was light on infected susceptible barberry bushes (alternate host for stem rust) growing in south-central Wisconsin. In early June, aecial infections were light on susceptible common barberry in southeastern Minnesota. In 2006, aecial infections on susceptible barberries were much lighter than during the years from 2003 to 2005 in southeastern Minnesota. Aecial infections from Minnesota and Wisconsin were mostly due to *P. graminis* f. sp. *secalis* (the form attaching rye) as *P. graminis* f. sp. *tritici* (the form attacking wheat) or *P. graminis* f. sp. *avenae* (attacking oats) was not identified from the barberry samples.

Wheat leaf rust (*Puccinia triticina)*. Southern Plains – Texas. The 2005 autumn and 2006 winter were the driest on record in the state of Texas. In late January, low levels of leaf rust were reported in irrigated central Texas wheat plots. In early March, leaf rust was found in varietal plots at College Station, TX. In a few of the susceptible cultivars, e.g. Jagger, leaf rust severities of 5% were observed on the flag leaves and in a few others, e.g. Cutter in an early planted test, 70% severities were observed on the lower leaves. In mid-March, only traces of leaf rust were found in the irrigated nursery at Castroville, TX. The wheat crop throughout south Texas was under severe drought stress. By the second week of April, the susceptible cultivars Jagelene and Jagger had 80% leaf rust severities in nurseries at Castroville and College Station, TX. In the highly resistant cultivars Fannin and Endurance, no infections were found. Only low levels of rust were reported in grower's fields in southern and central Texas because of the dry conditions (Fig. 1, p. 132).

Oklahoma. In mid-January, leaf rust was found in southern Oklahoma, but conditions were not conducive for infection, spread, and development of leaf rust. By the first week in March, a few pustules of leaf rust were observed on lower leaves in the wheat varietal plot at Stillwater, Oklahoma. In late March, low levels of leaf rust were reported in grower's fields in Oklahoma. On 1 May, traces of leaf rust were found in plots at Stillwater in northeastern Oklahoma. In 2006, leaf rust development was less than normal in Oklahoma because of drought conditions throughout the state.

Central Plains – Kansas. In mid-March, no rust pustules were found on wheat that previously had infections in late autumn in Kansas. In late April, traces of leaf rust were found in south-central Kansas where wheat was under extreme drought stress. In mid-May, low levels of leaf rust were found in fields and plots in central Kansas. During the third week in May, 1% severities were observed on flag leaves of susceptible cultivars in northeastern Kansas plots. This year leaf rust losses were less than normal in Kansas because of the persistent drought throughout much of the state (Table 4, p. 138).

Nebraska. In early March, traces of leaf rust were found on the lower leaves of wheat in plots and fields in central Nebraska. In mid-May, low levels of leaf rust were found on lower leaves of wheat plants in research plots in central Nebraska. By early June, leaf rust developed to 15 to 25% severity levels on flag leaves in central and eastern Nebraska, and in irrigated wheat in southwestern Nebraska. As in the southern Great Plains, continued hot dry weather slowed leaf rust development in the central Great Plains.

Northern Plains - Minnesota, South Dakota, North Dakota. On 8 May, leaf rust infections that had apparently overwintered were found on the lower leaves of the susceptible winter wheat Cheyenne at the Rosemount Experiment Station in east-central Minnesota. On 26 May, 5% severities were found on flag-2 leaves in susceptible winter wheat plots at Rosemount. In early June, traces of leaf rust were found on the spring wheat Alsen in Bottineau County in north-central North Dakota, which is near the Canadian border. Drier than normal conditions in May and June slowed leaf rust development in most areas of the northern plains. In late June, plots of susceptible winter wheat cultivars in east central Minnesota and east-central South Dakota had 60% rust severities, whereas resistant cultivars had only trace levels of infection on the flag leaves. By late June, spring wheat had leaf rust severities of trace to 1% on lower leaves in southern Minnesota and North Dakota fields (Fig. 1, p. 132). Susceptible spring wheat cultivars in southern Minnesota plots had 20% rust severities on the lower leaves.

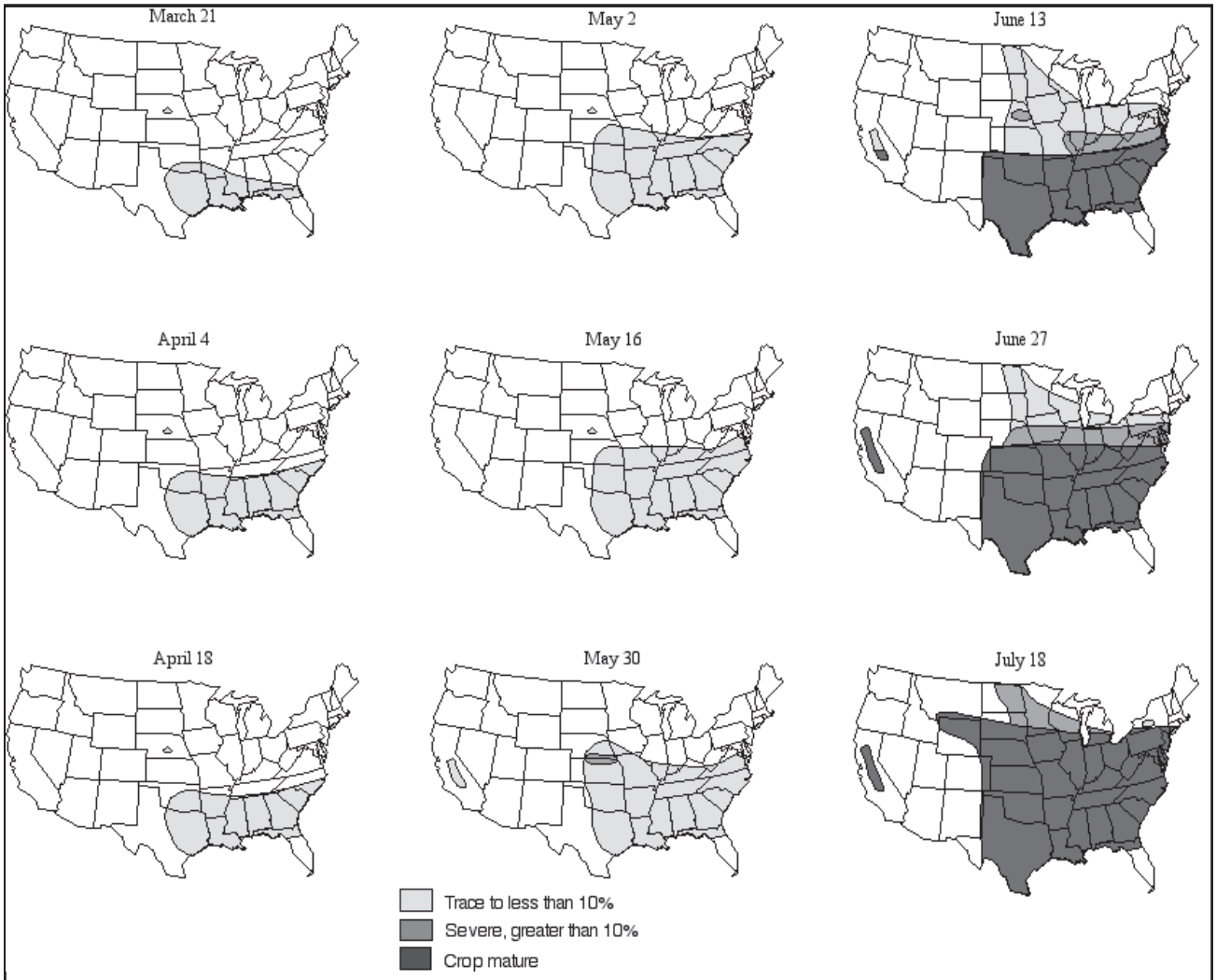

Fig. 1. Leaf rust severities in wheat fields in 2006.

In early July, high levels of leaf rust were found in susceptible winter wheat in plots in southeastern North Dakota and in mid-July high levels of infection were found in spring wheat fields in north-central North Dakota. By mid-July, trace to 60% leaf rust severities were observed on flag leaves of spring wheat cultivars in fields and plots from north-central South Dakota to west-central Minnesota (Fig. 1). In late July, wheat leaf rust was at trace to moderate severity levels in spring wheat fields in northern Minnesota and North Dakota. Plots of susceptible cultivars in the same area had moderate to high leaf rust severities.

Leaf rust was widespread in 2006, but at lower levels than normal in the upper Midwest on both spring (Table 5, p. 139) and winter wheat. Lower amounts of rust inoculum than in previous years arrived from the winter wheat region because of the persistent drought-like conditions in the southern plains, which reduced rust infections in the winter wheat. Hot and dry conditions in the northern plains in June and July also reduced the incidence and severity of leaf rust. Many spring wheat fields were sprayed with fungicide; further reducing leaf rust infections and also the incidence of leaf spot diseases.

Southeast – Louisiana. In mid-February, leaf rust was found on susceptible winter wheat cultivars throughout Louisiana in plots and fields. By early March, cultivars growing in plots in southeast Louisiana had up to 70% leaf rust severity. In late March in wheat plots at Alexandria, Louisiana, susceptible winter wheat cultivars had 20% leaf rust severities on the lower leaves. Some of the fields infected with rust were sprayed for rust control in the southern U.S. During the second week in April, plots in southern Louisiana had leaf rust severities up to 70%. By late April, plots of susceptible wheat cultivars in northeastern Louisiana had leaf rust severities up to 80% on flag leaves.

Arkansas. In early February, leaf rust had survived as far north as northeast Arkansas, however, a mid-February cold snap combined with freezing rain and snow appeared to kill the rust. In mid-March, leaf rust was light in the southern part of the state. By mid-April, leaf rust was found in areas of Arkansas that had sufficient moisture. In late April, plots in east-central Arkansas had 0–50% leaf rust severities. In Arkansas, leaf rust was more widespread than in the last few years, but the high severities occurred too late to cause much yield loss.

Table 2. Races of *Puccinia triticina* in the U.S. in 2006 determined by virulence to 20 near-isogenic lines of Thatcher wheat with leaf rust-resistance genes. Differentials used were 1a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 17, 30, B, 10, 14a, 18, 21, 28, 41, 42. An * indicates less than 0.6 %. For area designations, see Fig. 3 (p. 137).

Race	Virulence combination (ineffective *Lr* genes)	SE		NE		OH Valley		TX–OK		KS–NE		MN SD ND		CA		WA		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBDB	14a	0	0	0	2.9	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
CBLSG	3,3ka,B,10,14a,28	0	0	0	0	0	0	1	0.5	0	0	0	0	0	0	0	0	1	0.1
LBBTG	1,B,10,14a,18,28	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	0	0	1	0.1
MBBJG	1,3,10,14a,28	2	1.4	0	0	0	0	1	0.5	0	0	1	0.4	0	0	0	0	4	0.6
MBDSB	1,3,17,B,10,14a	3	2.1	0	0	0	0	8	3.9	2	6.7	5	2.2	0	0	0	0	18	2.5
MBGJG	1,3,11,10,14a,28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	30	3	0.4
MBPSB	1,3,3ka,17,30,B,10,14a	2	1.4	0	0	1	1.7	1	0.5	0	0	2	0.9	0	0	0	0	6	0.8
MBPSG	1,3,3ka,17,30,B,10,14a,28	0	0	0	0	0	0	3	1.5	0	0	1	0.4	0	0	0	0	4	0.6
MBRKG	1,3,3ka,11,30,10,14a,18,28	9	6.3	0	0	2	3.4	0	0	0	0	0	0	0	0	0	0	11	1.5
MCBJG	1,3,26,10,14a,28	0	0	7	20	0	0	0	0	0	0	0	0	0	0	0	0	7	1.0
MCDSB	1,3,26,17,B,10,14a	8	5.6	0	0	9	15.3	4	1.9	1	3.3	9	3.9	2	50	1	10	34	4.7
MCDSG	1,3,26,17,B,10,14a,28	0	0	1	2.9	0	0	0	0	0	0	0	0	0	0	4	40	5	0.7
MCJJG	1,3,26,11,17,10,14a,28	0	0	0	0	1	1.7	0	0	0	0	0	0	0	0	0	0	1	0.1
MCPSB	1,3,26,3ka,17,30,B,10,14a	0	0	5	14.3	2	3.4	0	0	3	10	3	1.3	0	0	2	20	15	2.1
MCPSC	1,3,26,3ka,17,30,B,10,14a,42	2	1.4	0	0	0	0	4	1.9	0	0	6	2.6	0	0	0	0	12	1.7
MCRKG	1,3,26,3ka,11,30,10,14a,18,28	0	0	0	0	5	8.5	0	0	0	0	1	0.4	0	0	0	0	6	0.8
MDBJG	1,3,24,10,14a,28	2	1.4	0	0	0	0	0	0	0	0	2	0.9	0	0	0	0	4	0.6
MFBJG	1,3,24,26,10,14a,28	6	4.2	0	0	0	0	4	1.9	0	0	0	0	0	0	0	0	10	1.4
MFBKG	1,3,24,26,10,14a,18,28	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
MFDSB	1,3,24,26,17,B,10,14a	2	1.4	5	14.3	0	0	4	1.9	0	0	2	0.9	0	0	0	0	13	1.8
MFGJG	1,3,24,26,11,10,14a,28	2	1.4	6	17.1	2	3.4	0	0	0	0	0	0	0	0	0	0	10	1.4
MFPSC	1,3,24,26,3ka,17,30,B,10,14a,42	5	3.5	3	8.6	2	3.4	24	11.7	3	10	18	7.8	0	0	0	0	55	7.7
MFRJG	1,3,24,26,3ka,11,30,10,14a,28	0	0	0	0	1	1.7	0	0	0	0	0	0	0	0	0	0	1	0.1
MFRKG	1,3,24,26,3ka,11,30,10,14a,18,28	0	0	3	8.6	0	0	0	0	0	0	0	0	0	0	0	0	3	0.4
MFTJG	1,3,24,26,3ka,11,17,30,10,14a,28	0	0	0	0	2	3.4	0	0	0	0	0	0	0	0	0	0	2	0.3
MJBJG	1,3,16,24,10,14a,28	0	0	0	0	0	0	0	0	0	0	14	6.1	0	0	0	0	14	1.9
MJBJH	1,3,16,24,10,14a,28,42	0	0	0	0	0	0	0	0	0	0	2	0.9	0	0	0	0	2	0.3
MLDSB	1,3,9,17,B,10,14a	6	4.2	0	0	2	3.4	33	16	6	20	16	6.9	2	50	0	0	65	9.1
PCMDG	1,2c,3,26,3ka,30,14a,28	2	1.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
SBDGG	1,2a,2c,17,10,28	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	0	0	1	0.1
SBDJG	1,2a,2c,17,10,14a,28	0	0	0	0	0	0	1	0.5	0	0	1	0.4	0	0	0	0	2	0.3

Table 2 (continued). Races of *Puccinia triticina* in the U.S. in 2006 determined by virulence to 20 near-isogenic lines of Thatcher wheat with leaf rust-resistance genes. Differentials used were 1a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 17, 30, B, 10, 14a, 18, 21, 28, 41, 42. An * indicates less than 0.6 %. For area designations, see Fig. 3 (p. 137).

Race	Virulence combination (ineffective *Lr* genes)	SE		NE		OH Valley		TX–OK		KS–NE		MN SD ND		CA		WA		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
TBBGG	1,2a,2c,3,10,28	0	0	0	0	0	0	1	0.5	0	0	1	0.4	0	0	0	0	2	0.3
TBBJG	1,2a,2c,3,10,14a,28	7	4.9	0	0	1	1.7	3	1.5	0	0	4	1.7	0	0	0	0	15	2.1
TBDSB	1,2a,2c,3,17,B,10,14a	3	2.1	0	0	0	0	0	0	0	0	7	3	0	0	0	0	10	1.4
TBNSB	1,2a,2c,3,3ka,17,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	0	0	1	0.1
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	5	3.5	0	0	2	3.4	0	0	0	0	0	0	0	0	0	0	7	1.0
TBTKG	1,2a,2c,3,3ka,11,17,30,10,14a, 18,28	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
TCDSB	1,2a,2c,3,26,17,B,10,14a	4	2.8	0	0	0	0	0	0	0	0	4	1.7	0	0	0	0	8	1.1
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a, 18,28	9	6.3	0	0	4	6.8	0	0	0	0	2	0.9	0	0	0	0	15	2.1
TCTDB	1,2a,2c,3,26,3ka,11,17,30,14a	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	0	0	1	0.1
TDBGG	1,2a,2c,3,24,10,28	6	4.2	0	0	0	0	20	9.7	0	0	37	16	0	0	0	0	63	8.8
TDBGH	1,2a,2c,3,24,10,28,42	0	0	0	0	2	3.4	2	1	0	0	2	0.9	0	0	0	0	6	0.8
TDBGK	1,2a,2c,3,24,10,28,41,42	0	0	0	0	0	0	0	0	0	0	2	0.9	0	0	0	0	2	0.3
TDBJG	1,2a,2c,3,24,10,14a,28	33	23.1	0	0	11	18.6	30	14.6	3	10	30	13	0	0	0	0	107	14.9
TDBJH	1,2a,2c,3,24,10,14a,28,42	7	4.9	0	0	1	1.7	31	15	6	20	18	7.8	0	0	0	0	63	8.8
TDBJK	1,2a,2c,3,24,10,14a,28,41,42	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
TDDJG	1,2a,2c,3,24,17,10,14a,28	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	0	0	1	0.1
TDDJJ	1,2a,2c,3,24,17,10,14a,28,41	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	2	0.3
TDDSB	1,2a,2c,3,24,17,B,10,14a	0	0	0	0	0	0	3	1.5	0	0	0	0	0	0	0	0	3	0.4
TFBGG	1,2a,2c,3,24,26,10,28	0	0	0	0	0	0	2	1	0	0	2	0.9	0	0	0	0	4	0.6
TFBGH	1,2a,2c,3,24,26,10,28,42	0	0	0	0	2	3.4	0	0	0	0	0	0	0	0	0	0	2	0.3
TFBJG	1,2a,2c,3,24,26,10,14a,28	7	4.9	0	0	2	3.4	6	2.9	2	6.7	1	0.4	0	0	0	0	18	2.5
TFBJH	1,2a,2c,3,24,26,10,14a,28,42	0	0	2	5.7	0	0	2	1	4	13.3	0	0	0	0	0	0	8	1.1
TGBJG	1,2a,2c,3,16,10,14a,28	0	0	0	0	0	0	0	0	0	0	2	0.9	0	0	0	0	2	0.3
THBJG	1,2a,2c,3,16,26,10,14a,28	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	0	0	1	0.1
TJBGG	1,2a,2c,3,16,24,10,28	0	0	0	0	0	0	0	0	0	0	12	5.2	0	0	0	0	12	1.7
TJBGJ	1,2a,2c,3,16,24,10,28,41	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	2	0.3
TJBJG	1,2a,2c,3,16,24,10,14a,28	0	0	0	0	0	0	1	0.5	0	0	12	5.2	0	0	0	0	13	1.8
TNRJJ	1,2a,2c,3,9,24,3ka,11,30,10,14a, 28,41	6	4.2	2	5.7	1	1.7	7	3.4	0	0	1	0.4	0	0	0	0	17	2.4

Mississippi, Georgia, Alabama, South Carolina. In mid-March, leaf rust was at low levels in southern Georgia plots. In early April, leaf rust was found on the lower leaves of the most susceptible cultivars in southwestern and south central Georgia. In late April, in the area from central Mississippi to central Georgia, plots of susceptible wheat cultivars had leaf rust severities up to 80%. Fields in the same area had severities from 0 to 10% (Fig. 1, p. 132). In mid-May, susceptible soft red winter wheat cultivars in northern Alabama plots had 60% severities. In early May, flag leaves of soft red winter wheat in central South Carolina plots had 5% leaf rust severity.

Leaf rust was widespread in the southeast U.S. in 2006.

Mid-Atlantic – North Carolina. In late March, the cultivar McCormick in southeastern North Carolina plots had low levels of leaf rust on lower leaves. In the second week in May, severe leaf rust infections were reported in plots at the Kinston station in east-central North Carolina. By late May, wheat leaf rust was widespread in the central Coastal Plain and particularly severe in the Neuse River basin; only traces of wheat leaf rust were observed in the Piedmont.

Table 2 (continued). Races of *Puccinia triticina* in the U.S. in 2006 determined by virulence to 20 near-isogenic lines of Thatcher wheat with leaf rust-resistance genes. Differentials used were 1a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 17, 30, B, 10, 14a, 18, 21, 28, 41, 42. An * indicates less than 0.6 %. For area designations, see Fig. 3 (p. 137).

Race	Virulence combination (ineffective *Lr* genes)	SE		NE		OH Valley		TX–OK		KS–NE		MN SD ND		CA		WA		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
TNRJK	1,2a,2c,3,9,24,3ka,11,30,10,14a, 28,41,42	2	1.4	0	0	4	6.8	6	2.9	0	0	5	2.2	0	0	0	0	17	2.4
Total		143		35		59		206		30		231		4		10		718	

Virginia. In the first week in May, severe leaf rust infections were reported in the wheat-breeding nursery at Warsaw in northeast Virginia. By mid-May, wheat leaf rust was widespread and severities up to 65% were reported on susceptible cultivars McCormick (*Lr24*) and USG3209 (*Lr26*), in plots on the eastern shore of Virginia. Leaf rust was earlier and more severe than normal across the state of Virginia. There appeared to be little virulence to the *Lr9* gene in the rust population, as Tribute, Coker 9835, and Coker 9663 were virtually clean. In contrast, there seemed to be significant virulence to genes *Lr24* and *Lr26* and to a lesser extent, *Lr18*.

Wheat leaf rust development was greater in 2006 than normal in the Mid-Atlantic States and losses occurred in a few areas.

Pennsylvania. In early June, leaf rust that over wintered was limited to the lower canopy of wheat in Pennsylvania.

New York. In early July, low levels of leaf rust were found in winter wheat plots at Ithaca, New York.

Midwest – In early June, wheat leaf rust was found in fields from east-central Missouri to southern Illinois at 20% severity on flag leaves. The first report of leaf rust in Ohio was during the second week in May in south-central Ohio, where the rust may have overwintered. By early June, trace levels of leaf rust were found on flag leaves of wheat in fields from northwestern Ohio to south-central Wisconsin. In mid-June, plots in west-central and northwestern Indiana had 40% severities on lower leaves. By mid-June, leaf rust was severe on the upper leaves of susceptible cultivars throughout the northern Ohio. More leaf rust was found in Ohio than in 2005, as moisture conditions throughout this area were conducive for rust development and some losses occurred in susceptible cultivars.

California – In mid-May, leaf rust severities up to 80% were observed in susceptible cultivar plots in Kern County and Madera County late in the growing season.

Washington – In mid-July, leaf rust was very light in experimental plots at Pullman and Mt. Vernon, WA. No leaf rust was found in farm fields.

Idaho – In early August, light to moderate levels of leaf rust were observed in spring wheat and triticale plots in Aberdeen, ID. The rust appeared to come in late as most infection was on late maturing lines.

Wheat leaf rust virulence. In 2006, 60 races of wheat leaf rust were found in the U.S. (Table 2, pp. 133-135). Races with virulence to *Lr24* increased in frequency throughout all wheat growing regions of the U.S. (Table 3, p. 136). Virulence to *Lr24* was highest throughout the Great Plains region, where a number of winter wheat cultivars have *Lr24*. Races with virulence to *Lr9* were found in all regions except for Washington State. Virulence to *Lr9* was highest in Texas and Oklahoma. Virulence to *Lr26* occurred in all regions of the U.S.,

Table 3. Virulence frequencies (%) of *Puccinia triticina* in the U.S. in 2006 to 20 differential lines of Thatcher wheat with leaf rust-resistance genes. Areas are described in Fig. 3.

Resistance gene	SE		NE		OH Valley		TX–OK		KS–NE		MN SD ND		CA		WA		U.S. Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	143	100	34	97.1	59	100.0	205	99.5	30	100.0	231	100.0	4	100.0	10	100.0	716	99.7
Lr2a	91	63.6	4	11.4	30	50.8	119	57.8	15	50.0	148	64.1	0	0.0	0	0.0	407	56.7
Lr2c	93	65.0	4	11.4	30	50.8	119	57.8	15	50.0	148	64.1	0	0.0	0	0.0	409	57.0
Lr3	143	100.0	34	97.1	59	100.0	205	99.5	30	100.0	228	98.7	4	100.0	10	100.0	713	99.3
Lr9	14	9.8	2	5.7	7	11.9	46	22.3	6	20.0	22	9.5	2	50.0	0	0.0	99	13.8
Lr16	0	0.0	0	0.0	0	0.0	3	1.5	0	0.0	43	18.6	0	0.0	0	0.0	46	6.4
Lr24	80	55.9	21	60.0	30	50.8	146	70.9	18	60.0	161	69.7	0	0.0	0	0.0	456	63.5
Lr26	48	33.6	32	91.4	32	54.2	50	24.3	13	43.3	50	21.6	2	50.0	7	70.0	234	32.6
Lr3ka	43	30.1	13	37.1	26	44.1	46	22.3	6	20.0	41	17.7	0	0.0	2	20.0	177	24.7
Lr11	34	23.8	11	31.4	24	40.7	13	6.3	0	0.0	10	4.3	0	0.0	3	30.0	95	13.2
Lr17	36	25.2	14	40.0	19	32.2	87	42.2	15	50.0	78	33.8	4	100.0	7	70.0	260	36.2
Lr30	43	30.1	13	37.1	26	44.1	45	21.8	6	20.0	40	17.3	0	0.0	2	20.0	175	24.4
LrB	35	24.5	14	40.0	16	27.1	85	41.3	15	50.0	75	32.5	4	100.0	7	70.0	251	35.0
Lr10	141	98.6	34	97.1	59	100.0	206	100.0	30	100.0	230	99.6	4	100.0	10	100.0	714	99.4
Lr14a	137	95.8	35	100.0	55	93.2	179	86.9	30	100.0	174	75.3	4	100.0	10	100.0	624	86.9
Lr18	25	17.5	3	8.6	13	22.0	0	0.0	0	0.0	4	1.7	0	0.0	0	0.0	45	6.3
Lr21	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Lr28	108	75.5	21	60.0	43	72.9	125	60.7	15	50.0	157	68.0	0	0.0	7	70.0	476	66.3
Lr41	9	6.3	2	5.7	5	8.5	17	8.3	0	0.0	8	3.5	0	0.0	0	0.0	41	5.7
Lr42	17	11.9	5	14.3	11	18.6	69	33.5	13	43.3	53	22.9	0	0.0	0	0.0	168	23.4
Total	143		35		59		206		30		231		4		10		718	

and was highest in the Northeast region. Virulence to *Lr16* occurred in only two regions, and was highest in the spring wheat region of Minnesota and North and South Dakota. Virulence to *Lr17* was found in all regions of the U.S., with the highest frequency in Kansas and Nebraska. Virulence to *Lr18* occurred in the southeast, northeast and Ohio valley, and was highest in the Ohio valley region where a number of soft red winter wheats have this gene. Virulence to *Lr21* was not found in any region, while virulence to *Lr41* was found in all regions except the central plains (Kansas and Oklahoma), California and Washington. Virulence to *Lr42* was found in all regions except California and Washington.

In the Southeast, the most common race, TDBJG (23.1%), had virulence to *Lr2a* and *Lr24*. In the Northeast, the most common race, MCBJG (20.0%) had virulence to *Lr26*. In the Ohio Valley, TDBJG (18.6%) was the most common race, which also was the most common race identified in the Southeast U.S. In Texas and Oklahoma, the most common race MLDSB (16.0%) had virulence to *Lr9 and Lr17*. In Kansas and Nebraska, MLDSB (20.0%) was also the most common race. In Minnesota, South Dakota, and North Dakota, the most common races MFPSC (7.8%) had virulence to *Lr24, Lr26, Lr17,* and *Lr42 and* TDBJH *(7.8%)* had virulence to *Lr2a, Lr24* and *Lr42*.

Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*). Southern Plains – In early March, wheat stripe rust was present at low levels on the upper leaves of a cultivar growing in a plot at College Station, TX. In mid-March, traces of stripe rust were found in the nursery at Giddings in central Texas. In late March, wheat fields and plots in southern and central Texas had low levels of wheat stripe rust (Fig. 2, p. 137). Conditions were not favorable for rust development (limited moisture and few cool nights). In early April, only traces of stripe rust were found in southern and central Texas. By mid-April, stripe rust had not been found in Oklahoma or states to the north. In late April, hot and dry conditions slowed stripe rust development in plots and fields throughout the southern U.S. (Fig. 2, p. 137). Stripe rust development in the southern plains in 2006 was much less than 2005 because of the limited moisture and high daytime temperatures. The southern states provided a reduced amount of inoculum for the northern regions of the U.S.

Fig. 2. Stripe rust severities in wheat fields in 2006.

Central Plains - On 22 May, traces of wheat stripe rust were found on the flag leaves of susceptible cultivars in plots at Manhattan, Kansas, but hot dry weather slowed further rust development. In early June, traces of stripe rust were found in a winter wheat nursery at Mead in east-central Nebraska and in winter wheat plots in northeast South Dakota. Stripe rust was very light in 2006 in the central and northern plains because inoculum from the southern plains was light and drought conditions persisted in much of the area.

Northern Plains - On 26 April, light amounts of stripe rust were reported on winter wheat in plots at St. Paul, Minnesota. This may have been an over-wintering site. In early May, stripe rust infections that had apparently over-wintered were observed on susceptible winter wheat cultivars in the Gallatin Valley in southwestern Montana. On 26 May, flag leaves of susceptible winter wheat in east-central Minnesota plots had 10% stripe rust severities.

By the third week in June, traces of stripe rust were found on a few winter wheat cultivars in east-central South Dakota and east-central Minnesota plots (Fig. 2). Hot weather slowed rust development in these plots. Many wheat fields were sprayed with fungicide to prevent losses due to rust and scab. By mid-July, hot dry weather had stopped most development of stripe rust on spring wheat in the northern Great Plains. Cool and wet weather the first half of June were favorable to stripe rust development in Montana winter wheat. In central and east-central Montana 15,000–20,000 acres of winter wheat were sprayed with fungicides. There were sporadic reports of stripe rust on spring wheat, but the severity was low. Dry and warm weather in early July slowed stripe rust development.

In mid-June, wheat stripe rust foci of 60–80% severity where observed in winter wheat nursery plots at Winnipeg, Manitoba, Canada. Infections were noted on lower leaves thus indicating that over wintering may have occurred. Very mild winter conditions with adequate snow cover occurred in 2005–06, and near normal spring temperatures were favorable for stripe rust infection.

Louisiana – In mid-February, stripe rust was increasing in wheat plots at Winnsboro in north-central Louisiana and by mid-March was severe throughout the plots. In mid-March, stripe rust was severe on a few susceptible cultivars in the nursery at Baton Rouge, LA. In late March, some fields were sprayed for rust control. In south-central Louisiana wheat

Fig. 3. Agroecological areas for *Puccinia tricina*.

Table 4. Estimated losses in winter wheat due to rust in 2006 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to Stem rust Percent	Stem rust 1,000 bushels	Leaf rust Percent	Leaf rust 1,000 bushels	Stripe rust Percent	Stripe rust 1,000 bushels
AL	45	58.0	2,610	0.0	0.0	1.0	26.4	T	T
AR	305	61.0	18,605	0.0	0.0	1.0	189.8	1.0	189.8
CA	250	58.0	14,500	0.0	0.0	1.0	172.6	15.0	2,529.1
CO	1,900	21.0	39,900	0.0	0.0	T	T	T	T
DE	45	67.0	3,015	0.0	0.0	T	T	0.0	0.0
FL	5	42.0	210	0.0	0.0	T	T	T	T
GA	120	49.0	5,880	0.0	0.0	T	T	T	T
ID	710	77.0	54,670	0.0	0.0	T	T	0.3	164.5
IL	910	67.0	60,970	0.0	0.0	T	T	T	T
IN	460	69.0	31,740	0.0	0.0	T	T	T	T
IA	18	66.0	1,188	0.0	0.0	T	T	0.0	0.0
KS	9,100	32.0	291,200	0.0	0.0	0.1	291.5	T	T
KY	320	71.0	22,720	0.0	0.0	1.0	229.5	T	T
LA	105	53.0	5,565	0.0	0.0	1.0	57.4	2.0	114.7
MD	125	68.0	8,500	0.0	0.0	T	T	T	T
MI	650	73.0	47,450	T	T	1.0	479.3	T	T
MN	45	62.0	2,790	0.0	0.0	1.0	28.2	T	T
MS	73	59.0	4,307	0.0	0.0	1.0	43.5	T	T
MO	910	54.0	49,140	0.0	0.0	1.0	496.4	T	T
MT	1,920	43.0	82,560	0.0	0.0	0.0	0.0	0.6	498.4
NE	1,700	36.0	61,200	0.0	0.0	0.1	61.3	0.0	0.0
NJ	22	60.0	1,320	0.0	0.0	0.0	0.0	0.0	0.0
NM	120	32.0	3,840	0.0	0.0	0.0	0.0	0.0	0.0
NY	95	61.0	5,795	0.0	0.0	1.0	58.5	0.0	0.0
NC	420	59.0	24,780	0.0	0.0	T	T	T	T
ND	180	44.0	7,920	0.0	0.0	2.0	161.6	0.0	0.0
OH	960	68.0	65,280	0.0	0.0	T	T	0.0	0.0
OK	3,400	24.0	81,600	0.0	0.0	T	T	0.0	0.0
OR	730	53.0	38,690	0.0	0.0	T	T	0.2	77.5
PA	150	59.0	8,850	0.0	0.0	T	T	0.0	0.0
SC	123	50.0	6,150	0.0	0.0	T	T	T	T
SD	1,150	36.0	41,400	0.0	0.0	1.0	418.2	T	T
TN	190	64.0	12,160	0.0	0.0	1.0	122.8	T	T
TX	1,400	24.0	33,600	T	T	T	T	T	T
UT	125	45.0	5,625	0.0	0.0	0.0	0.0	0.0	0.0
VA	155	68.0	10,540	0.0	0.0	T	T	T	T
WA	1,800	66.0	118,800	0.0	0.0	0.0	0.0	0.2	238.1
WV	6	61.0	366	0.0	0.0	T	T	0.0	0.0
WI	230	78.0	17,940	0.0	0.0	1.0	181.2	T	T
WY	135	27.0	3,645	0.0	0.0	T	T	0.0	0.0
Total	31,107	41.7	1,297,021		T		3,018.2		3,812.1
U.S.% Loss				T		0.23		0.29	
U.S. Total	31,117	41.7	1,298,081						

Table 5. Estimated losses in spring wheat due to rust in 2006 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to: Stem rust Percent	Stem rust 1,000 bushels	Leaf rust Percent	Leaf rust 1,000 bushels	Stripe rust Percent	Stripe rust 1,000 bushels
CO	19	85.0	1,615	0.0	0.0	0.0	0.0	0.0	0.0
ID	470	73.0	34,310	0.0	0.0	0.0	0.0	0.5	172.4
MN	1,650	47.0	77,550	0.0	0.0	1.0	783.3	0.0	0.0
MT	2,900	22.0	63,800	0.0	0.0	0.0	0.0	0.1	63.9
NV	2	88.0	176	0.0	0.0	0.0	0.0	0.0	0.0
ND	6,850	31.0	212,350	0.0	0.0	0.5	1,067.1	0.0	0.0
OR	115	50.0	5,750	0.0	0.0	0.0	0.0	0.5	28.9
SD	1,420	30.0	42,600	0.0	0.0	0.5	214.1	0.0	0.0
Utah	11	45.0	495	0.0	0.0	0.0	0.0	T	T
WA	425	50.0	21,250	0.0	0.0	0.0	0.0	0.5	106.8
WI	10	35.0	350	0.0	0.0	T	T	0.0	0.0
WY	6	39.0	234	0.0	0.0	0.0	0.0	0.0	0.0
Total from above									
	13,878	33.2	460,480		0.0		2,064.5		372.0
U.S. % loss				0.0		0.45		0.08	
U.S. total									
	13,878	33.2	460,480						

Estimated losses in durum wheat due to rust in 2006 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to: Stem rust Percent	Stem rust 1,000 bushels	Leaf rust Percent	Leaf rust 1,000 bushels	Stripe rust Percent	Stripe rust 1,000 bushels
AZ	74	100.0	7,400	0.0	0.0	0.0	0.0	0.0	0.0
CA	65	99.0	6,435	0.0	0.0	T	T	3.0	199.0
ID	15	89.0	1,335	0.0	0.0	0.0	0.0	0.0	0.0
MT	395	17.0	6,715	0.0	0.0	T	T	0.0	0.0
ND	1,260	25.0	31,500	0.0	0.0	T	T	0.0	0.0
SD	6	15.0	90	0.0	0.0	0.0	0.0	0.0	0.0
Total from above									
	1,815	29.5	53,475		0.0		T		199.0
U.S. % loss				0.00		T		0.37	
U.S. Total									
	1,815	29.5	53,475						

plots, susceptible cultivars had 60% stripe rust severities. Higher day and night temperatures during the last week of March slowed stripe rust development. In early April, high levels of stripe rust were observed in northeast Louisiana plots, but infections in fields were light.

Arkansas - In early February, wheat stripe rust was found throughout Arkansas. However, a mid-February cold snap slowed rust development in the state. By mid-March, only low levels of stripe rust in east-central Arkansas had been

found. In late March, stripe rust was at low levels in fields in southern Arkansas. By early April, stripe rust was increasing throughout Arkansas, but conditions did not favor development of high rust severities.

Southeast - In early April, stripe rust was found in southern Georgia. In late April, high severities of stripe rust were observed in late maturing susceptible cultivars in the nursery at Plains in southwestern Georgia. In the nursery, most of the stripe rust infections had occurred earlier in March and April when temperatures were cooler. By late April, leaf rust was the most prevalent rust on wheat at Plains. In mid-May, light levels of wheat stripe rust were found in Limestone county plots in north-central Alabama.

Midwest - In early May, plots in Urbana, IL, had low levels of stripe rust incidence and severity. The drier and warmer than normal weather in April and May slowed the increase and spread of stripe rust. In early June, traces of stripe rust were found in east-central Missouri fields. In early June, 40% wheat stripe rust severities were observed on flag leaves in plots in northwestern Indiana and trace severities were found in fields. The only report of stripe rust in 2006 in Ohio was in a wheat breeding line in northwestern Ohio. Stripe rust was found at a number of locations in Ohio in 2005.

North Carolina - Heavy stripe rust was reported in fields in the Albermarle/Pamlico Sounds region in east-central North Carolina in early May. Trace levels of wheat stripe rust were present throughout the Coastal Plain of North Carolina in 2006.

Virginia and Maryland – In mid-May, hotspots of stripe rust were found in wheat plots in the eastern shore of Virginia and Maryland.

California – In mid-March, low levels of stripe rust were found in plots in the southern San Joaquin Valley. In March, California had cool and very wet conditions, which were favorable for stripe rust development. In early April, the susceptible forage wheat cultivar Dirkwin had a stripe rust severity of 30% in the Imperial Valley. Infections also were noted in fields of Orita durum wheat in the Imperial Valley. Light infections of wheat stripe rust were reported in the southern portion of the San Joaquin Valley and more severe infections were reported from scattered areas further north in the San Joaquin Valley and throughout the Sacramento Valley. In some Sacramento Valley fields, 80% severities were recorded in hot spots. By late May, wheat stripe rust was severe throughout the Central Valley of California. The two most widely grown cultivars, Summit and Blanca Grande, are now both fully susceptible to the races of stripe rust that occur in California. Statewide, yield losses to wheat stripe rust were 15% in 2006 (Table 4, p. 138).

Pacific Northwest – By the second week in April, nursery plots at Mt. Vernon (northwestern Washington) had 40% stripe rust severity. Rust also was found in some surrounding fields. During the second week in April wheat stripe rust was not found from central to eastern Washington. By the third week in April, susceptible entries in winter wheat nurseries at Mount Vernon in northwestern Washington had 60% levels of stripe rust infection. In south-central and southeastern Washington, early planted winter wheat fields had 5% stripe rust severity. In this area, the initial stripe development was much later than 2005, but about normal for this area.

In late May, stripe rust was starting to increase on susceptible winter wheat entries in nurseries in the Palouse region of eastern Washington. Severities ranged from 1 to 10% with less than 1% of the plants infected. The stripe rust appeared one month later that 2005 in the Palouse region.

On May 22, stripe rust was found in a field in Franklin County, in southeastern Idaho, which is about 6 miles north of the Idaho-Utah border. Pustules were just beginning to show on the flag leaves.

By mid-June, stripe rust was widespread in eastern Pacific Northwest fields and plots. On 16 June, 30% severities were reported on susceptible winter wheat entries and 10% on susceptible spring wheat entries in disease monitoring nurseries at the Pendleton Experiment Station in Oregon. In nurseries near Walla Walla, WA, stripe rust severities reached 100% on susceptible entries in both winter wheat and spring wheat nurseries. Stripe rust was found in commercial spring wheat fields in the Palouse area, where 10% of the plants were infected with severities less than 5% on lower leaves. The wet and cool conditions the first three weeks in June were conducive for rust production.

By mid-July, stripe rust development had slowed in Pacific Northwest fields because of the hot dry weather. In early-July, 70-100% severities were reported on susceptible entries in plots where moisture was not limiting. Compared to 2005, wheat stripe rust was lighter in the Pacific Northwest (Table 4, p. 138).

Utah – In early June, light stripe rust was found on Garland wheat under irrigation in Logan, UT. Stripe rust was not found in the dry land area in northwestern Utah. This is typical, since rust is rarely seen in Utah. Last year (2005) was an anomaly with quite severe stripe rust in Logan which started much earlier in the growing season. Prior to last year, the previous year that had significant stripe rust (or any rust) was 1993 (which was similar in temperature and moisture to 2005).

NORTH DAKOTA

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Identification of a novel Fusarium head blight resistance QTL on chromosome 7A in tetraploid wheat.

Justin D. Faris, Sunil Kumar, and Timothy L. Friesen.

Fusarium head blight caused by *F. graminearum* is one of the most destructive diseases of durum and common wheat. Promising sources of FHB resistance have been identified among common (hexaploid) wheats, but the same is not true for durum (tetraploid) wheats. *Triticum turgidum* subsp. *dicoccoides*, or wild emmer wheat, is a potential tetraploid source of FHB resistance. A previous study indicated that chromosome 7A from *T. turgidum* subsp. *dicoccoides* accession PI478742 contributed significant levels of resistance to FHB. In this study, a genetic linkage map of chromosome 7A was constructed in a population of 118 recombinant inbred lines derived from a cross between the durum cultivar Langdon (LDN) and a disomic LDN–*T. turgidum* subsp. *dicoccoides* PI478742 chromosome 7A substitution line [LDN–DIC 7A(742)]. The population was evaluated for type-II FHB resistance in three greenhouse seasons. Interval regression analysis indicated that a single QTL designated *Qfhs.fcu-7AL* explained 19% of the phenotypic variation and spanned an interval of 39.6 cM. Comparisons between the genetic map and a previously constructed physical map of chromosome 7A indicated that *Qfhs.fcu-7AL* is located in the proximal region of the long arm. Combine *Qfhs.fcu-7AL* with the QTL *Qfhs.ndsu-3AS* in order to develop durum wheat germ plasm and cultivars with higher levels of FHB resistance would be beneficial.

The Stagonospora nodorum-wheat pathosystem is an inverse gene-for-gene system involving multiple, proteinaceous, host-selective toxins.

Timothy L. Friesen, Justin D. Faris, and Richard Oliver.

We have recently shown that *St. nodorum* produces multiple proteinaceous host selective toxins. These toxins include SnToxA, a host selective toxin first isolated from *P. tritici-repentis*, which has been implicated in a very recent horizontal gene transfer event from *St. nodorum* to *P. tritici-repentis*. Strong evidence has implicated SnToxA, as well as SnTox1, SnTox2, and SnTox3 as significant factors in SNB disease. Each toxin has been shown to interact either directly or indirectly with single dominant host sensitivity genes designated as *Tsn1* (SnToxA), *Snn1* (SnTox1), *Snn2* (SnTox2), and *Snn3* (SnTox3). Using mapping populations segregating for multiple toxin sensitivities, disease significance for each toxin sensitivity gene has been shown to account for as much as 60% of the disease caused by *St. nodorum* isolates producing each toxin. Other than SnToxA and SnTox1, 2, and 3, at least three additional host selective toxins and their host sensitivity genes have been identified and disease significance data is being collected. This work shows that the *S. nodorum* pathosystem is a model inverse-gene-for-gene system where at least seven proteinaceous host selective toxins produced by the pathogen interact directly or indirectly with dominant sensitivity/susceptibility genes in the host to cause disease.

Genomic analysis of the Snn1 locus on the short arm of chromosome 1B in wheat.

Leela Reddy, Timothy L. Friesen, Steven W. Meinhardt, Shiaoman Chao, and Justin D. Faris.

SnTox1 is a host-selective proteinaceous toxin produced by the wheat pathogen *St. nodorum*, and it is known to play a major role in causing disease. Sensitivity to SnTox1 is governed by a single dominant gene designated *Snn1*, which maps within a major gene rich region on the short arm of chromosome 1B. We conducted saturation mapping of the *Snn1* region using SSRs, RFLPs, and over 50 ESTs that map within deletion bin 1BSsat18-0.50-1.00. Flanking markers were used to initiate fine-mapping in a population of more than 8,000 gametes. The Langdon durum BAC library was used to construct a physical contig spanning about 500 kb at the *Snn1* locus. Comparisons between the physical and genetic distances indicate that recombination frequencies are highly variable within the region harboring *Snn1*. Sequencing and annotation of the BAC contig revealed that genes are not randomly distributed, but a number of the predicted genes are strong candidates for *Snn1*. The isolation of *Snn1* will allow us to begin the characterization of the interactions associated with the wheat–*St. nodorum* pathosystem.

Delineation of the wheat Tsn1 candidate-gene region.

Huangjun Lu, John P. Fellers, Steven W. Meinhardt, Timothy L. Friesen, and Justin D. Faris.

The wheat *Tsn1* gene confers sensitivity to the host-selective proteinaceous toxins Ptr ToxA and SnToxA produced by the pathogenic fungi *P. tritici-repentis* and *St. nodorum*, respectively. A positional cloning strategy is being used to clone this gene. An F_2 population consisting of 5,438 gametes was developed for high-resolution mapping. Multiple chromosome walking steps in conjunction with complete sequencing of BACs identified in the Langdon durum BAC library were performed. A total of 14 BACs were sequenced and assembled into two contigs that together spanned more than 1 Mb. Mapping results indicated that one contig spanned the *Tsn1* gene. The *Tsn1* candidate region is about 300 kb in size and contains nine putative genes. Four of the putative genes have been disproved to be *Tsn1* by comparative sequence analysis of Langdon EMS-induced *Tsn1*-disrupted mutants with the wild type. We are continuing the systematic testing of the remaining candidates to determine which candidate is *Tsn1*. The isolation of *Tsn1* will allow us to begin deciphering the molecular interactions and mechanisms associated with the wheat–*P. tritici-repentis* and wheat–*St. nodorum* pathosystems.

Molecular characterization of the AP2-like Q gene homoeoallele on chromosome 5D in hexaploid wheat.

Zengcui Zhang, Kristin J. Simons, and Justin D. Faris.

The *Q* gene of wheat is responsible for many morphological traits associated with domestication. *Q* is located on wheat chromosome 5A and it is a member of the AP2 class of transcription factors. Genotypes harboring the *q* allele on chromosome 5A have speltoid spikes, which include non free-threshing seed, tough glumes, and other primitive characteristics. Homoeoalleles of *Q* exist on chromosomes 5B and 5D, but their functions are unknown. Here, we initiated the structural and functional characterization of the 5D homoeoallele of the *Q* gene (5D*q*). Evaluation of deletion mutants indicated that 5D*q* also contributes to the suppression of speltoid characters, but to a lesser degree than does the *Q* allele on 5A. The genomic sequence of 5D*q* is 3,254 bp and is alternately spliced producing two transcriptional variants in spike tissue. One variant resulted from the splicing of ten exons that corresponded to the splicing structure of 5A*Q*/*q* alleles, and encodes a predicted protein of 452 amino acids. The other variant lacked the splicing of the first intron, which resulted in a frameshift that led to a stop codon within the first AP2 domain. Sequence alignments of 5A*Q* and 5D*q* indicated that they shared 90 and 94% identity at the nucleic acid and amino acid levels, respectively. RT–PCR experiments indicated that 5D*q* is expressed in immature spikes. Characterization of the *q* homoeoalleles will provide insights regarding polyploid gene regulation of genetic networks associated with domestication and morphology.

Molecular mapping of hybrid necrosis genes Ne1 and Ne2 in hexaploid wheat using microsatellite markers.

Chenggen Chu, Justin D. Faris, Timothy L. Friesen, Steven S. Xu.

Hybrid necrosis is the gradual premature death of leaves or plants in certain F_1 hybrids of wheat, and it is caused by the interaction of two dominant complementary genes *Ne1* and *Ne2* located on chromosome arms 5BL and 2BS, respectively. To date, molecular markers linked to these genes have not been identified and linkage relationships of the two genes with other important genes in wheat have not been established. We observed that the F_1 hybrids from the crosses between the bread wheat cultivar Alsen and four synthetic hexaploid wheat (SHW) lines (TA4152-19, TA4152-37, TA4152-44, and TA4152-60) developed at CIMMYT exhibited hybrid necrosis. This study was conducted to determine the genotypes of TA4152-60 and Alsen at the *Ne1* and *Ne2* loci and to map the genes using microsatellite markers in backcross populations. Genetic analysis indicated that Alsen has the genotype *ne1ne1Ne2Ne2*, whereas the SHW lines have *Ne1Ne1ne2ne2*. The microsatellite marker *Xbarc74* was linked to *Ne1* at a genetic distance of 2.0 cM on chromosome arm 5BL, and *Xbarc55* was 3.2 cM from *Ne2* on 2BS. Comparison of the genetic maps with the chromosome deletion-based physical maps indicated that *Ne1* lies in the proximal half of 5BL, whereas *Ne2* is in the distal half of 2BS. Genetic linkage analysis showed that *Ne1* was about 35 cM proximal to *Tsn1*, a locus conferring sensitivity to the host selective toxin Ptr ToxA produced by the tan spot fungus. The closely linked microsatellite markers identified in this study can be used to genotype parental lines for *Ne1* and *Ne2* or to eliminate the two hybrid necrosis genes using marker-assisted selection.

Molecular characterization of Langdon durum D-genome disomic substitution lines.

Jing Li, Daryl L. Klindworth, Xiwen Cai, Jinguo Hu, and Steven S. Xu.

The aneuploid stocks of durum wheat and common wheat have been developed mainly in the cultivars Langdon (LDN) and Chinese Spring (CS), respectively. The LDN–CS D-genome chromosome disomic substitution (LDN DS) lines, where a pair of CS D-genome chromosomes substitute for a corresponding homoeologous A- or B-genome chromosome pair of LDN, have been widely used for determining chromosomal locations of genes in tetraploid wheat. The LDN DS lines were originally developed by crossing CS nulli-tetrasomics to LDN followed by six backcrosses with LDN. They have subsequently been improved by five additional backcrosses with LDN. The objectives of this study were to characterize a set of the most recent 14 LDN DS lines and develop chromosome-specific markers using the newly developed TRAP (target region amplification polymorphism) marker technique. A total of 307 polymorphic DNA fragments were amplified from LDN and CS and 302 of them were assigned to individual chromosomes. Most of the markers (95.5%) were present on a single chromosome as chromosome-specific markers, but 4.5% of the markers mapped to two or more chromosomes. The number of markers per chromosome varied from a low of 10 (chromosomes 1A and 6D) to a high of 24 (chromosome 3A). There was an average of 16.6, 16.6, and 15.9 markers per chromosome assigned to the A-, B-, and D-genome chromosomes, respectively, suggesting that TRAP markers were detected at a nearly equal frequency on the three genomes. A comparison of the source of the ESTs used to derive the fixed primers with the chromosomal location of markers revealed that 15.5% of the TRAP markers were located on the same chromosomes as the ESTs used to generate the fixed primers. A fixed primer designed from an EST mapped on a chromosome or a homoeologous group amplified at least one fragment specific to that chromosome or group, suggesting that the fixed primers might generate markers from target regions. The TRAP marker analysis verified the retention of at least 13 pairs of A- or B-genome chromosomes from LDN and one pair of D-genome chromosomes from CS in each of the LDN DS lines. The chromosome-specific markers developed in this study provide an identity for each of the chromosomes and they will facilitate molecular and genetic characterization of the individual chromosomes, including genetic mapping and gene identification.

Chromosomal locations of genes for stem rust resistance in monogenic lines derived from tetraploid wheat accession ST464.

Daryl L. Klindworth, James D. Miller, Yue Jin, and Steven S. Xu.

The genetics of resistance to stem rust in durum wheat is not as well understood as for bread wheat. Our objective was to determine the chromosomal location of genes for stem rust resistance in four monogenic lines derived from the Ethiopian tetraploid landrace ST464. The four monogenic lines were crossed to a set of stem rust susceptible aneuploids based on the tetraploid line 47-1. We observed chromosome pairing in the hybrids and made testcrosses to Rusty durum. Monogenic lines ST464-A1 and ST464-A2 were observed to carry a 2A/4B translocation, and subsequent crosses proved that the translocation was derived from ST464. Testcross F_2 seedlings were inoculated with one of three stem rust pathotypes and classified for segregation for resistance to identify the critical chromosome for each monogenic line. The stem rust resistance genes in monogenic lines ST464-A1, ST464-A2, and ST464-C1 were located to chromosomes 6A, 2B, and 6A, respectively. The gene in ST464-B1 may be located to chromosome 4A, as it appeared it was not located on any of the other 13 chromosomes. The four ST464 monogenic lines and hexaploid lines carrying *Sr9e* and *Sr13* were then tested with eight stem rust pathotypes with the objective of postulating the genes present in the monogenic lines. The genes in ST464-A2 and ST464-C1 were postulated to be *Sr9e*, and *Sr13*, respectively.

Evaluation of genetic diversity and genome-wide linkage disequilibrium among US wheat germ plasm representing different market classes.

Shiaoman Chao, Wenjun Zhang, Jorge Dubcovsky, and Mark Sorrells.

Genetic diversity and genome-wide linkage disequilibrium (LD) were investigated among 43 U.S. wheat elite cultivars and breeding lines representing seven U.S. wheat market classes using 242 wheat genomic SSR markers distributed throughout the wheat genome. These lines were selected from 18 wheat breeding programs across the U.S. as part of a collaborative Wheat Coordinated Agricultural Project funded by USDA–CSREES (http://maswheat.ucdavis.edu/). Genetic diversity among these lines was examined using genetic distance-based and model-based clustering methods, and analysis of molecular variance. Four populations were identified from the model-based analysis, which partitioned each of the spring and winter populations into two subpopulations, corresponding largely to major geographic regions of wheat production in the US. This suggests that the genetic diversity existing among this U.S. wheat germ plasm was influenced more by regional adaptation than by market class, and the individuals clustered in the same model-based population shared related ancestral lines in their breeding history. For this germ plasm collection, genome-wide LD estimates were generally less than 1 cM for genetically linked loci pairs. This may result from the population stratification and small sample size that reduced statistical power. Most of the LD regions observed were between loci less than 10 cM apart. However, the distribution of LD was not uniform based on linkage distance and was independent of marker density. Consequently, LD is likely to vary widely among wheat populations and caution must be used in designing association studies in wheat.

Genetic stocks developed and maintained by the USDA-ARS Cereal Crops Research Unit, Fargo, ND.

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Summary of stocks maintained:

Langdon–*T. turgidum* subsp. *dicoccoides* substitution lines: 39
Langdon–*T. turgidum* subsp. *dicoccoides* homozygous recombinant mapping populations: 15
Langdon D–genome substitution lines: 14
Langdon–*Ae. tauschii* synthetics: 45
Durum T1AS-1AL·1DL translocation lines: 4
Triticale D-genome substitution lines: 10

Langdon durum–*T. turgidum* subpp. *dicoccoides* disomic substitution lines. Three sets of Langdon durum–*T. turgidum* subsp. *dicoccoides* (LDN-DIC) substitution lines were developed by Dr. Leonard R. Joppa using *T. turgidum* subsp. *dicoccoides* (DIC) accessions Israel-A, PI-481521 and PI-478742 as the chromosome donor in Langdon background (Table 1). In these lines, a pair of chromosomes from DIC was substituted for a pair of native homologous chromosomes in LDN. The LDN-DIC lines were produced by crossing each Langdon durum D-genome disomic substitution line (LDN D-genome DS) as female to each of three DIC accessions. Five to seven backcrosses were made to the LDN D-genome DS to restore the LDN genetic background, while retaining a single chromosome from DIC as a monosome. The LDN–DIC lines were selected after one generation of self-pollination of BC_5 to BC_7 plants. The sets based on PI-481521 and Israel-A have all 14 chromosome substitutions. But, three substitutions (2A, 3A, and 3B) in the set based on PI-478742 are not available.

Table 1. Abreviated chromosome designations for the 38 LDN-DIC disomic chromosome substitution lines.

	Israel-A	PI481521	PI478742
1A	LDN–DIC 1A(IsA)	LDN–DIC 1A(521)	LDN–DIC 1A(742)
2A	LDN–DIC 2A(IsA)	LDN–DIC 2A(521)	
3A	LDN–DIC 3A(IsA)	LDN–DIC 3A(521)	
4A	LDN–DIC 4A(IsA)	LDN–DIC 4A(521)	LDN–DIC 4A(742)
5A	LDN–DIC 5A(IsA)	LDN–DIC 5A(521)	LDN–DIC 5A(742)
6A	LDN–DIC 6A(IsA)	LDN–DIC 6A(521)	LDN–DIC 6A(742)
7A	LDN–DIC 7A(IsA)	LDN–DIC 7A(521)	LDN–DIC 7A(742)
1B	LDN–DIC 1B(IsA)	LDN–DIC 1B(521)	LDN–DIC 1B(742)
2B	LDN–DIC 2B(IsA)	LDN–DIC 2B(521)	LDN–DIC 2B(742)
3B	LDN–DIC 3B(IsA)	LDN–DIC 3B(521)	
4B	LDN–DIC 4B(IsA)	LDN–DIC 4B(521)	LDN–DIC 4B(742)
5B	LDN–DIC 5B(IsA)	LDN–DIC 5B(521)	LDN–DIC 5B(742)
6B	LDN–DIC 6B(IsA)	LDN–DIC 6B(521)	LDN–DIC 6B(742)
7B	LDN–DIC 7B(IsA)	LDN–DIC 7B(521)	LDN–DIC 7B(742)

LDN–DIC recombinant-inbred, chromosome-substitution lines (RICLs). Homozygous recombinant populations were developed by crossing each of the available LDN–DIC (Israel A accession) substitution lines with LDN as described in Joppa (1997; Crop Science 33:908-913). Maps have been generated for some of the populations (see Table 2). In addition, RIL populations have been developed for the LDN–DIC 5B (PI478742) and LDN–DIC 7A (PI478742) lines.

Table 2. Langdon–*T. turgidum* subsp. *dicoccoides* (LDN–DIC) recombinant-inbred, chromosome-line (RICL) populations.

Population	No. lines
LDN–DIC 1A(IsA) HR	92
LDN–DIC 1B(IsA) HR	93
LDN–DIC 2A(IsA) HR	107
LDN–DIC 3A(IsA) HR	83
LDN–DIC 3B(IsA) HR	91
LDN–DIC 4A(IsA) HR	136
LDN–DIC 4B(IsA) HR	117
LDN–DIC 5A(IsA) HR	95
LDN–DIC 5B(IsA) HR	136
LDN–DIC 6A(IsA) HR	89
LDN–DIC 6B(IsA) HR	85
LDN–DIC 7A(IsA) HR	166
LDN–DIC 7B(IsA) HR	148
LDN–DIC 5B(742) RI	125
LDN–DIC 7A(742) RI	125

Langdon D-genome substitution lines. The Langdon D-genome substitutions were developed by crossing the Chinese Spring nullisomic-tetrasomic series to Langdon durum wheat. The Chinese Spring aneuploids have four copies of a chromosome and have no copies of a homoeologous chromosome. Thus, CS N1A/T1D can be crossed to Langdon durum, a tetraploid that does not have the D-genome chromosomes. The F_1 from this cross has 14 pairs of chromosomes, including a pair of 1D chromosomes and also has seven univalent chromosomes including a monosome for 1A. Selfing and selecting will result in plants with 14 pairs of chromosomes and no monosomics. These plants will be disomic for 1D and nullisomic for 1A. All possible combinations of plants with the disomic D-genome chromosomes and nullisomic for the A- and B-genome homoeologues were obtained.

In order to eliminate the genes contributed to the A and B genomes by the CS parent, the plants were backcrossed to Langdon 12 times. We hope that almost all contribution to these lines from CS has been eliminated except for the contribution of the homozygous D-genome chromosomes.

In some cases, the D-genome chromosomes fail to completely compensate for the loss of the homoeologous A- or B-genome chromosomes. A description of these lines follows. If a line is not mentioned, it should be assumed that it is normal.

LDN-4D(4A). The plants nullisomic for chromosome 4A do not germinate and no plants of this constitution have ever been observed. The line is maintained as 13" + 1"$_{4D}$ + 1'$_{4A}$. Selfing these plants results in plants like the parent except for occasional plants with 15" (4D disomic additions). These plants should always be used as the female in crosses and the progeny will almost always be 13" + 2' (i.e., M4A, M4D).

LDN-5D(5A). Plants nullisomic for chromosome 5A have very low fertility. Consequently, this line is maintained as disomic for 5D and monosomic for 5A. The 14" + 1' plants produce progeny like the parent (i.e. 14" + 1'). There are occasional 15" plants. We usually discard these plants using root tip analysis of seedlings.

LDN-3D(3B). Sears reported that chromosome 3B contains a gene that is necessary to prevent asynapsis at MI of meiosis. The 3D(3B) line must have the short arm of 3B and we maintain the line as the disomic 3D, monosomic 3B. Transmission of the 3B chromosome is low. Thus, it is necessary to look at root tips to find plants with the 3B monosome. Plants that are disomic for both 3D and 3B are possible to obtain, but they are abnormal and very hard to maintain. We continue to search for better plants and for plants with a telosomic 3B chromosome.

LDN-5D(5B). The *Ph1* gene is on the long arm of chromosome 5B. When this gene is absent, pairing between non-homologous chromosomes is observed. Selfing plants nullisomic for chromosome 5B results in the line running out after a few generations; due to translocations, duplications, and deficiencies. The line is maintained as disomic for 5D and monosomic for 5B. Transmission of the monosomic 5B chromosome averages about 50 percent in selfed plants.

LDN-6D(6B). Plants nullisomic for 6B and disomic for 6D have very low fertility. Examination of the heads reveals that many of the anthers resemble pistils (i.e., plants are pistilloid). We maintain this line with a telosomic 6BS chromosome. Transmission of the 6BS telosome through the male gamete is close to 100 percent. Occasional plants disomic for 6BS are observed. Because of the male transmission of this telo, crosses should be made with the 6D(6B) line as the female. The telo is seldom transmitted through female gametes.

LDN-7D(7B). The group-7 chromosomes have genes governing chlorophyll production. Chromosome 7D does not completely compensate for either 7A or 7B, but the problem is greater in the case of 7B. The plants tend to be somewhat weak. At heading, the leaves develop a progressive necrosis that eventually leads to plant death, but this does not occur before the plants set seed. Pollen for crossing is sometimes difficult to obtain. Seed production is adequate for most purposes.

Langdon durum-*Ae. tauschii* synthetic hexaploid wheat. Dr. Joppa developed a number of spontaneous synthetic hexaploid wheat from partially fertile hybrids between LDN and different *Ae. tauschii* accessions in 1980s. We recently developed three new synthetic lines from the crosses between LDN and *Ae. tauschii* accessions PI 476874 (tough rachis), CIae19, and AL8/78. Some *Ae. tauschii* accessions were received from National Small Grains Collection (NSGC), Aberdeen, ID, others were provided respectively by Dr. E.R. Kerber (Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada), Dr. E. Nevo (University of Haifa, Haifa, Israel), and Dr. B. Keller (University of Zurich, Zurich, Switherland). Except that the synthetic line from cross LDN/PI 268210 was named as Largo and released as greenbug-resistant germplasm, other lines have not been characterized previously. These synthetics have recently been evaluated for resistance to tan spot, Stagonospora leaf blotch, leaf and stem rust, and Hessian fly. We currently are evaluating their resistance to FHB and seed storage protein compositions. The synthetics that are available for seed distribution are listed in Table 3 (p. 147).

Durum wheat T1AS·1AL-1DL translocation lines carrying *Glu-D1d*. Four translocation lines having the pedigree Langdon1D(1A)/Len//Langdon/3/2*Renville and carrying glutenin subunits 1Dx5 and 1Dy10 from the *Glu-D1d* allele are available. These lines were produced in an effort to develop dual-purpose (good baking and pasta quality) durum wheat. The lines are identified as L092, L252, S99B33, and S99B34. Three of the lines carry the LMWII banding pattern derived from Renville and conditioned by the *Glu-B3* gene. The fourth line, L252, carries the LMWI banding pattern derived from Langdon. Quality tests have indicated L252 has better mixing traits and slightly better loaf volume than the translocation lines carrying LMWII. In trials conducted in North Dakota from 2000-2002, S99B33 and S99B34 were the highest yielding of the translocation lines and similar in yield to Renville. These lines should be useful to breeders attempting to produce dual-purpose durum or for cereal chemists studying effects of *Glu-D1d* in a durum background.

Hexaploid triticale D-genome, disomic substitution lines. A partial set of 10 hexaploid triticale D-genome disomic substitution lines except for 2D(2A), 5D(5A), 3D(3B), and 5D(5B) were developed from crosses between Langdon

durum D-genome disomic substitution lines and 'Gazelle' rye (Table 3). The triticale substitution lines 4D(4A) and 6D(6B) were produced from colchicine treatment of F_1s and other eight lines were selected from partially fertile F_1s. Most of the triticale D-genome substitutions had reduced seed fertility except that 1D(1A), 1D(1B), and 7D(7B) substitutions had the same high level of fertility as the LDN triticale. Because these hexaploid triticale D-genome disomic substitutions have a uniform genetic background, they could be used to evaluate the effects of each of the D-genome chromosomes on economically important traits of hexaploid triticale, such as grain shriveling, seed quality, and productivity.

Table 3. Langdon durum–*Aegilops tauschii* synthetic hexaploid wheat lines (NSGC is the National Small Grains Collection).

Line No.	Pedigree	Source of *Ae. tauschii*
1	Langdon/*Ae. tauschii* CIae 1	NSGC, Aberdeen, Idaho
2	Langdon/*Ae. tauschii* CIae 5	NSGC, Aberdeen, Idaho
3	Langdon/*Ae. tauschii* CIae 9	NSGC, Aberdeen, Idaho
4	Langdon/*Ae. tauschii* CIae 11	NSGC, Aberdeen, Idaho
5	Langdon/*Ae. tauschii* CIae 14	NSGC, Aberdeen, Idaho
7	Langdon/*Ae. tauschii* CIae 22	NSGC, Aberdeen, Idaho
8	Langdon/*Ae. tauschii* CIae 25	NSGC, Aberdeen, Idaho
9	Langdon/*Ae. tauschii* CIae 26	NSGC, Aberdeen, Idaho
10	Langdon/*Ae. tauschii* H80-101-4	Haifa, Israel
11	Langdon/*Ae. tauschii* H80-114-1	Haifa, Israel
12	Langdon/*Ae. tauschii* H80-115-3	Haifa, Israel
13	Langdon/*Ae. tauschii* PI 220331	NSGC, Aberdeen, Idaho
14	Langdon/*Ae. tauschii* PI 220641	NSGC, Aberdeen, Idaho
15	Langdon/*Ae. tauschii* PI 317392	NSGC, Aberdeen, Idaho
16	Langdon/*Ae. tauschii* RL 5003	Winnipeg, Manitoba, Canada
17	Langdon/*Ae. tauschii* RL 5214	Winnipeg, Manitoba, Canada
19	Langdon/*Ae. tauschii* RL 5259	Winnipeg, Manitoba, Canada
20	Langdon/*Ae. tauschii* RL 5261	Winnipeg, Manitoba, Canada
21	Langdon/*Ae. tauschii* RL 5263	Winnipeg, Manitoba, Canada
22	Langdon/*Ae. tauschii* RL 5266-1	Winnipeg, Manitoba, Canada
23	Langdon/*Ae. tauschii* RL 5271	Winnipeg, Manitoba, Canada
24	Langdon/*Ae. tauschii* RL 5272	Winnipeg, Manitoba, Canada
25	Langdon/*Ae. tauschii* RL 5286	Winnipeg, Manitoba, Canada
26	Langdon/*Ae. tauschii* RL 5392	Winnipeg, Manitoba, Canada
27	Langdon/*Ae. tauschii* RL 5393	Winnipeg, Manitoba, Canada
28	Langdon/*Ae. tauschii* RL 5492	Winnipeg, Manitoba, Canada
29	Langdon/*Ae. tauschii* RL 5498	Winnipeg, Manitoba, Canada
30	Langdon/*Ae. tauschii* RL 5527	Winnipeg, Manitoba, Canada
32	Langdon/*Ae. tauschii* RL 5532	Winnipeg, Manitoba, Canada
34	Langdon/*Ae. tauschii* RL 5544	Winnipeg, Manitoba, Canada
35	Langdon/*Ae. tauschii* RL 5552	Winnipeg, Manitoba, Canada
36	Langdon/*Ae. tauschii* RL 5555	Winnipeg, Manitoba, Canada
37	Langdon/*Ae. tauschii* RL 5557	Winnipeg, Manitoba, Canada
38	Langdon/*Ae. tauschii* RL 5560	Winnipeg, Manitoba, Canada
39	Langdon/*Ae. tauschii* RL 5561	Winnipeg, Manitoba, Canada
40	Langdon/*Ae. tauschii* RL 5562	Winnipeg, Manitoba, Canada
41	Langdon/*Ae. tauschii* RL 5570	Winnipeg, Manitoba, Canada
44	Langdon/*Ae. tauschii* PI 476874	NSGC, Aberdeen, Idaho
52	Langdon/*Ae. tauschii* CIae 17	NSGC, Aberdeen, Idaho
53	Langdon/*Ae. tauschii* PI 268210	NSGC, Aberdeen, Idaho
55	Langdon/*Ae. tauschii* RL 5257	Winnipeg, Manitoba, Canada
56	Langdon/*Ae. tauschii* RL 5258	Winnipeg, Manitoba, Canada
57	Langdon/*Ae. tauschii* RL 5270	Winnipeg, Manitoba, Canada
58	Langdon/*Ae. tauschii* AL8/78	Zurich, Switzerland
59	Langdon/*Ae. tauschii* CIae 19	NSGC, Aberdeen, Idaho

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OKLAHOMA

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Wheat extension and wheat management research.

Jeff T. Edwards.

Drought was a major hindrance to Oklahoma wheat research and production in 2006. Our research efforts are frequently hampered by drought but to have a large portion of our wheat plots emerge and then die due to moisture limitations was a new experience and was hopefully a one-time event.

A major thrust of our research and extension efforts centered on sensor-based nitrogen recommendations (see www.nue.okstate.edu for more information). We were successful in creating over 600 nitrogen-rich strips in farmer's fields in the autumn of 2006. These strips will be sensed by county educators in the spring of 2007 and nitrogen recommendations will be given to producers. We will record grower adoption of sensor recommendations and use these data to retool extension efforts where appropriate.

Our work evaluating early-season radiation use efficiency (RUE) and canopy closure of wheat cultivars continued in 2006. We found that RUE of our most popular wheat cultivars ranged from 2.0 to 2.8 g/MJ. Our data also revealed a 150 Cd difference in thermal time until canopy closure among wheat cultivars, which resulted in a 114 g/m^2 difference in wheat forage production by 1 November. We will continue this research in 2007 and 2008 to further evaluate how early-season wheat physiology affects wheat forage production.

Finally, we established no-till versus conventional till wheat cultivar comparisons in the autumn of 2006. This research will evaluate the effect of no-till systems on wheat forage and grain yield of approximately 20 wheat cultivars and investigate insect predator/prey relationships in no-till systems. Although commonplace in many areas, no-till wheat production is still a relatively new practice in the southern Great Plains, so research and demonstration efforts are needed by producers.

Cultivar development and breeding research.

Brett F. Carver.

The Oklahoma Wheat Improvement Team, the Oklahoma Agricultural Experiment Station, and the USDA–ARS announced the release of **Duster** and **Centerfield** HRWW cultivars in late 2006.

Centerfield has the pedigree 'TXGH12588-105*4 / FS4 // 2*2174'. The germ plasm indicated by FS4 originated with BASF Corporation (formerly American Cyanmid) and provides tolerance to imazamox herbicide. Centerfield is moderately resistant to WSSMV and WSBMV and should exhibit insignificant losses to these viral diseases. Though susceptible in the seedling stage, Centerfield shows moderate to high adult-plant resistance to wheat leaf rust caused by races of *P. triticina* present in Oklahoma and Texas from 2004 to 2006. Centerfield appears to be at least moderately resistant to *P. striiformis* f. sp. *tritici* in the field. Seedling tests in the greenhouse indicate a susceptible reaction to tan spot and to *S. tritici* leaf blotch and a moderately susceptible reaction to powdery mildew. Centerfield shows a heterogeneous reaction (46 % resistant : 54 % susceptible) to biotype-E greenbug. Field ratings in Oklahoma indicate a tolerant reaction to Hessian fly, similar to those of Chisholm, 2174, and Ok102, although its seedling reaction in the greenhouse is heterogeneous. Early seeding of Centerfield is not recommended because of its heat-sensitive germination response. Milling and baking characteristics are an improvement over those of Okfield and AP502CL, current imazamox-tolerant cultivars grown in Oklahoma, with above-average kernel size and grain-volume weight, good dough strength, and moderately high wheat protein content of (13.0 %, 12 % m.b.).

Wheat producers in the southern Plains who are shifting to conservation-tillage practices while planting early for forage production in a graze-plus-grain (dual-purpose) management system are increasingly challenged by Hessian fly infestations. The majority of cultvars grown in this area possess no Hessian fly-resistance genes. A driving force in the release of **Duster** was its resistance to the Great Plains biotype of Hessian fly. As a high-tillering cultivar, it also exhibits excellent biomass accumulation prior to autumn grazing and canopy regeneration during grazing, and exceptional recovery from grazing. These are characteristics we continue to emphasize in our *GRAZE*n*GRAIN* breeding system. Hence, it is positioned for all areas inclusive of and immediately adjacent to Oklahoma, particularly those featuring a dual-purpose management system. Duster originated from the cross 'W0405 / NE78488 // W7469C / TX81V6187', which was produced in the HRWW-breeding program of Pioneer Hi-Bred International, Inc. Duster is resistant to WSSMV and to WSBMV. Although susceptible to leaf rust in the seedling stage, Duster exhibited a resistant adult-plant reaction in the field in Oklahoma and Texas during the three crop seasons of 2004–06. Reaction to stripe rust has varied from intermediate to moderately susceptible in the Great Plains. Thus, reaction to stripe rust may be highly dependent on the environment and/or races of the pathogen present. Based on combined greenhouse and field observations, Duster is moderately susceptible to tan spot but shows an intermediate reaction to Septoria leaf blotch and an intermediate to moderately resistant reaction to powdery mildew. Aside from kernel size being intermediate (kernel diameter of 2.2 mm), Duster shows excellent mixing tolerance at a intermediate protein level (wheat protein, 12.4 %, 12 % m.b.), and it exhibits a unique but desirable farinograph pattern of short peak time (<5 min) and long stability time (>15 min). Duster contains alleles which encode HMW-glutenin subunits 2* at the *Glu-A1* locus, 7+8 at *Glu-B1*, and 5+10 at *Glu-D1*.

Two experimental HWWW lines are under breeder-seed production in the 2006–07 crop season, **OK00514W** and **OK00611W**. The former is a reselection of OK Bullet (HRWW cultivar) with agronomic and quality characteristics

almost identical to OK Bullet. OK00611W was a sister selection to OK Bullet and features a moderately high level of preharvest sprouting tolerance and postharvest seed dormancy that is accentuated by high soil temperature. With their foliar disease resistance and ability to tolerate acid soils, both lines may be positioned for the Central Plains, offering a HWWW alternative in an area dominated heavily by HRWW cultivars. A release decision for one of these will be made in June 2007. Currently, we allocate 80 % of our resources in the latter stages of selection to HRWW line development, although 50 % of the crosses made each year involve HWWW parentage to varying degrees. About 20 % of the crosses made each year involve strictly HWWW parentage.

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 coöperation with Dr. Liuling Yan (Oklahoma State University molecular geneticist). Target traits currently under watch are Hessian fly resistance, acid-soil tolerance, pre-harvest sprouting tolerance, resistance to leaf rust, WSMV, and BYDV.

Personnel.

The Wheat Improvement Team at OSU currently has ten members: Brett Carver (team leader), Liuling Yan (molecular genetics), Bob Hunger (pathology), David Porter (USDA–ARS; aphid 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 (physiology). Dr. Yan is our newest addition to the team, having recently moved from a postdoctoral position in wheat molecular genetics at the University of California–Davis. His research will focus on identification and cloning of genes responsible for agronomically and economically important traits in wheat and other cereal crops. Projects already in progress include genetic analysis of variation in vernalization requirement and duration among winter wheat cultivars and establishment of a genome-scale gene network for flowering time in wheat and barley. Molecular markers will be developed to assist breeding programs to select gene combinations that maximize plant adaptation to different environments.

USDA–ARS–SPA WHEAT, PEANUT AND OTHER FIELD CROPS RESEARCH UNIT
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Cheryl A. Baker, John D. Burd, Norman C. Elliott, Yinghua Huang, Dolores W. Mornhinweg, David R. Porter, Gary J. Puterka, and Kevin A. Shufran.

Predicting the impact of predators and parasities.

In conjunction with collaborators from Oklahoma State University, we continued research to develop a predictive model for the predatory impact of Coccinellidae on the greenbug. During the previous year, we conducted field and laboratory studies to quantify the spatially explicit population dynamics of the greenbug in relation to parasitism by *L. testaceipes* and predation by Coccinellidae and other predators and initiated development of a preliminary spatially explicit simulation model. The research has potential to improve pest management practices for the greenbug in wheat. If successful, treatment decisions will be more accurate and based on improved knowledge of the potential for biological control.

Remote sensing of cereal aphids.

In conjunction with collaborators from the Texas Agricultural Experiment Station and SST Development Group Inc., we are developing remote sensing technology to detect and monitor greenbug infestations in winter wheat. During the previous year we documented that multi-spectral remote sensing differentiated stressed areas in production winter wheat fields caused by greenbug infestation from non-stressed areas. Remote sensing technology has the potential to markedly

improve pest management practices for the greenbug in winter wheat because infestations in fields will be efficiently detected and delineated at an early stage, which could result in more economically and environmentally sound management.

Distribution of RWA biotypes.

Approximately 370 RWA clones we collected from 70 sites in Texas, Oklahoma, New Mexico, Colorado, Nebraska, and Wyoming in 2005. The collections were made primarily from wheat with the exception of a few from wild grasses and a majority collected from barley in northern Wyoming. The clones were evaluated on *Dn4* and *Dn7* resistance in wheat in replicated trials. A subsample of 30% of the collections were evaluated on *Dn1–Dn9* RWA resistance in wheat and STARS 9301B and 9577B RWA resistance in barley for a complete biotype determination. Colorado, Texas, Oklahoma, Kansas and Nebraska had equal proportions of RWA clones virulent and avirulent to *Dn4*. New Mexico had 76% of the samples avirulent to *Dn4* (RWA1) while Wyoming had 70% of the samples virulent to *Dn4*. No clones were found to be virulent to *Dn7* or the two sources of RWA resistance in barley. The subsamples tested were found to be either RWA1 or RWA2, based on chlorosis ratings. Therefore, our survey indicates the RWA2 is now present in significant levels in the wheat and barley growing regions RWA infests.

Genetic variation of Russian wheat aphid biotypes and populations in the U.S.

Diuraphis noxia biotypes RWA1 and RWA2 (10 clones each) were subjected to RAPD and COI mtDNA sequence analysis. No variation was found within or between biotypes. Zero nucleotide variation in the COI was found in an additional 40+ field collected individuals of unknown biotype (collected from 2003 to 2005 in TX, CO, NM, KS, NE, OK, and WY). COI sequences from the USA were identical to those from Canada, Ethiopia, Turkey, Syria, and the Czech Republic as reported in GenBank by Belay and Stauffer (AY241697–AY241705). Microsatellite analysis revealed US populations were made up of multiple clones. Clonal variation was found within and between RWA1 and RWA2, however no biotype specific loci or alleles were found. Microsatellite markers are being used to study gene flow in US populations.

Greenbug ecology and biotypic diversity.

Biotypic diversity of the greenbug, was assessed among populations collected from cultivated wheat and sorghum, and their associated noncultivated grass hosts. Greenbugs were collected during May through August from 30 counties of Kansas, Nebraska, Oklahoma, and Texas. Discounting the presumptive biotype A, five of the remaining nine letter-designated greenbug biotypes were collected; however biotypes C, F, J, and K were not detected. Biotypes E and I exhibited the greatest host range and were the only biotypes collected in all four states. Sixteen greenbug clones, collected from eight plant species, exhibited unique biotype profiles. Eleven were collected from noncultivated grasses, three from wheat, and two from sorghum. The most virulent biotypes were collected from noncultivated hosts. The great degree of biotypic diversity among noncultivated grasses supports the contention that the greenbug species complex is composed of host-adapted races that diverged on grass species independent of, and well before the advent of modern agriculture.

Greenbug was first discovered damaging seashore paspalum (*Paspalum vaginatum*) turfgrass in November 2003 at Belle Glade, Florida. Several golf courses with seashore pasplaum in central and southern Florida were subsequently infested by April 2004. Damage symptoms progress from water soaked lesions surrounding feeding sites within 24 hours to chlorosis and necrosis of leaves within 96 hours. Problems caused by greenbug feeding were initially misdiagnosed as fertilizer, disease or water management problems because aphids previously were not found on warm season turfgrasses in Florida. The Florida greenbug isolate exhibited a unique biotypic profile, which was most similar to the profiles of biotypes F, G, and H. These biotypes are typically not abundant on cultivated crops, but are commonly found on Kentucky bluegrass lawns and/or noncultivated grass hosts. Moreover, the Florida isolate was virulent to all currently available resistant sorghums and GRS1201, which is resistant to the principal agricultural biotypes that attack small grains.

Russian wheat aphid resistant wheat.

At the 2005 WERA-066 meeting, it was determined that there was a pressing need for specific guidelines to be set and followed when screening for resistance to Russian wheat aphid. These guidelines were published in the 2005 WERA-066 Annual Meeting Minutes, which are available at the following link:
http://www.oznet.ksu.edu/entomology/wera-066/WERA-066report.pdf.

Included in the guidelines were recommendations for establishing set plant differentials for use as screening tools, thereby eliminating one of the obvious sources of variability in our screening techniques. In order to standardize the seed source, we determined that these plant differentials would be available to RWA researchers via Stillwater USDA-ARS, as soon as sufficient seed is available. We hope that enough seed will be available for small screening tests, and if larger amounts of seed are required for an individual program, then starter seed can be obtained from Stillwater, and seed can then be increased as needed at the various locations. In order to establish this uniform set of differentials, the suggested differential lines were screened for homogeneity for RWA1 resistance, and plants were then grown and harvested with an eye for uniform maturity, height, and other observable characteristics. Off-types were discarded. Progeny screening will be done prior to further increases.

In addition, it was determined that Stillwater ARS would be the official source for the RWA1 biotype and Colorado State University would be the official source for RWA2. When research is to be done with either of these biotypes, it would be advantageous to know that we are all working with the same aphids and not relying on new field collections of aphids. For example, if a new RWA collection is virulent on *Dn4* wheat, it must be noted that it does not logically follow that the new aphid is RWA2- it merely confirms that it is not RWA1. Other additional biotypes have been collected that are also virulent on *Dn4*, so the use of a small number of differentials may not successfully distinguish between biotypes.

We have continued with the development of our breeding lines that are resistant to RWA1. Even though they may not be useful as germ plasm or cultivar releases in the near future with the current prevalence of RWA2, different sources of RWA1 resistance that are due to different genes may provide additional differentials for screening against new RWA biotypes that may develop.

In addition, screening current breeding lines for resistance to RWA2 also is underway, as space and conditions allow. Several of our winter breeding lines containing *Dn7* appear to be resistant to all of the RWA biotypes against which they have been tested. A germplasm release is planned for this autumn.

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IV. CULTIVARS AND GERM PLASM

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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 (March 2007).

Character	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
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

Table 1 (continued). Wheat descriptors with data currently in GRIN (Febraury 2007).

Character	Years	Location	Accessions
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	2003–06	Ft. Collins, CO	12,322
Cereal Leaf Beetle	1963–70	Indiana, Michigan	16,347
AGRONOMIC, TAXONOMIC, AND QUALITY DESCRIPTORS.			
Growth Habit	1987–06	Aberdeen, ID	54,552
Lysine Content	1966–69	Lincoln, NE	10,367
Awn Color	1983–97	Aberdeen, ID & Maricopa, AZ	22,650
Awn Type	1983–97	Aberdeen, ID & Maricopa, AZ	26,561
Glume Color	1983–97	Aberdeen, ID & Maricopa, AZ	22,812
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, 2005–06	Aberdeen, ID & Maricopa, AZ	27,039
Kernels/Spike	1983–94	Aberdeen, ID & Maricopa, AZ	3,666
Kernel Weight	1983–94, 2005–06	Aberdeen, ID & Maricopa, AZ	12,712
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	Aberdeen, ID & Maricopa, AZ	15,823
Spikelets/Spike	1995	Maricopa, AZ	2,502
Spike Type	1983–97	Aberdeen, ID & Maricopa, AZ	15,551
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

The authors wish to acknowledge the important contributions of the NSGGRF staff in this effort, with special thanks to Glenda B. Rutger, Scott McNeil, Carol Mortenson, Kay Calzada, and Kim Wilson.

PI Assignments in Triticum, Secale, and X Triticosecale, January 2006 – March 2007.

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. *Crop Science*-registered accessions are available by contacting the developers.

Table 2. PI assignments in *Triticum, Secale,* and *X Triticosecale* from January 2006–March 2007.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
641952	*Triticum aestivum* subsp. *aestivum*	Allegiance	United States	Kentucky
641961	*Triticum aestivum* subsp. *aestivum*	Elissavet	Greece	
642003	*X Triticosecale* sp.	342	United States	Florida
642020	*Triticum turgidum* subsp. *durum*	Alkabo	United States	North Dakota
642021	*Triticum turgidum* subsp. *durum*	Divide	United States	North Dakota
642022	*Triticum turgidum* subsp. *durum*	Grenora	United States	North Dakota
642171	*Triticum aestivum* subsp. *aestivum*	Trooper	United States	North Dakota
642315	*Triticum aestivum* subsp. *aestivum*	Ledger	United States	Montana
642361	*Triticum aestivum* subsp. *aestivum*	UI Cataldo	United States	Idaho
642362	*Triticum aestivum* subsp. *aestivum*	UI Winchester	United States	Idaho
642363	*Triticum aestivum* subsp. *aestivum*	UI Pettit	United States	Idaho
642364	*Triticum aestivum* subsp. *aestivum*	IDO630	United States	Idaho
642365	*Triticum aestivum* subsp. *aestivum*	IDO629	United States	Idaho
642366	*Triticum aestivum* subsp. *aestivum*	Vida	United States	Montana
642367	*Triticum aestivum* subsp. *aestivum*	Howard	United States	North Dakota
642373	*Triticum aestivum* subsp. *aestivum*	Grande Doro	United States	North Dakota
642376	*Triticum aestivum* subsp. *aestivum*	Snow Crest	United States	Montana
642378	*Triticum aestivum* subsp. *aestivum*	UI Alta Blanca	United States	Idaho
642379	*Triticum aestivum* subsp. *aestivum*	IDO672	United States	Idaho
642380	*Triticum aestivum* subsp. *aestivum*	IDO673	United States	Idaho
642381	*Triticum aestivum* subsp. *aestivum*	IDO674	United States	Idaho
642382	*Triticum aestivum* subsp. *aestivum*	IDO675	United States	Idaho
642383	*Triticum aestivum* subsp. *aestivum*	IDO676	United States	Idaho
642384	*Triticum aestivum* subsp. *aestivum*	IDO677	United States	Idaho
642385	*Triticum aestivum* subsp. *aestivum*	IDO678	United States	Idaho
642386	*Triticum aestivum* subsp. *aestivum*	IDO679	United States	Idaho
642405	*Triticum aestivum* subsp. *aestivum*	N97L9534	United States	Nebraska
642406	*Triticum aestivum* subsp. *aestivum*	N97L9522	United States	Nebraska
642407	*Triticum aestivum* subsp. *aestivum*	N97L9531	United States	Nebraska
642408	*Triticum aestivum* subsp. *aestivum*	NO2Y5078	United States	Nebraska
642409	*Triticum aestivum* subsp. *aestivum*	NO2Y5106	United States	Nebraska
642410	*Triticum aestivum* subsp. *aestivum*	NW97S2181t	United States	Nebraska
642411	*Triticum aestivum* subsp. *aestivum*	NW97S139-1	United States	Nebraska
642415	*Triticum aestivum* subsp. *aestivum*	OK Bullet	United States	Oklahoma
642416	*Triticum aestivum* subsp. *aestivum*	NC06BGTAG12	United States	North Carolina
642417	*Triticum aestivum* subsp. *aestivum*	NC06BGTAG13	United States	North Carolina
642780	*Triticum aestivum* subsp. *aestivum*	Traverse	United States	South Dakota
642781	*Triticum aestivum* subsp. *aestivum*	ND 751	United States	North Dakota
642794	*Triticum aestivum* subsp. *aestivum*	Bess	United States	Missouri
642799	*Triticum aestivum* subsp. *aestivum*	Bakker Gold	Germany	
642800	*Triticum aestivum* subsp. *aestivum*	Fireball	Germany	
642856	*Triticum aestivum* subsp. *aestivum*	Ada	United States	Minnesota
642936	*Triticum aestivum*	Armor 3015	United States	Virginia

Table 2 (continued). PI assignments in *Triticum, Secale,* and *X Triticosecale* from January 2006–March 2007.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
642937	*Triticum aestivum*	Dominion	United States	Virginia
642938	*Triticum aestivum*	XW04C	United States	Indiana
642939	*Triticum aestivum*	XW04A	United States	Indiana
642952	*Triticum aestivum* subsp. *aestivum*	CJ 8809	United States	Michigan
642965	*Triticum aestivum* subsp. *aestivum*	NW03Y2016	United States	Nebraska
642966	*Triticum aestivum* subsp. *aestivum*	NW03Y2022	United States	Nebraska
642967	*Triticum aestivum* subsp. *aestivum*	NW03Y2023	United States	Nebraska
643087	*Triticum aestivum* subsp. *aestivum*	OKField	United States	Oklahoma
643089	*Triticum aestivum* subsp. *aestivum*	NuDakota	United States	Kansas
643090	*Triticum aestivum* subsp. *aestivum*	NuGrain	United States	Kansas
643091	*Triticum aestivum* subsp. *aestivum*	Kelby	United States	Kansas
643092	*Triticum aestivum* subsp. *aestivum*	Coker 9553	United States	Kansas
643093	*Triticum aestivum* subsp. *aestivum*	Postrock	United States	Kansas
643094	*Triticum aestivum* subsp. *aestivum*	AgriPro Paladin	United States	Kansas
643095	*Triticum aestivum* subsp. *aestivum*	9511	United States	Kansas
643133	*Triticum aestivum* subsp. *aestivum*	Guymon	United States	Oklahoma
643139	*Triticum aestivum* subsp. *aestivum*	Foragemax	United States	Kansas
643142	*Triticum aestivum* subsp. *aestivum*	WB-528	United States	Montana
643143	*Triticum aestivum* subsp. *aestivum*	TAM 112	United States	Texas
643399	*Triticum aestivum* subsp. *aestivum*	Stars 0601W	United States	Oklahoma
643400	*Triticum aestivum* subsp. *aestivum*	MAS 21-3	United States	Montana
643401	*Triticum aestivum* subsp. *aestivum*	MAS 21-10	United States	Montana
643402	*Triticum aestivum* subsp. *aestivum*	MAS 22-5	United States	Montana
643403	*Triticum aestivum* subsp. *aestivum*	MAS 22-16	United States	Montana
643404	*Triticum aestivum* subsp. *aestivum*	MAS 3G-BB	United States	Montana
643405	*Triticum aestivum* subsp. *aestivum*	MAS 3G-AA	United States	Montana
643406	*Triticum aestivum* subsp. *aestivum*	MAS 3B-BB	United States	Montana
643407	*Triticum aestivum* subsp. *aestivum*	MAS 3B-AA	United States	Montana
643408	*Triticum aestivum* subsp. *aestivum*	MAS 71-3	United States	Montana
643409	*Triticum aestivum* subsp. *aestivum*	MAS 71-1	United States	Montana
643410	*Triticum aestivum* subsp. *aestivum*	MAS 70-3	United States	Montana
643411	*Triticum aestivum* subsp. *aestivum*	MAS 70-15	United States	Montana
643412	*Triticum aestivum* subsp. *aestivum*	MAS 46-8	United States	Montana
643413	*Triticum aestivum* subsp. *aestivum*	MAS 46-10	United States	Montana
643414	*Triticum aestivum* subsp. *aestivum*	MAS 47-1	United States	Montana
643415	*Triticum aestivum* subsp. *aestivum*	MAS 47-5	United States	Montana
643416	*Triticum aestivum* subsp. *aestivum*	MAS 141-5	United States	Montana
643417	*Triticum aestivum* subsp. *aestivum*	MAS 141-4	United States	Montana
643418	*Triticum aestivum* subsp. *aestivum*	MAS 142-8	United States	Montana
643419	*Triticum aestivum* subsp. *aestivum*	MAS 142-7	United States	Montana
643423	*Triticum aestivum* subsp. *aestivum*	Eddy	United States	Montana
643425	*Triticum aestivum* subsp. *aestivum*	DPC05	United States	Missouri
643426	*Triticum aestivum* subsp. *aestivum*	Rush	United States	Montana
643427	*Triticum aestivum* subsp. *aestivum*	176	United States	Virginia
643428	*Triticum aestivum* subsp. *aestivum*	Yellowstone	United States	Montana
643429	*Triticum aestivum* subsp. *aestivum*	Bynum	United States	Montana
643430	*Triticum aestivum* subsp. *aestivum*	Norris	United States	Montana
643433	*Secale cereale*	Maton II	United States	Oklahoma
643435	*Triticum aestivum* subsp. *compactum*	Cara	United States	Washington
643454	*X Triticosecale* sp.	TS1	Spain	
643455	*X Triticosecale* sp.	TS10	Spain	

Table 2 (continued). PI assignments in *Triticum, Secale,* and *X Triticosecale* from January 2006–March 2007.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
643456	*X Triticosecale* sp.	TS41	Spain	
643935	*Triticum aestivum* subsp. *aestivum*	Chesapeake	United States	Maryland
643974	*X Triticosecale* sp.	Bunker	Canada	Alberta
643975	*X Triticosecale* sp.	Tyndal	Canada	Alberta
643978	*Triticum aestivum* subsp. *aestivum*	Hyalite	United States	Montana
643981	*Triticum aestivum* subsp. *aestivum*	Patwin	United States	California
643982	*Triticum aestivum* subsp. *aestivum*	Platte 2	United States	Kansas
643987	*X Triticosecale* sp.	98	United States	California
643988	*X Triticosecale* sp.	116	United States	California
644016	*Triticum aestivum*	Duster	United States	Oklahoma
644017	*Triticum aestivum*	Centerfield	United States	Oklahoma
644020	*Triticum aestivum* subsp. *aestivum*	951079-2E31	United States	Georgia
644021	*Triticum aestivum* subsp. *aestivum*	Concept	United States	Washington
644065	*Triticum turgidum* subsp. *durum*	Havasu	United States	Arizona
644066	*Triticum aestivum* subsp. *aestivum*	Joaquin	United States	Arizona
644067	*Triticum aestivum* subsp. *aestivum*	Solano	United States	Arizona
644068	*Triticum aestivum* subsp. *aestivum*	Dash 12	United States	Arizona
644072	*Triticum aestivum* subsp. *aestivum*	USG 3342	United States	Virginia
644080	*Triticum aestivum* subsp. *aestivum*	*Pina-D1b*/*Pinb-D1a*	United States	Washington
644081	*Triticum aestivum* subsp. *aestivum*	*Pina-D1a*/*Pinb-D1b*	United States	Washington
644082	*Triticum aestivum* subsp. *aestivum*	*Pina-D1a*/*Pinb-D1c*	United States	Washington
644083	*Triticum aestivum* subsp. *aestivum*	*Pina-D1a*/*Pinb-D1d*	United States	Washington
644084	*Triticum aestivum* subsp. *aestivum*	*Pina-D1a*/*Pinb-D1e*	United States	Washington
644085	*Triticum aestivum* subsp. *aestivum*	*Pina-D1a*/*Pinb-D1f*	United States	Washington
644086	*Triticum aestivum* subsp. *aestivum*	*Pina-D1a*/*Pinb-D1g*	United States	Washington
644113	*Triticum aestivum* subsp. *aestivum*	CITR2492-sel-fhb	United States	Minnesota
644114	*Triticum aestivum* subsp. *aestivum*	CITR11215-sel-fhb	United States	Minnesota
644115	*Triticum aestivum* subsp. *aestivum*	CITR12021-sel-fhb	United States	Minnesota
644116	*Triticum aestivum* subsp. *aestivum*	CITR12470-sel-fhb	United States	Minnesota
644117	*Triticum aestivum* subsp. *aestivum*	PI57364-sel-fhb	United States	Minnesota
644118	*Triticum aestivum* subsp. *aestivum*	PI132856-sel-fhb	United States	Minnesota
644119	*Triticum aestivum* subsp. *aestivum*	PI163429-sel-fhb	United States	Minnesota
644120	*Triticum aestivum* subsp. *aestivum*	PI163439-sel-fhb	United States	Minnesota
644121	*Triticum aestivum* subsp. *aestivum*	PI168716-sel-fhb	United States	Minnesota
644122	*Triticum aestivum* subsp. *aestivum*	PI168727-sel-fhb	United States	Minnesota
644123	*Triticum aestivum* subsp. *aestivum*	PI182568-sel-fhb	United States	Minnesota
644124	*Triticum aestivum* subsp. *aestivum*	PI182583-sel-fhb	United States	Minnesota
644125	*Triticum aestivum* subsp. *aestivum*	PI182586-sel-fhb	United States	Minnesota
644126	*Triticum aestivum* subsp. *aestivum*	PI182591-sel-fhb	United States	Minnesota
644127	*Triticum aestivum* subsp. *aestivum*	PI184512-sel-fhb	United States	Minnesota
644128	*Triticum aestivum* subsp. *aestivum*	PI185380-sel-fhb	United States	Minnesota
644129	*Triticum aestivum* subsp. *aestivum*	PI192219-sel-fhb	United States	Minnesota
644130	*Triticum aestivum* subsp. *aestivum*	PI192498-sel-fhb	United States	Minnesota
644131	*Triticum aestivum* subsp. *aestivum*	PI192660-sel-fhb	United States	Minnesota
644132	*Triticum aestivum* subsp. *aestivum*	PI203083-sel-fhb	United States	Minnesota
644133	*Triticum aestivum* subsp. *aestivum*	PI213833-sel-fhb	United States	Minnesota
644134	*Triticum aestivum* subsp. *aestivum*	PI256958-sel-fhb	United States	Minnesota
644135	*Triticum aestivum* subsp. *aestivum*	PI264927-sel-fhb	United States	Minnesota
644136	*Triticum aestivum* subsp. *aestivum*	PI264940-sel-fhb	United States	Minnesota
644137	*Triticum aestivum* subsp. *aestivum*	PI264946-sel-fhb	United States	Minnesota
644138	*Triticum aestivum* subsp. *aestivum*	PI264998-sel-fhb	United States	Minnesota

Table 2 (continued). PI assignments in *Triticum, Secale,* and *X Triticosecale* from January 2006–March 2007.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
644139	*Triticum aestivum* subsp. *aestivum*	PI294975-sel-fhb	United States	Minnesota
644140	*Triticum aestivum* subsp. *aestivum*	PI349534-sel-fhb	United States	Minnesota
644141	*Triticum aestivum* subsp. *aestivum*	PI351221-sel-fhb	United States	Minnesota
644142	*Triticum aestivum* subsp. *aestivum*	PI351256-sel-fhb	United States	Minnesota
644143	*Triticum aestivum* subsp. *aestivum*	PI351476-sel-fhb	United States	Minnesota
644144	*Triticum aestivum* subsp. *aestivum*	PI351743-sel-fhb	United States	Minnesota
644145	*Triticum aestivum* subsp. *aestivum*	PI351748-sel-fhb	United States	Minnesota
644146	*Triticum aestivum* subsp. *aestivum*	PI351993-sel-fhb	United States	Minnesota
644147	*Triticum aestivum* subsp. *aestivum*	PI360869-sel-fhb	United States	Minnesota
644148	*Triticum aestivum* subsp. *aestivum*	PI382144-sel-fhb	United States	Minnesota
644222	*Triticum aestivum* subsp. *aestivum*	Ripper	United States	Colorado
644223	*Triticum aestivum* subsp. *aestivum*	Alice	United States	South Dakota
644224	*Triticum aestivum* subsp. *aestivum*	Darrell	United States	South Dakota
645483	*Triticum turgidum*	DGE-1	United States	North Dakota
645605	*Triticum aestivum* subsp. *aestivum*	Xerpha	United States	Washington
645606	*Triticum aestivum* subsp. *aestivum*	WA007970	United States	Washington
645607	*Triticum aestivum* subsp. *aestivum*	WA007971	United States	Washington
646183	*Triticum aestivum*	Bigg Red	United States	Montana
646184	*Triticum aestivum*	Smoky Hill	United States	Montana
646185	*Triticum aestivum*	Shocker	United States	Montana
646196	*Triticum aestivum*	Cabernet	United States	California

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2007 SUPPLEMENT

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The most recent edition of the Catalogue, produced and presented at the 10th International Wheat Genetics Symposium is available on CD. MacGene was produced by Y. Yamazaki (yyamazak@lab.nig.ac.jp) in collaboration with R.A. McIntosh. The Catalogue and the 2004, 2005, 2006, and 2007 Supplement are displayed on the GrainGenes Website: http://wheat.pw.usda.gov.

INTRODUCTION

Recommended Rules

9. Laboratory Designators

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cmw Chinese wheat eSSR Fu et al. 2006 TAG 112: 1239-1247.

cnl Cornell University eSSR Yu et al. 2004 Genome 47: 805-818.

hbd SSR loci from sequences in DDBJ {10330}.

hbe EST sequence based SSR {10330}.

hbg Genomic SSR {10330}.

Gene Symbol

Add to gene symbols list:

Almt. Malate transporter (GeneBank AB081803)**.**

***Nam1*.** Regulation of senescence and grain maturity. Pleiotropic effects in grain protein and nutrient content (iron and zinc).

Lvl. Loaf volume.

***Vrt-2*.** Mads-box (GenBank DQ022679) {10294}.

1. Gross Morphology: Spike characteristics

Insert at the end of the introductory paragraph: In a large study of six agronomic traits in a AC Karma / 87E03-S2B1 DH populaton, 24 QTL were detected in 12 chromosomes {10434}.

5.5. Purple grain/pericarp

Pp1.7BL {10392}. **v:** Novosibirsk 67 {10392}. Note, this cultivar has white pericarp.
v2: Purple K49426 *Pp3a* {10392}; Purple Feed *Pp3b* {10392}.
ma: *Xgwm983-7B* – 15.2 cM – *Pp1* – 11.3 cM – *Xgwm767-7B* {10392}.

Pp2. Add note: *Pp2* was renamed *Pp3b*.

Pp3 {10392}. 2A, not 6A {0066; 10392}.

Pp3a {10392}. **v2:** Purple K49426 *Pp1* {10392}.
ma: *Xgwm328-2AS* – 2.7 cM – *Pp3a* – 3.2 cM – *Xgwm817-2AL* {10392}.

Pp3b {10392}. *Pp2*.
v2: Purple Feed {0066, 10392}.
ma: *Xgwm328-2AS* – 5.2 cM – *Pp3b*/*Xgwm817*/*Xgwm912-2A* – 3.6 cM – *Xgwm445-2A* {10392}.

pp1pp3. **v:** Saratovskaya 29 {10392}. Note, this cultivar has red pericarp.

6. Awnedness

6.1.2. Tipped 1

B1. **ma:** Correct the first entry to: *Xgwm410.2-5A* – 8.2 cM – *B1* – 12.2 cM – *Yr34* {10040}. Add: *Xgwm291-5A.3* – 5.3cM – *B1* {10330}.

9. Brittle Rachis

Br-D1. ***Br^{61}*** {10362}. **v:** R-61 {10362}.

17. Dormancy (Seed)

QTL: After Zenkoujikomugi/CS add:
Zenkoujikomugi/Spica: White-seeded wheats with the dormancy-related QTL, *QPhs-3AS* from Zenkoujikomugi were more resistant to PHS than counterparts with the contrasting allele from Spica {10377}. White-seeded wheats with contrasting alleles of *QPhs-4AL* were not different {10377}.
Diploid wheat
QTL: *T. monococcum* subsp. *monococcum* KT3-5 (nondormant) / *T. monococcum* subsp. *aegilopoides* KT1-1 (dormant): RIL population: QTL on chromosome 5A^{m}L, *Xcdo1326c-5A* - *Xabc302-5A*), R^2 = 0.2 - 0.27. Weaker QTL were found on 3A^m (*TmAB18* – *Xwmc102-3A* and *Xrz444-3A* – *TmABF*) and 4A^m (*Xrz261-4A* – *Xrz141-4A*) {0892}. The 3A^m QTL co-located with *TmABF* and *TmAB18* {10417}, derived from othologous ABA signaling genes in *Arabidopsis*. The 5A QTL may be orthologous to the barley dormancy gene *SD1* {10417}.

23. Frost Resistance

QTL: Norstar (tolerant) / Winter Manitou (nontolerant: DH population: Norstar possessed major and minor QTL for tolerance on chromosomes 5A and 1D. The 5A QTL was 46 cM proximal to the *vrn-A1* locus (R^2 = 0.4); its peak coincided with *Xwmc206-5A and Xcfd2-5A,* and expression of C-repeat Binding Factor genes with strong homology to *Cfb14* and *Cfb15* located at the *Fr-2* locus in *T. monococcum* subsp. *monococcum* {10414}.

27. Glume Colour and Awn Colour

Black glumes are now included in the following homoeologous series with red/brown/bronze glumes.

27.1. Red (brown/bronze/black) glumes

The majority of studies report a single dominant gene for red glume colour. A few papers report two factors {1009, 1477, 1520}. Red glume colour in Swedish land cultivars is apparently associated with hairy glumes {1277} suggesting, because *Hg* is located in chromosome 1A, that a red glume factor different from *Rg1* was involved in the Swedish stocks. Nothing was known of the possible association of such a gene with *Bg*, another glume colour gene on 1A. See {1640} for review. A chromosome 1A gene, *Rg3*, was eventually identified by linkage with *Gli-A1* {1405} and shown to cosegregate with *Hg* {624}.

Rg-A1 {10378}. *Rg3* {924,562}. 1AS {924, 562, 9906}.

Rg-A1a {10378}. **v:** TRI 542 {10378}; white-glumed genotypes.
dv: DV92 {282}; G2528 {10378}.

Rg-A1b {10378}. *Rg3*. **i:** Saratovskaya 29*3 // F2 CS mono 1 / Strela {924}.

v: CS / Strela Seln {9906}; Iskra {9906}; L'goskaya-4 {1405}; L'govskaya-47 {1405}; Zhnitsa {9906, 10378}.

v2: Milturum 553 *RgB1b* {9906}; Milturum 321 *Rg-B1b* {9906}; Strela *Rg-B1b* {9906, 924}; Sobko & Sozinov {1405, 1406} reported a further group of 30 international wheats which, by inference from their *Gli-A1* alleles, probably carry *Rg-A1b*.

ma: A linkage order of *Glu-A1* – cent – *Hg* – *Rg-A1b* was reported {1405}.

Rg-A1c {10378}. *Bg* {282, 1304}, *Bg(a)* {282}[3]. 1A {282,1304}.

i: ANK-22A {10378}; S29BgHg {10378}.

s: CS*7/Indian 1A {1304}.

dv: G1777 {282}; G3116 {282}.

ma: *Rg-A1c(Bg)* and *Nor9* co-segregated in *T. monococcum* subsp. *monococcum* {282}[3]; *Xutv1391-1A* (distal) – 3 cM – *Rg-A1c(Bg)* – 1.6 cM – *Hg* – 2.4 cM – *Gli-A1* (proximal) {9959}[2]. *Xgwm1223-A1* – 0 & 0.6 cM – *Rg-A1c* – 4.7 & 4.6 cM – *Xgwm0136-1A* {10378}. Five of six wheats with *Rg-A1c* possessed a 264-bp allele at *Xgwm0136-1A* {10378}.

Rg-A1d. [*Bg(b)* {282}[3]]. **dv:** G3116 {282}.

At the diploid level, *Rg-A1c* (*Bga*) and *Rg-A1d* (*Bgb*) were dominant and caused a solid black glume and a black line at the margins of the glume, respectively {282}. A single factor for black glumes was reported in diploid, tetraploid, and hexaploid wheats {1347}. Linkage with *Hg* was demonstrated at all levels of ploidy, indicating a common gene on chromosome 1A; *Bg* is epistatic to *Rg*.

Rg-B1 {10378}. *Rg1*, *Rg*. 1B {1517}. 1BS {369}.

Rg-B1a {10378}. **v:** TRI 542 {10378}; white-glumed genotypes.

dv: *T. turgidum* subsp. *dicoccoides* acc. MG4343 {9959}.

Rg-B1b {10378}. *Rg1*. **s:** CS*5/Red Egyptian 1B {1304}.

v: Diamant I {9906}; Federation 41 {1517}; Highbury {1121}; Red Egyptian {1304}; *T. petrapavlovskyi* {9906}.

v2: Milturum 321 *Rg-A1b* {9906}; Milturum 553 *Rg-A1b* {9906}; Strela *Rg-A1b* {9906}.

tv: Messapia {9959}; Ward {792}.

ma: *Xytv1518-1B* (distal) – 7.7 cM – *RgB1b* – 0.8 cM – *G1i-B1* (proximal) {9959}. *Xgwm1078-1B* – 1.5 cM – *Rg-B1b* – 3.1 cM – *Xgwm0550-B1* {10378}. *Xutv1518-1B* (distal) – 7.7 cM – *Rg-B1b* – 0.8 cM – *Gli-B1* (proximal) {9959}[2].

Rg-D1 {10378}. *Rg2*. 1DL {769,1241}. 1DS.

Rg-D1a {10378}. **v:** Novosibirskaya 67 {10378}; L301 {10378}; white-glumed genotypes.

Rg-D1b {10378}. *Rg2*. Derived from *Aegilops tauschii*.

i: Saratovskaya 29*5 // *T. timopheevii* subsp. *timopheevii* / *Ae. tauschii* {9906}.

v: Synthetic Hexaploid-11 {10128}; (*Triticum turgidum* subsp. *dicoccoides* / *Ae. tauschii*) {769}; (*Tetra Canthatch* / *Ae. tauschii* var. *strangulata* RL 5271), RL 5404 {1240}; (*Tetra Canthatch* / *Ae. tauschii* var. *meyeri* RL 5289), RL 5406 {648, 1240}.

dv: *Aegilops squarrosa* accessions.

QTL: *QRg.ipk.1D* was mapped in the Opata/W-7984 (ITMI) mapping population {0255}; Linkage with *Gli-D1* implied *Rg2*. This QTL coincided with a QTL for awn color, *QRaw.ipk-1D* {0255}.

ma: *Xpsp2000-1D* – 9.3 cM – *Rg-D1b* – 21.2 cM – *Xgwm106-1D*{10128}.

Rg-D1c {10378}. Brown or smokey-grey phenotype {729}. *Brg* {729}.

i: ANK-23 = Novosibirskaya 67*10 / K-28535 {729}.

v: Golubka {10378}; K-28535 {729}; K-40579 {729}; *T. aestivum* botanical varieties *cinereum*, *columbina*, and *albiglaucum* {10378}.

ma: *Xgwm1223-1D* – 1.5 cm – *Rg-D1c* – 13.1 cM – *Xbarc152-1D* {10378}. *Xbarc149-1D* – 6.3 cM – *Rg-D1c* – 26.5 cM – *Xbarc152-1D* {10378}.

With the deletion of section 27.2 and its incorporation into 27.1, the following sections' are renumbered as follows:

27.2. Pseudo-black chaff

27.3. Black-striped glumes

27.4. Inhibitor of glume pigment

27.5. Chocolate chaff

27.6. Awn colour

28. Grain Hardness / Endosperm Texture
In the preamble paragraph 2 line 5, correct reference from '0380' to '0384'; that is: 'Friabilin is also referred to by the name 'Grain Softness Protein' (GSP) {0384}, and was later shown to be comprised primarily of puroindoline a and puroindoline b {0295}.'

29. Grain Quality Parameters
In a comprehensive study of 46 quality-related traits in a 'RL4452 / AC Domain' RIL population, 99 QTL involving 41 traits were located in 18 chromosomes {10361}; 14 QTL clustered in the *Glu-1B* region (50 cM), 20 QTL occurred in the *Xwmc617-4D – Xwmc48-4D* region (30 cM), 10 QTL mapped to the *Xgwm130-7D – Xwmc405-7D* region (14 cM), and 66 QTL were dispersed {10361}.

In a large study of 11 seed quality traits in a 'AC Karma / 87E03-S2B1' DH population, 26 QTL were detected in seven chromosomes {10434}; six were clustered in the *Glu-D1* region, and five were clustered in the *Rht-D1* region.

QTL analyses of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility, and mixograph properties) in the ITMI population grown in Mexico, France, and USA (California) are reported in {10436}.

29.2. Flour, semolina and pasta colour
QTL: W9262-260D3 (low yellow colour) / Kofa (high colour): Four QTL identified on chromosomes 2A (*Xgwm425-2A*), 4B (*Xgwm495-4B*), 6B (*Xgwm193-6B*), and *Psy-B1* (chromosome 7BL) {10230}. See also Enzymes: Phytoene synthase.

31. Grain Weight
Rye Selection 111 (high GW) / CS (low GW) RIL: two definitive QTL *QGw.ccsu-2B.1* and *QGw.ccsu-7A.1* and one tentative QTL, *QGw.ccsu-1A.1,* were detected by CIM analysis{10363}. The chromosome 7A QTL co-located with a QTL for early heading {10363}.

39. Height
Add at end of section: Genotypes of Indian semi-dwarf wheats based on the Ellis et al. {0378} markers are given in {10404}.

40. Hybrid Lethalities
41.1. Hybrid necrosis
Ne1. Following the chromosome location insert:

	ma:	*Xbarc216-5B* – 8.3 cM – *Ne1* – 2 cM – *Xbarc74-5B* {10334}.
Ne1s.	**v:**	Add: Synthetics TA4152-19, TA4152-37, TA4152-44, TA4152-60 {10334}.

Ne2. Following the chromosome location insert:

	ma:	*Xgwm148-2B* – 6.7 cM – *Ne2* – 3.2 cM – *Xbarc55-2B* {10334}.
Ne2m.	**v:**	Alsen {10334}.

47.Male Sterility
47.1. Chromosomal
ms1g {10355}. 4BS {10354}. **v:** Lanzhou Mutant 257A {10354,10355}.

Insert the following after the present entries:

Photoperiod and/or temperature-sensitive male sterility (PTGMS)

wptms1 {10332}. 2B {10332}. **v:** BNY-S {10332}.
ma: E: AAG/M: CTA_{163} – 6.9 cM – *wtms1* – 4.8 cM – *Xgwm374-2B* {10332}.
Described as a thermo-sensitive gene (TGMS), giving complete sterility at less than 10°C, but fertile at higher temperatures {10332}.

wptms1 {10333}. 5B {10333}. **v:** Line 337S *wptms2* {10333}.
ma: *Xgwm335-5B* – 4.2 cM – *wptms1* – 24.4 cM – *Xgwm371-5B* {10333}.
wptms1 produces sterility only in the presence of *wptms2*.

wptms2 {10333}. 2B {10333}. **v:** Line 337S *wptms1*{10333}.
ma: *Xgwms374-2B* – 6.9 cM – *wptms2* – 20.9 cM – *Xgwm120-2B* {10333}.
wptms2 produces sterility only in the presence of *wptms1*.
wptms1 and *wptms2* were analyzed and mapped under long photoperiod/high temperatures, but an earlier study indicated a single gene for male sterility under short photoperiod/low temperatures. Although mapping data are different, a possible relationship between *wptms2* and *wptms1* needs to be resolved.

57. Polyphenol Oxidase (PPO) Activity

Chara (mod high) / WW2449 (low): DH population: PPO activity Associated with *Xgwm294b-2A* ($R^2 = 0.82$), *Xwmc170-2A*, *Xhwm312-2A*, and *Xwmc178-2A* ($R^2 > 0.7$) {10410}.

A multiplex of markers *PPO33* and *PPO16* was reliable for selecting genotypes with low PPO activity {10418}.

60. Response to Photoperiod

QTL: Trident (early) / Molineux (late): In addition to an effect associated with chromosome 2B, three QTL were designated as follows: *QPpd.agt-1AL* (*Xwmc304 – Xgwm497*), *QPpd.agt-7AS* (*Xbarc154 – Xbarc108*) and *XPpd.agt-7BS* (*Xgwm46 – Xgwm333*) {10382}. The QTL in chromosome 1A is possibly orthologous to *Ppd-H2* in barley.

61. Response to Salinity

61.2. Salt tolerance

QTL: Opata 85 / W7984. 77 QTL effective at different growth stages were mapped to 16 chromosomes {10384}.

63. Response to Vernalization

Replace the existing material in the *Vrn-3* section with the following and eliminate the *Vrn-B4* section:

Vrn3.

Vrn-B3 {10421}. [Synonymous with *Vrn-B4* {279} and *Vrn5, eHi*{769,771} {769,779}].
7BS {768,769,771}. **s:** CS (Hope 7B) *Vrn-D1a* {768}.
v2: Hope *Vrn-A1a* {1424}.
ma: *Vrn-B3* is completely linked to *TaFT* and 1 cM distal to *Xabc158-7B* on the region of 7BS proximal to the translocation with homoeologous group 5 {10421}.
The dominant *Vrn-B3* allele in Hope has a retrotransposon insertion in the *TaFT* promoter (GenBank DQ890165) {10421}. Transformation of the winter wheat Jagger with the dominant *Vrn-B3* significantly accelerated flowering {10421}. Different Hope seed sources were heterogeneous for this insertion {10421}. The retrotransposon insertion in the *TaFT* promoter is present in the CS (Hope 7B) {10421}.

Vrn-H3{10421}. [Synonymous to *Sh3*].
ma: Completely linked to *HvFT* and 1 cM distal to *Xabc158* on 7HS. Originally mapped incorrectly on 1H based on loose linkage {1455, 1316}.

vrn-B3. **v**: Chinese Spring *Vrn-D1* (GenBank DQ890162) {10421}.
In both wheat and barley *Vrn-3* is completely linked with a flowering promoter gene homologous to Arabidopsis *FLOWERING LOCUS T* (*FT*) {10421}.

Vrn-B4. Synonymous with *Vrn3* and will be deleted {10421}.

69. Stem Solidness

Insert introductory note: Solid stem confers resistance to wheat stem sawfly. See also Reaction to *Cephus* spp.

Qsst.msub-3DL. [*Qss.msub-3DL* {10395}]. 3DL {10395}.

Associated with *Xgwm645-3DL* (R^2 = 0.31), *Xwmc656-3DL* (R^2 = 0.1), and *Xcfd9-3DL* (R^2 = 0.13) {10395}. This gene acted as an enhancer of *Qsst.msub-3BL* {10395}.

Tetraploid wheat

Qsf.spa.-3B {10351}. Kyle*2 / Biodur (solid stem) // Kofa (hollow) DH population: *Qsf.spa-3BL* was located to a 21.3 cM interval flanked by *Xgwm247-3B* and *Xgwm114-3B* {10351}. Mapped as a single gene, *Xgwm247-3B* – 6.9 cM – *Qsf.spa-3B* – 14.4 cM – *Xgwm114-3B* {10351}. This location was confirmed in two other crosses involving G9580B-FE1C and Golden Ball as the solid stem parents{10351}.

72. Tiller Inhibition

tin3 {10329}. 3A^{m}L {10329}. **dv:** *T. monococcum* subsp. *monococcum* TA 4443 = TA4342-96 mutant {10329}.
ma: *Xbcd131*/*Xbcd1431*-3A – 9.6 cM – *tin3*/*Xpsr1205-3A* – 4.7 cM – *Xcfa2076-3A* {10329}.

Proteins

77. Proteins

77.1. Grain protein content

Gpc-B1a. *QGpc.ndsu.6Ba* {623}.

This allele, fixed in cultivated durum, is a nonfunctional, frame-shift mutation {10438}. A similar nonfunctional allele, or a complete deletion of *Gpc-B1,* is fixed in hexaploid wheat {10438}.

Gpc-B1b.

Cointinue from 2006 supplement: *Gpc-B1*, the functional allele {10438} in *T. turgidum* subsp. *dicoccoides,* affects senescence and maturity in addition to grain protein content, accelerating senescence and maturity {10298}. *Gpc-B1* is a NAC transcription factor designated *Nam-B1* {10438}. A paralogous copy of this gene is present in homoeologous group 2 (*Nam2*).

Add at end of section: Durum: In '3BIL-85 (high protein introgressed from *T. turgidum* subsp. *dicoccoides*) / Latino' QTL were detected in chromosomes 2AS (associated with *Xcfa2164-2A*, R^2 = 17%), 6AS (*Xp39M37*$_{250}$*-6A,* R^2 = 17%), and 7BL (*Xgwm577-7B*, R^2 = 9%) {10338}.

77.2. Enzymes

77.2.1. Acid phosphatase

Acph-D2 {10407}. **tv:** *Aegilops tauschii* {10407}.

77.2.32. Phytoene synthase

Psy1-B1. **ma:** *Xcfa2040-7B* – 12 cM – *Psy-B1* – 5 cM – *Xgwm146-7B* {10230}.

Psy2-B1. **ma:** *Xgwm312-5B* – 17 cM – *Psy-B2* {10230}.

77.2.34. Polyphenol oxidase

Ppo-A1 {10386}. *PPO-2A* {10385}. 2AL {10385}.
ma: Detected with STS markers PPO18 (10385) and PPO33 {10418}. *Xgwm312-2A* – 1.4 cM – *Ppo-A1* – 5.8 cM – *Xgwm294-2A* {10385}.

Ppo-A1a {10386}. *PPO-2Aa* EF070147{10385}.
v: Zhongyou 9507 {10385,10386}; others {10386}.
ma: 876 bp – wheats with this allele tend to have lower PPO activity {10385, 10386}.

Ppo-A1b {10386}. *PPO-2Ab* EF070148 {10385}.
v: CA 9632 {0758,10386}, others {10386}.
ma: 685 bp (AY596268) – wheats with this allele tend to have lower PPO activity {0758, 10386}.

Ppo-D1 {10386}. 2D {10386}.
ma: Detected with primers PPO16 and PPO29. *Xwmc41-2D* – 2.0 cM – *Ppo-D1* {0759, 10418}.

Ppo-D1a {0759}. EF070149 {10384}.
v: Zhonghou 9507 {0759}; others {0759}.
ma: 713 bp with primer PPO16; wheats with this allele tend to have higher PPO activity {0759}.

Ppo-D1b {0759}. EF070150{0759}.
v: CA 9632 {0759}; others {0759}.
ma: 490 bp with primer PPO29; wheats with this allele tend to have higher PPO activity (0759).

74.2.34. Protein disulfide isomerise (E.C. 5.3.4.1).
Pdi-A1 [{10422}]. 4AL {10422}. **v:** {10422}.

Pdi-B1 [{10422}]. 4DS {10422}. **v:** {10422}.

Pdi-D1 [{10422}]. 4BS {10422}. **v:** {10422}.

The genes for PDI and their promoters were sequenced in {10423}. A related sequence on 1BS was shown to be a partial, nonexpressed copy in {10424}, but not detected in {10409}. PCR-RFLP markers for [*TaPDI-4A*] and [*TaPDI-4B*] were designated [*Xvut(PDI)-4A*] and [*Xvut(PDI)-4B*] in {10409}. These also were closely associated with Germin (oxalate oxidase {10441}) genes (10409).

Endosperm Storage Proteins

77.3.1. Glutenins
77.3.1.1. Glu-1
Glu-B1
Add:
Glu-B1bn [{10425}]. 7+19 {10425}. **v:** Triticales: Lasko, Dagno, Tewo, Vision, Dato {10425}.
Glu-B1bo [{10425}]. 7+26 {10425}. **v:** Triticales: Presto, Modus {10425}.
The number 26 was also used to designate a subunit encoded by *Glu-A1k* and *Glu-A1-1k*.

Glu-D1
Add:
Glu-D1br [{10426}]. 5*t+10.1t {10426}. **tv:** *Ae. tauschii* TD 81 {10426}.

Glu-E1
HMW glutenin y-type subunit Ee1.5 encoded by this locus was sequenced {10439} and compared with other y-type subunits, particularly subunit 1Dy10. It has major deletions in its middle region and is one of the smallest known HMW-glutenin subunits. It has an additional Cys residue in the middle of the repetitive domain, but lacks one Cys residue commonly found towards the end of this domain. These changes may influence inter- or intramolecular disulphide bond formation.

Add after the *Glu-V2* section:
Glu-Ta1 {10449}. **al:** *Taenitherum crinitum* PI 204577 {10449}.
Glu-Ta1a [{10449}]. **al:** *Ta. crinitum* PI 204577 {10449}.
Glu-Ta1b [{10449}]. **al:** *Ta. crinitum* PI 205590 {10449}.
Glu-Ta1c [{10449}]. **al:** *Ta. crinitum* PI 561094, *Ta. asperum* PI 561091, PI 561092 {10449}.
Glu-Ta1d [{10449}]. **al:** *Ta. caput-medusae* PI 598389 {10449}.
Glu-Ta1e [{10449}]. **al:** *Ta. caput-medusae* PI 577708 {10449}.
Glu-Ta1f [{10449}]. **al:** *Ta. caput-medusae* PI 577710 {10449}.

Each allele identified to date encodes two subunits, an x-type and a y-type. The x-type subunits are slower or equal in mobility to subunit Dx2 of wheat, whereas the y-type subunits are faster than subunit Dx12 {10449}. Phylogenetic analysis based upon the sequence of two genes designated *Tax* and *Tay* isolated from *Ta. crinitum* PI 204577 suggest that the *Tax* subunit was most closely related to Ax1, Cx (*Ae. caudata*), Ux (*Ae. umbellulata*) and Dx5, and the *Tay* subunit to Ay, Cy, and Ry (*Secale cereale*) {10449}.

Add at the end of the *Glu-D1* section:
Subunit 10.1t possesses a mobility slightly lower than subunit 10 in SDS-PAGE, and its deduced amino acid sequence is similar to subunit 12 (eight amino acid differences) {10426}; the authors used the complete coding sequence to make phylogenetic comparisons with 19 other subunits including both x-type and y-type subunits and concluded that the *Glu-1* gene duplication event probably occurred about 16.83 million years ago.

77.5.6 Waxy proteins

Following the formal gene lists, the paragraph 'Various hard and soft wheats .....' Add: 'Fifteen percent of Chinese wheats possessed *Wx-B1* null alleles {10357}.'

To the string of references in the following paragraph add: ',10437'}.

77.5.8. Puroindolines and grain softness protein

Pina-D1. After CS, add: (GenBank DQ363911) {03108}. Capitole (GenBank X69914) {03110}.

Pina-D1a. add: **v:** Capitole (GenBank X69914) {03110}; Renan (GenBank CR626934) {10440}.
dv: *Ae. tauschii* unidentified accession (GenBank AJ249935) {03103}; *Ae. tauschii* CPI 10799 (GenBank CR626926) {10440}.

Pina-D1b. add: **i:** PI 644080 (Alpowa / ID377s // 7*Alpowa) {10429}.
v: Glenlea (GenBank AB262660) {10431}.

This allele is now defined as a 15,380 bp deletion versus other possible puroindoline a nulls {10428, 10391}.

Pina-D1c. add: **dv:** *Ae. tauschii* TA10 (GenBank AY649746) {03108}.

Pina-D1d. add: **dv:** *Ae. tauschii* TA1704 (GenBank AY649744) {03108}.

Pina-D1k. add: homonym: *Pina-D1b*/*Pinb-D1h(t)*:
v: Bindokku {10305}; Cheyenne-A {10305}**;** Chosen 68 {10305}; Gaiyuerui {10316}; KT020-584 {10432}; Saiiku 18 {10305}; Saiiku 44 {10305}; Sifangmai {10316}; Tachun 2 {10316}; ZM2851 {10316}; ZM2855 {10316}.

This allele is currently used to denote a large deletion of undetermined size that involves *Pina-D1, Pinb-D1*, and *Gsp-D1* {10077}. The deletion of both puroindolines is associated with harder kernel texture than other known puroindoline hardness alleles {10077, 10305, 10432}.

Pina-D1m. Revise ref. {101208} in the 2005 Supplement to {10208}.

Pina-D1n **v:** Hongheshang, add: (GenBank EF620907) {10208}.
v: Xianmai, add: (GenBank EF620908) {10208}.

New entries:

Pina-D1q {10316}. **v:** U29 (GenBank AB181238) {10316}; u-27 (homonym 'a2', *Pina-D1p*) {10316}.

Pinb-D1.Change '(GenBank X69914)' to '(GenBank X69912)'.

Pinb-D1b. add: **i:** PI 644081 (Alpowa / ND2603 // 7*Alpowa) {10429}.
v: Cheyenne (GenBank DQ363914) {10315}; Renan (GenBank CR626934) {10440}.

Pinb-D1c. add: **i:** PI 644082 (Alpowa / Red Bobs // 7*Alpowa) {10429}.

Pinb-D1d. add: **i:** PI 644083 (Alpowa / Mjølner // 7*Alpowa) {10429}.
add: **v:** Soissons (homonym 'b1') {10433}.

Pinb-D1e. add: **i:** PI 644084 (Alpowa / Canadian Red // 7*Alpowa) {10429}.
add: **v:** Yunxianxiaomai {10427}.

Pinb-D1f. add: **i:** PI 644085 (Alpowa / Sevier // 7*Alpowa) {10429}.
add: **v:** Abyssinia AV12.4 {10430}.

Pinb-D1g. add: **i:** PI 644086 (Alpowa / Andrews // 7*Alpowa) {10429}.

Pinb-D1h. add: **dv:** TA10 (GenBank AY649748) {03108} CPI110799 (GenBank AY159804) {10037}.

Pinb-D1i. add: **dv:** *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747) {03108, 10315}; *Ae. tauschii* isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440}.

Q03-002, TA1704, and TA2381 were incorrectly assigned *Pinb-D1w* in the 2006 supplement.

Pinb-D1j. add: **dv:** *Ae. tauschii* TA1691 (GenBank AY251946) {03108}.

Pinb-D1l. add: Note: {10208} reported *Pinb-D1b* in Gaocheng 8901.

Pinb-D1p. Change reference '{10121}' in three places under this heading to '{10208}'.
Add note: The single nucleotide A deletion occurs in the AAAA at position 210-213 and is assigned to the last position at 213.
add: homonym: *Pinb-D1i(t)* {10305}.
v: Qindao landrace 1{10305}; Qitoubai {10305}; Shijiazhuang 34 {10305}; Zigan {10305}.

This homonym sequence (allele) was incorrectly assigned *Pinb-D1v* in the 2006 supplement.

add: homonym: *Pinb-D1z, 'b3', Pinb-D1u.*
v: Dahuangpi (GenBank AY581889) {10316}.

Pinb-D1q. **v:** Jingdong 11 (GenBank EF620909){10313}.

This allele was used originally (2004 Supplement) in combination with *Pina-D1k* and *Gsp-D1i* to denote the large deletion that encompasses *Pina-D1, Pinb-D1*, and *Gsp-D1* {10077} (*cf. Pina-D1k*). The haplotype nomenclature of this deletion is under review; *Pinb-D1q* is currently used to denote the C-to-G SNP at position 218 {10313}.

Pinb-D1t. add after Guangtouxiamai: (GenBank EF620910).

Pinb-D1u. add after Tiekemai: (GenBank EF620911).

Pinb-D1v. **v:** Tachun 3 {10316}, homonym 'b5' {10316}.

The original assignment of this allele in the 2006 supplement was incorrect; the sequence/varieties in {10305} are *Pinb-D1p* as listed above for that allele. The following variety/sequence was assigned *Pinb-D1y* in the 2006 supplement; but the original assignment of {10316} is now unchanged.

Pinb-D1w add: **v:** Jing 771 (GenBank AY640304, AB180737){10316}, homonym 'b4' {10316}. This variety/sequence was incorrectly assigned *Pinb-D1x* in the 2006 supplement; the original assignment of {10316} is now unchanged.

Ae. tauschii isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747){10315}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440} were incorrectly assigned this allele in the 2006 supplement; they are *Pinb-D1i* as listed above.

Pinb-D1x.

The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Jing 771 {10305} is *Pinb-D1w* as listed above. Currently there is no assignment for this allele.

Pinb-D1y.

The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Tachun 3 in {10305} is *Pinb-D1v* as listed above. The original assignment of {10316} is now unchanged. Currently there is no assignment for this allele.

Pinb-D1z.

This allele/sequence is identical to, and listed under *Pinb-D1p*. Currently there is no assignment for this allele.

New entries:

Pinb-D1u {10427}. **v:** Tiekamai) {10427}; 31 hard Yunnan endemic wheats (*T. aestivum* subsp. *yunnanense* King) {10427}.

Possesses a G deletion at position 127 leading to a shift in ORF {10427}.

Pinb-D1aa {10391}. **v:** Changmangtoulongbai (GenBank EF620912) {10391}; Hongtutou 1 {10391}; Hongtutou 2 {10391}.

Pinb-D1ab {10432}. **v:** KU3062 {10432}; KU3069 {10432}.

77.5.9. Grain softness protein

Gsp-D1i. Change reference '{10120}' to '{03105}' in two places.

77.7.1 Polygalacturonidase-inhibiting proteins

PGIPs are LRR proteins involved in plant defence as inhibitors of fungal polygalacturonases {10390}.

Pgip1 {10390}.	7BS {10390}.	**v:** CS ditelo 7BL {10390}.
		v2: Chinese Spring *Pgip2* {10390}.
		tv: Langdon {10390}.
Pgip2 {10390}.	7DS {10390}.	**v:** CS ditelo 7DL {10390}.
		v2: Chinese Spring *Pgip1* {10390}.

Pathogenic Disease/Pest Reaction

79. Reaction to *Blumeria tritici*

79.1. Designated genes for resistance

33 NILs, including 22 resistance genes and three genetic backgrounds are listed in {10389}.

Pm2. **ma:** *Xcfd81-5D* – 2.0 cM – *Pm2* {10366}.

Pm3.

Add note at beginning of section: Following the cloning and sequencing of *Pm3d* {10064}, six other alleles were sequenced {10405}. The Chinese Spring (susceptible) allele, *Pm3CS,* considered to be ancestral and present in many hexaploid and tetraploid wheats was also transcribed {10405, 10406}. Other wheats possessed a truncated sequence

(e.g., Kavkaz), or were null {10405, 10406}. Unique markers were developed for all eight transcribed alleles and for individual alleles {10405}.

Pm3b. *Pm3j*{10405}.

Pm3c. *Pm3i* {10405}. Sequence DQ251587, DQ517917 {10405}.

Pm3d. *Pm3h* {10405}. Sequence DQ251488, DQ517518 {10405}.

Pm3e.

Pm3g. Sequence DQ251489, DQ517919 {10405}.

Pm3h. Delete and add to *Pm3d*.

Pm3i. Delete and add to *Pm3c*.

Pm3j. Delete and add to *Pm3b*.

Genotype list for *Pm3*: Add: {',10405, 10406'}

Pm35 {10342}. 5DL {10342}. **v:** NC96BGTD3 = PI 603250 = Saluda*3 / TA2377 {10342}.
dv: *Ae. tauschii* ssp. *strangulata* TA2377 {10342}.
ma: *Xcfd26-5D* – 11.9 cM – *Pm35* {10342}.

Pm36 {10356}. 5BL {10356}. **tv:** MG-FN14999, a durum backcross line 5BIL-29 {10356}: *T. turgidum* subsp. *dicoccoides* MG29896 {10356}.
ma: Less than 15 cM linkage with three SST and one EST-SSR markers on chromosome 6BL {10356}.

Pm37 {10372}. 7AL {10372,10274}. **v:** NC99BGTAG11 = *T. timopheevii* subsp. *ameniacum* {10372}.
tv: PI 427315 = *T. timopheevii* subsp. *ameniacum* {10372}.
ma: *Pm37* (*PmAG11*) was about 15 cM proximal to a cluster of markers that earlier co-segregated with *Pm1* {10372}. A cross indicated linkage between *Pm37*and *Pm1* {10372}.

Pm38 {10373}. Adult plant resistance. 7DS {10374}.
i: RL6058 = Tc*6 / PI58458 {10374}.
v: Lines with *Lr34/Yr18* – see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*.
ma: *Xgwm1220-7D* – 0.9 cM – *Lr34/Yr18/Pm38* – 2.7 cM {10374}. See also Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*.

79.3. Temporary designated genes for resistance to *Blumeria graminis*

Mlm3033 {10393}. 7AL {10393}. **dv:** *T. monococcum* subsp. *monococcum* TA2033 {10393}.
ma: *Xmag1757/Xmag2185* – 2.7 cM – *Mlm2033/Xmag2185* – 1.3 cM – *Xgwm344-7A* {10393}; *Xmag1757* – 5.9 cM – *Mlm2033/mag2185/Xgwm344/Xgwm146-7A* – 4.7 cM – *Xmag1986* {10393}; *Xmag1757/Xmag1714/Xmag1759 – Mlm2033* – 0.9 cM – *Xmag2185/Xgwm344-7A* {10393}.

Mlm80 {10393}. 7AL {10393}. **dv:** *T. monococcum* subsp. *aegilopoides* M80 {10393}.
ma: *Xmag1757/Xmag1759* – 3.6 cM – *Mlm80* – 0.7 cM – *Xmag2166/Xgwm344-7A* {10393}.

Mlm2033 and *Mlm80* appeared to be allelic and their relative locations suggest they are allelic with *Pm1* {10393}.

PmY39 {10367}. 2U(2B) {10367}. **su:** Laizhou 953*4 / Am9 (Am9 = *Ae. umbellulata* Y39 / *T. turgidum* subsp. *carthlicum* PS5) {10367}.
dv: *Ae. umbellulata* Y39 {10367}.
ma: Associated with 2U markers *Xgwm257, Xgwm296*, and *Xgwm319* {10367}.

79.4. QTL for resistance to *Blumeria graminis*

Add at end of section:

Fukuho-Komugi / Oligoculm, DH population. QTL for adult-plant resistance located on 1AS (R^2 = 22%, *Pm3* region, *Xgdm33 – Xpsp2999*), 2BL (R^2 = 8%, *Xwmc877.1 – Xwmc435.1*), and 7DS (R^2 = 10%) derived from Fukuho-komugi, and 4BL (R^2 = 6% at one of two sites, *Xgwm373-Xgwm251*) from Oligoculm {10335}. The QTL on 7DS, flanked by *Xgwm295.1-7D* and *Ltn,* is likely to be *Lr34/Yr18*.

CI 13227 (S) / Suwon 92 (R), SSD population: APR (field resistance) was closely associated with *Hg, Xpsp2999-1A* and *Xpm3b.1* and *Xpm3B.2* designed from the *Pm3b* sequence {10340}.

RE9001 (R) / Courtot (S) RIL population: *QPm.inra.2B* (R^2 = 10.3 – 36.6 %), in the vicinity of *Pm6*, was consistent over environments {10360}. Eleven QTL, detected in at least one environment were identified by CIM {10360}.

XX. Reaction to *Cephus spp.*
Pest: Wheat stem sawfly. North American species *C. cinctus*; European species *C. pygmeus*. Resistance to wheat stem sawfly is associated with solid stem (see also: Stem solidness).

Tetraploid wheat
Qsf.spa-3B {10351}. See Stem Solidness.

81. Reaction to *Diuraphis noxia*
***Dn4*.** **i:** Yumar {10397}.
v: Ankor {10397}; Prairie Red {10397}.

***Dn5*.** Add ref 10396 to 7DL.
Add note: 'Genetic mapping indicated that *Dn5* is located in chromosome 7DS, but cytological analysis showed it was located in 7DL {10396}. It also was suggested {10396} that the Palmiet Dn5 line {0004} may not have *Dn5* {10396}.'.

82. Reaction to *Fusarium graminearum*
82.1. Disease: Insert: 'Fusarium head blight' as an additional disease name. Fusarium head scab, scab
Fhb1 {add: ',10403'}**.** **i:** HC374 / 3*98B69-l47 {10214}; Sumai 3*5 / Thatcher {10214}.
v: HC-l47-126 {10444}.
v2: BW278 *Fhb2* {10225}; Sumai 3 *Fhb2* 10314}.
ma: *XSTS3B-80* – 0.2 cM – *Fhb1* – 1.1 cM – *XSTS3B-142* {10214}. Placed in a 1.2-cM interval flanked by *XSTS3B-189* and *XSTS3B-206* {10403}.
The relationship of *Fhb1* to *Fhs1* or *Fhs2* {1096}is unknown.
***Fhb2*.** Change '6B' to '6BS'. **v:** pbE85 {10444}.
v2: Sumai 3 *Fhb1* {10225}.
ma: Change present entry to: '*gwm133-6B* – 4 cM – *Fhb2* – 2 cM – *Xgwm644-6B* {10225}.'
Add note: The relationship of *Fhb2* to *Fhs1* or *Fhs2* {1096}is unknown.

In the third paragraph following the listing of *Qfhs.ifa-5A* (relates to Ning 7840 / Clark) add: Three RGA sequences putatively assigned to chromosome 1A explained 3.37–12.73% of the phenotypic variation in FHB response among F7 and F10 populations {10364}. STS marker FHBSTS1A-160 was developed from one of the RGA.

Following the entry for 'Frontana / Remus' add:
'Frontana (MR) / Seri 82 (S)', F3 and F3:5 populations: QTL were located in chromosomes 1BL (R^2 = 7.9%), flanked by AFLP markers, 3AL (R^2 = 7.7%), flanked by *Xgwm720-3A* and *Xgwm121-3A* , 7AS (R^2 = 7.6%), flanked by an AFLP and *Xgwm233-7A* {10349}.

Following 'Wangshuibai /Alondra' add:
'Wangshuibai / Annong 8455': RIL population: CIM analysis over 2 years detected QTL for FHB response on chromosomes 3B (R^2 = 0.17) and 2A (R^2 = 0.12), and for DON levels in 5A (R^2 = 0.13), 2A (R^2 =0.85), and 3B (R^2 = 0.06) {10447}. The regions involved were *Xgwm533.3B – Xbarc133-3B, Xgwm425-2A,* and *Xgwm186-5A – Xgwm156-5A* {10447}

In a reciprocal backcross analysis of' Chris monosomics / Frontana', Frontana chromosomes 3A, 6A, and 4D reduced visibly diseased kernels, kernel weight and DON content, whereas Frontana chromosomes 2A, 2B, 4B, and 7A increased the same traits {10398}.

At end of section add:
Tetraploid wheat
Qfhs.crc-2BL {10445}. **tv:** Strongfield {10445}.
ma: Spanning 16 cM, this QTL peaking on *Xgwm55-2B* explained 23% of the phenotypic variation {10445}.
Qfhs.ndsu-3AS {10402}. **sutv:** LDN–DIC3A {10402}.
tv: *T. turgidum* subsp. *dicoccoides* {10402}.
ma: Located in an interval spanning 29.3 cM, this QTL accounted for 37% of the phenotypic variation; peak marker, *Xgwm2-3A* {10402}.

Qfhs.crc.6BS {10445}. **tv:** *T. turgidum* subsp. *carthlicum* cv. Blackbird {10445}.
ma: Spanning 23 cM and peaking on *Xwmc397,* this QTL accounted for 23% of the phenotypic variation {10445}.

Qfhs.fcu-7AL {10401}. **sutv:** LDN–DIC 7A {10401}.
tv: *T. turdidum* subsp. *dicoccoides* PI 78742 {10401}.
ma: Located in an interval spanning 39.6 cM, this QTL accounted for 19% of the phenotypic variation in a RIL population of 'Langdon / LDN–DIC 7A'; nearest marker *Xbarc121-7AL* {10401}.

'Strongfield / *T. turgidum* subsp. *carthlicum* (Blackbird)': Field resistance identified in chromosome 2BL (*Xgwm55-2B*), and 6BL (*Xwmc397-6B*) (coincident with *Fhb2* {10225}).

82.2. Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* species.
Add: W21MMT70 / Mendos: DH population: three consistent QTL for seedling resistance were identified with CIM; there were located in chromosomes 5D and 2D (resistance alleles from W21MMT70) and 2B (resistance allele from Mendos) {10358}.

83.Reaction to *Heterodera avenae*Woll.

Cre5. **v:** Continue present text with: However a contribution of the *Cre5* region was detected in 'Trident / Molineux' {10343}.
ma: Associated with the *Xgwm359-2A* (R^2 = 8%) – *Xwmc177-2A* (R^2 = 7%) region in 'Trident / Molineux' {10343}.

Cre8. **ma:** Associated with the *Xgdm147-6B* (R^2 =24%) – *Xcdo247-6B* (R^2 = 12%) region in 'Trident / Molineux' {10343}.

QTL: *Qcre.srd-1B* was located to the *Xwmc719-1B* (R^2 = 12%) – *Xgwm140-1B* (R^2 = 12%) region in 'Trident / Molineux' (10343).

85. Reaction to *Mayetiola destructor*

H13. 6DS {10388}. **v:** PI562619 {10388}; SW34 = Langdon / *Ae. tauschii* RL 5544 {10388}.
ma: *Xcfd132-6D* – 3.7 cM – *H13* {10388}.

H22. 1D {1199}, 1DS {10381}.
v: KS85WGRC01 = *Ae. tauschii* TA1644 / Newton // Wichita {1199}; PI572542 {10388}.
ma: *Xgdm33-1D* – 1.0 cM – *H22* – 0.3 cM – *Xhor2KV-1D* – 0.5 cM – *Xgpw7082-1D* {10381}.

H23. **v:** PI535766 {10388}.

H24. **v:** PI535769 {10388}.

H26. 3DL {10388}. **v:** SW8 = Langdon / *Ae. tauschii Clae* 25 {10388}.
ma: *Xcfd211-3D* – 7.5 cM – *H26* – 2.9 cM – *Xwgc7330-3D* – 4.0 cM – *Xgwm3-3D* {10388}.

87. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

Stb6. **v:** Amigo {10448}; Arina {10448}; Amada {10448}; Atlas 66 {10448}; Ble Seigle {10448}; Bon Fermier {10448}; Chinese Spring {10448}; Gene {10448}; Heines Kolben {10448}; Hereward {10448}; Poros {10448}; Senat {10448}; Shafir m{10448}; Tadinia {10448}.
v2: Bulgaria 88 *Stb1* {10448}. Veranopolis *Stb 2* {10448}. Israel 493 *Stb3*{10448}.

Stb10. 1D. Kavkaz-4500 L.6.A.4.

Stb11. 1BS. **v:** TE9111, JIC W 9996.

Stb12. 4AL. Kavkaz-4500 L.6.A.4.

Stb13 {10347}. Confers resistance to Canadian cultures MG96-13 and MG2 {10347}.
7BL {10347}. **v:** DH line 90S05B*01 {10347}; DH line 98S08C*03 {10347}.
v2: Salamouni *Stb14* {10347}.
ma: *Xwmc396-7B* – 9 cM – *Stb13* 10347}; *Xwmc396-7B* – 7 cM – *Stb13* {10347}.

Stb14 {10348}. Confers resistance to Canadian isolate MG2 but not to MG96-13 {10347}.
3BS {10348}. **v:** DH line 98S08A *09 {10348}.

v2: Salamouni *Stb13* {10347}.
ma: *Xwmc500-3B* – 2 cM – *Stb14* – 5 cM – *Xwmc632-3B* {10348}.

Stb15 {10341}. Confers resistance to Ethiopian culture IPO88004 {10341}.
6AS {10341}.
v: Riband {10341}.
v2: Arina *Stb6* {10341}.
ma: *Stb15* – 14 cM – *Xpsr904-6A* {10341}.

QTL:
A weak QTL, *QStb.psr-7D.1*, giving partial resistance to Portuguese isolate IPO92006, was detected in the *Xcdo475b-7B* – *Xswm5-7B* region in chromosome 7DS {10341}.

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

89.2. Sensitivity to SNB toxin
Replace or update present entries with the following**:**

Snn1 {10008}. Sensitivity to toxin SnTox1 is dominant {10008}. 1BS {10008}.
s: CS-DIC 1B {10008}.
v: CS {10008}; Grandin {10008}; Kulm {10008}; ND 495 {10008}.
ma: *Snn1* – 4.7 cM – *XksuD14-1B* {10008}.

snn1. **v:** Br34 {10008}; Erik {10008}; Opata 85 {10008}.

QTL: ITMI population: A major QTL, coinciding with *Snn1*, was located in chromosome 1BS (R^2 = 0.58, 5 days after inoculation); minor QTL were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL, and 7BL (10009).

90. Reaction to *Puccinia graminis*

Sr31. **ma:** A SCAR marker, SCSS30.2_{576} was developed {10359}.

91. Reaction to *Puccinia striiformis*
91.1. Designated genes for resistance to stripe rust

Yr3a. **i:** Taichung 29*6 / Vilmorin 23 {10370}.
Yr3 (*YrV23*) – *Xwmc356-2B*, 9.4 cM {10370}.

Yr5. **ma:** Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310 {10435}.

Yr7. **i:** Taichung 29*6 / Lee {10371}.
ma: *Yr7 – Xgwm526-2B,* 5.3 cM {10371}.

Yr9. **ma:** *Yr9* – 3.7cM – *Xgwm582-1BL* {10365}.

Yr15. **v:** Boston {0330}; Cortez {0330}; Legron {0330}.

Yr17. **v:** Kris {10336}.
ma: Characterized by null alleles for *Xwmc382-2A* and *Xwmc407-2A* {10336}.

Yr24. *YrCH42*. **v:** Chuanmai 42 {10339}; Synthetic 769 {10339}.
tv: Decoy 1 {10339}.
ma: *Xbarc187-1B* – 2.3 cM – *Yr24* – 1.6 cM – *Xgwm498-1B* {10339}.

Yr24 is identical to *Yr26* {10339, 939}.

Yr26.
Yr26 is identical to *Yr24* {10339, 939}.

Yr32. **v:** Deben {10336}.

Yr34. Change to: **v:** AUS22857 {10040}; WAWHT2046 = AUS91389 {10040}.
ma: Change current entry to:'*Xgwm410.2-5A* – 8.2 cM – *B1* – 12.2 cM – *Yr34* {10040}'.

Yr39 {10416}. HTAP resistance. 7BL {10416} .
v: Alpowa {10416}.
ma: Closely linked to several RGAP markers {10416}.

Yr40 {10328}. Derived from *Aegilops geniculata*. 5DS (T5DL·5DS-T5MS^{G}) {10328}.
v: TA5602 {10328}; TA5603 {10328}.
al: *Ae. geniculata* (= *ovata*) ($U^{s}U^{s}M^{g}M^{g}$) TA10437 (10328).
ma: Completely linked with distinctive alleles of *Gsp, Xfbb276*, and *Xbcd873* {10328}.

Completely linked with *Lr57* {10328}.

At end of section add: Genotype list: Chinese common wheats {10369}.

Yr1Ap {10416}. 1BS {10416}. **v:** Alpowa *Yr39*{10416}.
ma: *YrAlp* – 15.2 cM – *Xgwm18-1B* – 1.1 cM – *Xgwm11-1B* (10416) and more closely linked to RGAP markers {10416}.

YrSp {10352}. *YrSp* {10353}. 2B {10352,10353}, probably 2BL.
i: 'Avocet*3 / Spaldings Prolific' {10353}; 'Taichung*6 / Spaldings Prolific' {10352}.
v: Spaldings Prolific {10352,10353}.
ma: *YrSp – Xwmc-2B* 12.1cM {10352}.

YrV23 {10370}. Presumed to be *Yr3a*. **v:** Vilmorin 23 {10370}.

YrZH84 {10331}. 7BL {10331}. **v:** Annong 7959 {10331}; Zhoumai 11 {10331}; Zhoumai 12 {10331}.
v2: Zhou 8425B *Yr9* {10331}.
ma: *Xwmc276-7B* – 0.6 cM – *Xcfa2040-7B – YrZH84* – 4.8 cM – *Xbarc32-7B* {10331}.

Yrns-B1. **ma:** As a QTL, *Yrns-B1* was located in a 3 cM interval between *Xgwm493-3B* and *Xgwm1329-3B* {10383}.

91.3. Stripe rust QTLs

Multi-cross analyses detected QTL in chromosomes 2AS (*Yr17*), 2AL (*Yr32*), 2BL (*Yr5*/*Yr7*) region, and 6BL {10336}. 'Avocet S / Pavon76': QTL identified in 1BL (*Xgwm259*), 3BS (PstAATMseCAC2), 4BL (*Xgwm495*), 6AL (*Xgwm617*), 6BL (PstAAGGMseCGA1) {10443}.

92. Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr1. **ma:** Add: 'Mapped to a 0.7 cM interval in *Ae. tauschii* and a 0.075 cM interval in wheat {10408}. A candidate gene for *Lr1*, *Lr1RGA1,* encoding a CC-NBS-LRR protein co-segregated with *Lr1* {10408}.'.

Lr3c. **v:** Blava {10345}.

Lr10. **ma:** *Lr10* was cloned – it has a CC-NBS-LRR structure, syn, *T10rga1* GeneBank AY270157 {10442}.

Lr17a. **v:** Jagger {10346}.

Lr17b. **v2:** Contra *Lr13* {10345}; Kalasz *Lr13* {10345}; Riband *Lr13* {10345}; Sarka *Lr13*{10345}.

Lr19. **ma:** RAPD, SCAR and SSR markers co-inciding with, or flanking, *Lr19* in a derivative of Knott's Agatha Mutant 28 (C80.1) were reported in {10379}.

Lr21. *Lr40* {1200, 10415}.
v2: WGRC16 = 'TAM107*3 / *Ae. tauschii* TA 2460' *Lr39* {220, 10415}.
dv: *Ae. tauschii* TA2460 *Lr39* {220, 10415}.
ma: *Xksu-1D* is part of *Lr21* {10420}. *Lr21* was cloned and shown to have a NBS-LRR structure {10420}.

Lr22a. **ma:** *Xgwm296-2DS* – 2.0 cM – *Lr22a* {10446}.

Lr24. **ma:** SCAR markers were developed in {10368}.

Lr34. **v:** Arina*3/Forno {10380}; Bezostaya {10387}; Condor {10387}; Cook {10387}; Forno {10066, 10380, 10387}; Fukuho-Komugi {10387}; Otane {10387}.
ma: *Lr34……XsfrBF473324* – 0.5 cM – *Xsfr.cdo475*-7D – 0.7 cM – *Xswm10*-7D {10380}. A 150-bp allele (b) of STS *CsLV34*, derived from wEST BQ788742 was identified in most wheats with *Lr34*; *CsLV34a* – 0.4 cM – *Lr34* {10387}.

Lr39. Add existing **v:** and **dv:** entries from *Lr41* and add ',10415' after each reference.
v2: WGRC16 = 'TAM107*3 / *Ae. tauschii* TA 2460' *Lr39* {220, 10415}.
dv: *Ae. tauschii* TA2460 *Lr21* {220, 10415}.

Lr40 {1200}. Deleted. Shown to be *Lr21* {10415}.

Lr41 {215}. Deleted. Shown to be *Lr39* {10415}.

Lr43 {218}. Deleted. WGRC16 shown to have *Lr21* and *Lr39* {10415}.

Lr57 {10328}. Derived from *Aegilops geniculata*. 5DS (5DL·5DS-T5MS^{G} {10328}.
v: TA5602 {10328}; TA5603 {10328}. Since TA5602 and TA5603 are fourth backcross selections to WL711, they likely also carry *Lr13*.

al: *Ae. geniculata* (= *ovata*) ($U^SU^SM^GM^G$ TA10437) {10328}.
ma: Completely linked with distinctive alleles of *Gsp*, *Xfbb276* and *Xbcd873* {10328}. Completely linked with *Yr40* {10328}.

Lr58 {10375}. Derived from *Aegilops triuncialis*. 2BL {10375} = T2BS·2BL-2^tL(0.95).
v: TA5605 = WL711*4 / Ae. triuncialis TA10438 *Lr13* {10375}.
al: *Ae. triuncialis* TA10438 {10375}.
ma: TA5605 possesses *Ae. triuncialis* alleles of RFLP markers *XksuH16*, *XksuF11* and *Xbg123* in the terminal region of chromosome 2BL {10375}.

Lr59 {10399}. 1AL (probable centric fusion {10399}.
v: Line 0306 {10399} = *Ae. peregrina*-680 / 2*CS // 5*W84-17 {10399}.
al: *Ae. peregrina* (UUSS, 2n = 28) 680 {10399}.

Lr60 {10400}. *LrW2* {0305}. 1DS {10400}.
v: RL6172 {0305} = Thatcher*3/V860.

At the end of section: Under Genotype lists; to references after European cultivars add: {',10345'}.

92.3. QTLs for reaction to *P. triticina*

Avocet S / Pavon76: QTL identified included: 1BL (PstAFAMseCAC1&2), 4BL (*Xgwm368*), 6AL (*Xgwm617*), and 6BL (PstAGGMseCGA1) {10443}.

93. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

93.1. Insensitivity to tan spot toxin

***tsn1*.** **ma:** Replace the last entry with: *Xfgcg7-5B* – 0.4 cM – *Tsn1*/*Xfcg17-5B* – 0.2 cM – *Xfcg9-5B* {10207}; *Xfcg17-5B* – 0.2 cM – *Tsn1* – 0.6 cM – *Xfcg9-5B* {10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM {10337}. *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1*/*XBE425878*/*Xfcc*/*XBE443610* {10413}.

Add note: According to {10376} the same dominant allele, presumably *tsn1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN 2137 in crosses with 6B-365.

Tsn2 {10344}. Conditions resistance to race 3 {10344}. 3BL {10344}.
sutv: LDN (DIC-3B) {10344}.
tv: *T. turgidum* no. 283, PI 352519 {10344}; *T. turgidum* subsp. *dicoccoides* Israel-A {10344}.
ma: Identified as a QTL in region *Xgwm285-3B* - *Xwmc366.2-3B* (R2 = 91%) {10344}. Also classified as a single gene: *Xgwm285-3B* – 2.1 cM – *tsn2* – 15.2 cM – *Xwmc366.2-3B* {10344}.

tsn3 {10394}. 3D {10394}, 3DS {10419}.
v: XX41 = [Langdon / *Ae. tauschii* CI 00017] {10394}; XX45 {10394}; XX110 {10394}
dv: *Ae. tauschii* CI 00017 {10394}.
ma: *Xgwm2a – tsn3*, 15.3 cM, 14.4 cM, and 9.5 cM in CS / XX41, CS / XX45, and CS /XX110, respectively {10419}.

Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant – all three were hemizygous-effective {10394}. The genes were given different temporary designations {10394, 10419}, but all will be considered to have a common gene until they are shown to be different.

tsn4 (10350). Resistance to race 1 (culture ASC1a) {10350}. 3A {10350}.
v: Salamouni {10350}.

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Updates

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10008. Change '2003' to '2004' and 'Abstr.' to ' Phytopathology 94: 1056-1060.
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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
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. recondita* f.sp. *tritici = *Puccinia recondita* f.sp. *tritici* = leaf rust fungus
P. striiformis* f.sp. *tritici = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus
P. graminis = *Polymyxa graminis* = wheat soilborne mosaic virus vector
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. peregrina = *Aegilops peregrina* = *Aegilops variabilis* = *Triticum peregrinum*
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. ventricosa = *Aegilops ventricosa* = *Triticum ventricosum*
S. cereale = *Secale cereale* = rye
T. aestivum = *Triticum aestivum* = hexaploid, bread, or common wheat
T. dicoccon = *Triticum dicoccon* = *T. dicoccom*
T. durum = *Triticum durum* = durum, pasta, or macaroni wheat
T. macha = *Triticum macha*
T. militinae = *Triticum militinae*
T. monococcum* subsp. *aegilopoides = *Triticum boeoticum*
T. monococcum* subsp. *monococcum = *Triticum monococcum*
T. 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. *dicoccom = *Triticum dicoccum*

T. urartu = *Triticum urartu*
Th. bessarabicum = *Thinopyrum bassarabicum*

Scientific journals and publications:

Agron Abstr = Agronomy Abstracts
Ann Wheat Newslet = *Annual Wheat Newsletter*
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 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
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

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X. VOLUME 54 MANUSCRIPT GUIDELINES.

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CONTRIBUTIONS MAY INCLUDE:

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—Wheat stocks; lines for distribution, special equipment, computer software, breeding procedures, techniques, etc.

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Follow the format in volume 44–53 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.

All text will be entered in computer files; therefore, please submit manuscript in any of the above formats. Mail hard copy to W. John Raupp, Department of Plant Pathology, Throckmorton Hall, Kansas State University, Manhattan KS 66506-5502, or submit by E-mail to jraupp@ksu.edu.

DISTRIBUTION:

The primary method of distribution of Volume 54 will be CD-ROM in HTML format. These files can be read with any internet browser. A hard copy will be sent only if requested by 1 April, 2008, and will cost $40.

The *Annual Wheat Newsletter* will continue to be available (Vol. 37–53) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/ and Internet gopher access at "http://wheat.pw.usda.gov/GG2/index.shtml".

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