ANNUAL WHEAT NEWSLETTER

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IN DEDICATION TO DR. ROBERT J. METZGER

The following tribute was written by Bob's daughter, Debra (Metzger) Lee and her husband Michael. Reflecting on his life, she wrote 'I have reflected on the life's lessons I learned from Dad. The ones that stood out most strongly include always try to do your best, don't be satisfied with seemingly obvious answers, there is dignity in all forms of labor, and share your time, your abilities, and your good fortune with others'. Bob will be missed as a colleague and friend by many.

Robert J. Metzger died on 24 June, 2008, in Albany, Oregon, at age 83. Bob was born on 11 April, 1925, near Cerro Gordo, Illinois. He spent his youth with his parents and five sisters on several farms in this area. He enjoyed a long life with his family, friends, and colleagues around the world. He is survived by his former wife, Barbara, daughter Debbie Lee (Michael), son David (Laura), and four grandsons.

Bob was the first person in his family to attend college and was able to attend through benefit of a Future Farmers of America scholarship. His undergraduate studies were interrupted by service in the Army Air Corp. He earned B.S., M.S., and Ph.D. degrees from the University of Illinois, in 1946, 1948, and 1952, respectively. After Illinois, Bob worked briefly as a plant breeder at Clemson University in South Carolina, working on forage legume species. In 1954, Bob accepted a USDA wheat geneticist position at Oregon State University, where he worked until his retirement in 1986.

As one of his colleagues described him, Bob was a 'wheatologist' who had broad knowledge of the breeding and biology of wheat, relatives of wheat, wheat pathogens, and wheat researchers. At OSU, his wheat research emphasized genetic investigations of disease resistance and germ plasm enhancement using exotic wheat and wheat relatives. He worked directly with wheat breeders on varietal development (e.g., Stephens), and with basic researchers on more fundamental aspects of taxonomy, the biology of flowering and vernalization, and novel methods of wheat improvement. During his career, Bob consulted extensively with the wheat-breeding program at the International Center for Maize and Wheat Improvement (CIMMYT) and the Food and Agriculture Organization of the United Nations and was a leader of germ plasm collection trips throughout Turkey and Pakistan.

Bob lived his life with passion and zest. Every day provided a new opportunity to learn. Bob was an enthusiastic traveler. He loved being among plants, either in research plots, in the greenhouse, or on the roadside. His hobbies

and community service activities included public school committees, Boy Scout leadership, reading, and rhododendron breeding.

Bob enjoyed a long and active retirement that allowed him to focus his research energy on triticale. From 1986 through 2008, he collaborated with local and global networks of researchers and friends to learn and to genetically improve triticale. Those efforts produced much camaraderie, some solid basic information, more than a few good 'Bob' stories, and some successful varieties. In his final weeks, Bob made a road trip to California. He was joined by colleagues who made it possible for him to view the research plots for one more evaluation. Bob made his last visit to his beloved triticale nursery in Oregon just a few days before he died. He described it as 'the best nursery in 50 years'.

Based on the attendance at his 80th birthday party, the many kind visits and assistance as his health declined, and communication from students and colleagues from around the world, Bob was obviously loved and respected by his family, friends, and colleagues. His presence and spirit will be missed.

I. SPECIAL REPORTS

MINUTES OF THE NATIONAL WHEAT IMPROVEMENT COMMITTEE (NWIC) MEETING.
5 December, 2007.
Raleigh, NC, USA.

Attendence.

NWIC Members and Proxies: C. J. Peterson, Oregon State University (chair), Robert Graybosch (secretary); David Van Sanford, University of Kentucky; Edward Souza, USDA–ARS; Tom Shanower, USDA–ARS; Christina Cowger, USDA–ARS; Elias Elias, North Dakota State University; Jose Costa, University of Maryland; David Marshall, USDA–ARS; Barry Morton, National Association of Wheat Growers; Jon Raupp, Kansas State University; Allan Fritz, Kansas State University; Jackie Rudd, Texas A&M University; Hans Braun, CIMMYT; Mohamed Mergoum, North Dakota State University; Jane Demarchi, North American Millers Association; David Garvin, USDA–ARS; Yue Jin, USDA–ARS Brett Carver, Oklahoma State University; Elizabeth Maghirang, USDA–ARS; Floyd Dowell, USDA–ARS; Bob Bowden, USDA–ARS; Dave Matthews, USDA–ARS; Robert Zemetra, University of Idaho; Kim Garland Campbell, Washington State University; Mike Davis, American Malting Barley Association; and Kay Simmons, USDA–ARS.

Informational items.

Barry Morton has assumed the position of scientific liaison for the National Association of Wheat Growers (NAWG). Main scientific topics of concern for NAWG are GMO wheat, carbon sequestration, wheat as a source of cellulosic ethanol, and practical spin-offs from agricultural research.

UG99 screening in Kenya. The USDA–ARS continues to facilitate, under the guidance of Yue Jin, Cereal Disease Laboratory, St. Paul, MN, the screening of resistance to the stem rust race UG99 in Kenya. The main effective genes found in current U.S. advanced breeding lines are *SrTmp*, *Sr24*, *Sr36* and an unknown gene on the Amigo T1AL·1RS wheat-rye chromosomal translocation. Virulence was noted to *Sr24* and *Sr26*. These efforts will continue, and the NWIC thanks Yue Jin for his diligence in this area.

Rust in the Great Plains. Bob Bowden, USDA–ARS, noted good control of leaf rust in the southern and central Great Plains remains elusive. Approximately two-thirds of the SW Kansas wheat acreage was treated with fungicide in 2007. Stripe rust continues to impact wheat production in this region.

Annual Wheat Newsletter. According to Jon Raupp, editor, both financial and research contributions have been dropping. Readers are urged to encourage their colleagues to contribute research updates from their programs.

GrainGenes update. GrainGenes has added a web page with updated information on the stem rust race Ug99. Web analysis revealed the GrainGenes receives approximately 30,000 unique users each month.

Wheat genomics subcommittee. The NWIC has established a Wheat genomics subcommittee to provide guidance in this area. Established priorities are: databases, physical maps, and increased number of available markers. P. Stephen Baenziger, University of Nebraska, presently serves as the chair. Additional information may be found at the following website: http://wheat.pw.usda.gov/NWIC/.

Research priorities.

NWIC members voted, in order of decreasing preference, the following research areas as high priority items for increased attention:

a. Wheat rusts
b. Wheat genotyping efforts
c. Wheat quality screening
d. National Small Grains Collection, Aberdeen, ID
e. Hessian Fly resistance

Resolutions.

Germ plasm exchange issues. The National Wheat Improvement Committee urges the USDA–ARS to establish and fund a position, affiliated with the National Small Grains Collection at Aberdeen, ID, to coördinate the import, increase, and distribution of wheat germ plasm (defined as seed and related articles) from CIMMYT-coördinated international nurseries. Due to the urgent need to access novel germ plasm and disease resistance genes, the National Wheat Improvement Committee urges USDA–APHIS to develop protocols to allow the importation and distribution of wheat seed and related articles from CIMMYT international nurseries.

Chair. It was moved that C.J. Peterson continue in his current role as chair of the NWIC for a second term. NWIC unanimously approved this motion, and thank Dr. Peterson for his continued efforts. The current term shall expire in December 2010.

Approved amendment to NWIC by-laws.

The scientific liaison of the National Association of Wheat Growers (position occupied, as of this writing, by Barry Morton) shall be an *ex officio* member, with voting privileges, of the National Association of Wheat Growers.

Next annual meeting of the NWIC.

Members approved a tentative plan to meet in January, 2009, in conjunction with the annual Plant and Animal Genome Meetings, in San Diego, CA.

R. Graybosch, Secretary, 31 March, 2008.

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December 2007.

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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

Publication: Genomics-assisted Crop Improvement.

Two volumes of ***Genomics-assisted Crop Improvement*** (GACI) have been recently published by Springer. Volume 1, entitled '**Genomics Approaches and Platforms'**, presents state-of-the-art genomic resources and platforms and also describes the strategies and approaches for effectively exploiting genomics research for crop improvement (http://www.springer.com/home?SGWID=5-102-22-173739833-0). Volume 2, entitled '**Genomics Applications in Crops**', presents a number of case studies of important crop and plant species that summarize both the achievements and limitations of genomics research for crop improvement (http://www.springer.com/dal/home?SGWID=1-102-22-173739832-0).

More than 90 authors, representing 16 countries from five continents have contributed 16 chapters for Volume I and 18 chapters for Volume II. Each article shows how structural and/or functional genomics can improve our capacity to unveil and deploy natural and artificial allelic variation for the benefit of plant breeders. The editors hope that these two volumes, while providing new ideas and opportunities to those working in crop breeding, will help graduate students and teachers to develop a better understanding of the applications of crop genomics to plant research and breeding.

Contents of Volume 1

1. Genomics-assisted crop improvement: an overview; *RK Varshney, R Tuberosa*.
2. Genic molecular markers in plants: development and applications; *RK Varshney, T Mahender, RK Aggrawal, A Börner.*
3. Molecular breeding: maximizing the exploitation of genetic diversity; *AP Sørensen, J Stuurman, JR van der Voort, J Peleman*.
4. Modeling QTL effects and marker-assisted selection in plant breeding; *M Cooper, DW Podlich, L Luo*.
5. Applications of linkage disequilibrium and association mapping in crop plants; *ES Ersoz, J Yu, ES Buckler*.
6. Exploitation of natural biodiversity through genomics; *S Grandillo, S D Tanksley, D Zamir*.
7. Genomeless genomics in crop improvement; *KJ Lim, V Fey, S Rudd*.
8. Comparative genomics of cereals; *J Salse, C Feuillet*.
9. Cloning QTLs in plants; *S Salvi, R Tuberosa*.
10. Use of serial analysis of gene expression (SAGE) for transcript profiling in plants; *PC Sharma, H Matsumura, R Terauchi*.
11. Genetical genomics: successes and prospects in plants; *M Kirst, Q Yu*.
12. Analysis of salt stress-related transcriptome fingerprints from diverse plant species; *A Pareek, SL Singla-Pareek, SK Sopory, A Grover*.
13. Auxin and cytokinin signaling component genes and their potential for crop improvement; *JP Khurana, M Jain, AK Tyagi*.
14. Statistical advances in functional genomics; *RW Doerge*.
15. TILLING and EcoTILLING for crop improvement; *BJ Till, L Comai, S Henikoff*.
16. Characterization of epigenetic biomarkers using new molecular approaches; *M-V Gentil, S Maury.*

Contents of Volume 2

1. Microsatellite and SNP markers in wheat breeding; *MW Ganal, MS Röder*.
2. Molecular markers and QTL analysis for grain quality improvement in wheat; *D Lafiandra, MC Sanguineti, M Maccaferri, E Deambrogio*.
3. Molecular approaches and breeding strategies for drought tolerance in barley; *M Baum, M van Korff, P Guo, B Lakew, SM Udupa, H Sayed, W Choumane, S Grando, S Ceccarelli*.
4. Molecular markers for gene pyramiding and disease resistance breeding in barley; *W Friedt, F Ordon*.
5. Cloning genes and QTLs for disease resistance in cereals; *B Keller, S Bieri, E Bossolini, N Yahiaoui*.
6. Maize breeding and genomics; *M Lee*.
7. Molecular markers and marker-assisted selection in rice; *DJ Mackill*.
8. Application of genomics for molecular breeding in rice; *NK Singh, T Mohapatra*.
9. Marker-assisted selection in sorghum; *G Ejeta, JE Knoll*.
10. Molecular genetics and breeding of grain legume crops for the semi-arid tropics; *RK Varshney, DA Hoisington, HD Upadhyaya, PM Gaur, SN Nigam, K Saxena, V Vadez. NK Sethy, S Bhatia, R Aruna, MVC Gowda, NK Singh*.
11. Genomics approaches to soybean improvement; *TD Vuong, X Wu, MS Pathan, B Valliyodan, HT Nguyen*.

12. Application of genomics to forage crop breeding for quality traits; *T Lübberstedt*.
13. Molecular mapping, marker-assisted selection and map-based cloning in tomato; *MR Foolad*.
14. Genomics for improvement of Rosaceae temperate tree fruit; *P Arús, S Gardiner*.
15. DNA markers: development and application for genetic improvement of coffee; *PS Hendre, RK Aggarwal*.
16. Genomics of root nodulation in soybean; *K Van, MY Kim, S-H Lee*.
17. Genomics of wheat domestication; *C Pozzi, F Salamini*.
18. Transcriptome analysis of the sugarcane genome for crop improvement; *P Arruda, T Rezende e Silva*.

1–2 December, 2007.
Kansas City, MO, USA.

Note: Speaker abstracts are followed by the poster abstracts.

IWGSC: A physical map and sample sequencing of the homoeologous group-3 chromosomes of wheat.

Bikram S. Gill [1], Wanlong Li [1], Sunish K. Sehgal [1], Justin D. Faris [2], Leela Reddy [3], Katrien M. Devos [4], Pablo Rabinowicz [5], Robin Buell [6], Piotr Gornicki [7], Jaroslav Dolezel [8], H. Simkova [8], Yaqin Ma [9], Frances Chen [9], Frank M. You [9], and Ming-Cheng Luo [9].

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Hexaploid wheat (*Triticum aestivum*) presents a challenge in constructing physical maps, which are prerequisite for genome sequencing and annotation, mainly due to its large genome size (~17 Gb), polyploid nature, and repetitive sequence content (>90%). The complexity of the analysis can be reduced by establishing physical maps and sequences of isolated chromosome BAC libraries using flow cytometry and wheat aneuploids developed in Chinese Spring wheat (CS) by the late E.R. Sears. Under the auspices of the IWGSC, a pilot project on chromosome 3B was initiated in France, and a new project on the physical map of chromosome 3D has been funded by the EU. The USDA–CSREES funded a pilot project on chromosome arm 3AS in the U.S. with the specific objectives to (1) develop an anchored physical map for the short arm of chromosome 3A, fingerprint BAC libraries constructed from a 3AS telosomic chromosome isolated by flow cytometry, assemble the fingerprints using the FPC program, and anchor the FPC contigs to the cytogenetic and genetic maps using a combination of EST, RFLP, and SSR markers and markers derived from BAC-end sequences (BES); (2) generate 18.4 Mb of sequence from the chromosome 3AS BAC libraries, sequence 48 targeted BAC clones (5.8 Mb) to 8X sequence coverage and BAC end sequence 10,000 random clones (12.6 Mb), annotate these sequences for repeats and genes using a combination of automated and manual annotation, and identify chromosome-specific markers from the BES for physical and genetic mapping; (3) perform comparative sequence analysis in wheat, compare the 3AS BAC sequences (objective 2) with sequences already (and to be) generated from homoeologous chromosome arm 3BS for new insight into structural and functional specificities of the genomes in a polyploid context, and perform comparative analyses with rice, a related cereal for which finished sequence is available; (4) further wheat genome annotation and bioinformatics and construct an expanded wheat genome annotation resource; and (5) train and educate the wheat community in genomics and hold two workshops. From a BAC library for CS 3AS from flow-sorted chromosomes with 12× chromosome equivalent, 55,584 BAC clones were fingerprinted and assembled into 1,677 contigs (10-fold 3AS coverage) and 11,939 singletons. Ten thousand random BACs were end sequenced and 16,795 high-quality BESs with an average read-length of 500 bp and a total of 8.3 Mb of genomic sequences. Microsatellite primers were successfully developed from 598 SSRs found in the BES and, on average, 20 and 11 % of markers were polymorphic in *T. monococcum* and *T. turgidum* species, respectively. Another 504 genic sequences were identified from the BES and screened in the 3AS BAC fingerprint database. Primers were developed from 279 genic sequences that were present in contigs and will be used for anchoring BAC contigs to genetic map. EST–STS markers are being developed from 3AS EST bin-mapped markers. In addition to already bin mapped ESTs, another 250 ESTs were designed on the basis of similarity with rice chromosome 1 and are being used to physically anchor the BAC contigs using 190 six-dimensional pools. Progress is being made on the construction of 20 Mb BAC-contig for comparative sequencing of *Fhb1*/*Rph7* region.

Wheat: A challenging genome to study.

Katrien M. Devos, Department of Crop and Soil Sciences and Department of Plant Biology, University of Georgia, Athens, GA 30602, USA.

The hexaploid nature (2n=2x=42) and large genome size (C=17,000 Mb) of wheat make genomic analyses in this crop challenging. Nevertheless, a large number of resources have been built over the past five years, including BAC libraries of diploid, tetraploid and hexaploid wheats, more than 1 million expressed sequenced tags, and partial physical maps of the *Ae. tauschii* genome and of selected chromosomes of hexaploid wheat. Large-scale mapping of ESTs, and sequence analysis of regions carrying traits of interest and of randomly selected BAC clones has greatly increased our understanding of the organization of the wheat genome. The next big challenge will be to sequence the entire wheat genome. The development in recent years of new sequencing technologies has made sequencing the 17,000 Mb wheat genome an attainable goal. The short sequence reads associated with these techniques, however, make sequence assembly extremely challenging. My presentation will contain information on our current knowledge of the wheat genome, and some food for thought on strategies for wheat genome sequencing.

Wheat domestication and genetic diversity.

Jan Dvorak [1], Eduard D. Akhunov [5], Alina R. Akhunova [5], Olin D. Anderson [2], James A. Anderson [3], Nancy Blake [5], Michael T. Clegg [4], Devin Coleman-Derr [1], Emily J. Conley [3], Curt C. Crossman [1], Karin R. Deal [1], Jorge Dubcovsky [1], Bikram S. Gill [5], Yong Q. Gu [2], Jakub Hadam [5], Hwayoung Y. Heo [6], Naxin Huo [2], Gerard R. Lazo [2], Karen E. Lundy [4], Ming-Cheng Luo [1], Ya Q. Ma [1], David E. Matthews [7], Patrick E. McGuire [8], Peter Morrell [4], Calvin O. Qualset [8], James Renfro [1], Susan Reynolds [3], Dindo Tabanao [3], Luther E. Talbert [6], Chao Tian [1], Dona Toleno [4], Marilyn Warburton [9], Frank M. You [1], and Wenjun Zhang[1].

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Domestication of diploid einkorn wheat and tetraploid emmer wheat (*Triticum turgidum* subsp. *dicoccoides*, genomes AABB) was one of the key events during the emergence of agriculture in southwestern Asia. Emmer was the source of durum wheat and the tetraploid ancestor of hexaploid common wheat. Although einkorn wheat may have been domesticated in several places, genetic evidence based on single-locus and multilocus genotypes of restriction fragment length polymorphism at 131 loci suggest that domesticated emmer and the rest of the tetraploid wheats have a monophyletic origin. Emmer was domesticated west of Diyarbakir in southeastern Turkey. Subsequently, gene flow from wild emmer to domesticated emmer occurred across the entire distribution of wild emmer and enhanced its genetic diversity. This process was important particularly in southern Levant. Consequently, the Mediterranean emmer population has the highest genetic diversity of all domesticated emmer populations. Durum is closely related to the Mediterranean and Ethiopian domesticated emmer populations and probably originated in the eastern Mediterranean. Common wheat originated in Transcaucasia. Gene flow from domesticated tetraploid wheat and wild emmer wheat greatly enhanced genetic diversity in the A and B genomes. Gene flow from *Ae. tauschii* to the D genome was sporadic, and the D genome shows low gene diversity. Genetic diversity was estimated in 942 genes in one, two, or all three *T. aestivum* genomes, and the loci were mapped in *Ae. tauschii*. Genetic diversity varied among *T. aestivum* chromosomes in the A, B, and D genomes, the greatest diversity is in chromosomes 1A, 1B, and 2D, and the lowest in 4A, 4B, and 5D. Selection during domestication of tetraploid wheat or evolution of hexaploid wheat is principally responsible for variation in diversity among wheat chromosomes.

Exploring the functional roles of the Q gene homoeoalleles in wheat.

Zengcui Zhang [1,2], Kristin J. Simons [2], Bikram S. Gill [3], and Justin D. Faris [2].

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The *Q* gene on chromosome 5A (*Q-A1*) has been referred to as a super gene in wheat, because it governs the free-threshing character and square spike phenotype. *Q* also pleiotropically affects many other traits associated with wheat development and domestication. The function of the *Q* homoeoalleles on chromosomes 5B (*q-B1*) and 5D (*q-D1*) is less understood. In this study, we further investigated the function of *Q-A1* through comparison of the wild type *Q-A1* allele with an EMS-induced *Q-A1*-knockout mutant in the hexaploid wheat cultivar Bobwhite. The phenotypic comparison confirmed the numerous pleiotropic effects of *Q-A1*. Relative quantitative-PCR (RQ-PCR) analysis revealed that the mutant allele, which has a premature stop codon, was transcribed at a lower level than the wild type. This result provided additional evidence that the amino acid at position 329 is important for homodimer formation, which may be a mechanism of self-regulation. We also initiated the functional analysis of the *q* homologs on chromosomes 5B and 5D. The genomic and cDNA sequences of *Q-A1*, *q-B1*, and *q-D1* share >90% similarity. Chinese Spring *q-B1* and *q-D1* deletion lines (5BL-14 and 5DL-5) had semispeltoid spikes instead of square spikes as observed in euploid Chinese Spiring. We developed a double deletion line lacking both *Q-A1* and *q-D1*, which exhibited more extreme speltoid spikes and tougher glumes compared to the single-gene deletion lines. In addition, alternatively spliced transcriptional variants were found for both *q-B1* and *q-D1* in spike tissues. Specific RQ-PCR assays were developed for each homoeoallele and their transcriptional variants, and the results suggested the presence of complex interactions among the homoeoalleles. This study demonstrated that the *q* homoeoalleles on 5B and 5D contributed to the suppression of speltoid characters and glume toughness but to a lesser degree than does the *Q-A1* allele on 5A. The mutation in *q-A1* that gave rise to *Q-A1* played a key role in the modern wheat evolution.

The Brachypodium genome structure and its potential as a model for wheat.

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Research in the grass crops, including wheat, has suffered from the lack of an appropriate model system and, thus, have not benefited from the potentials of such models similar to how *Arabidopsis* has revolutionized general plant biology. Although *Arabidopsis* has application to the grasses in areas of basic plant biology, *Arabidopsis* is a dicot, and a more appropriate tool for the dicots and less so for the monocots such as the grasses. Rice was originally proposed to fill this need for the grasses, but for a number of reasons, rice has not proven sufficient for all grasses. For example, rice has a longer life-cycle, is tropic/semitropic, is difficult to achieve flowering in most regions of the U.S., and is larger than appropriate for a model. In place of rice, the grass *Brachypodium distachyon* has been proposed as a more appropriate model system. Among its attributes, *Brachypodium* has an 8–10 week life cycle, a small genome (~320 Mb), can be transformed by *Agrobacterium* at a high efficiency, and is in the process of having the complete genome sequenced. As an added bonus for the Triticeae, taxonomic relatedness puts *Brachypodium* within a sibling tribe to the Triticeae and, thus, far closer in evolutionary distance to wheat than is rice. An overview will be given of what is known of the structure of the *Brachypodium* genome, an update on progress at developing tools necessary for *Brachypodium* to serve as a model system, the available results on how *Brachypodium* DNA sequences compare with available wheat genome information, and speculations on how *Brachypodium* will assist wheat research.

Wheat Stem Rust Genome Project: First look under the hood.

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Puccinia graminis f. sp. *tritici*, the casual agent of stem rust of wheat, has caused major epidemics over the last century. Renewed awareness of the threat to wheat production posed by this disease has occurred with the emergence of a new, virulent race (TTKS) in Eastern Africa. *P. graminis* is a dikaryotic fungus with five spore stages and two plant hosts. Whole-genome shotgun coverage (12X) has been generated by paired-end sequencing from three libraries generated by randomly sheared, total genomic libraries. A 6.8 X draft assembly containing 392 supercontigs (N50 911 kb) and covering 89 Mb was constructed. A restriction fingerprint map containing 1,969 contigs (10.8 X) was generated from approximately 22,000 fosmid clones. The restriction fingerprint map and draft sequence assembly are highly similar with 99% of the sequence assembly being placed on the fingerprint map. Annotation of the draft assembly predicted 20,567 genes, with approximately one-half of the gene calls supported by homology to sequence data in public databases and/or *P. graminis* EST database. Approximately 57,000 ESTs were generated from three cDNA libraries (urediniospores, germinated urediniospores, and teliospores), which were assembled into 6,465 synthetic contigs. Thirty-six percent of the EST contigs could be annotated using GO categories. The majority of the EST synthetic contigs were stage-specific, with only 8% common to all three libraries.

Genomic and metabolic analysis of *R* gene-mediated defense pathways in wheat.

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Plant defense involves three major steps: surveillance, signal transduction, and the production of defense chemicals. A great deal of information on signal perception and transduction has been revealed in numerous plant-parasite systems. Here we investigated changes in metabolic pathways that might lead to accumulation of defense chemicals using genomic and metabolic profiling. The wheat-Hessian fly interaction was used in this study. Hessian fly is an insect but shares many features with plant pathogens, being sessile during feeding stages and having avirulence genes that match plant resistance genes in gene-for-gene relationships. Many genes involved in carbon/nitrogen metabolism were differentially regulated during compatible and incompatible interactions. During compatible interactions, the attacking site became a carbon sink. Photoassimilates were transported to the attacking site from other parts of the plant. Part of the transported photoassimilates were converted into amino acids through coördinated activation of key metabolic pathways including glycolysis, the tricarboxylic acid cycle, and amino acid synthesis pathways. In contrast, the attacking site became a nitrogen sink during incompatible interactions. Nitrogen was transported to the attacking site from other parts of the plant in the form of asparagine. The transported nitrogen was likely converted into defensive secondary metabolites. Our data suggested that the formation of a carbon sink and the conversion of C-compounds into N-compounds at the feeding site is a necessary condition for Hessian fly larvae to survive and develop in susceptible plants, whereas the formation of a nitrogen sink and the increase in phenylpropanoids and other secondary metabolites may be part of the resistance mechanism.

Fine mapping of the Lr46/Yr29 locus in wheat.

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Rust diseases, including leaf rust (*Puccinia triticina*), stripe rust (*P. striiformis* f. sp. *tritici*), and stem rust (*P. graminis* f. sp. *tritici*) are globally the most important diseases of wheat. Genetic resistance is the best form of control but frequent race changes typically render new varieties susceptible within a few years after release. For typical resistance genes, the

mechanism of resistance and the basis of race specificity are due to gene-for-gene interactions. However, some disease resistance genes are thought to be durable, because they are not dependent on the recognition of a single *Avr* gene product from the pathogen by an R gene. The adult-plant resistance gene *Lr46* has provided non-race-specific resistance to leaf rust that has remained effective for more than 30 years. The gene also has a pleiotropic effect on resistance to stripe rust (*Yr29*). Using recombinant, chromosome substitution line populations, we previously located *Lr46* on the terminal region of the long arm of chromosome 1B that is syntenic to chromosome 5L of rice. To fine map the *Lr46* gene region, high resolution mapping (HRM) populations were developed that represent 4,100 gametes. The EST-derived, STS marker *XSTS3680* that co-segregated with *Lr46* in the original mapping populations was mapped 0.15 cM distal to *Lr46* in the HRM populations. A BAC contig of the *Lr46* region is being constructed. New SSR and SNP markers identified from the BAC clones and linked to *Lr46* have been evaluated on a set of diverse wheat lines to determine their usefulness for marker-assisted selection. Gene expression studies can complement map-based cloning efforts, because expression data can be used for identifying candidate genes, identifying expression markers, and for generating and testing hypotheses about genetic resistance mechanisms. To identify transcripts associated with *Lr46*-mediated adult-plant resistance, the Affymetrix Wheat GeneChip Microarray was used to identify transcriptional changes in isogenic lines with and without *Lr46*. Considering the increasing worldwide use of *Lr46* and other adult-plant genes for durable rust resistance, it is essential to obtain a greater understanding of their mechanisms of resistance. Also essential is obtaining the best possible markers for breeding for durable resistance.

Genetic analysis of host-toxin interactions in the wheat–Stagonospora nodorum pathosystem.

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Stagonospora nodorum, causal agent of Stagonospora nodorum blotch (SNB) in wheat, produces multiple necrosis-inducing host-selective toxins (HSTs) that interact with dominant host sensitivity genes to cause disease. Absence of either the toxin or the dominant host gene precludes recognition and results in an incompatible (resistant) response. Therefore, these host-toxin interactions are mirror images of classical gene-for-gene interactions. One of the first HSTs identified in this system was SnToxA, which was horizontally transferred from *S. nodorum* to the tan spot pathogen *Pyrenophora tritici-repentis* around 1941. This event is considered to have been significant for the establishment of tan spot as a pathogen. Sensitivity to SnToxA is governed by the *Tsn1* gene on the long arm of chromosome 5B. To date, eight additional toxins, designated SnTox1 through SnTox8, have been identified, and their corresponding host sensitivity genes, designated *Snn1* through *Snn8,* have been mapped to wheat chromosome arms 1BS, 2DS, 5BS, 4BL, 5BS, 6AL, 5DS, and 3DL, respectively. Genetic analysis of several host-toxin interactions indicates that they play important roles in the development of disease in adult plants as well as seedlings, and their effects are mostly additive. To gain a better understanding of compatible host-toxin interactions at the molecular level, we have embarked on the positional cloning of two host-sensitivity genes: *Tsn1* on 5BL and *Snn1* on 1BS. Toward the map-based cloning of *Tsn1* on chromosome 5B, we sequenced and assembled chromosome 5A and 5B BAC contigs spanning the gene. Evaluation of gene content and micro-colinearity between the orthologous regions of 5A, 5B, and rice chromosome 9 indicated the 5A region and rice share a higher level of micro-colinearity than the 5B region does with rice due to the presence of numerous transpositions, deletions, and rearrangements present in the wheat 5B region. In addition, the 5B *Tsn1* candidate region is nearly 4 times larger than the corresponding region of 5A due to the presence of additional genes and transposable elements. At least ten genes exist within the 350 kb *Tsn1* candidate-gene region, and they are currently being validated by comparative sequence analysis of *Tsn1*-disrupted mutants and virus-induced gene silencing. An important applied by-product of this research is the development of efficient PCR-based markers for *Tsn1*, which are being used to introgress SnToxA insensitivity into adapted germ plasm. Overall, this research demonstrates the potential of the wheat–*S. nodorum* pathosystem to be an excellent toxin-based inverse gene-for-gene model.

Toward a better understanding of a major FHB resistance QTL in tetraploid wheat.

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Fusarium head blight (FHB), mainly caused by the fungus *Fusarium graminearum*, is a destructive disease of wheat and poses a serious threat to wheat production and health of wheat consumers worldwide. Partial resistance to FHB has been identified in common wheat (*Triticum aestivum*). A source of effective resistance to FHB, however, has not been found in durum wheat (*T. turgidum* L. subsp. *durum*). A major FHB resistance QTL, *Qfhs.ndsu-3AS,* was identified and mapped to chromosome 3A of *T. turgidum* L. subsp. *dicoccoides*, a wild relative of durum wheat, in a previous study. This QTL explains 42% of the phenotypic variation for FHB resistance and is not homoeologous to *Qfhs.ndsu-3BS*, a major FHB-resistance QTL identified in the Chinese common wheat cultivar Sumai 3. We have saturated the genomic region harboring the QTL using EST-derived TRAP (target region amplified polymorphism), STS (sequence tagged site), and SSR (simple sequence repeat) markers and are developing a high-resolution map of this FHB-resistance QTL. We used the genomic sequences from 10 PACs on the short arm of rice chromosome 1, which are collinear with the chromosomal regions harboring *Qfhs.ndsu-3AS*, to search the wheat EST pool and identified 404 unmapped wheat ESTs for marker development. To date, a total of 58 new molecular marker loci have been detected on chromosome 3A. Five new EST-derived STS markers mapped to a chromosomal interval of 10.7 cM harboring the QTL in a population of 83 recombinant inbred chromosome lines (RICLs). One of the STS markers was derived from the EST of a gene from which expression was induced by the FHB pathogen *F. graminearum* in the common wheat cultivar Frontana. This STS marker mapped 0.6 cM proximal to *Xgwm2*, an SSR marker closely linked to the QTL peak. Frontana also contains a major FHB-resistance QTL on chromosome 3A. In addition, we have been genotyping a large F_2 population (>2,000 individuals) derived from the cross between Langdon durum and a RICL that has a small *T. turgidum* subsp. *dicoccoides* chromosomal fragment (10.7 cM) harboring *Qfhs.ndsu-3AS* for fine mapping of the QTL. This research facilitates the use of *Qfhs.ndsu-3AS* in wheat breeding and germ plasm development through marker-assisted selection and map-based cloning of the QTL.

Linkage disequilibrium and association mapping for wheat improvement.

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Knowledge of the level of genetic diversity and historical relationships among elite wheat germ plasm is very useful for association mapping (AM) and the exploitation of genetic variation in wheat. Linkage disequilibrium (LD), or nonrandom association of alleles at adjacent loci throughout the genome within a population forms the basis for AM strategies. The power of association analysis is affected by the patterns of LD, the extent of LD in the genome, and the variation in LD from one population to another. Linkage disequilibrium is affected by mating system, recombination rate, population structure, population history, genetic drift, directional selection, and gene fixation. Linkage disequilibrium estimates for cultivated wheat and barley have indicated that LD decays over 5 to 40 cM, a much slower rate than reported for outcrossing species. Germ plasm can be broadly classified into three categories: exotic accessions from germ plasm bank collections, intermating populations, and elite lines. These classes of germ plasm can be used for different purposes according to their genetic expectations. A core collection from a germ plasm bank may be used to screen high heritability traits, whereas elite lines are usually evaluated for low heritability traits in replicated, multi-environment trials. Intermated progenies of a segregating population are evaluated in different ways depending on the recurrent selection method and traits. The genetic expectations for an exotic core collection are low LD, low to medium population structure, and high allelic diversity. Linkage disequilibrium is high in the early generations of a segregating population and declines with additional cycles of intermating and selection. Elite lines have high LDs and population structure. Exotic germ plasm is typically used as a source of novel alleles in a marker-assisted backcross scheme, whereas elite lines are intermated and marker-assisted selection is used in the segregating progenies in a forward-breeding strategy. Intermated segregating populations offer a favorable balance of power and precision for association analysis and would allow mapping of quantitative traits with increasing resolution through cycles of intermating.

Association analysis and complex trait dissection can be integrated into conventional breeding programs using molecular tools and information to facilitate marker-assisted selection of parents and segregating populations. Breeding programs are dynamic, complex genetic entities that require frequent evaluation of marker/phenotype relationships. Biparental cross populations sometimes involve poorly adapted parents, exhibit maximum linkage disequilibrium, and are limited to two alleles per locus. Association mapping can be conducted directly on the breeding material greatly facilitating the practical use of information in a crop improvement program. Because there is more genetic variation in a breeding program than in a biparental cross, phenotypic variation and marker polymorphism are much higher. Genotypic data can be combined with phenotypic data from routine screening and variety trial evaluations to facilitate selection for low heritability traits. Probably the most important advantage for a breeding program is that novel alleles can be identified and the relative allelic value can be assessed as often as necessary. To minimize statistical error, correction for population structure is critical in a collection of genotypes, especially in a breeding program where relationships are highly variable. Simulations suggest potential problems associated with unknown marker/QTL relationships and can be used to forecast the response to marker-assisted selection.

The Wheat–CAP Project: Wheat applied genomics.

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The Wheat Coordinated Agricultural Project (WheatCAP) is a consortium funded by USDA–CSREES National Research Initiative that includes public breeders from 25 states and four USDA–ARS genotyping centers, and integrated with GrainGenes. Because public wheat cultivars account for 78% of the wheat production in the United States, this project has a significant economic impact. The competitiveness of US public wheat breeding is being increased by the incorporation of marker-assisted selection (MAS). With input from regional stakeholders, each breeder has determined the most important traits to select through MAS and has access to 5,000 analyses per year. During the first two years of the project, the high-throughput, USDA–ARS genotyping centers have generated more than 190,000 datapoints. The traits selected include disease and pest resistance genes (65%), quality traits (17%), tolerance to abiotic stresses (12%), and agronomic or special purpose traits (9%). Molecular markers for new traits are being identified using QTL analysis in 18 segregating populations created by the breeding programs using parental lines adapted to the different U.S. wheat-growing regions. As part of our outreach efforts, we are informing growers and end-users of the economic advantage of lines developed by MAS through field days and demonstration plots. We are training over 90 students at all levels in agricultural sciences and breeding as part of our educational objectives. Through September 2007, the WheatCAP participants have published 25 papers in peer-reviewed journals, presented 71 lectures and posters, and organized three experiential trips and 51 workshops and field days. For further information see http://maswheat.ucdavis.edu.

Wheat SNP markers: Discovery and utilization.

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For the purposes of marker-assisted selection, association mapping, genetic mapping, and positional cloning, the availability of a large number of molecular markers is critical. In the foreseeable future, single nucleotide polymorphisms (SNPs) will become the marker of choice for all the above-listed applications. Polyploidy, large genome size, and low level of polymorphism make the development of wheat SNP markers very challenging. However, recent advances in high-throughput sequencing and genotyping led to the development of technological platforms that could easily overcome all the limitations of the wheat system. New sequencing platforms could be used to discover the required number of SNPs over larger regions of the wheat genome; new genotyping platforms could overcome the limitations caused by polyploidy and allow genotyping a large number of plants at large number of SNP loci. New technologies, combined with new methods of statistical analysis, are extremely powerful tools for studying wheat at the whole-genome level and dissecting the genetic basis of complex traits. An overview of recently developed wheat SNP resources and their application to the analysis of wheat genome will be presented.

Using BSMV–VIGS for functional genomics in wheat.

Steven Scofield, USDA–ARS Crop Production and Pest Control Unit, West Lafayette, IN 47907, USA.

Our laboratory has gained significant experience using the barley stripe mosaic virus system for virus-induced gene silencing (BSMV-VIGS) as a tool for functional genomics in wheat. This presentation will summarize our experiences using the BSMV-VIGS system to functionally identify genes with essential roles in disease resistance pathways and, in particular, it will focus on the design considerations for successful VIGS experiments.

Development of resources for reverse-genetic analysis in Triticum monococcum.

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Reverse genetics is a powerful tool to discover gene function by identifying modifications in specific genes. Mutagenized populations are generated using either chemical, physical, or biological methods and screened for lesions for the desired gene of interest to identify its functional role. The goal of this project is to develop a mutagenized population of *Triticum monococcum* and screening systems for lesions in genes of interest using DNA pooling and PCR-based approaches as a reverse-genetic resource for the scientific community. We have generated mutagenized populations using 1,2,3,4-diepoxybutane (DEB) or trimethylpsoralen along with a UV treatment (TMP/UV) as a pilot study with chemical concentrations that lead to 20–25% survival rates. Experiments were conducted to identify the relative efficiency of these chemicals in a) creating mutations and b) detecting deletions/lesions using forward and reverse-genetic approaches.

We have generated approximately 1,000 M_2 families from each chemical treatment. Initial observations from five germinating seeds per M_1 plant indicated 2% albinos in 250 M_2 families per chemical treatment. DNA was isolated using a filter-based method from individual plants and, currently, is pooled to 1:8 and 1:16 times and used for screening using different methods. A total of 424 DEB-treated, M_2 families were advanced to the M_3 generation to observe visible mutant phenotypes and determine forward mutation frequency for this chemical treatment. Many phenotypic mutants, such as dwarf, early and late flowering, bushy, oligoculm, small spike, purple plants, and disease mimic were observed in this M_3 population. The percent of phenotypic mutants in the M_2 as observed in the M_3 families was 0.94% to 8.02 % for ten different phenotypes. The results of the screening for lesions in the mutagenized population will be presented, which will strengthen the use of this approach for developing reverse-genetic resources in wheat.

Poster 1. A detailed, comparative sequence analysis on the HMW-glutenin locus regions of eight genomes from diploid and polyploid wheats.

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Wheat is the most widely grown crop worldwide and feeds one-third of the world's population. As a result, wheat is foremost among the world's crops both in regards to its importance as a staple of mankind and its economic significance. Despite several successes in sequencing several plant genomes, the complex wheat genome might still represent challenges in genome-sequencing projects. Compared to most other cereals, bread wheat (*Triticum aestivum*) has an extremely large genome (~16,000 Mb); more than 30-fold greater than the rice genome. Furthermore, bread wheat is an allohexaploid species consisting of three related subgenomes (A, B, and D). To study the structural organization of wheat genomes, we sequenced large genomic regions harboring HMW-glutenin genes from eight Triticeae genomes including the D genome from diploid *Ae. tauschii*, the A^m genome from diploid *T. monococcum* subsp. *monococcum*, the A and B genomes from tetraploid *T. turgidum*, the A, B, and D genomes from hexaploid wheat, and the H genome from barley. The in-depth sequencing of the HMW-glutenin locus regions allowed us to compare sequence changes among the three

homoeologous A, B, and D genomes and analyze the types and rates of sequence evolution between homologous wheat genomes. Our detailed comparative sequence analyses of HMW-glutenin regions among the different wheat genomes provided molecular mechanisms underlying the rapid sequence changes among the A, B, and D genomes and revealed extensive sequence conservation between homologous HMW-glutenin genomic regions. The results from this study also provided useful knowledge on designing effective strategies to decipher the complex wheat genome.

Poster 2. Meta-analyses of QTL associated with Fusarium head blight resistance.

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Quantitative trait loci (QTL) associated with different types of Fusarium head blight (FHB) resistance have been identified from various sources. Because of differences in genetic backgrounds, experimental factors, and analysis methods, the marker loci orders on chromosomes and significance are not consistent across studies. Such discrepancies in the proposed chromosome location and the effect of putative QTL on FHB as well as differences in the amount of variation explained by markers associated with a QTL make it difficult to select common flanking markers that will be most diagnostic when applied in marker-assisted selection (MAS) and breeding. Meta-analysis has been used to estimate the confidence intervals (CI) of identified QTL in plant and animal genomes. The objective of this study is to estimate the CIs of 63 QTL associated with different types of FHB resistance and align them onto the consensus ITMI map to determine if different QTL on the same chromosomes from different studies overlap. Forty-seven QTL associated with FHB resistance types I, II, III, and IV from various sources were classified into 15 clusters on 10 chromosomes. Thirty-nine QTL are significant QTL (LOD > 4.0). Two clusters on 3BS and 5A contain confirmed QTL from Sumai 3 and Wangshuibai. Markers flanking a QTL cluster may help breeders to pyramid QTL more efficiently in marker-assisted selection.

Poster 3. Whole genome mapping and QTL analysis in a doubled-haploid population derived from the cross between a synthetic hexaploid wheat and hard red spring wheat.

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Quantitative trait loci analysis allows the identification of genomic regions associated with quantitative traits, which provides an estimation of the number and chromosomal location of genes involved and leads to the identification of molecular markers suitable for marker-assisted selection. In this research, we used the 'wheat × maize' method to develop a doubled-haploid population derived from the synthetic hexaploid wheat line TA4152-60 and the North Dakota hard red spring wheat line ND495. The population consisted of 213 lines, and a subset of 120 lines was randomly selected and used to construct linkage maps of all 21 chromosomes. The maps consisted of 626 markers, including 408 SSRs and 218 TRAPs, and spanned 3,811.5 cM with an average density of one marker per 6.1 cM. Telomere, sequence-based fixed TRAP primers were used to define the ends of seven linkage groups. Novel tan spot resistance QTL were identified on chromosomes 2A, 5A, and 5B. In addition to *Tsn1* and *Snn1*, a new *Stagonospora nodorum* blotch toxin-sensitivity gene identified on chromosome 3D was found to be significantly associated with the disease. Major QTL for days to heading, plant height, coleoptile color, glume toughness, and seed threshability also were identified. The DH population and genetic map will be a useful tool for the identification of other disease resistance QTL and agronomically important loci and aid in the identification and development of markers for marker-assisted selection.

Poster 4. Development of markers from BAC-end sequences (BESs) for anchoring 3AS BAC contigs in wheat.

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In an effort to develop wheat resources for genomics studies, we are constructing a BAC-based physical map for the chromosome arm 3AS of hexaploid wheat cultivar Chinese Spring. In total, 16,795 high-quality BAC-end sequences showing an average read-length of 500 bp with a total of 8.3 Mb of genomic sequence were obtained from 9,984 clones. To accelerate the integration of the bacterial clone resources with the genetic map for the International Wheat Genome Sequencing Project, we searched all available markers from these sequence data. A total of 1,057 simple sequence repeats (SSR) were identified out of which 189 had more than nine repeats. Microsatellite primers were successfully developed from 598 SSRs, and a subset was screened for polymorphism in both *T. monococcum* and *T. turgidum* species. On average, 20 and 11 % of the markers were polymorphic in *T. monococcum* and *T. turgidum*, respectively. Most of the primers showed simple amplification patterns indicating their utility in genetic mapping. Efforts are underway to map these markers for physical anchoring the BACs to the genetic map. Another 504 genic sequences were identified from the BES and were screened in the 3AS BAC fingerprint database. Primers were developed from 249 genic sequences that were present in contigs and will be used for anchoring BAC contigs to genetic map.

Poster 5. Validation of six QTL associated with Fusarium head blight resistance in adapted soft red winter wheat.

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This study was conducted to validate molecular markers linked to six FHB resistance QTL previously identified in different biparental populations using elite breeding lines with incorporated FHB resistance to initial infection, spread, and DON accumulation in different genetic backgrounds. A total of 129 SSRs were characterized in the 145 breeding lines. Forty-four unrelated SSRs (four SSRs/chromosome) were used in background selection and the remaining 85 SSRs were used to validate the target QTL. The 145 wheat lines also were evaluated in yield performance trials at two locations, Blacksburg and Warsaw, VA, and for type I, type II, and DON resistance in a scab nursery at Blacksburg, VA, in 2005 and 2006. Molecular markers linked to scab resistance genes located on wheat chromosomes 2BS, 2DS, 3AS, 3BS, 5AS, and 6BS were confirmed and the allelic effect of associated marker loci was analyzed. Adapted, resistant lines with novel alleles different from known exotic sources were characterized. Renwood 3260 and its derived lines have good overall resistance and high yield potential. These lines have unique resistance with alleles differing from those of known resistance sources W14 and Sumai 3 at marker loci GWM429, GWM120, GWM261, BARC33, and GWM186 in the chromosome 2BS, 2DS, 3BS, and 5AS QTL regions, respectively. Ernie and its derived lines also have good overall resistance but did not produce promising grain yields in Virginia. These lines have unique resistance comprised of same resistance alleles as Renwood 3260 at loci GWM429, GWM120, and GWM261 in the 2BS and 2DS QTL regions. Both the Ernie and Renwood 3260 derivatives contain the same resistance alleles as the donor parent W14 at loci WMC264, BARC133, and BARC117 in 3AS, 3BS, and 5AS QTL regions, respectively. In addition, these lines have unique resistance alleles in their background at GWM493 and WMC152 in 3BS and 6BS QTL regions. This is the first study to validate six FHB QTL in elite breeding lines. QTL markers validated in the current study have been used widely in parental selection, gene pyramiding, and in postulating and selection of FHB resistance of progeny derived from such newly developed FHB-resistant lines. This also is the first study evaluating the effects of allelic differences and genetic backgrounds on FHB resistance. Newly developed, FHB-resistant lines with unique QTL/allele combinations have been used as parental lines in most Eastern U.S. wheat-breeding programs. Some of these lines will be released as cultivars and/or adapted germ plasm. The newly developed FHB-resistant lines and unique QTL/marker allele profiles identified

in this study will set the stage for using MAS not only for FHB resistance but also in combining FHB resistance with other important agronomic traits.

Poster 6. Molecular mapping of leaf rust resistance genes Lr41 and Lr42 in wheat.

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Leaf rust, caused by *Puccinia triticina* Erikss., is an important foliar disease of wheat worldwide. Pyramiding of major rust-resistance genes into a single cultivar by aid of molecular markers is an effective strategy to control the disease. Two leaf rust resistance genes, *Lr41* and *Lr42*, have been widely transferred from *Ae. tauschii* into wheat germ plasm lines. Recent mapping work located *L41* on 2DS, but markers for *Lr42* have not been reported to date. In this study, two sets of NILs were developed by backcrossing the two *Ae. tauschii* accessions TA2460 (*Lr41*) and TA2450 (*Lr42*) to the leaf rust-susceptible hard winter wheat cultivar Century. To identify new markers for *Lr42* and verify the markers for *Lr41*, two populations of 95 $BC_3F_{2:6}$ lines were analyzed with microsatellite markers. Four markers from chromosome 2DS were linked to *Lr41*, and two markers on chromosome 1DS were tightly linked to *Lr42*. The marker *Xbarc124* on 2DS was located 0.3 cM proximal to *Lr41*, and marker *Xwmc432* on 1DS was located 0.6 cM proximal to *Lr42*. Physical mapping of the markers using Chinese Spring nulli-tetrasomic and ditelosomic genetic stocks confirmed that markers linked to *Lr41* and *Lr42* were on 1DS and 2DS, respectively. Closely linked markers to *Lr41* and *Lr42* genes are new markers for these genes identified in this study and can be used for marker-assisted gene pyramiding in breeding programs.

Poster 7. Mapping of QTL for heat tolerance of wheat in response to high temperature.

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In cereals, heat stress during seed formation is critical factor in lowering yield. This study identified and mapped QTL for heat tolerance in wheat in response to two heat treatments (short and long term) during seed formation using recombinant inbred lines derived from the cross '7C'(heat resistant)/SERI M 82(heat susceptible)'. Yield components, such as kernel number, kernel weight, and grain filling duration were used as indicators of heat susceptibility. The phenotypic variation of individual yield components was normally distributed in response to heat stress suggesting that they have quantitative heritability. Transgressive segregation compared to the parents also was observed, suggesting that genetic variation from an optimal recombination of favorable loci from both parents occurred in the progeny population. One hundred thirteen SSR markers out of 320 were polymorphic between the 7C and SERI M 82 parental lines with a linkage coverage of 2,609 cM and average interval map distance of 25 cM throughout the whole genome. QTL for heat tolerance and their genetic effects were analyzed by association of percent reduction of each phenotypic trait of yield components with polymorphism in the 62 RILs. Eleven and 22 QTL for heat tolerance under short-term and long-term heat stress, respectively, were detected for each yield component phenotypic trait. Phenotypic variation was 93% for short-term and 86% under long-term heat stress.

Poster 8. Identification of seed dormancy for four populations derived from synthetic hexaploid wheat.

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Seed dormancy is a key adaptive trait for wild species and is also a major domestication-related trait for crop species. Cereal cultivars have been selected for rapid, uniform germination during domestication and breeding. Consequently, they generally have an insufficient degree of seed dormancy to resist preharvest sprouting (PHS). To seek dormancy genes from the wheat wild relative *Ae. tauschii*, we have identified four populations of doubled haploid (DH) or recombinant inbred (RI) lines derived from synthetic hexaploid wheat. The four populations, coded as DH1, DH2, DH3, and RI1, were developed from crosses between different synthetic hexaploid wheat lines and the nondormant line ND495. Plants were grown in field conditions during summer seasons of 2006 and 2007. Seeds/panicles were harvested at physiological maturity, air-dried in a greenhouse for 7 days, and then stored in the cold room (4–5°C) prior to dormancy testing. The degree of dormancy was measured by germinating threshed seeds (refer to threshed seed germination) and seeds on the intact panicles (refer to intact seed germination) at 20°C. Threshed seed germination for the DH1, DH2, DH3, and RI1 populations was 46.0 ± 23.9, 77.7 ± 16.5, 95.6 ± 7.4, and 66.7 ± 24.0 (%), respectively, after a 7-day incubation, and 55.8 ± 22.2, 82.7 ± 13.6, 97.7 ± 4.3, and 68.0 ± 23.0 (%), respectively, after a 14-day incubation. An overwhelming majority of lines from the populations displayed stronger dormancy with the threshed seeds than the nondormant parent ND495 (germination rate >93%) under the same conditions, suggesting that *Ae. tauschii*-derived, synthetic hexaploid wheat could be a novel source of seed dormancy genes imparting PHS resistance to common wheat. In a preliminary experiment, a subpopulation of 60 lines from the DH1 population harvested in 2007 displayed 39.9 ± 26.2 and 27.5 ± 27.5 (%), respectively, for threshed and intact seed germination after a 10-day incubation. The threshed and intact seed germination rates were highly correlated with $r = 0.784$ and $r^2 = 0.61$, respectively. This result implies that the seed covering tissues in the synthetic wheat-derived lines may also have germination inhibitors enhancing PHS resistance. We are using a QTL analysis strategy to identify dormancy genes from the above populations.

Poster 9. Markers linked to the adult-plant, leaf rust resistance gene Lr12 in bread wheat.

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The resistance gene *Lr12* provides adult-plant, race-specific resistance to wheat leaf rust caused by *Puccinia triticina*. A population of 115 F_3 families segregating for resistance was generated from a cross between Thatcher and the Thatcher isoline containing *Lr12*. At anthesis, flag leaves were inoculated with leaf rust isolate PRTUS25, which is avirulent on *Lr12*. Resistance segregated as a single qualitative gene. The simple sequence repeat marker *Xgwm251* was located 0.9 cM proximal to the *Lr12* locus and *Xgwm149* was 1.9 cM distal. These markers can be used in marker-assisted selection to combine leaf rust resistance genes in wheat. Using wheat deletion stocks, we located *Lr12* in the deletion bin 4BL-5 (0.84–0.89) that comprises 5% of the 4BL arm. We are developing a high-resolution mapping population for fine mapping of *Lr12*.

Poster 10. Association of seed dormancy with red pericarp color in weedy rice arises from pleiotropy of a predicted transcription factor.

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Seed dormancy has been associated with grain color in wheat and rice, with the red-colored genotypes being more dormant than white-colored. However, whether the association arises from pleiotropy or linkage remains uncertain. We introduced a segment of chromosome harboring a cluster of QTL for seed dormancy (*qSD7-1*) and pericarp color (*qPC7*) from weedy into cultivated rice to clone and characterize their underlying gene(s). High-resolution mapping narrowed the QTL to the same locus of *Os07g11020* (a predicted transcription factor) and obtained a rare recombinant intragenic to the transcription factor. Sequence comparison for the 6,445-bp region identified 33 point mutations between alleles from the weedy and cultivated lines and that intragenic recombinant retains a segment of 2,000 bp from the weedy rice. A pair of dormant and nondormant isogenic lines was developed from the recombinant. These lines differed in seed dormancy, pericarp color (red vs. white), grain weight, and abscisic acid (ABA) content at about 10 days of seed development. The transcripts of the dormancy gene were detected in both seed and leaf tissues from the isogenic lines. Sequence comparison between the genomic DNA and the full-length cDNA identified eight exons and the 14-bp deletion in exon 7 that accounts for the molecular lesion for the aforementioned natural variation. We conclude that the above association in rice is a pleiotropic effect of the predicted transcription factor, and the dormancy allele cannot be used to improve white pericarp-colored varieties for resistance to preharvest sprouting. This research also suggests that the *qSD7-1* underlying gene may regulate the natural variation in seed dormancy and pericarp color by ABA- and pigment-related physiological pathways, respectively, and may have other effects on the traits expressed in the vegetative tissues.

Poster 11. GrainGenes: Serving the wheat community for 15 years, over a billion served.

David E. Matthews [2], Gerard R. Lazo [1], Victoria Carollo Blake [3], David L. Hane [1], and Olin D. Anderson [1].

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GrainGenes (graingenes.org) is a comprehensive database for molecular and genetic information on wheat, barley, rye, and oats. In addition, the GrainGenes project helps coördinate wheat community research projects, such as the International Triticeae EST Cooperative (ITEC), the mapping of ESTs in Chinese Spring deletion lines, development of the D-genome physical map, development of genome-specific SNPs, and analysis of Triticeae repeat sequences (TREP). The GrainGenes map collection comprises 165 mapping studies including genetic, consensus, and physical maps, viewable using the CMap comparative map display. Additional database tools are in development to build genotype, trait and QTL relationships for germ plasm to assist in wheat marker-assisted selection (Wheat CAP project, maswheat.ucdavis.edu). Other tools, such as preformatted Quick Queries, advanced SQL, and Batch Queries have been updated to aid user access to the database. The web log shows that 30,000 different people use GrainGenes per month. Most of you have not told us what you do not like about GrainGenes, either what data should be there that is not or questions about how to find what is there. Please speak up.

Poster 12. Influence of flanking sequences on transgene expression levels in the endosperm of transformed wheat.

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There is often no relationship between transgene copy number and expression levels in different transgenic plants transformed with the same DNA construct. We hypothesized that expression of the integrated DNA can be influenced

by the surrounding genome sequences, a phenomenon known as position effects. Matrix attachment elements (MAR) are segments of DNA that anchor chromosomes to the nuclear matrix. Inclusion of a MAR upstream and/or downstream of genes in transformation constructs has sometimes resulted in higher and/or more copy-number dependent transgene expression levels. MAR elements have been identified in the 5' flanking regions of the *Glu-D1* genes that encode high-molecular-weight glutenin subunits Dx5 and Dy10. To test the effects of flanking sequences on transgene expression in wheat endosperm, we transformed Bobwhite wheat with four constructs that express the *uidA* (GUS) marker gene under control of the promoter of the wheat *1Dy10* HMW-glutenin gene. One construct consists of the GUS-coding region flanked by about 2,800 bp upstream of the start codon of the native *1Dy10* gene and about 2,000 bp downstream of the stop codon of the native *1Dx5* HMW-glutenin gene. The second construct contains a 425-bp version of the 5' flanking sequence that comprises the *1Dy10* gene promoter but lacks the MAR region upstream. The third construct has the nopaline synthase transcription terminator (Nos 3') in place of the 3' regions from the *1Dx5* gene. The fourth construct contains GUS flanked by the 425-bp version of the promoter and the Nos 3' transcription terminator. Fifteen to twenty independent transgenic events for each construct were identified and characterized in detail. Transgene inheritance and homozygous progeny were identified for each event by histochemical staining of endosperm. GUS enzyme activities in homozygous mature seeds of each event were measured using a fluorimetric substrate. GUS transgene copy numbers were measured by quantitative real-time PCR, using *PinB* as a single-copy reference gene. The relationship of copy number to expression level for each of the four plant populations will be discussed. These comparisons will show whether inclusion of large regions of flanking DNA in transformation constructions can buffer position effects in transgenic wheat.

Poster 13. The genetic basis of variation in vernalization requirement duration in winter wheat.

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The transition from vegetative to reproductive development in wheat is mainly determined by the three vernalization genes *VRN1*, *VRN2*, and *VRN3*. These genes have been cloned and characterized in recent studies on allelic variation that occurs between winter wheat, which requires exposure to low temperatures to accelerate the developmental transition (vernalization), and spring wheat, which requires no vernalization. However, little is known about allelic variation in the flowering process among winter wheat cultivars that are practically categorized, based on their various requirements to vernalization, as weak winter, semi-winter, and strong winter types. We developed a mapping population using a cross between the two winter wheat cultivars Jagger (low vernalization requirement) and 2174 (high vernalization requirement) and mapped 96 $F_{7:8}$ recombinant inbred lines using approximately 200 SSR markers. Our preliminary results have shown that the vernalization requirement and flowering date were controlled by a major genetic locus and several minor modifiers. Identification of genes located on this major locus controlling the vernalization requirement in winter wheat is in progress.

Poster 14. A novel source of resistance in wheat to Pyrenophora tritici-repentis race 1.

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Tan spot, caused by the fungus *Pyrenophora tritici-repentis*, causes serious yield losses in wheat and many other grasses. Race 1 of the fungus, which produces the necrosis toxin Ptr ToxA and the chlorosis toxin Ptr ToxC, is the most prevalent race in the U.S. Great Plains. Wheat genotypes with useful levels of resistance to race 1 have been deployed, but this resistance only reduces damage by 50-75%. Therefore, new sources of resistance to *P. tritici-repentis* are needed. Recombinant inbred lines developed from a cross between the Indian spring wheats WH542 (resistant) and HD29 (moderately-susceptible) were evaluated for reaction to race 1 of the fungus. Composite interval mapping revealed QTL on the short arm of chromosome 3A explaining 23% of the phenotypic variation and the long arm of chromosome 5B explaining 27% of the variation. Both resistance alleles were contributed by the WH542 parent. The QTL on 5BL is probably *tsn1*, which was described previously. The 3AS QTL (*QTs.ksu-3AS)* on 3AS is a novel QTL for resistance to *P. tritici-repentis*,

race 1. The QTL region is located in the most distal bin of chromosome 3AS in a 2.2-cM marker interval. Flanking markers *Xbarc45* and *Xbarc86* are suitable for marker-assisted selection for tan spot resistance.

Poster 15. Computer tools for high-throughput wheat genome data analysis.

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The GrainGenes (graingenes.org) database project has worked alongside many Triticeae research projects over the years, and has developed several computer tools which have assisted in wheat genome research. Initial applications have dealt mainly with sequence processing and archiving (e.g., SQPR), and clone identification and selection (e.g., Hybsweeper). These software were important toward generating EST collections and assisting in clone picking methods for furthering genetic research within the laboratory. Other applications have been applied toward extracting high information content fingerprint traces (e.g., GenoProfiler) used for constructing physical mapping scaffolds of and viewing (e.g., FPC WebViewer) the wheat genome. These tools have been useful in determining the linear order of cloned genes and have helped to build a linear order of clones along a chromosome. Additional applications have been developed for sequence data analysis used for generating genome primers (e.g., BatchPrimer3) and reporting sequence alignments (e.g., SNPreporter) to distinguish germ plasm differences. This collection of tools has been useful in the development of genome-specific primers and new molecular markers. Other applications serve to report analysis in a database format (e.g., WheatDB and SNPdb). These resources have proven useful as a starting point for the design of many genetic experiments and surveys. Other projects under development attempt to assist gene discovery using gene-mining algorithms (e.g., CCV). For these and other examples, please visit the GrainGenes demonstration page at wheat.pw.usda.gov/demos. These and other tools from community resources can assist in the study of the wheat genome.

Poster 16. Structural characterization of the model Brachypodium genome and the observation of synteny conservation with wheat.

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Because of its small genome size (~350 Mb) and several desirable attributes, *Brachypodium distachyon* is emerging as a model system for temperate grasses, including important crops like wheat and barley. Analysis of 10.9% of the *Brachypodium* genome based on 64,696 BAC end sequences (BES) revealed that the genome consists of ~18.4% repetitive elements (TEs), with 11% known TEs and 7.4% unique *Brachypodium* TEs. Sequence analysis indicated that approximately 21.2% of the *Brachypodium* genome represents coding sequence. The BESs were integrated into the BAC-based physical maps of the *Brachypodium* genome, which allows for comparison of gene order and contents with that of another grass model genome, *Oryza sativa* (rice), at a genome-wide level. Large, conserved genomic regions were readily identified between the two small grass genomes. We also analyzed the sequence conservation at the microcolinearity level by comparing sequenced *Brachypodium* BACs with the orthologous regions from rice. Genomic rearrangements, differential gene amplification, and deletion appeared to be the common evolutionary events that caused variations of microcolinearity at different orthologous genomic regions. Our conclusions also were supported by a preliminary analysis of the 4X whole-genome sequence produced by the *Brachypodium* sequencing project at the DOE Joint Genome Institute. In addition, several annotated genes in *Brachypodium* BACs have matches to the wheat deletion bin-mapped ESTs. In some cases, genes in the same BACs matched to wheat ESTs that were mapped to the same wheat deletion bins, suggesting that the *Brachypodium* genome will provide useful information in placing the order of mapped wheat ESTs within the deletion bins and developing specific markers in the targeted regions of wheat chromosomes.

Poster 17. Mapping adult-plant resistance to powdery mildew in soft red winter wheat.

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The soft red winter wheat cultivar USG3209 contains adult-plant resistance (APR) to powdery mildew (PM), *Blumeria graminis* (DC.) E.O. Speer f. sp. *tritici*. Because of its quantitative nature, APR to PM can be difficult to assess phenotypically, yet its durability compared to that of single, race-specific major genes makes it very desirable to wheat breeders especially in the eastern and southern U.S. soft wheat region where favorable environmental conditions create substantial PM losses. A QTL analysis for PM resistance was completed on a 'USG3209/Jaypee' recombinant inbred line mapping population in seven field environments and one greenhouse environment from 2002–07. The preliminary genetic linkage map of the 'USG3209/Jaypee' population identifies QTL for APR to PM on chromosomes 1B, 2B, and 2A. The QTL on chromosome 1B is located in the same region as the APR leaf rust gene *Lr46* near molecular marker *Xgwm259*. The QTL located on the long arm of chromosome 2A is located in the same region as the single, major PM resistance gene *Pm4*. The QTL located on chromosome 2B is located in the same region as the single, major stem rust gene *Sr36* near molecular marker *Xgwm501* and the single, major PM resistance gene *Pm6*. An updated genetic linkage map of the QTL for APR to PM contained within this population will be presented.

Poster 18. QTL for preharvest sprouting resistance in a hard white winter wheat Rio Blanco.

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Preharvest sprouting (PHS) is a major constraint for wheat production worldwide. To identify QTL for PHS resistance, a population of 170 recombinant inbred lines (RIL) from the cross between the PHS-resistant hard white wheat Rio Blanco and the PHS-susceptible line NW97S186 was evaluated for PHS under controlled moist conditions in three greenhouse experiments (2005–07) in Kansas and one field experiment (2006) in Nebraska. After 1,430 SSR primers were screened between the two parents and two bulks, 112 polymorphic markers were analyzed in the RIL population. Five QTL were detected for PHS resistance. One QTL, *QPhs.rio-3A*, with a major effect on PHS resistance was mapped in the distal region of chromosome 3AS and explained up to 38.7% of the total phenotypic variance. The second QTL on chromosome 2B, *QPhs.rio-2B.1*, explained 19.2% and 11.2% phenotypic variation in two greenhouse experiments. The third QTL also on 2B, *QPhs.rio-2B.2,* explained 15.3% and 9.8% phenotypic variation in 2006 greenhouse and field experiments, respectively. Additional two minor QTL on 1A and 5B were significant only in one experiment. The major QTL *QPhs.rio-3A* was validated in another RIL population from 'Rio Blanco/NW97S078' in all three greenhouse experiments. Because Rio Blanco is a popular parent used in many hard winter wheat breeding programs, SSR markers linked to the QTL have great potential to be used for marker-assisted selection of wheat cultivars with improved PHS resistance.

Poster 19. Using Affymetrix array to discover single nucleotide polymorphisms in wheat .

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Gene expression arrays have been used to discover single nucleotide polymorphism (SNP) in several crop species. This study was designed to explore the possibility of using the Affymetrix Wheat Genome Array for the discovery of SNP in wheat. Complementary DNAs synthesized from mRNA isolated from the seedlings of six wheat cultivars of diverse origins (Ning 7840, Clark, Jagger, Encruzilhada, Chinese Spring, and Opata 85) were hybridized to the Affymetrix Wheat Genome Array. Cluster analysis of array data selected a total of 396 genes/probe sets with a signal intensity of at least 200, p value of $< 1e^{-10}$ and overall $R^2 > 0.8$ for SNP confirmation through DNA sequencing. Sequencing results

confirmed that 87 probe sets had at least one SNP within the probe sequences. In addition, SNPs also were identified in 21 genes, but they were detected outside the probe sequences. A total of 387 SNPs were discovered from the 108 genes. One SNP was selected from each gene to design primers for SNP analysis in a mapping population using a SNaPshot kit (Applied Biosystems, Foster City, CA, USA). Forty-two SNP markers were further analyzed in 96 F_{8-12} recombinant inbred lines from the cross of 'Ning 7840/Clark', and 25 markers were integrated into the existing SSR map of the population. The result shows that Affymetrix arrays can be used to discover SNP markers in wheat.

Poster 20. Mapping rice centromere genes to wheat and Triticeae and their sequence conservation between monocots and dicots.

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Most eukaryotic centromeres consist of megabases of DNA of repetitive sequences and are generally known to be devoid of genes. However, the sequencing of centromere of rice (*Oryza sativa*) chromosome 8 revealed active genes in the centromere. These rice centromeric genes are useful to study centromere synteny between wheat and rice by comparative mapping and sequencing, and RT-PCR. The seven cDNA clones of rice centromeric genes from rice centromere 8 (*Cen8*) were directly hybridized to the genomic DNA of a set of wheat nulli-tetrasomics, ditelosomics, wheat-alien ditelosomic addition lines, and deletion lines. Four could be mapped to wheat chromosomes. One rice cDNA clone 6733.t9 located close to the end of the *Cen8* virtual contig was mapped to the distal regions of the group-3 chromosomes. However, the other three cDNA clones, 6729.t09, 6729.t10, and 6730.11, located in the kinetochore region of *Cen8*, were mapped to centromeric regions of the wheat group-7 chromosomes. Three wheat ESTs, BJ301191, BJ305475 and BJ280500 with sequences similar to those of rice centromeric genes were also mapped to the same regions as these rice clones. A possible pericentric inversion on chromosome 7D was detected by three clones, which were mapped to the long arm of chromosomes 7A and 7B but to the short arm of the chromosome 7D. The loci of four rice cDNA clones and three wheat ESTs were also detected in the corresponding homoeologous chromosomes of *Ae. speltoides*, barley, and rye using wheat-alien disomic addition lines. A pericentromeric inversion was also found in rye chromosome 7R. The PCR amplification with RT-PCR primer of 6730.t11 was conducted in the genomic DNA isolated from Triticeae species, including *T. urartu*, *T. monococcum* subsp. *monococcum* and *aegilopoides*, *Ae. speltoides*, *Ae. tauschii*, barley, rye, and *Haynaldia villosa*; the rice cultivars (*O. sativa* subsp. *Japonica*) 'Nipponbare' and (*O. sativa* subsp. *Indica*) 'IRRB7'; maize; soybean; tomato; and *Arabidopsis*. A 211-bp sequence was amplified from Nipponbare, an original source for rice genomic sequencing. Of eight plasmid clones of PCR products sequenced from IRRB7, six have the same 211-bp sequence as that in Nipponbare and two have a 202-bp sequence, which shares 100 percent and 87 percent similarity in first 38 and last 72 nucleotides with 211-bp sequence respectively. Surprisingly, the 202-bp sequence amplified from IRRB7 was found in all monocots and dicots species used in this study except Nipponbare. The sequence similarity ranges from 99% to 100% when compared to the 202-bp sequence in IRRB7. However, no sequence similar to this 202-bp sequence was found in the sequence database for the species used in this study. This sequence may be located in the centromere region, a difficult region for sequencing in most species. The RT-PCR results from CS cDNA with primers of 6729.t09, 6729.t10, and 6730.t11 indicated that the three rice centromeric genes were expressed in wheat leaf tissue. Our data demonstrate strong selection pressure for the conservation of the genes in the kinetochore region although their functional role is not clear as yet.

Poster 21. Wheat–rice collinearity and chromosome walking at the Snn1 locus in wheat.

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The wheat fungal pathogen *Stagonospora nodorum* causes Stagonospora nodorum blotch (SNB) and produces multiple host-selective toxins that interact with specific host genes to cause disease. *Snn1* is a dominant gene that confers

sensitivity to the host selective toxin SnTox1. Previous genetic and cytogenetic analysis showed that *Snn1* maps to a gene rich region on the short arm of chromosome 1B and was located distal to the 1BS-18 deletion breakpoint. We developed a saturated map of the *Snn1* region using RFLPs, SSRs, and bin-mapped ESTs, which contained 51 markers spanning a genetic distance of 64.6 cM. Markers closely linked to *Snn1* were used to develop a high-resolution map of the locus in a population of 4,255 F_2 plants. *Snn1* was delineated to a 0.46 cM interval and two ESTs were found to co-segregate with *Snn1*. Of the 44 ESTs mapped within the *Snn1* region, 20 had homology with rice sequences on nine different chromosomes. Eight of these ESTs had homology to genes on rice chromosome 5 but were not collinear due to numerous complex chromosomal rearrangements in wheat compared to rice. We initiated chromosome walking at the *Snn1* locus using the Langdon durum BAC library and assembled a 595-kb contig. BAC sequencing and annotation revealed 10 possible candidates for *Snn1*. Genetic analysis using contig-derived markers indicated variable recombination frequencies within the *Snn1* region. Functional validation of the candidate genes using virus-induced gene silencing is in progress.

Poster 22. QTL analysis of drought tolerance in a spring wheat population.

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Water availability is commonly the most limiting factor to crop production, especially in drought prone areas like the Midwest. This study mapped QTL involved in drought tolerance in wheat to enable their use for marker-assisted selection in breeding. A population of F_7-derived, recombinant inbred lines from a cross between Dharwar Dry and Sitta, spring wheat lines with contrasting drought tolerances, was analyzed using amplified fragment length polymorphism (AFLP) techniques to create a QTL map. QTL with relatively large effects or involving several traits were selected to design STS markers. Of the 256 AFLP primer combinations evaluated, 151 were found to be polymorphic on the parents and were used to screen the population. The AFLP data was combined with the SSR data and a linkage map of 32 groups was used to create a QTL map that identified QTL in 20 of these groups. A major QTL located on chromosome 4AS was found to affect eight traits, including biomass (R^2=.35) and yield (R^2=.44) under reduced irrigation. Further results will be presented.

Poster 23. Surveying expression level polymorphism and single-feature polymorphism in near-isogenic wheat lines differing for the Yr5 stripe rust resistance locus.

Tristan E. Coram [1, 2], Matthew L. Settles [3], Meinan Wang [2], and Xianming Chen [1, 2].

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DNA polymorphisms are valuable for several applications including genotyping, molecular mapping, and marker-assisted selection. The Affymetrix Wheat GeneChip was used to survey expression level polymorphisms (ELPs) and single-feature polymorphisms (SFPs) between two near-isogenic wheat genotypes (BC_7:F_4) that differ for the *Yr5* stripe rust resistance locus, with the objective of developing genetic markers linked to *Yr5*. Ninety-one ELP probe sets and 118 SFP-containing probe sets were identified between isolines, of which just nine ELP probe sets also contained SFPs. The proportion of the transcriptome estimated to be variable between isolines from this analysis was 0.30% for the ELPs and 0.39% for the SFPs, which correlated to the theoretical genome difference between isolines of ~0.39%. Using wheat–rice synteny, both ELPs and SFPs mainly clustered on long arms of rice chromosomes four and seven, which are syntenous to wheat chromosomes 2L (*Yr5* locus) and 2S, respectively. The strong physical correlation between the two types of polymorphism indicated that the ELPs may be regulated by cis-acting DNA polymorphisms. Twenty SFPs homologous to rice 4L were used to develop additional genetic markers for *Yr5*. Physical mapping of the SFP probe sets to wheat chromosomes identified nine on the target chromosome 2BL, thus, wheat–rice synteny greatly enhanced the selection of SFPs that were located on the desired wheat chromosome. Of these nine, four were converted into polymorphic cleaved amplified polymorphic sequence (CAPS) markers between the *Yr5* and *yr5* isolines, and one was mapped within 5.3 cM of the *Yr5* locus. This study represents the first array-based polymorphism survey in near-isogenic genotypes, and the results are applied to an agriculturally important trait.

Poster 24. High-throughput sequencing to assess the microbial diversity in Hessian fly.

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Recently, oceans and soils have been explored for their large unknown microbial genomic resources. Insects could prove another avenue for genomic innovations as majority of insects are known to harbor the symbionts. The objective of this work was to estimate the microbial diversity associated with the Hessian fly, a serious pest of wheat, using 454 pyrosequencing. Insect fat body and midguts from three different larval stages were dissected out. Following DNA extraction, the V3, the most hypervariable region (corresponding to positions 341-534 in *E. coli*) of the 16S rRNA gene was amplified and sequenced. These 454 tag sequences (total of ~6,000) served as query against reference database (V3RefDB) and the phylotype assignments were made according to V3RefDB sequences that display the minimum distance to the query. The most abundant group associated with Hessian fly is γ-*Proteobacteria* followed by β-*Proteobacteria* and *Bacteroidetes*. For assignment of similarity based operational taxonomic units (OTUs), sequences were aligned and distance matrices were calculated by using ARB software, and clustering was done by DOTUR. At the lowest level of dissimilarity, a total of 951 OTUs were recorded. A relatively large number of different populations dominate all samples, which count for observed phylogenetic diversity.

Poster 25. Recurrent deletions of puroindoline genes at the grain hardness locus in four independent lineages of polyploid wheat.

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Polyploidy is known to induce numerous genetic and epigenetic changes but little is known about their physiological bases. In wheat, grain texture is determined by the hardness (*Ha*) locus consisting of genes *Pina* and *Pinb*. These genes are conserved in diploid progenitors but were deleted from the A and B genomes of tetraploid *T. turgidum* (AB). We now report the recurrent deletions of *Pina-Pinb* in other lineages of polyploid wheat and discuss a physiological basis of this phenomenon. We analyzed the *Ha* haplotype structure in 90 diploid and 300 polyploid accessions of *Triticum* and *Aegilops* species. *Pin* genes were conserved in all diploid species and deletion haplotypes were detected in all polyploid *Triticum* and most of the polyploid *Aegilops* species. Two *Pina-Pinb* deletion haplotypes were found in hexaploid *T. aestivum* (ABD). *Pina* and *Pinb* were eliminated from the G genome, but maintained in the A genome of tetraploid *T. timopheevii* (AG). Subsequently, *Pina* and *Pinb* were deleted from the A genome but retained in the A^m genome of hexaploid *T. zhukovskyi* (A^mAG). Comparison of deletion breakpoints demonstrated that the *Pina-Pinb* deletion occurred independently and recurrently in the four polyploid wheat species. The PIN proteins have α-amylase inhibitor activity and bind to the surface of starch granules in the endosperm. We hypothesize that the sudden gene dosage-driven increase in PIN proteins in a neopolyploid would constrain the embryos obtaining nutrition from the endosperm during seed germination. Therefore, deletions of *Pin* genes would be favored for early stand establishment during polyploid speciation.

Poster 26. The finished genomic sequence of the Septoria tritici blotch pathogen Mycosphaerella graminicola.

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Mycosphaerella graminicola is the haploid ascomycete that causes Septoria tritici blotch, one of the most important diseases of wheat worldwide. This pathogen is phylogenetically distinct from other fungi that have been sequenced and is hemibiotrophic; early infection is biotrophic, followed by a switch to nectrophic growth just prior to symptom expres-

sion. More than 15 genes for resistance have been identified and named in wheat, some of which have been shown to interact in a gene-for-gene relationship. However, the trigger for the switch from biotrophic to nectrotrophic growth of the pathogen and the mechanisms of resistance in the host are not known. To better understand the biology of this pathosystem, the genome of the pathogen was sequenced completely by filling in the gaps in an 8.9× draft sequence. The essentially finished sequence contains 18 chromosomes from telomere to telomere, plus five fragments. Four of the five fragments contain telomeres so they presumably make up two additional chromosomes for a total of 20. A comparative bioinformatics analysis of *M. graminicola* with seven other sequenced fungal genomes revealed that *M. graminicola* possessed fewer enzymes than expected for degrading plant cell walls. Analyses of grass-infecting pathogens *versus* those from other hosts indicated that the suites of cell wall-degrading enzymes were tailored to break down the cell wall compositions of their particular hosts. The frequency of transposable elements in the genome of *M. graminicola* was intermediate between those of other sequenced fungi. Many long (> 10 kb) retrotransposons were identified in the finished genome compared to the draft sequence, indicating the need for finishing of other fungal genomes. Availability of the finished genome for *M. graminicola* should greatly aid research on this organism and will help to understand its interaction with wheat**.**

Poster 27. Transcriptome analysis of high-temperature adult-plant resistance conditioned by Yr39 during the wheat-Puccinia striiformis f. sp. tritici interaction.

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Stripe rust (caused by *Puccinia striiformis* Westend. f. sp. *tritici* Eriks. (*Pst*)) is a destructive disease of wheat worldwide. High-temperature, adult-plant resistance (HTAP) to stripe rust is non-race-specific, inherited quantitatively, and is often more durable than race-specific resistance. Previously, we identified and mapped the single *Yr39* HTAP stripe rust resistance gene in the spring wheat cultivar Alpowa, which was identified on chromosome 7BL and accounted for 64.2% of the variation in HTAP resistance. To identify transcripts associated with *Yr39*-mediated HTAP resistance, we selected two recombinant inbred lines from an 'Alpowa/Avocet Susceptible' cross that differed at the *Yr39* locus to represent an incompatible (*Yr39*) and compatible (*yr39*) interaction with *Pst*. Using the Affymetrix Wheat GeneChip, we profiled the transcription changes occurring in flag leaves of these two lines over a time-course after treatment with *Pst* urediniospores and mock-inoculation. This time-course study identified 107 and 10 transcripts that were significantly induced and repressed during *Yr39*-mediated HTAP resistance, respectively. Only one transcript was induced during the compatible interaction. The temporal pattern of transcript accumulation showed a peak at 48 h after infection, which was supported by quantitative PCR assays that showed a rapid increase in fungal biomass after this time in the compatible interaction. Most (64%) of the annotated transcripts specifically induced during HTAP resistance were involved in defense and/or signal transduction, including transcripts associated with pathogenesis-related protein production, phenylpropanoid (lignin) and anthocyanin biosynthesis, and receptor-protein-kinase signalling. As expected for non-race-specific resistance, no transcripts associated with an oxidative burst and/or hypersensitive response were identified. This study represents the first transcript profiling of HTAP resistance to stripe rust in wheat, and we conclude that *Yr39*-mediated HTAP resistance involves substantial gene expression changes associated with known nonspecific defense mechanisms.

Poster 28. Interdisciplinary approaches to understanding the mechanisms of cereal crop–aphid pest interactions using a wheat–greenbug system.

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The greenbug, *Schizaphis graminum* (Rondani), is an important aphid pest of small grain crops, especially wheat and sorghum in the Southern Plains of the U.S. No host resistance gene against aphid pests in cereal crops has been cloned, and the mechanisms of host resistance against aphid feeding are not well understood. At the Texas Agricultural Experiment Station – Amarillo, we have a research program aimed at understanding the mechanisms of interaction between the

phloem-feeding aphid pests and cereal crop hosts using the wheat–greenbug as a model system. Recent results from our research on the following projects follow. (1) Toward map-based cloning of the *Ae. tauschii*-derived greenbug resistance gene *Gb3* in wheat. *Gb3* was mapped in the distal bin of wheat chromosome arm 7DL. Fine genetic mapping for *Gb3* is under way. Marker enrichment has identified over 30 *Gb3*-linked SSR, AFLP-, EST-, or RFLP-converted STS markers in the distal bin. Two STS markers flanking *Gb3* are being used to screen an *Ae. tauschii* BAC library to initiate chromosome walking. (2) Expression profiling of host defense responses against greenbug feeding. In a 2-genotype (bulked segregant R and S super pools), 3-time-point (0, 24, and 48 hours after infestation, hai), 3-replicate experiment, 18 Affymetrix GeneChips were used to investigate *Gb3*-mediated defense responses upon greenbug feeding. Of the 55K transcripts surveyed, 48 showed significant differences in constitutive expression between the R and S pools ($P = 0.05$). Among more than 6,000 transcripts with significant changes in expression level in both genotypes at 24hai, 165 were significantly up-regulated in the R pool as compared with those in the S pool at either 24 hai or 48 hai or both. Defense responses to greenbug feeding appear to be more similar to plant pathogens, in which the jasmonic signaling pathway seems to play important roles. (3) Development of cross-species transferable microsatellite markers for evaluation of biotypic diversity in the greenbug. Over 100 SSR markers were developed through database mining of the pea aphid and green peach aphid EST and genomic resources. Cross species transferability of these markers was high. Sixty SSRs were used to evaluate genetic diversities among six greenbug biotypes. Host-associated genotypic variation and geographical differentiation among these clones were revealed.

Poster 29. Haplotype structure and genetic diversity at Fusarium head blight resistance QTL in soft winter wheat germ plasm.

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Several quantitative trait loci for resistance to *Fusarium* head blight (FHB) have been mapped in wheat. Haplotyping strategies make use of previous QTL mapping and molecular marker information. We selected markers reported to be near FHB resistance QTL mapped in Sumai 3, Wuhan 1, and Ernie to haplotype a large set of Eastern soft winter wheat lines submitted by breeders. The objectives of this research were to (1) determine the genetic relationship among soft winter wheat lines with native and exotic sources of resistance using simple sequence repeat (SSR) marker data, (2) compare the SSR marker haplotypes of soft winter wheat lines with those of Sumai 3, Wuhan 1, and Ernie at known FHB-resistance QTL, and (3) identify lines with novel sources of FHB resistance. Reaction of the soft winter wheat entries evaluated was skewed toward resistance, with 59 lines classified as resistant, 116 moderately resistant, and 28 intermediate. Only 12 and 18 lines were considered moderately susceptible and susceptible, respectively. Of the resistant lines, 24 have exotic sources of resistance in the pedigree and the remaining resistant lines had only soft winter germ plasm in their pedigrees. Entries were grouped into 16 clusters that were generally based on breeding program or geographic origin of lines. The Chinese wheat cultivars having the *Fhb1* resistance gene were grouped separately from all other entries. The eight soft winter wheat entries in this study that have the *Fhb1*-resistance gene based on haplotype data were resistant in the field evaluation. The *Xsts3B-256* and *Xgwm533* markers can be clearly used to identify lines with the *Fhb1*-resistance gene. However, fine mapping is needed in other regions in which FHB resistance QTL have been located; particularly for resistance from Ernie, because allele sizes of Ernie for markers in the 5A and 4BL QTL intervals are common among Eastern soft wheat germ plasm. A number of soft winter wheat breeding lines did not share any haplotype at known QTL evaluated in this study. These lines likely carry novel sources of FHB resistance.

Poster 30. Genotyping U.S. wheat germ plasm for the presence of stem rust resistance genes Sr2, Sr24, Sr26, Sr36, and Sr1RS-Am.

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Wheat germ plasm from throughout the U.S. was surveyed for the stem rust resistance genes *Sr2*, *Sr24*, *Sr26*, *Sr36*, and the T1AL·1RS rye translocation that have conferred resistance to race TTKS of *Puccinia graminis* f.sp. *tritici* identified in Uganda and Kenya. A collection of 804 cultivars and breeding lines of wheat and 12 lines of durum wheat from all growing regions of the United States were screened with simple sequence repeat (SSR) and sequence tag site (STS) markers linked to stem rust resistance genes to determined frequencies of these genes U.S. wheat germ plasm. None of the U.S. lines surveyed possess the *Th. ponticum*–derived gene *Sr26*. In general, the marker analysis revealed less resistance in the spring wheat germ plasm than in U.S. winter wheats. The *Sr24*/*Lr24* translocation is present in 11% of lines tested and is most frequent in hard winter wheat lines from the Great Plains. The T1AL·1RS translocation that confers resistance to TTKS was present in 7% of the winter wheat lines surveyed and was not present in any spring wheat germ plasm. Eastern soft winter wheat germ plasm has been the primary source of *Sr36*. The SSR marker *Xgwm533* was not predictive of the presence of *Sr2*, and new markers are being tested to screen for this gene. For 413 lines, phenotypic data from evaluation of seedlings with stem rust was used to validate the genotypic data. In general, the molecular marker data was consistent with phenotypic observations. Identification of the principle sources of stem rust resistance genes in U.S. germ plasm effective against the TTKS race of stem rust will aide in the development of more diverse and durable resistance profiles.

Poster 31. A simple, bead-based assay for multiplex SNP analysis in wheat.

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Single nucleotide polymorphisms (SNPs) are the most abundant form of DNA polymorphism and are highly suitable for automated analysis. These polymorphisms can be used in plants as simple genetic markers for many breeding applications and are useful for cultivar identification, genetic mapping, trait association, and marker-assisted selection. With the influx of various SNP genotyping assays in recent years, there has been a need for an assay that is robust, yet cost effective, and suited to marker-assisted selection. The Luminex system is a simple, bead-based assay that utilizes a fluorescent microsphere sorter and can be used for low to medium throughput genotyping projects capable of analyzing anywhere from one SNP in one individual up to 100 SNPs in an unlimited number of individuals. This device uses FlexMAP beads that are fluorescent microspheres comprising 100 unique color codes enabling individual beads to be identified using a Luminex 100 instrument. This instrument is capable of analyzing either single-base extension (SBE), allele-specific primer extension (ASPE) or direct hybridization (DH) assays. Here, we present preliminary data on mapping SNPs in wheat and its potential uses in developing a high-throughput system for analyzing multiple SNPs in any given assay.

CONTRIBUTIONS FROM PRIVATE COMPANIES

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The use of foliar fertilizers under rain-fed conditions.

Nicolás Casanova and Ricardo Maich (College of Agriculture FCA-UNC) and Diego Righi (Stoller Argentina S.A.).

The objective of this study was to measure the effects of four foliar fertilization treatments on grain yield and its principal components. The commercial cultivar Baguette Premium 11 (winter type) was sown according to the no-till and para-till practices. A completely randomized block design with three replications was used. The treatments and their chemical and operational aspects are presented in Table 1.

Table 1. Treatments used in assessing the efficacy of foliar fertilizers under rain-fed conditions.

	Treatment	Application	Amount (L/ha)
T_0	Untreated		
T_1	BioForge® (antioxidants)	Anthesis	1.2
T_2	Flower Power® (B, Co, Mo, Zn)	Anthesis	2.4
T_3	Sugar Mover® + CoMo® (B, Mo) + (Co, Mo)	Double ridge	2.4 + 1.0
T_4	Sugar Mover® (B, Mo)	Double ridge	3.5

The mean values of the different measured traits are shown in Table 2 (no-till practice) and Table 3 (p. 32) (paratill practice).

Table 2. Comparison of four foliar fertilizer treatments on eight traits of non-till cultivated wheat. Means in a column with different letters are significantly different at 0.05 probability level (Duncan test). BY: biological yield, GY: grain yield, HI: harvest index, TKW: 1,000-kernel weight, GN: grain number, PN: plant number, SN: spike number, and SS: seed number/spike.

Treatment	**BY** (g/m^2)	GY (g/m^2)	HI (%)	TKW (g)	GN ($n°/m^2$)	PN ($n°/m^2$)	SN ($n°/m^2$)	SS ($n°$)
T_0	1,234.33 A	388.67 A	31.70 A	33.33 A	11,859.00 A	160.00 A	519.33 A	23.00 A
T_1	1,358.33 A	422.67 A	31.33 A	33.00 A	12,867.33 AB	151.00 A	512.33 A	25.67 A
T_2	1,461.33 A	457.67 A	31.40 A	31.67 A	14,447.00 B	175.67 A	614.67 A	24.00 A
T_3	1,318.33 A	416.67 A	31.80 A	32.33 A	12,850.67 AB	146.33 A	533.00 A	24.33 A
T_4	1,353.00 A	433.00 A	32.10 A	33.00 A	13,247.00 AB	151.67 A	559.67 A	24.00 A

No significant differences were noted between treatments for grain yield in both agronomical practices. However, the Flower Power® treatment during anthesis with the micronutrients B, Co, Mo, and Zn generated a significant increase in grain number/m^2 with respect to the untreated experimental unit in the no-till trial.

For the para-till experiment, the Flower Power® foliar fertilizer significantly increased the 1,000-kernel weight when compared to the control. In conclusion, both principal grain-yield components showed significant and positive changes in response to foliar fertilization.

Table 3. Comparison of four foliar fertilizer treatments on eight traits of paratill cultivated wheat. Means in a column with different letters are significantly different at 0.05 probability level (Duncan test). BY: biological yield, GY: grain yield, HI: harvest index, TKW: 1,000-kernel weight, GN: grain number, PN: plant number, SN: spike number, and SS: seed number/spike.

Treatment	BY (g/m^2)	GY (g/m^2)	HI (%)	TKW (g)	GN (n^o/m^2)	PN (n^o/m^2)	SN (n^o/m^2)	SS (n^o)
T_0	1,224.67 A	394.33 A	32.20 A	31.40 A	12,576.33 A	177.33 A	485.00 A	26.00 B
T_1	1,280.67 A	389.67 A	30.63 A	32.93 AB	11,758.67 A	167.33 A	544.33 A	23.00 AB
T_2	1,289.33 A	387.33 A	30.33 A	32.93 B	11,758.67 A	168.00 A	535.00 A	23.33 AB
T_3	1,247.33 A	400.33 A	32.10 A	31.87 AB	12,564.00 A	168.00 A	517.33 A	24.33 AB
T_4	1,231.67 A	359.67 A	29.50 A	31.17 A	11,537.67 A	164.33 A	528.33 A	22.00 A

ITEMS FROM AFGHANISTAN

CIMMYT
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Mahmood Osmanzai, M. Aziz Osmanzai, and Tom Payne.

The 2007 harvest of wheat in Afghanistan was good, due to normal environmental conditions during both winter and spring. The extent of drought and high temperature was typical for Afghanistan. Consequently, yield levels were normal. Yellow rust levels on wheat were low to high at various testing sites. Cereal balance at the national level in 2007 is presented in Table1.

Table1. Cereal balance in Afghanistan in 2007.

Crop	Area ($x10^6$ ha)	Production ($x10^6$)	Surplus/deficit ($x10^6$ t)
Irrigated wheat	1,071	2,878	
Rain-fed wheat	1,395	1,606	
All wheat	2,466	4,484	-433
Rice	170	370	-93
Maize	137	360	0
Barley	236	370	0
All cereals	3,009	5,584	-526

The overall wheat price was $250/t in October 2006 and increased to $320/t, an increase of 13.4% on the previous month and 29.8% increase on the same month of last year.

Wheat is the number one staple crop in Afghanistan and is grown almost everywhere in the country. Winter wheat is grown in central areas where winters are cold. A small number of hectares of spring-sown wheat is grown in areas where it is too cold for winter wheat or when autumn planting is missed. Mainly spring and facultative types are sown in the autumn in most parts of the country. Most of the rain-fed crops are grown in early spring. Maize and rice are important summer cereal crops in Afghanistan, but because of two decades of unrest and 5 years of drought, maize and rice have received less attention. Six-row barley is grown and mainly used for feeding horses in the northern provinces where they are used for transport. Hulless barley is used in central areas as food either direct or mixed with faba bean for the preparation of special breads

The seed policy now calls for certified seed production to be grown by farmers. The total amount of certified wheat seed produced in 2007 was 7,900 t by NGOs, and the public and private sectors. Five NGOs, six Improved Seed Enterprises, Agriculture Research Institute of Afghanistan (ARIA) farms, and 12 recently established, private seed enterprises in 10 provinces with initial support from the FAO continue to produce certified wheat seed. Breeder and foundation seed in 2007 was produced by implementing partners such as the FAO and ARIA.

Two wheat lines have been released by the ARIA and the Ministry of Agriculture, Irrigation and Livestock (MAIL) with technical support of CIMMYT–Afghanistan. **Darulaman-07**, from the cross WEAVER/4/NAC/TH.AC//*3PVN/3/MIRLO/BUC (origin 23rd ESWYT #30) and **Ariana-07** (PASTOR/3/KAUZ*2/OPATA//KAUZ, origin 23rd ESWYT #34).

In collaboration with ARIA, three lines of bread wheat were identified as candidate cultivars for release consideration in 2008 (Table 2). These lines have been tested at multiple locations in Afghanistan for the past 4 years. To further confirm their performance, these lines are being tested at 10 sites in the National Uniform Trial (NUT) in Afghanistan. Four promising bread wheat lines were identified based on their performance in the 2004–05, 2005–06, and 2006–07 yield trials by a project in collaboration with ARIA and the FAO. These lines are being further tested in advanced yield trials at multiple sites (Table 2).

Table 2. Bread wheat lines in consideration for cultivar release in 2008 or under Advanced Yield Trials.

Cross	Origin
Lines considered for release in 2008	
Prl/2*Pastor	24th ESWYT#47
CROC_1/AE.SQUARROSA (205)//KAUZ/3/ATTILA	35th IBWSN#157
SW89.5181/Kauz	35th IBWSN#228
Lines from advanced yield trials:	
SW89.5181/KAUZ	25th ESWYT#5
Cal/NH//H567.71/3/Seri/4/Cal/NH//H567.71/5/2*Kauz/6/WH576/7/WH542	25th ESWYT#8
Fiscal	25th ESWYT#13
Yubileinaya75/3/Agri/Bjy//Vee/4/Pyn/Bau	24th ESWYT#47

Table 3. High-yielding bread wheat lines with adult-plant resistance for stem rust in testing at ten sites in Afghanistan in 2006–07.

Cross	Origin
WBLL1*2/4/YACO/PBW65/3/KAUZ*2TRAP//KAUZ	2nd EBWYT#9
WBLL1*2/KURUKU	2nd EBWYT#10
WBLL1*2/KUKUNA	2nd EBWYT#14
CAL/NH//H567.71/3/SERI/4/CAL/NH/H567.71/5/2*KAUZ/6/PASTOR	2nd EBWYT#17
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR	2nd EBWYT#19
MILAN/KAUZ//PASTOR/3/PASTOR	2nd EBWYT#27

Several high-yielding bread wheat lines with adult-plant resistance or specific resistance genes were identified and are being tested in the National U Trial at 10 diverse sites in Afghanistan (Table 3). These lines will provide high-yielding, stem rust-resistant cultivars to the farmers in the next 2 years.

Yellow rust.

The wheat-cropping seasons of 2003–04 and 2005–06 were dry, making assessment of yellow rust during these seasons impossible. However, the 2004–05 and 2006–07 cropping seasons were conducive to yellow rust infection in the eastern and central regions of Afghanistan. The 2007 data shows susceptibility of PBW 343, which indicates the presence of new virulence to *Yr27*. We found that it was useful to keep the plots for rust evaluation under frequent irrigation and demonstrated to ARIA. In 2006–07, 28 lines of Avocet were planted at the Kunduz, Heart, Nangarhar, and Kabul research stations.

Ug99 is a threat, and concerned people and partners are informed. Selected lines with adult-plant resistance are being tested further for adaptation and yield. High-yielding bread wheat lines with adult-plant resistance or specific

resistance genes were identified and are being tested in the NUT at 10 diverse sites in Afghanistan in hopes of making high-yielding, stem rust-resistant cultivars available to the farmers in the next 2 years.

ITEMS FROM ARGENTINA

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The usefulness of crossing methods in recurrent selection schemes.

R.H. Maich.

During 20 days of September and October 2007, one technician emasculated and approach pollinated 229 wheat and 125 triticale spikes. A total of 17,482 fertile florets were emasculated and 13,767 hybrid seeds were obtained, with a seed set of 78.7%. Approximately 39 hybrid seeds per spike or parent combination enabled a field evaluation of the S_0 progenies that were evaluated under rain-fed and no-till field conditions using one-row plots, 1.3-m long and spaced 0.20 m apart, with a seeding rate of 100 seeds/m^2. In order to obtain the next cycle of the recurrent selection scheme applied in both species, a selection index consisting of 11 traits was used. At the moment, we are in the sixth (triticale) and ninth (wheat) cycles of recurrent selection.

Morphophysiological changes of wheat seedlings after six cycles of recurrent selection.

G.B. Melchiore and R.H. Maich.

The objective of this study was to measure the genetic progress for several seedling morphophysiological wheat traits after six cycles of a recurrent selection scheme conducted under rain-fed conditions. The cycles were characterized through eight variables measured in laboratory: length of the first leaf, number and length of seminal roots, dry weight of the radical system, dry weight of the aerial biomass, and the relation of root to shoot. Except for the seminal radical system dry weight, the remaining traits showed significant differences between the mean values corresponding to the different cycles. Among the recurrent selection cycles evaluated, a negative tendency was verified for both dry weights. In conclusion, the seedling aspects were not neutral with respect to the selection pressure applied to the more conspicuous grain-yield components. A probable progressive adaptation was attained in order to diminish the consumption of water before anthesis, conserving more water for the period in which the number of seed is determined.

An agronomical approach to higher performance in rain-fed bread wheat.

A.C. Masgrau and R.H. Maich.

The results reported here were obtained from an experience carried out during 2006 at Monte Cristo (Province of Cordoba). No-till bread wheat was cultivated on soybean and corn residue. The stored soil water (0.0–1.6 m) was estimated by means of gravimetric measurements. The soil moisture contents were 133.6 mm (soybean residue) and 147.2 mm (corn residue). The soybean residue soil analysis included organic matter (2.55 %), N–NO_3^- (9.6 ppm), S-SO_4^- (1 ppm), and phosphorus (21.9 ppm).

Three bread wheat genotypes were evaluated. On soybean residue, each genotype was cultivated under the following treatments: normal seeding rate (90 kg/ha) with and without phosphorus and at a low-seeding rate (45 kg/ha) with and without phosphorus. On corn residue each genotype was cultivated under a normal and low-seeding rate (without phosphorus). Each treatment was 1 ha. For phosphorus fertilization (15 kg P/ha), triple superphosphate was used. Bread wheat cultivated on soybean residue performed better than that cultivated on corn residue (two q/ha). De-

spite the source of residue, the effect of the seeding rate on grain production was insignificant; 2.014 kg/ha (125 seed/m^2) for soybean versus 1.948 kg/ha (250 seed/m^2) for corn residue. Maintaining a constant seed weight, the normal seeding rate sustained production through the spike number/m^2; on the other hand, the number of seed/spike sustained production in the low seeding rate. With respect to the phosphorus fertilization, genotypes with a higher agronomical performance produced 2 q/ha more than the treatment without phosphorus. The number of spikes/m^2 was the grain yield component that best explained this difference; however, a diminution of the number seed/spike and seed weight was denoted.

Tillage effects on soil properties and wheat rain-fed production.

A.C. Masgrau, P. Petit, J. Godoy, and R.H. Maich.

Subsoiling a compacted soil should loosen it, improve the physical conditions, and increase nutrient availability and crop yields. The aim of this work was to compare the effects of no tillage and the use of the para-till subsoiler on the physical properties of soil and rain-fed wheat productivity. A split-plot design consisting of five fertilization treatments and two tillage subtreatments was used. Physical properties in the top layers of the soil and wheat grain yield were determined. Vertical tillage reduced the bulk density values (1.29 to 1.19 g/cm^3), infiltration rate increased to ~40%, and penetration resistance was diminished by 56% in the 10–25 cm layer. Differences in wheat yields were attributed only to differences in the NP fertilization. Production under water-stress conditions was independent of the two tillage systems evaluated.

Genetic progress for forage production in triticale.

F. Ripoll, G. Vallverdu, and R.H. Maich.

A recurrent-selection program was used to improve forage production in triticale. One cycle/year was obtained since 2000. During 2007, a forage yield trial was performed comparing five cycles of recurrent selection. A completely randomized block design with four replications was used. Each plot was seven rows, 5-m long and 0.20 m apart, with a seeding rate of 250 seed/m^2. On three occasions, green matter was clipped and dried at 65ºC for at least 48 hrs to determine the total dry matter production. A significant linear regression between cycles and forage production was found. An increase of 135.1 kg of dry mater/ha/cycle was estimated. Genetic progress of 4.1 % per year was obtained after five cycles of recurrent selection for forage production in triticale.

The effects of nitrogen and seeding rates on agronomic performance of wheat grown under rain-fed conditions.

L.R Carraro and R.H. Maich.

During 2007, a seeding and N fertilization trial was performed under no-till conditions. Nitrogen fertilization rates were 0, 20, 40, 60, and 80 N kg/ha; seeding rates were 60 and 120 kg of seed/ha. A commercial cultivar and an experimental line were evaluated. Two treatments of foliar fertilizer were applied. No significant differences between seeding rates were found. The higher number of spikes/m^2 at the higher seeding rate was compensated for by a higher number of seed/spike and a higher number of spikes/plant at the lower seeding rate. The results from N fertilization are not clear. The progressive drought stress typical of the region during the critical period of wheat anthesis must be taken in consideration when seeding and N fertilization rates are examined in detail. These preliminary results suggest that under rain-fed conditions with a regional mean production between 2–3 t/ha, diminishing seeding rates and nearly no N fertilization are two strategies to be considered. However, some evidence about the rational use of both types of fertilization (mineral and foliar) through the partition of N is plausible. Finally, 'genotype x management' interactions are responsible for the difficulty of establishing absolute rules for the dryland production of wheat.

The effect of the introgression of exotic germ plasm on the probability of obtaining superior genetic materials.

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

We are working with several types of recurrent selection programs. In some (A and B), only local germ plasm is used; in others (C and D), the introgression of exotic germ plasm is facilitated. In population A, the parents of the next cycle are those pertaining to the same cycle of recurrent selection. In the case of the population B, germ plasm originating from diverse cycles of recurrent selection are crossed. For population C, crosses between local and exotic germ plasm is promoted. Finally, population D is constituted only with exotic germ plasm. Superior S_0 progenies are those with higher yields than the check cultivars. Our results suggest that only those populations with and within local germ plasm yield populations with a higher level of adaptability to the local environmental conditions and give the highest percentage of superior genetic material (Fig. 1).

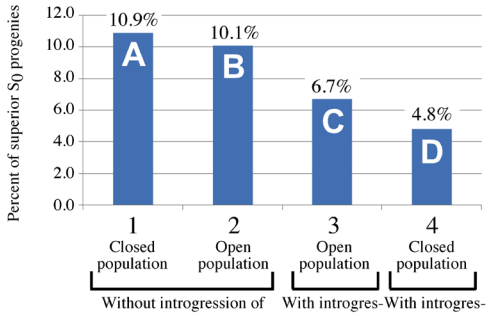

Fig. 1. The effect of introgression of exotic germ plans on the probablility of obtaining superior genetic matierials.

Changes of the realized heritability estimates during a cyclical process of selection and recombination.

J.A. Isaía and R.H. Maich.

This study estimated the realized heritability for several agronomic traits along three consecutive cycles of recurrent selection in bread wheat (C6, C7, and C8) and hexaploid triticale (C3, C4, and C5). The response to selection from divergent selection schemes is in Table 1.

Table 1. Heratibility for several agronomic traits for bread wheat and triticale during three consecutive cycles of selection. An * indicates significance and ns indicates nonsignificance.

	Bread wheat			Hexaploid triticale		
	C6	C7	C8	C3	C4	C5
Grain yield	*	*	ns	ns	ns	ns
Biological yield	*	*	ns	ns	ns	ns
Spike number	*	*	ns	*	ns	ns
1,000-kernel weight	ns	*	ns	ns	ns	*
Harvest index	*	*	*	ns	ns	*
Grain number	*	*	ns	ns	ns	ns

In the bread wheat breeding program, only harvest index maintained significant differences between the higher and lower selected groups. Moreover, the estimated heritability in the more advanced cycle (C8) was higher than those of the previous cycles (C6 and C7). Considering the hexaploid triticale program, controversial results are generated from harvest index (positive response) and 1,000-kernel weight (negative response). There was general agreement in both the sign and magnitude of response to selection for harvest index in both the bread wheat and hexaploid triticale program. Based on these results, the physiological process of partitioning dry matter to grain production could be improved.

ITEMS FROM AUSTRALIA

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Jason Sheedy and John Thompson, and Jon Raupp (Wheat Genetic and Genomic Resources Center, Kansas State University, 4711 Throckmorton Hall Manhattan KS 66506-5502).

Identifying resistance to root-lesion nematodes (Pratylenchus thornei & P. neglectus) in wild relatives of wheat from the genera Triticum and Aegilops.

Common or bread wheat is an allohexaploid comprised of three genetically related genomes (A, B, and D) that originated as a hybrid of emmer wheat (BBA^uA^u) and *Ae. tauschii* (DD). *Pratylenchus thornei* and *P. neglectus* are migratory root-endoparasitic nematodes that feed and reproduce in the cortex of wheat and can reduce yield by up to 50% in intolerant wheat cultivars. Although wheat is their preferred host, they attack a range of crops including chickpea (*Cicer arietinum*), mungbean (*Vigna radiata*), and sorghum (*Sorghum bicolor*). The estimated annual value of wheat production lost in the northern Australian grain region from *P. thornei* and *P. neglectus* is up to \$46 and \$23 x 10^6, respectively.

The first aim of this research was to test the A, BA, and closely related progenitors of wheat to determine if resistance to *P. thornei* is present on these genomes. The second aim was to screen Chinese Spring–*Ae. speltoides* and related *Aegilops* species addition lines for resistance to both root-lesion nematodes (RLN).

To achieve the first aim, 148 wild wheat accessions obtained from Kansas State University via the Australian Winter Cereals Collection in Tamworth were tested for resistance over 2 years to *P. thornei*. This group of wild relatives included *Ae. speltoides* (S genome), *T. urartu* (A^u genome), *T. monococcum* (A^m genome), *T. timopheevii* (GA^u genomes), and *T. turgidum* (BA^u genomes).

Generally, all of the *Ae. speltoides* accessions that were tested were found to be resistant or partially so. Eight accessions (AUS26952, AUS26983, AUS26957, AUS26948, AUS26984, AUS26954, AUS26955, and AUS26951), however, were more resistant (produce lower *P. thornei* multiplication) than the current common wheat resistance standard GS50a in both experiments. None of these accessions were significantly better over both years, but AUS26948, AUS26952, and AUS26983 were significantly ($P < 0.05$) more resistant in Experiment 1.

Of the *T. urartu* accessions, nine (AUS26978, AUS26979, AUS26935, AUS26946, AUS26947, AUS26937, AUS27033, AUS26941, and AUS26932) performed consistently better than GS50a. Although none of the accessions were significantly better than GS50a over both years, AUS26935 was significantly ($P < 0.05$) more resistant in Experiment 1.

Twenty-two accessions of *T. monococcum* subsp. *aegilopoides* and one of *T. monococcum* subsp. *monococcum* were screened during this research. None of the accessions were found to be particularly susceptible in either experiment, but eight accessions (AUS27049, AUS27037, AUS27036, AUS27090, AUS27041, AUS27050, AUS27046, and AUS27091) produced lower *P. thornei* populations than GS50a in both experiments.

AUS27081 was the only *T. timopheevii* subsp. *armeniacum* accession in Experiment 1 to produce fewer *P. thornei* than GS50a. Unfortunately, none of the accessions tested in both Experiments 1 and 2 were able to out-perform GS50a over both years of testing.

Thirty accessions of *T. turgidum* subsp. *carthlicum*, 25 accessions of *T. turgidum* subsp. *dicoccoides* and one accession of *T. turgidum* subsp. *turanicum* were tested for resistance in Experiments 1 and 2. None of the *T. turgidum* subsp. *carthlicum* or *T. turgidum* subsp. *turanicum* accessions were found to be resistant. In fact, the majority of accessions were quite susceptible with only a few producing *P. thornei* populations similar to the resistant durum Yallaroi. The *T. turgidum* subsp. *dicoccoides* accessions also produced a wide range of results from quite susceptible through

to resistant. A number of accessions appeared to be moderately resistant with AUS27025 proving to be as resistant as GS50a over both years of testing.

In all, 148 wild wheat accessions were screened with 134 (91%) of these able to be screened over two years. Of the 134 accessions, 26 (19%) proved to be more resistant than the current best source of resistance, GS50a. Interestingly, 25 (96%) of the 26 elite accessions were from the diploid relatives of wheat.

Because resistant accessions were found among both *T. urartu* and *T. monococcum*, we have confirmed that there are one or more resistance genes on the A genome. A number of resistant accessions were also found among the *Ae. speltoides* accessions. Although *Ae. speltoides* is an S-genome diploid, it is thought to be the B-genome donor of modern bread or common wheat and, therefore, it is reasonable to hypothesize that resistance genes found on the S genome could be introduced into the B genome of domestic wheat. Thompson and Haak (1997) also have identified *P. thornei*-resistant accessions of the D-genome donor to wheat, *Ae. tauschii*. Theoretically resistance genes could be introduced into all three genomes (A, B, and D) of domestic bread wheat and combined to produce a higher level of resistance.

To achieve the second aim, two experiments determined the resistance of seven Chinese Spring–*Ae. speltoides* disomic addition (DA) lines, their parents, and four parental lines of other addition populations to the RLNs *P. thornei* and *P. neglectus*. *Pratylenchus thornei* multiplied more readily than *P. neglectus*, but statistically significant differences between resistant and susceptible checks were observed in both experiments. *Aegilops speltoides* (TA2780; S genome) was significantly more resistant to both RLN than Chinese Spring (TA3008). Resistance to *P. thornei* resistance statistically equal to that of *Ae. speltoides* was observed in TA7694 (DA 6B) and TA7693 (DA 5B). Additionally, TA7693 (5B), TA7690 (2B), and TA7695 (7B) for *P. neglectus*. Additionally, TA7692 (DA 4B), TA7690 (DA 2B), and TA7691 (DA 3B) were significantly more resistant to *P. thornei* than Chinese Spring but more susceptible than *Ae. speltoides*, indicating the presence of minor resistance genes. *Pratylenchus neglectus* resistance statistically equal to *Ae. speltoides* was identified in TA7963 (DA 5B), TA7690 (DA 2B), and TA7695 (DA 7B). *Aegilops searsii* (TA2355, S^s genome) and *Ae. biuncialis* (TA2782, UM genomes) were resistant to both RLN, whereas *Ae. longissima* (TA1910, S^l genome) was resistant to *P. neglectus* and moderately susceptible to *P. thornei*. *Triticum turgidum* subsp. *dicoccoides* (TA106) was susceptible to both species of RLN. Resistance to *P. thornei* has been reported on chromosomes 2B (Schmidt et al. 2005; Thompson et al. 1999; Toktay et al. 2006; Zwart et al. 2005, 2006) and 3B (Schmidt et al. 2005; Toktay et al. 2006), but these *Aegilops* accessions appear to possess several novel resistances for both *P. thornei* and *P. neglectus*, making them valuable for wheat breeding.

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Daryl Mares, Kolumbina Mrva, Robert Asenstorfer, 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 in 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.

Dormancy in white-grained wheat: mechanisms and genetic control.

Daryl Mares, Judith Rathjen, and Kolumbina Mrva, and Judy Cheong (SARDI, GPO Box 397, Adelaide SA 5001, Australia).

Grain dormancy is a major component of resistance to PHS resistance in red- and white-grained wheat. A QTL on chromosome 4A of both types has been associated with a component of this dormancy that is reflected in sensitivity of the embryo to ABA. Genetic studies involving reciprocal F_1s and doubled haploids suggest that two or more genes are involved in dormancy in white-grained wheat and that at least one is expressed in the seed coat. By analogy, it is tempting to suggest that the seed coat effect in white-grained wheats may be similar to that in red wheat and be controlled by a gene(s) on one of the group-3 chromosomes. A doubled-haploid population involving parents that both contain the 4A QTL but vary in dormancy phenotype was analyzed, and a new QTL was located on chromosome 3B close to the likely position of *R-B1a*. This QTL appeared to be linked to increased expression of genes controlling key enzymes in the flavonoid pathway and a significantly greater accumulation of soluble flavonoids. Interaction between a factor produced by the dormant seed coat and the ABA-sensitive embryo during early imbibition would appear to explain a significant part of dormancy in white-grained wheat and be consistent with the evolution of white wheat.

Pathway for water movement into dormant and nondormant wheat grain.

Judith R. Rathjen and Daryl J. Mares, and Ekaterina V. Strounina (Centre for Magnetic Resonance, University of Queensland, Brisbane, Qld 4072, Australia).

The movement of water into harvest-ripe grains of dormant and nondormant genotypes of wheat was investigated using magnetic resonance micro-imaging (MRMI). Neither the rate of increase in water content nor the pattern of water distribution within the grain was significantly different in closely related dormant and nondormant genotypes during the first 18 h. Water entered the grain through the micropyle. By 2 h, water was clearly evident in the micropyle channel, embryo, and scutellum. After 12 h, embryo structures such as the coleoptile and radicle were clearly visible and water had accumulated between the inner and outer layers of the seed coat as well as in the crease. Varying the point of access

to water, distal versus proximal end of the grain, did not affect the pattern of water distribution significantly. Germination was, however, delayed significantly in grains imbibed from the distal compared to proximal end, and this effect was more pronounced in the dormant genotype. This observation suggested that dormant genotypes may contain an inhibitor in the seed coat that is transferred to the embryo by water during imbibition.

Late maturity α-amylase: semidwarfing genes impose a cool temperature shock requirement.

Kolumbina Mrva and Daryl Mares, and Judy Cheong (SARDI, GPO Box 397, Adelaide SA 5001, Australia).

Late maturity α-amylase (LMA) in wheat involves the premature synthesis of high pI α-amylase isozymes during the middle to later stages of grain development. Expression of LMA in wheat is dependent on QTL on chromosomes 7B and 3B, however, the level of expression is affected by a range of factors that include genotype (GA insensitivity genes, T1B·1R translocation), environment (temperature, light), and agronomy. GA insensitive/semidwarfing genes, *Rht1* and *Rht2,* reduce expression of LMA and appear to introduce a requirement for a cool temperature shock as a trigger for α-amylase synthesis. For the majority of LMA-prone genotypes, exposure to a significant temperature differential (i.e., a cool temperature shock), rather than cool temperature alone appears to be important for consistent and maximum expression of LMA. The aims of this study were to investigate LMA expression in synthetic wheats with and without a semidwarf (*Rht1*) phenotype, to define the window of sensitivity to cool temperature shock, to determine the minimum duration of cool temperature for initiation of α-amylase synthesis and finally to examine the quantitative relationship between the duration of the cool temperature shock and α-amylase activity.

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ITEMS FROM BRAZIL

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Spring triticale breeding program at EMBRAPA, Brazil.

Alfredo do Nascimento Junior.

Although triticale production costs through the years were slightly lower than wheat, mainly due to a superior resistance to foliar diseases, the rainy environment associated with a no-till system with more humidity and stubble on the soil surface resulted in an increase in disease selection pressure. Many released cultivars previously characterized as resistant to foliar diseases are now moderately susceptible to susceptible. For more than a century, rye and wheat have been bred and grown in Brazil, contributing to the accumulation of favorable genes through natural selection. The adaptive value of these genes and genetic variability should be brought into national triticale-breeding programs. Developing new hexaploid triticales will certainly need improved octoploid types. Crosses among these improved octoploid and hexaploid triticales, rye, or wheat genotypes by backcrosses to hexaploid triticale cultivars need to be made continuously in order to guarantee better selection efficiency. The major challenges for Brazilian triticale-breeding programs are increasing grain yield potential, disease resistance, and nutritional value; reducing preharvest sprouting; and improving or maintaining the adaptation to acid soils.

Each year we make 250–300 crosses between hexaploid triticales. Germ plasm introduction is important for increasing the genetic variability and used to be the main source for developing new cultivars in Brazil but, currently, the genetic basis is increased and new triticale genotypes are developed by crossing wheat and rye cultivars adapted to Brazilian conditions. Field selection for plant type and disease resistance is carried out from the F_2 onwards, followed by severe screening for grain formation. Due to the great environment pressure, selection for disease resistance is possible under natural conditions in early generations. In advanced stages (F_6 or greater), all lines selected are artificially inoculated for evaluation to scab, spot blotch, tan spot, and blast, and for agronomic evaluations and characterizations parallel to the yield and official trials.

The cultivars Embrapa 53 (LT1117.82/Civet//Tatu), BRS 148 (Yogui/Tatu), and BRS 203 (LT-1/Rhino) developed by Embrapa Trigo with CIMMYT's coöperation, represented more than 70% of the available triticale seed in Brazil in 2004. In 2005, BRS Minotauro, the first truly Brazilian triticale cultivar, was registered.

New lines have been improved by crosses and selections to fulfil the requirements of cereal growers aiming at resistance or tolerance to the most important diseases, grain quality, and broad adaptation. The genetic gain of the breeding program for grain yield, since 2000, was 124.6 kg/ha/year.

Acknowledgements. The author thanks the devotion of Dr. Augusto Carlos Baier, researcher retired of National Wheat Research Center, for the triticale progress in Brazil. Certainly the phrase 'Triticale in Brazil' it will always come associated with the humble and diligent person of Dr. Baier.

BRS Minotauro, the first truly Brazilian triticale cultivar.

Alfredo do Nascimento Junior, Márcio Sóe Silva, Eduardo Caierão, Pedro Luiz Scheeren, and Luiz Eichelberger.

Triticale (X *Triticosecale* Wittmack) is an important crop for the winter growing season in Southern Brazil. The total triticale area in 2005 was approximately 131,000 ha and the same area is estimated for 2006 in Brazil. The average grain yield was 2,200 kg/ha in 2005, without irrigation. Despite this, due to the seed availability, four very similar cultivars are responsible for more than 95% of growing area. Cereal growers have a few cultivars to choose and cultivate annually.

The genetic base of today's triticale in the world and Brazilian-released triticale genotypes is narrow and should be increased; all recommended triticale cultivars originated from a coöperative program with CIMMYT. At Embrapa Trigo, the triticale-breeding program is focused on obtaining triticale cultivars with specific aim at characteristics for adaptation to local climate and increase in genetic variability.

BRS Minotauro is derived from a cross, made at Embrapa Trigo in the winter of 1991, between the Brazilian hexaploid wheat line PF 89358 (BR 35*3//BR 14*2/LARGO) and the Brazilian rye Centeio BR 1, followed by doubling the F_1 plant chromosomes using colchicine to produce the new primary octoploid OCTO 92-3. This octoploid line was crossed with the hexaploid triticale Triticale BR 4 (Beagle/Cinamon//Muskox) in 1995.

Annual selections of individual plants were performed according to the generation in a modified-pedigree method. In 1998, after mass selection, the spring hexaploid line PFT 008 was selected and agronomic evaluation started in 1999. Breeder's seed was increased in 2000 and 2001. In 2002 and 2003, the population was described for 'Distinctness, Uniformity and Stability' according to UPOV and evaluated in field trials under distinct environments.

BRS Minotauro yields 3,790 kg/ha of grain on average, 9% above the check cultivars, and showed an outstanding test weight and Hagberg Falling Number. The new triticale cultivar was registered in 2005. BRS Minotauro has a medium–tall stature and medium ear emergence and maturity cycle; is tolerant to soil aluminum toxicity; resistant to leaf rust, stem rust, powdery mildew and lodging; moderately resistant to spot blotch, Septoria leaf blotch, and BYDV; and moderately susceptible to scab and preharvest sprouting.

BRS Serrano – the first Brazilian dual-purpose rye cultivar.

Alfredo do Nascimento Junior, Renato Serena Fontaneli, Henrique Pereira dos Santos, Luiz Eichelberger, Sandra Patussi Brammer, Eliana Maria Guarienti, Maria Imaculada Pontes Moreira Lima, Pedro Luiz Scheeren, Márcio Sóe Silva, and Eduardo Caierão.

Rye has been grown for years in the southern states of Brazil, first introduced in the country by Polish and German immigrants two centuries ago. The cropping area has decreased substantially in the last five decades, but rye still presents important potential in cereal production, mainly as pasture or soil cover and for human food. Our breeding efforts aim at yield improvement (grain and green forage), health, and wide adaptation. **BRS Serrano** is derived from a cross made at Embrapa Trigo during the winter of 1998 between Garcia rye and Bagé rye populations. These populations were selected in a field trial of colonial rye genotypes for agronomic and forage evaluation. After three cycles of open pollination, the population of BRS Serrano was established. The genetic seed multiplication process began in 2000 and continued until 2001. Between 2002 and 2004, the population was described for 'Distinctness, Uniformity and Stability' according to UPOV and evaluated in field trials for dual-purpose (forage and grain production) in seven distinct environments. During this period, BRS Serrano produced 10,700 kg/ha dry matter, 30% greater than the yield of rye BR 1 (check cultivar), and the potential was higher than 120 dt/ha. BRS Serrano is diploid and a spring type, has a high stature, and is medium–late in ear emergence and maturity. BRS Serrano is highly tolerant to soil aluminum toxicity; resistant to leaf rust, powdery mildew, spot blotch, Septoria leaf blotch, and BYDV; moderately resistant to scab and grain shedding; susceptible to stem rust and lodging.

ITEMS FROM CROATIA

BC INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS
Marulicev trg 5/1, 10000 Zagreb, Croatia.

Technological quality estimates of the new winter wheat lines developed by the Zagreb Bc Institute.

Slobodan Tomasović, Rade Mlinar, Ivica Ikić, Branko Palaveršić, and Katarina Jukić.

The main objective of the wheat breeding in the Bc Institute is development of the high-yielding cultivars with good rheological and baking flour quality. In the breeding process, quality presents a very complex and variable quantitative trait that are greatly affected by ecological factors. The estimate of the final value estimate of a wheat cultivar does not depend on a large number of genes controlling only quality, but on the genes controlling different resistance traits, which is why progress in breeding is a demanding and long process. During 2004–05, 16 new winter wheat lines were tested for production characteristics in small-scale trials at three locations (Botinec, Rugvica, and Lovas). The experimental material included the following wheat lines: Bc 5204/02, Bc 9327/99, Bc 9362/99, Bc 5320/02, Bc 5308/02, Bc 319/01, Bc 306/01, Bc 5325/02, Bc 9345/99, Bc 5263/02, Bc 5137/02, Bc 5167/02, Bc 1553/01, Bc 5090/02, Bc 5210/02, and Bc 5227/02. These lines were tested and compared against the standard cultivars for yield, Sana and Soissons, and grain quality, Žitarka and Renan. After the average values of the most important agronomic traits were analyzed, two lines, Bc 9327/99 and Bc 9362/99, were separated prior to submission for testing by the Croatian Board for Registration, Approbation and Protection of Varieties. Based on the final test results, these new Bc lines combine high yield capacity (Table 1) and desirable grain and flour traits (Tables 2 and 3 (p. 44)) and were released for production under the names **Bc Mira** and **Bc Renata**.

Table 1. Grain yield analysis of new winter wheat cultivars Bc Renata and Bc Mira in comparison with checks (Source: Commission for Varieties Recognition in the Republic of Croatia from 2005–07).

Cultivar	Year of study (t/ha)			Average	Divana	Žitarka	Sana
	2004–05	2005–06	2006–07	(t/ha)	(= 100)	(= 100)	(= 100)
Bc Renata	8,054	8,341	6,726	7,707	141.96	105.49	104.52
Bc Mira	7,769	7,867	7,315	7,650	140.91	104.71	103.74
Sana	6,600	8,399	7,123	7,374			100.00
Žitarka	7,636	7,326	6,955	7,306		100.00	
Divana	6,076	5,918	4,294	5,429	100.00		

Table 2. Results of kernel and flour quality testing of new winter wheat cultivars Bc Renata and Bc Mira in comparsion with checks at Osijek, Croatia, 2006 (Source: Commission for Varieties Recognition in the Republic of Croatia, 2006).

	Bc Renata	Bc Mira	Sana	Žitarka	Divana
Protein (%)	11.96	12.77	11.86	12.60	15.38
Sedimentation (ml)	42	42	28	35	66
Quality class	II	II	III	II	I
Wet gluten (%)	23.5	30.0	23.7	28.6	33.0
Dry gluten (%)	8.54	9.10	8.54	9.92	11.40
Milling value (%)	70.9	68.5	69.3	65.6	68.9
Falling number (sec)	386	406	376	403	428
Water absorption (%)	59.5	65.0	63.5	69.0	67.5
Degree of softening (FJ)	110	80	140	95	30
Quality number	45.3	58.3	36.0	53.3	74.6
Quality group	B-2	B-1	C-1	B-2	A-2
Energy (cm^2)	142.8	90.9	72.9	93.7	145.3
Extensibility (mm)	157	174	147	153	193
Resistance (EJ)	450	250	280	320	290
O/E	2.9	1.4	1.9	2.1	1.5
Maximum viscosity (AJ)	1,280	1,280	1,780	1,190	1,510

From the obtained results of preliminary and official results, developing new wheat cultivars at the Bc Institute has been successful. These newly registered, highly productive cultivars produce excellent technological results and, therefore, deserve attention by the agricultural community and production.

Table 3. Results of kernel and flour quality testing of new winter wheat cultivars Bc Renata and Bc Mira in comparsion with checks at Zagreb, Croatia, 2006 (Source: Commission for Varieties Recognition in the Republic of Croatia, 2006).

	Bc Renata	Bc Mira	Sana	Žitarka	Divana
Protein (%)	11.56	13.48	10.79	12.15	14.73
Sedimentation (ml)	44	42	35	35	66
Quality class	II	I	III	III	I
Wet gluten (%)	22.8	31.8	28.3	28.3	33.9
Dry gluten (%)	7.94	9.61	9.87	9.87	10.93
Milling value (%)	73.0	71.1	73.3	73.3	72.0
Falling number (sec)	331	400	357	357	376
Water absorption (%)	58.5	66.0	64.5	68.0	68.5
Degree of softening (FJ)	85	70	110	65	20
Quality number	56.4	60.4	50.6	66.7	83.7
Quality group	B-1	B-1	B-2	B-1	A-2
Energy (cm^2)	161.9	68.5	67.9	78.7	123.5
Extensibility (mm)	190	179	175	171	222
Resistance (EJ)	390	200	200	245	230
O/E	2.1	1.1	1.2	1.4	1.1
Maximum viscosity (AJ)	1,130	1,100	1,550	950	1,320

Selection of winter wheat lines with good resistance to Fusarium head blight.

Fusarium head blight is one of the most serious fungal diseases occurring in wheat production. In addition to reducing the yield, FHB affects grain quality because certain mycotoxins have a harmful effect on the health of humans and domestic animals. Breeding for resistance to FHB by producing resistant cultivars is the most effective means of control. We tested new wheat lines for resistance to *F. graminearum* by artificial inoculation before submitting them for official testing and to select resistant lines for further use in our breeding efforts. The new wheat lines were tested for resistance at the experimental field in Botinec. Most lines were tested in preliminary trials without replication, and the most promising were tested in exact small-scale trials. In the preliminary trial that included 194 genotypes, evaluation was made using the visual index (VRI %). The most FHB-resistant lines were 2692/05 (0.0), 5601/06 (0.13), 5597/06 (0.13), 2512/04 (0.25), 5561/06 (0.25), 5608/06 (0.25), 2417/04 (0.5), 6068/06 (0.5), 7739/05 (0.75), 4888/06 (1.38), 2559/05 (1.5), and 6065/04 (1.88) (Table 4). The small-scale trial included 25 genotypes and also included standards for resistance (Roazon, Poncheau, and $(D48 / 42x6)_2$ (Fig. 1). The following lines were resistant: 9362/99 (0.54), 5377/05 (1.15), 6045/04 (2.0), 2596/05 (6.17), 9327/99 (7.08), and 2368/05 (9.71). Selection of lines under artificial inoculation with FHB proved as an effective additional criteria for value determination of individual winter wheat lines.

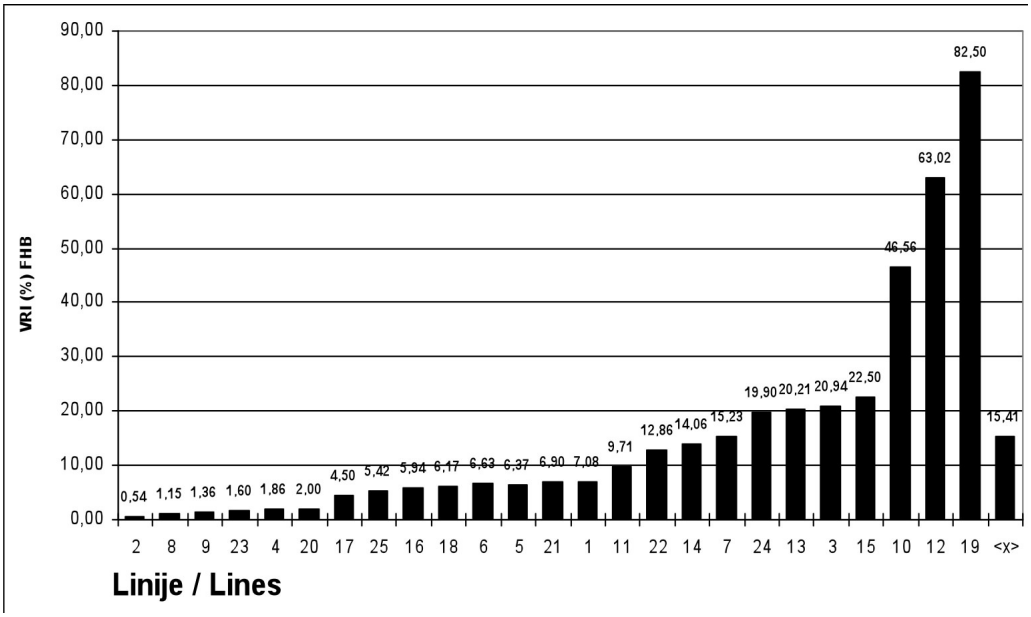

Fig. 1. Investigation results of resistance to Fusarium head blight of prospective winter wheat lines from exact variety trial in comparison with sources of resistance in conditions after artificial infection, Botinec, 2007.

Table 4. Resistance to Fusarium head blight (FHB) after artificial infection of prospective winter wheat lines from the Exact Variety Trial, Botinec, 2007. R, resistant; MS, moderately resistant; MS, moderately susceptible; S, susceptible; VS, very susceptible; 4, Poncheau; 13, Roazon; and 16, $(S_{48X42X6})_2$.

	FHB VRI (%)	Score
2	0.54	R
8	1.15	R
9	1.36	R
23	1.60	R
4	1.86	R
20	2.00	R
17	4.50	MR
25	5.42	MR
16	5.94	MR
18	6.17	MR
6	6.63	MR
5	6.73	MR
21	6.90	MR
1	7.08	MR
11	9.71	M
22	12.86	MS
14	14.06	MS
7	15.23	MS
24	19.90	S
13	20.21	S
3	20.94	S
15	22.51	S
10	46.56	VS
12	63.02	VS
19	82.50	VS

able lines. Breeding material (F_1–F_{12}) consisting of 659 combinations and 2,350 ear progenies was established. In 2006, six lines were selected from preliminary investigations for exact variety trial for further work in 2006-07 (standard Clercal). Analysis of the trials showed that the best line in 2007 was Bc 6315/06; with a yield of 5,636 kg/ha, it was superior to the standard cultivar Clerical by 21.6% (4,636 kg/ha). This line is being tested by the Croatia Board for Registration, Approbation and Protection of Varieties. Good results were ob-

Breeding winter triticale in the Zagreb Bc Institute.

The winter triticale breeding program was initiated at the Bc Institute in early 1990 and was aimed at developing variety with high and stable yields and good grain quality. The genetic base consisted of 1,156 genotypes and was formed and tested for several years both in the experimental field in Botinec and in the laboratory. Selected material was crossed followed by breeding using the pedigree method for testing agronomically valu-

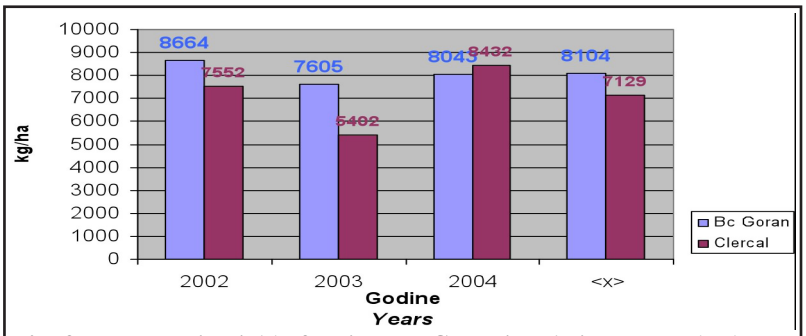

Fig. 2. Mean grain yield of variety Bc Goran in relation to standard variety Clercal in investigations of the Croatia Board for Registration, Approbation and Protection of Varieties, 2002-04.

Table 5. Mean grain yield (kg/hl) of Bc Goran at five locations (Lovas, Osijek, Kutjevo, Nova Gradiška, and Zagreb) in relation to standard cultivar Clercal in investigations of the Croatia Board for Registration, Approbation and Protection of Varieties, 2002–04.

	Cultivar		Relative yield (Clerical=100%)	Difference (in kg) to Clercal
	Bc Goran	Clercal		
2002	8664	7552	11,72	+1112
2003	7605	5402	140,78	+2203
2004	8043	8432	95,39	-389
Mean	8104	7129	116,96	+975

Table 6. The description of the cultivar Bc Goran.

Type of spike	cylindrical with a clear awn
Vegetation	mid–early
Height (cm)	115–121
Resistance to low temperatures	clearly winter type
Resistance to drought	very good
Resistance to lodging	very hard, elastic stem
Resistance to diseases	very good
1,000-kernel weight (g)	45–47
Hectoliter weight (kg/hl)	71–76
Protein (%)	14.31
Fiber (%)	2.43
Lipid (%)	2.11
Minerals (%)	1.84
NET easily utilized carbohydrates (%)	79.31
Use	humans and domestic animal feed and industrial processing
Optimal sowing time	1–20 October
Sowing rate (viable kernels/m^2)	500–550

tained by the following lines in an extremely dry season in 2007: Bc 6322/06 (7,168 kg/ha), Bc 2791/05 (6,316 kg/ha), Bc 6310/06 (5,324 kg/ha), and Bc 1276/99 (4,700 kg/ha), which will all be used in further breeding. Triticale breeding results at the Bc Institute so far include the registered cultivar Bc Goran, the production of which has already spread (Fig. 2 and Table 6, p. 45). Additionally, there has been a considerable interest in this variety also in the neighboring countries of Bosnia and Herzegovina and Slovenia.

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ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK
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A. Börner, O. Dobrovolskaya, E.K. Khlestkina, S. Landjeva, U. Lohwasser, P. Martinek, S. Navakode, M.S. Röder, A. Voylokov, A. Weidner, and K. Zaynali Nezhad.

Spike morphology genes.

Genes determining spike morphology in wheat (multirow spike; MRS) and rye (monstrosum; mo) were studied. Phenotypic analysis revealed segregation ratios of 3 (wild type) : 1 (mutant) in both species. Applying molecular markers, the mutants were mapped in comparable positions on the short arms of chromosomes 2D and 2R of wheat and rye, respectively. The distance to the centromere is about 10 cM. We suggest that the loci are homoeoallelic. Furthermore, it should be noted that a spike morphology gene from a *T. turgidum* supernumerary spikelet stock has been described on the short arm of chromosome 2A at a highly comparable distance from the centromere.

Anthocyanin pigmentation.

Different organs of the plant, including anthers, auricles, coleoptiles, culm, grains, or leaves, can show anthocyanin pigmentation. Anthocyanins are secondary metabolites playing an important role in UV protection of plant tissues. Molecular-mapping studies suggested that two groups of genes for anthocyanin pigmentation exist in wheat. The first group includes genes *Rc*, *Pc*, *Pan*, *Plb*, and *Pls* determining anthocyanin pigmentation of coleoptile, culm, anthers, leaf blades, and leaf sheath, respectively. They are closely linked to each other and represent homoeoloci on the short arms of chromosomes 7A, 7B, and 7D, and a putative homoeologous set for the same traits on chromosomes 5A, 4B, and 4D, all corresponding to the probable candidate genes coding for Myb protein homologous to the maize gene *C1*. The second group includes *Pp* and *Ra*, which determine anthocyanin pigmentation of the pericarp and auricles, respectively. These genes do not cluster with the others (and not one to another), no homoeoloci have been found for them yet, and

their gene product remained unknown. Another specific characteristic of the second group of genes may be the complementary effect, not found for the genes of the first group.

Flowering time and protein content on chromosome 7B.

Two related segregating populations were used to detect QTL underlying the vernalization response, the photoperiod response, and grain protein content. The QTL *QVrn.ipk-7B* (vernalization response) was identified in a cross between the single chromosome intervarietal substitution line Chinese Spring–Hope 7B and TRI 2732, a Gatersleben genebank accession. *QVrn.ipk-7B* maps close to the centromere of chromosome arm 7BS and probably is identical to *Vrn5*. The QTL underlying the photoperiod response (*QPpd.ipk-7B*) and grain protein content (*QGpc.ipk-7B*) were identified in a cross between Favorit and Favorit/F26-70 7B. Both are linked and map ~20 cM distal from the centromere on the same chromosome arm. Because of the absence of any correlation between grain protein content and grain size in the segregating population, we concluded that *QGpc.ipk-7B* may be involved in nitrogen uptake and/or translocation.

Post anthesis drought tolerance.

QTL analysis was carried out with a set of 114 RILs from the International Triticeae Mapping Initiative (ITMI) population of 'W7984/Opata 85' to identify genomic regions controlling traits related to post-anthesis drought tolerance of wheat. In two experiments performed in Gatersleben in two consecutive years, the amount stem reserves mobilization was estimated by measuring of changes in the 1,000-grain weight after chemical-desiccation treatment. QTL for stem reserves mobilization (*Srm*) were mapped on chromosomes 2D, 5D, and 7D. Comparing the data with studies on drought tolerance performed previously, QTL for drought tolerance preferentially appeared in homoeologous regions at distal parts of the group 7L chromosomes.

In a second study, Iranian bread wheat accessions including 70 winter and 70 spring genotypes were selected from the genebank of IPK Gatersleben being representatives of wheat grown area in Iran. These accessions were evaluated based on Augmented Randomize Complete Block Design in field experiments at IPK Gatersleben in 2006. Chemical desiccation was applied as simulator to induce post-anthesis drought stress. Morphological characters such as plant height, spike length, spike weight, number of seeds/spike, seed weight/spike, awn length, glume hairiness, seed length, seeds width, days-to-flowering, and 1,000-kernel weight were measured and the stress tolerance index was calculated. Significant differences were found for all morphological characters as well as for the stress tolerance index. In both winter and spring type awn length showed highest amount of coefficient of variation while days to flowering had the lowest of this value. Spring genotypes showed more variation than winter forms for most of the traits. Correlations for 1,000-kernel weights at normal and stress conditions were low in both winter and spring wheat. This confirmed that selection against drought stress can be performed under drought stress conditions only. Genetic diversity of these accessions based on SSR markers, its correlation to morphological characters, and its relationship to geographical distributions are under study.

Osmotic stress response in Rht wheat seedlings.

Sets of near-isogenic *Rht* lines in five varietal backgrounds (April Bearded, Berseé, Maris Huntsman, Maris Widgeon, and Mercia) were subjected to osmotic stress induced by polyethylene glycol (PEG 6000). To assess growth responses, the length of longest root, coleoptile, and longest leaf (shoot) was measured and the root-shoot length ratio and tolerance index were calculated. Seedling growth response to osmotic stress was significantly affected by *Rht* allele, other unidentified genes, determined by the different varietal background, and the stress level. Treatment with increasing concentrations of PEG caused gradual reduction in root and shoot length, but elongation of coleoptile at milder stress, followed by coleoptile length decrease at higher stress level. The general trend observed was that genotypes with longer roots, coleoptile, and shoots, as determined by the *Rht* alleles (*Rht-B1b*, *Rht-D1b*, and their combination) and varietal background (April Bearded and Maris Widgeon), had the highest tolerance index and keep maintaining the highest absolute values under stress, whereas genotypes with lower seedling vigor (*Rht-B1*c, *RhtB1c+RhtD1b*; Berseé and Mercia) were affected in a greater degree.

Aluminum tolerance.

Previous studies on aluminum tolerance exploiting 'Chinese Spring (CS)/Synthetics' single-chromosome substitution lines and based on a nutrient solution culture approach revealed chromosome 3B of CS influences the trait positively. As a consequence, a set of doubled-haploid lines derived from the cross between 'CS/Synthetic 3B//CS' was developed and used for QTL analysis. One locus having a LOD score >7 was detected on the long arm of chromosome 3B, close to the centromere. This QTL accounted for 49% of the phenotypic variation.

Preharvest sprouting / dormancy.

A set of seven, disomic Chinese Spring wheat–Imperial rye addition lines was evaluated for preharvest sprouting and dormancy. For the wheat-rye addition lines, chromosomes 4R and 7R could be identified for the traits preharvest sprouting and dormancy in a first test. For wheat, a major QTL for both traits could be localized on chromosome 4AL in the ITMI population. Comparing homoeologous regions between wheat and rye chromosome arm 7RS is comparable to 4AL.

Disease resistance originating from Ae. markgrafii.

Aegilops species possess a valuable potential of resistance against economically important diseases like powdery mildew, yellow rust and leaf rust. The *Ae. markgrafii* accession S740-69 is characterized by resistance against leaf rust and powdery mildew. The accession was used in different prebreeding programs that resulted in either leaf rust-resistant or powdery mildew-resistant introgression lines, because the resistance genes were located on different chromosomes.

In order to combine both resistances in one genotype, a total of six powdery mildew-resistant introgression lines were crossed with one leaf rust-resistant line. The F_2 generations were tested at the seedling stage on leaf samples for both diseases. Special sets of isolates/races were used for the inoculation. These sets are normally applied for the official resistance tests before releasing a new cultivar. Segregation analyses for the inheritance of powdery mildew resistance resulted in at least one dominant gene and some minor factors for three F_2 families tested. Two families were characterized by one recessive gene and one family by two recessive genes that are responsible for the resistance. With the exception of one family, the leaf rust resistance in the plant material was inherited by two dominant genes. In one family, only two recessive genes for leaf rust resistance were found.

For the detection of the number and location of responsible genes, a total of five resistant introgression lines showing different expression of powdery mildew resistance were crossed with the susceptible wheat cultivar Kanzler. The F_2 generations were tested at the seedling stage against powdery mildew as described above. Segregation analyses for the inheritance of the resistance resulted in one dominant gene and some minor factors with respect to three F_2 families tested and, for the remaining F_2 families, two and three recessive genes.

DNA analyses of the plant material has started to find segments of *Ae. markgrafii* in the wheat background by means of microsatellite markers. The aim is the verification of the leaf rust QTL on chromosome 2AS and the localization of the powdery mildew-resistance genes.

Seed longevity.

Genetic variation in seed germinability, seed vigor and deterioration, and seedling performance after long-term natural ageing was evaluated in 135 *Triticum* species accessions stored for up to 33 and 15 years at 0°C and ambient room temperature (RT), respectively, in the Seed Genebank at IPK, Gatersleben. To assess the effects of storage temperature, seeds of identical accessions stored at 0°C and RT were investigated. Standard germination, electrical conductivity of seed leachate, accelerated ageing, and seedling growth tests were performed. The study revealed a considerable genetic variation in seed vigor and longevity, determined by the genotype, duration, and temperature of storage. After 33 years of storage at 0°C, more than half of the accessions still had high germinability (about 60 %). No clear trend between increasing the conductivity of seed leachate with increasing the duration of storage was established. This trait was shown to be mostly genotype-dependent (R2=0.94). However, the conductivity of seed leachate of 0°C seed lots was lower

compared with the RT seed lots (P<0.001). A significant negative correlation was established between conductivity of seed leachate and germinability in five- and seven-year-old accessions, but no correlation was observed between the two traits with seed ageing. Seedling growth traits were significantly affected by the genotype, duration, and temperature of seed storage. Subjecting the he 0°C seed lots to accelerated ageing resulted in deterioration effects comparable to those caused by storage of seeds at RT. In addition, the accelerated ageing tests provided tools to differentiate between higher and lower vigor accessions among the high-germinating ones.

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ITEMS FROM HUNGARY

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Wheat season. The 2006–07 season started with a drier than average autumn, which had a negative effect on the uniformity of emergence and on autumn tillering. The long period of warm weather helped virus vectors to survive, so in many places, especially where emergence was patchy, the stands suffered virus infection. The unusually warm, dry weather continued during the winter and the lack of frost during the winter months meant that the plants developed continuously, without a dormant period. After rainfall in late winter, April again was very dry and from the second half of May, extreme heat damaged the stand. A severe powdery mildew epidemic in spring was terminated by the hot, dry weather. The level of natural leaf rust infection was negligible. The wheat harvest was not disturbed by rain or any other unfavorable conditions, so although the national yield average was lower than usual (3.6 t/ha), the crop was of very good quality.

Breeding.

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

Breeding. Three winter wheat cultivars were registered in Hungary in 2007, and the winter wheats Mv Toborzo and Mv Regiment and the winter durum Mv Makaroni were registered in Romania.

Mv Laura (Mv 11-04) is an early maturing, awnless cultivar with good abiotic stress resistance, selected from the cross 'BR918/Ukrainka//Dropia/Ukrainka'. The frost resistance level determined in phytotron tests is very good. Mv Laura has below-average protein content, with excellent gluten quality. The HMW-glutenin composition is 1, 7*+8, 5+10; the LMW composition is c, b, c; and the cultivar does not have T1B·1R. Mv Laura is moderately resistant to powdery mildew, resistant to leaf rust and stem rust, and has good field resistance to yellow rust.

Mv Lucia (Mv 15-04) is a mid-early, hard red cultivar with a high yield level and wide adaptability to very different geographical regions. The head type is awned, plant height is optimal (90-95 cm), and lodging resistance reliable. Mv Lucia has good frost tolerance and winter hardiness. The cultivar was selected from the cross 'Csornoc/Odesskaya 132'. Mv Lucia has acceptable field resistance against powdery mildew and good resistance to leaf rust and good baking quality; the dough strength and stability, especially, are excellent. The HMW-glutenin composition is 2*, 7+9, 5+10 and the LMW is d, b, b.

Mv Zelma (Mv 17-04) was selected from a single cross (C30-2-3-5/Magvas) and was registered as a mid-late maturing bread wheat cultivar. The grain type is HR and the quality is good. One advantage of this new cultivar is that despite the later maturity, it has good yield stability even in hot, dry years. The HMW-glutenin composition is 2*, 7+8, 5+10 and the LMW is c, b, b.

Disease-resistance studies. Within the framework of two international projects (Bioexploit-EU FP6 and NAP-BIO-NEWSEED) molecular marker-assisted selection is being used to incorporate known resistance genes (*Lr9*, *Lr10*, *Lr21*, *Lr24*, *Lr25*, *Lr29*, *Lr37*, and *Lr37*) into the Martonvásár wheats Mv Emma, Mv Madrigál, Mv Magvas, and Mv Pálma with good adaptability to Hungarian conditions. The presence of the resistance genes is detected using public PCR-based (STS and SCAR) markers in various backcross generations. In field populations sown for phenotypic testing, selection is made for progeny resembling the recurrent cultivar but possessing leaf rust resistance. Work also has begun on the pyramiding of leaf rust-resistance genes. Various gene combinations are stabilized in progeny plants using the doubled haploid technique.

Research on Fusarium head blight is focussed on identifying genetic factors determining the resistance of the B9086-95 line derived from a population of the old Hungarian cultivar Bánkúti 1201. In earlier field trials, this line was found to have exceptionally good FHB resistance. Two-year data on the type-II resistance of 250 SSD lines originating from a cross between B9086-95 and the cultivar Mv Magvas gave values between 5.0 and 72.3% for the spike infection, thus providing adequate variation for the identification of QTL regions responsible for FHB resistance.

The degree of infection exhibited by genotypes carrying known leaf and stem rust resistance genes was tested in artificially inoculated nurseries. Genes *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr28*, *Lr29*, *Lr35*, *Lr37*, and *Lr47* continue to provide effective protection against leaf rust in Martonvásár in 2007, wheras cultivars with gene *Sr36* were still resistant to stem rust. The resistant reaction type and a severity of below 20% were observed for genes *Sr7a*, *Sr9d*, *Sr11*, *Sr27*, *Sr30*, and *SrDr* and for genotypes carrying the gene combination *Sr5+6+8+17*.

Powdery mildew isolates collected in the Martonvásár area were used to determine the race composition of the pathogen population, the degree of virulence, and the efficiency of known resistance genes. The races dominant in 2007 (and their frequency) were as follows: 51 (41.7%), 76 (27.2%), and 77 (12.6%). The number of virulence genes in the pathogen population was calculated as 6.12, which was higher than in any previous year. Almost complete protection against the tested wheat powdery mildew isolates was provided by the resistance gene *Pm4a+* (Khapli).

Plant samples exhibiting symptoms of virus infection were collected from experiments on winter wheat, winter barley, durum wheat, winter oats, and triticale in order to identify the virus species and their incidence. Wheat dwarf virus (WDV) was detected on 100% of the infected durum wheat plants and on 92% of the winter wheat samples. Compared with the previous year, a significant increase in the extent of WDV infection on winter barley was observed (2006, 4%; 2007, 60%). This pathogen was identified on 40% of the triticale samples. None of the oat samples collected in 2007 (25 winter and 25 spring genotypes) were infected with WDV, but the level of BYDV infection was higher than the long-term mean.

Abiotic stress resistance studies. The effect of heat stress on the quantity and quality of cereal grain yields was studied in phytotron chambers. Considerable differences were recorded in the quality parameters of the grain yield from stress-treated wheat plants. Heat stress caused a significant increase in the protein content of the grain. This relative rise in the protein content could be explained by the decline in the 1,000-kernel weight, grain weight, and grain size when high temperature occurred during the grain-filling phase, and by a drastic reduction in the grain number and grain yield per plant when heat stress affected young plants, because high temperature during shooting leads to a substantial drop in the number of spikelets. Despite the increase in the protein content of the grain, the quality of the grain was generally poor, due to the decrease in the insoluble polymer protein fraction and in the glutenin/gliadin quantity. Changes indicative of quality deterioration were chiefly observed at the highest temperature (41°C).

The effect of weather components on the biomass and grain production of cereals and on the quality of the grain yield is investigated in long-term experiments. The results achieved in 2007 indicated that drought stress generally reduced the disease resistance of cereals, whereas a combination of water deficiency and pathogens led to a drastic drop in the grain yield. Although the protein content was higher after drought and severe infection, due to the smaller yield, the gluten content was lower.

In a series of model experiments in the phytotron, correlations between drought stress and increased atmospheric CO_2 concentration were examined on various cereal species and cultivars. Drought stress in the early stages of ripening inhibited biomass accumulation, leading to forced ripening, an increase in the number of sterile kernels and a reduction in the grain mass, resulting in an average 40% reduction in the grain yield per plant. The smaller kernels had a relatively high protein content at the cost of the starch fraction. An increase in the atmospheric CO_2 concentration improved the drought tolerance of cereals; the biomass and grain number per plant exhibited values similar to the control values (normal CO_2 level and water supplies) in drought-stressed plants grown at twice the normal atmospheric CO_2 concentration. The protein content of the kernels increased to a moderate extent due to the opposing effects of high CO_2 level and drought stress.

Studies were made on the effect of the weather conditions and plant pathogens in the 2006–07 growing season on the functioning of the antioxidant enzyme system in cereals. Four of the five enzymes tested gave similar patterns over time for each cultivar, with only slight deviations, whereas a more intense genotype effect was observed at the various sampling dates for the ascorbate peroxidase enzyme, and a general tendency was less noticeable. The results achieved so far suggest that the functioning of this enzyme may be correlated with resistance to powdery mildew.

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Genetic and physiological studies

G. Galiba, G. Kocsy, T. Janda, E. Páldi, G. Szalai, and A. Vágújfalvi.

Identification of candidate genes for frost tolerance. Cbf genes recently have been shown to code for transcription factors and are the most likely candidate genes for frost tolerance in wheat. Frost tolerance tests on a newly developed, einkorn mapping population proved the involvement of three Cbf genes, *Cbf12*, *Cbf14*, and *Cbf15*, in the genetic control of frost tolerance. The Cbf genes regulate the expression of several cold-inducible target genes. Besides Cbfs, other cold-responsive genes selected by cDNA-macroarray were investigated to discover whether there were cold-specific.

Physiological changes during low temperature hardening. The research is investigating the regulatory processes involved in the development of stress tolerance in cereals, with special regard to antioxidant systems that regulate the quantity of reactive oxygen species. Light plays a role in the achievement of maximum frost resistance in wheat. In this connection, changes occurring in various antioxidants, in the salicylic acid metabolism, and in membrane lipids during low temperature hardening were investigated under varying light conditions. We found that when studying the role of salicylic acid-dependent signal transduction pathways, it is important to consider not only salicylic acid itself, but also changes in its precursors.

Publication.

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ITEMS FROM INDIA

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Rapid identification of a hidden, co-migratory AP-PCR marker in wheat by band-stab PCR-RFLP.

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Abstract. Analysis of bread wheat genotypes for AP-PCR markers linked to rust resistance gene *Sr31* identified a ~580-bp band that showed high intensity ($SS30.2_{580(H)}$) among the resistant genotypes. Further analysis of this band by band-stab PCR followed by restriction analysis, revealed presence of two co-migratory bands, $SS30.2_{580(ad)}$ and $SS30.2_{580(L)}$. Band $SS30.2_{580(L)}$ was present among all the genotypes, irrespective of the status of the *Sr31* gene, whereas $SS30.2_{580(ad)}$ was present specifically among the *Sr31*-carrier genotypes. Band $SS30.2_{580(ad)}$ was identified from clones of $SS30.2_{580(H)}$, sequenced, and converted into a SCAR marker linked to the *Sr31* gene. The method reported here allows use of intensity difference of bands, which could be due to a hidden co-migratory band in PCR profiles for marker development.

Introduction. Molecular markers are useful for MAS in breeding of crop plants (Tanksley et al. 1989). A large number of markers for various traits have been reported for several crops in the last decade (Mohan et al. 1997). In wheat, molecular markers such as RFLP, RAPD, STS, SCAR, and AFLP have been reported for a number of traits (Gupta et al. 1999 and MASwheat web site http://maswheat.ucdavis.edu). Arbitrary primers (as in RAPD, DAF, and AP-PCR) are commonly used for developing DNA markers. The marker for MAS should be easy to score, highly reproducible, and should be specific. Hence, a marker identified by the above-mentioned methods is generally converted into SCAR marker before its use for MAS (Paran and Michelmore 1993).

While scoring DNA markers, generally the bands that show unambiguous polymorphism are considered, whereas differences in the intensity of bands among the parents and/or accessions are ignored. Intensity differences among bands are generally observed among accessions and is likely to be due to small variations in the amount of genomic DNA or PCR per se or both. We present data to show that among wheat accessions where polymorphism is low, even a difference in intensity of band should be analyzed. We describe a method to identify and characterize bands that show difference in intensity, due to the presence of more than one co-migratory band. The method involves band-stab PCR and restriction analysis in which a hidden co-migratory band present within a high intensity band could be identified and characterized.

Materials and Methods. DNA was isolated from wheat leaves according to Krishna and Jawali (1997). Arbitrarily Primed-PCR (AP-PCR) was performed using long primers (>15 mer) as described by Saini et al. (2004). Amplification products were resolved on 2% agarose gel in 1 X TBE buffer, stained with ethidium bromide and visualized under UV light and photographed.

Selective reamplification of the DNA band of interest from the agarose gel was carried out by band-stab method (Bjourson and Cooper 1992). Agarose gels were stained with ethidium bromide and DNA fragments were visualized on a UV transilluminator. The DNA band of interest was stabbed with a sterile needle (22 gauge), briefly dipped into a PCR tube containing 25 µl reaction mix and subjected to PCR amplification using same primer and thermal cycling conditions.

The band-stab amplified products (500 ng) were digested by 10 restriction enzymes (Bangalore Genei Pvt. Ltd., India) including *Taq*I and *Alu*I in a total reaction volume of 20 µl, according to the conditions specified by the manufacturers. The digested products were analysed on a 2.5% agarose gel as explained above.

The band-stab PCR products were polished using Vent DNA polymerase (Exo+: New England BioLabs Inc., Beverley, MA, USA.) and ligated into vector plasmid Bluescript at the *EcoR*V site using the Rapid DNA ligation kit (Ro-

che Molecular Biochemicals, Germany). Transformation of E. coli (DH5α) cells with ligation product and identification of the colonies carrying recombinant plasmid was done according to standard protocols (Sambrook et al. 1989).

The insert DNA from the recombinant plasmid was amplified by colony PCR as follows. Colonies carrying the recombinant plasmid were stabbed with a fine sterile needle tip and briefly immersed into a PCR tube containing 25-µl PCR reaction mixture and plasmid specific primers M13F (5′ CGACGTTGTAAAACGACGGCCAGT 3′) and M13R (5′ CACAC-AGGAAACAGCTATGACCATG 3′). PCR amplification was carried out under the following cycling conditions: 95ºC–5 min, 60ºC–1 min, 72ºC–1.5 min (one cycle); 35 cycles of 95ºC–1 min, 60ºC–1 min and 72ºC–1.5 min followed by final extension of 72ºC–10 min. Where mentioned, the colony PCR product was subjected to restriction analysis.

Results and Discussion. From the AP-PCR profile of 45 wheat genotypes, a ~580-bp band with high intensity (designated as SS30.2580(H)) was found to be present only among genotypes carrying *Sr31* (Fig.1A), and a band of similar size with low intensity (designated as $SS30.2_{580(L)}$) was detected among the genotypes not carrying *Sr31*.

Whether $SS30.2_{580(H)}$ and $SS30.2_{580(L)}$ were a) same sequence amplified to different extent, b) two different sequences of similar size, c) mixture of different sequences was investigated. Band $SS30.2_{580(H)}$ from PBW-343 (an *Sr31* carrier) and $SS30.2_{580(L)}$ from Kalyansona (a noncarrier of *Sr31*) were amplified individually by band-stab PCR method. Because the products were indistinguishable on the basis size (Fig. 1B, lanes 3 and 4), they were digested with restriction enzymes and the profiles were analyzed. Results showed that profiles obtained after digestion with *Taq*I and *Alu*I, could distinguish the two products. The profiles of the two bands after digestion with *Taq*I is shown in Fig. 1B (lanes 5 and 6). The $SS30.2_{580(L)}$ consisted of a single DNA band that yielded fragments 'b'(~360 bp), and 'c' (~220 bp), whereas $SS30.2_{580(H)}$ was a mixture of two DNA bands that yielded four fragments, 'a' (~420 bp), 'b' (~360 bp) 'c' (~220 bp), and 'd' (~160 bp). Comparison of the two profiles showed that $SS30.2_{580(H)}$ band consisted of two bands, i.e., $SS30.2_{580(L)}$ consisting of fragments 'b' and 'c' and a second band designated as $SS30.2_{580(ad)}$ consisting of fragments 'a' and 'd'. These results suggested that the DNA fragment $SS30.2_{580(ad)}$ may be associated with *Sr31* gene.

To confirm the above findings, $SS30.2_{580(H)}$ and $SS30.2_{580(L)}$, bands from the remaining 42 wheat cultivars were amplified by band-stab PCR and the

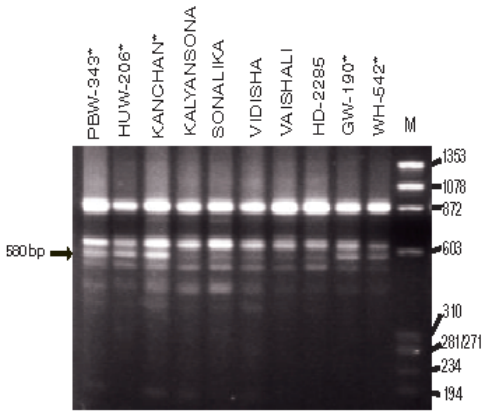

Fig. 1A

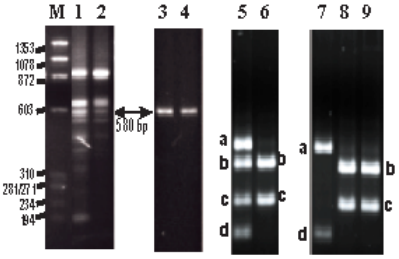

Fig. 1B

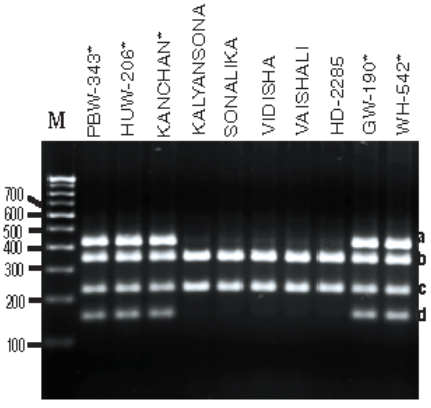

Fig. 1C

Fig. 1A. AP-PCR profiles of wheat genotypes obtained using primer SS30.2. The names of the genotypes are shown on top of the lanes. An '*' indicates genotypes carrying *Sr31* gene. An arrow indicates the position of ~580 bp band. Lane 'M' indicates molecular size marker (PhiX174 digested with *Hae*III).

Fig. 1B. Analysis of band stab-amplified ~580-bp bands from resistant and susceptible genotypes: Lanes 1 and 2, AP-PCR profiles of resistant and susceptible genotypes using SS30.2 primer; Lanes 3 and 4, band stab-amplified 580-bp bands from resistant and susceptible genotypes; Lane 5, restriction profile of $SS30.2_{580(H)}$ fragment by *Taq*I; Lane 6, restriction profile of $SS30.2_{580(L)}$ by *Taq*I; Lanes 7 and 8, *Taq*I restriction profiles of two different types of clones of 580 bp from resistance genotype; Lane 9, *Taq*I restriction profile of single type clone of 580 bp from susceptible genotype.

Fig. 1C. *Taq*I restriction profiles of band-stab amplified 580-bp band from wheat cultivars (carrier and noncarrier of *Sr31*). An '*' indicates genotypes carrying *Sr31* gene. Lane 'M' indicates the 100-bp DNA

products obtained were subjected to *Taq*I analysis. As an example, the profile obtained from a few cultivars is shown in Fig. 1C (p. 55). The results showed that both $SS30.2_{580(ad)}$ and $SS30.2_{580(L)}$ were present among all *Sr31* carriers, whereas only $SS30.2_{580(L)}$ was present among the noncarriers of Sr31, establishing that $SS30.2_{580(ad)}$ is associated with *Sr31*.

To further establish that the $SS30.2_{580(H)}$ contains $SS30.2_{580(ad)}$ and $SS30.2_{580(L)}$, and $SS30.2_{580(L)}$ is a single fragment, the band-stab PCR amplified products were cloned and the insert DNA from several clones were analyzed as mentioned in materials and methods using *Taq*I. The analysis revealed that the clones obtained from $SS30.2_{580(H)}$ band consisted of two types: inserts $SS30.2_{580(ad)}$ and $SS30.2_{580(L)}$ that yielded either fragments 'a' and 'd' (Fig. 1B, lane 7, p. 55) or 'b' and 'c' (Fig. 1B, lane 8, p. 55), whereas $SS30.2_{580(L)}$ clones carried one type of insert that yielded fragments 'b' and 'c' (Fig. 1B, lane 9, p. 55). These results confirmed that $SS30.2_{580(H)}$ consisted of two bands of same size of which $SS30.2_{580(ad)}$ was associated with *Sr31*. Furthermore, the $SS30.2_{580(ad)}$ band has been sequenced, and SCAR primers designed and validated (Das et al. 2006).

In this paper we have described a method for identification and characterization of a band that is polymorphic due to differing intensity. This method allows the quick identification of the sequence dissimilarity between two similar sized bands or a band without the use of time consuming Southern hybridization technique that is generally needed for such analyses. This study stresses the need for careful analysis of DNA marker profiles for intensity differences, while looking for markers linked to traits of interest particularly among the crop species such as wheat in which the diversity is poor.

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

B.K. Das and S.G. Bhagwat (Nuclear Agriculture & Biotechnology Division).

Improvement of wheat for quality in Indian wheat background is being carried out using HMW-glutenin subunits as a selection criterion. 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. Progenies from several intervarietal crosses, in different generations such as F_2, F_3, and F_4 were sown and selections are being developed.

Marker-assisted selection for rust resistance genes and quality related genes.

B.K. Das and S.G. Bhagwat (Nuclear Agriculture & Biotechnology Division).

Marker-assisted breeding for combing *Sr24*, *Sr31*, and *Glu-D1d* (coding for HMW-glutenin subunits 5+10) was carried out in intervarietal crosses. In the F_2, 174 plants were analyzed by SCAR markers. Plants carrying three genes were selected and will be advanced further.

For transferring *Sr24* and *Glu-D1d* into the good cultivar HD-2189, backcross breeding was adopted. Twenty-two BC_2F_1 plants were grown and, DNA from leaves of four weeks old individual plants were extracted and screened by SCAR markers for these two genes. Two plants carrying both the genes were identified and backcrossed with the recurrent parent HD-2189.

Assessment of allelic variation with microsatellite marker Xgwm261 and its effects on agronomic traits in heat stress and nonstressed locations in Indian wheat cultivars.

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

The need for genes/alleles in wheat cultivars to improve their performance in heat-stress environments is urgent. The gene *Rht8* is reported to confer tolerance to heat stress. Allelic variation was analyzed with microsatellite marker *Xgwm261* in wheat cultivars. The analyses showed that 165-bp and192-bp alleles were more frequent as compared to 174-bp allele. The 192-bp allele, which is supposed to be associated with *Rht8* gene, is present in 45% of the tested cultivars. All the tested cultivars were grown in heat-stress and nonstressed locations for assessing their allelic advantage in respective environments. Cultivars with the 192-bp allele did not show significant height reduction over the 165-bp and 174-bp alleles in both environments, indicating presence of height neutral 192-bp allele. Although pedigree analyses did indicate involvement of Akakomughi, the donor of *Rht8* gene in the pedigrees of Indian cultivars, the 192-bp fragment that was found in the Indian wheat cultivars was not the one associated with *Rht8* from Akakomughi. The 192-bp fragment appeared to be the one that is contributed by 'Norin10 / Brevor' lines. The parentage information from literature, molecular analyses, and agronomic data in the present study indicated absence of *Rht8* gene in Indian cultivars.

Callus induction and regeneration in wheat.

Chun Mei Chang, P. Suprasanna, and S.G. Bhagwat (Nuclear Agriculture & Biotechnology Division).

Callus induction was attempted from different tissue explants such as nodes, immature rachis, and mature and immature embryos of the wheat cultivars HD2189 and Unnath C306. A MS medium containing 2 and 4 mg/L 2-4D along with casein hydrolysate was found to be favorable for high frequency callus induction. Regenerating calli were obtained only from immature embryos. The regenerated plants were hardened and transplanted to soil. The regenerants showed normal plant morphology and grain filling.

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Evaluation of near-isogenic wheat lines carrying various stripe rust-resistance genes.

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A total of 28 NILs are available in the genetic background of two Indian wheat cultivars HW 1015 and HD 2408. These lines, which carry one or more rust-resistance genes (leaf rust, stem rust, or stripe rust) present either singly or in combination, were evaluated for rust resistance and yield performance. Fourteen different wheat donor parents contributing a total of 17 stripe rust-resistance genes (*Yr5, Yr8+Yr19, Yr9, Yr10, Yr11, Yr12, Yr13, Yr14, Yr15, Yr3a+Yr4a+Yr16, Yr17, Yr28, Yr29, Yr30*), present either singly or in linked condition with the same stripe rust-resistance genes or other wheat rust-resistance genes, are involved in the NILs. Both the Indian wheat parents are completely susceptible not only to stripe rust but also to stem and leaf rust. The severity of stripe rust in these cultivars ranged from 70S (HW 1015) to 90S (HD 2408). Chemically treated control plants were found completely free from all the three types of wheat rust. Except for *Yr28* in HW 1015 and HD 2408 and *Yr8+Yr19* and *Yr17* in HD 2408, all other stripe rust-resistance genes provided high degree of resistance (F to 10R reaction) in both the Indian wheat cultivars. Near-isogenic lines with *Yr28* showed a 10MS type of moderate susceptibility in both the Indian wheats. Similarly, the stripe rust resistance gene complex *Yr8+Yr19* and stripe rust-resistance gene *Yr17* did not provide adequate resistance in HD 2408. These lines exhibited a 10MS to 20S type of susceptible reaction to stripe rust. Chemically treated control plants exhibited a higher grain yield compared to the untreated control. The grain yield of the NILs with various stripe rust-resistance genes showed a significant increase in grain yield when compared to both the untreated and chemically treated control. The degree of increase in grain yield in the NILs was considerably higher when compared to the untreated control. In some NILs, grain yield was less than that of the chemically treated control.

Confirmation of specific rust-resistance gene Lr19 through use of a molecular marker.

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

In a backcross-breeding program, genes conferring rust resistance were transferred into several Indian hexaploid wheat cultivars. The constituted NILs with leaf rust-resistance gene *Lr19* together with the respective recurrent wheat parents HW 517, HD 2135, HD 2204, and UP 301 and the donor source stocks were screened for polymorphism at the molecular level using RAPD primers. Primer S73 showed polymorphism corresponding to all the resistant NILs including the donor, compared to the recurrent parents. One band of 728 bp was present in the source stock and in all the NILs but was absent in the recurrent parents.

Rheologic and baking performance of composite flours.

V.R.K. Reddy.

Composite flour samples were prepared by blending commercial wheat flour 'resultant atta' (a mixture of part of clear/tail end flour, fine bran, and germ) with various legumes, i.e., sorghum, soya, and maize in different proportion to study their rheologic and baking performance. Sixteen treatments were prepared by blending commercial wheat flour with the above materials in different proportions for the preparation of chapatti and parota. Rheological behaviour of the composite flours showed decrease in water absorption and increase in dough development time. The dough rheological properties of the different flours, including Farinographic and Extensographic properties, also were studied for correlating with their protein compositions. Sensory attributes of chapatti, such as color, flavor, taste, texture, chewing ability, and folding ability, decreased during the storage period. We noticed that soya gives a whiter look and puffiness to the chapaties and parota.

Genetic divergence in bread and durum wheat.

K.Thamayanthi and V.R.K. Reddy.

We evaluated 150 genotypes of bread and durum wheat, including Indian and exotic collections, for various agronomic characters following a nonhierarchical Euclidean cluster analysis. Genotypes were grouped into 13 clusters with a variable number of genotypes. Heterogenous genotypes of original place of release and different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. On the basis of the data on genetic divergence and mean performance of yield and other traits, five diverse and superior genotypes were selected, HI 1077, WH 147, WH 542, HD 2285, and UP 262. These genotypes may be involved in multiple crossing program to recover transgressive segregates.

HMW-glutenin subunit composition in Indian hexaploid wheat cultivars.

V.R.K. Reddy.

Thirty-two cultivars of bread wheat were analyzed for allelic variation in the HMW-glutenin subunits by SDS-PAGE. A total of nine alleles were identified in the 32 cultivars. At the *Glu-A1* locus, the alleles a and b encoded 1, 2-HMW-glutenin subunits. The HMW-glutenin subunits 2* was found in 22 of the 32 cultivars. Ten cultivars had subunit 1 (the a allele). At the *Glu-B1* locus, the alleles a, b, c, and d encoded glutenin subunits 7, 7+8, 7+9, and 6+8, respectively. Eight cultivars had glutenin subunit 7, four had subunit 7+8, 16 had the subunits 7+9, and four had subunits 6+8. At the *Glu-D1* locus, the alleles a, b, c, and d encoded HMW-glutenin subunits 2+12, 3+12, and 5+10, respectively. The *Glu-1* quality score 8 is present in a large number of cultivars.

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Development and use of molecular markers for wheat genomics and breeding.

Construction of framework linkage maps using trait specific intervarietal RIL populations. Three framework linkage maps using three mapping populations have been prepared in our laboratory for QTL interval mapping of various agronomically important traits. The three mapping populations were originally prepared for the following three traits: (i) grain protein content (GPC); (ii) grain weight (GW), and (iii) preharvest-sprouting tolerance (PHST).

Updating the framework linkage map of the GPC population. We earlier prepared a framework linkage map for the GPC population using 171 SSR markers. The map spanned a genetic distance of 3,272.4 cM and had large gaps in certain regions, which adversely affected the precision of QTL mapping studies. In view of this, the following two exercises were undertaken.

(a) Genotypic data on a set of 39 markers (including ISSR, SSR, and RAPD markers) was procured from the NCL, Pune (India), as a collaborative activity.

(b) An additional set of 124 SSRs was used to study polymorphism between parents of GPC population (WL711 and PH132). Forty-six of the above 124 SSRs showed polymorphism and were used for genotyping of RILs.

Using the genotypic data on above 85 markers, a total of 47 markers could be added to the existing framework map of GPC population. While updating the framework map, three markers from the existing map were eliminated, making the total number of markers in the map to 217. The map now spans a total genetic distance of 3,868 cM.

Framework map for the PHST population. A framework linkage map for a solitary chromosome (3A) was prepared earlier for the PHST population using genotyping data for 124 molecular markers (11 SSR, 76 AFLP, and 37 SAMPL) on 100 RILs of the above population. Only 13 of the 124 markers could be assigned to 3A, and an average genetic distance of 21.47 cM between any two markers was observed. This map of 3A was prepared for QTL interval mapping, because chromosome 3A is known to carry genes for PHST.

To develop the whole-genome framework linkage map of the PHST population, an additional 778 SSR primers were tested on parents of the mapping population, i.e., SPR8198 and HD2329. A total of 233 SSRs covering all the 21 chromosome of bread wheat were polymorphic between the two parents. These 233 SSRs were further used to screen a subset of 90 RILs of the mapping population. Further, 16 AFLP and 9 SAMPL primer combinations were tried for detection of polymorphism between the two parental genotypes; 23 AFLP and 91 SAMPL polymorphic markers were identified. The genetic map was composed of 214 loci (198 SSR, 5 AFLP, and 11 SAMPL loci), which were distributed on all 21 chromosomes with an average of 10.19 loci/chromosome. The map spanned a genetic distance of 3,972 cM. For all mapped loci, a maximum of 77 were in the A genome (11 loci/chromosome), followed by 73 loci in the B genome (10.42 loci per chromosome), and 64 in the D genome (9.14 loci/chromosome).

Framework map for the GW population. To prepare a framework linkage map for GW, a set of 836 primer pairs, including 337 WMC, 288 GWM, 90 BARC, 48 PK, 30 CFD, 25 CFA, and 18 GDM primers, were used to detect polymorphism between the two parent genotypes (RS111 and CS) of the RIL mapping population. Of the 836 SSR primer pairs, only 270 (32.3%) were found polymorphic between the two parental genotypes and were subsequently used for genotyping of the GW mapping population. In addition to SSR markers, 299 AFLP and 120 SAMPL polymorphic markers also were used. Using the genotyping data, a total of 294 loci, including 194 SSR, 86 AFLP, and 14 SAMPL loci, were mapped on all 21 chromosomes of wheat genome (average 14 loci/chromosome) covering a map length of 5,211 cM.

Genome-wide, single-locus and two-locus QTL analysis for PHST and GW. Using the data on the linkage map and PHS collected over six environments, genome-wide, single-locus and two-locus QTL analyses were conducted for preharvest sprouting tolerance. A single-locus analysis following composite interval mapping (CIM) revealed a total of seven QTL on 1A, 2A, 2D, 3A, and 3B, including one major QTL each on 2A and 3A. The PVE by individual QTL (R^2) ranged from 15.22% to 45.11%. Three of these QTL also were detected following two-locus analysis, which resolved a total of four main-effect QTL (M-QTL) and 12 epistatic QTL (E-QTL) involved in seven QTL × QTL interactions. These QTL could be efficiently utilized for marker-assisted selection for enhancing PHST in bread wheat.

For the genome-wide genetic dissection of GW in bread wheat, the genotypic data and GW data recorded on RILs over six environments (three locations × 2 years) were used for the genome-wide, single-locus QTL analysis using inclusive composite interval mapping (ICIM) and two-locus QTL analysis using QTL Network to identify main effect QTL (M-QTL) and epistatic QTL (E-QTL). Single-locus QTL analysis identified 11 QTL above threshold LOD values (3.95 to 32.0), which contributed significantly to the phenotypic variation (maximum PV in individual environments varied from 4.37% to 82.0%) for GW. These QTL included four major and stable QTL (explaining >20% PV; available in 50% environments), one each located on chromosomes 1A, 1B, 5A, and 6B. The major QTL on chromosome 1B (LOD value =10.7-32.0) explained a maximum (26.0-82.0%) PV in individual environments. Two-locus QTL analysis resolved a total of 30 QTL, which included three M-QTL (also detected by single-locus analysis) and 27 E-QTL involved in digenic Q × Q interactions; no Q × E and Q × Q × E interactions were detected. However, the level of PV explained by QTL identified through two-locus analysis was relatively low. The four, major QTL identified through single-locus analysis can be utilized for marker-assisted selection for improving GW in bread wheat.

Single- and two-locus QTL analysis for yield and yield contributing traits. The GPC and ITMI mapping populations were used to identify QTL for nine yield traits including plot yield and its components, using single- and two-locus QTL analysis. Framework linkage maps, consisting of 217 and 1,345 markers for the GPC and ITMI populations, respectively, and phenotypic data from four environments at two locations, were used for QTL analysis using QTL Cartographer and QTLNetwork software. Composite interval mapping using QTL Cartographer identified a total of 71 and 109 QTL located on 19 (except chromosome 5A and 6D) and 20 (except chromosome 7D) chromosomes in the GPC and ITMI populations respectively. QTLNetwork identified a total of 89 and 155 QTL, which included QTL with significant main effect and/or significant interaction effect (epistatic QTL or QTL involved in interaction with the environment), located

on 19 (except chromosome 6D and 7D) and 21 chromosomes in GPC and ITMI populations, respectively. In this study, a major QTL was identified on chromosome arm 2DS in both the GPC and ITMI populations for six yield traits each. In the ITMI population, this QTL was detected for plot yield, spike weight, spike length, spikelets/spike, seed weight, and 1,000-kernel weight (explaining from 13.00% to 37.85% PV for individual trait), whereas in the GPC population, this QTL was detected for plot yield, tiller number, spike length, spike compactness, number of seeds, and 1,000-kernel weight (explaining from 8.93% to 19.81% PV for individual trait).

The above QTL was physically mapped to distal bin (2DS5-0.47-1.00) covering 53% region of 2DS. Comparative mapping revealed that the genomic region with this QTL could be an orthologue of a major QTL for spikelets/panicle (*qSSP7*) located in a 912.4-kb region of rice chromosome 7. This information may prove useful for high-resolution mapping leading to map-based isolation of the above major QTL. The study revealed that epistatic interaction contributes significant portion of the phenotypic variation for these yield traits. Another important finding was that for about half (54 out of 106) of the epistatic interactions detected in both mapping populations, interactions between alleles from different parents (recombinant types) resulted in better trait values. This finding supports the suggestion that epistasis for yield traits in wheat may contribute to heterosis. In that case, marker-assisted selection can prove very successful to fix the portion of heterosis owing to QQ effects. The MAS strategy would, therefore, be a promising approach for utilizing heterosis. For some yield traits, environmental interactions also play an important role. The results of this study suggest that while selecting for increased yield, one also must pay attention to the best two locus QTL combinations as well as major genes and nonenvironment specific QTL.

Genetic diversity and population structure analysis among Indian bread wheat cultivars. As a first step towards association mapping in wheat, we analyzed the genetic diversity and structure in a collection of 134 Indian wheat cultivars that were released over a period of ~100 years (1910 to 2006). We used a set of 42 SSR markers, one each from each arm of 21 individual chromosomes. The 42 SSRs had a total of 257 alleles, which included 71 (27.6%) rare alleles occurring at a frequency of <5%. The number of alleles/locus ranged from 1 to 13, indicating considerable genetic diversity in the cultivars studied. The cultivars formed two groups, one with 31 cultivars released previous to the Green Revolution period and the other with 103 cultivars released after the Green Revolution period. The average number of alleles/locus in the cultivars from post-Green Revolution period was relatively higher (5.29 versus 4.76 alleles/locus), but genetic diversity did not differ (0.63, 0.62), indicating that Green Revolution did not lead to any loss of genetic diversity. Furthermore, analysis of molecular variance showed that the proportion of the variance among cultivars within groups accounted for 94.4% but between the groups only 5.6% of the overall molecular variance. The model-based, structure analysis identified a total of ten subpopulations including two subpopulations, from pre-Green Revolution cultivars and the remaining eight from post-Green Revolution cultivars.

An integrated physical map of 2,072 SSRs loci (gSSR and EST-SSRs). As many as ~2,800 genomic SSRs (gSSRs) and ~300 EST-SSRs have been genetically mapped so far world over. Of these, only 1,320 gSSRs have been physically mapped. As many as 270 of these mapped gSSRs and an additional set of 275 EST-SSRs (not used earlier for genetic/physical mapping) were physically mapped in our laboratory, which leaves a very large number of genetically mapped/unmapped gSSRs and EST-SSRs that are yet to be physically mapped. We extended our studies further, so that in our laboratory altogether we physically mapped as many as ~1,500 SSR loci (~800 gSSR loci + ~700 EST-SSR loci) involving all the 21 wheat chromosomes. This physical map was integrated with all other available SSR containing physical maps in wheat. In the integrated physical map, a maximum of 776 loci (37.45%) were mapped on B subgenome followed by D subgenome with 672 loci (32.43%) and A subgenome with 624 loci (30.11%).

To further enrich the physical map, we plan to map 132 class I gSSRs derived from the ~14 Mb of available genomic sequences belonging to wheat and its relatives (http://www.tigr.org//tdb/e2k1/tae1/info.shtm).

Molecular marker-assisted selection for improvement of GPC. Grain protein content is a major nutritional quality trait in bread wheat. Most of the Indian bread wheat cultivars have low to medium GPC (10.90% to 12.14%) and, thus, are relatively poor in their nutritional value. In order to improve the GPC of Indian bread wheat genotypes, a bread wheat genotype Yecora Rojo carrying a high GPC QTL (*GPC-B1*) was used as the donor parent in marker-assisted backcross breeding. For three successive backcross generations, the foreground selection for *GPC-B1* QTL was made using the STS marker *Xuhw89*, which is tightly linked (0.1 cM) to the *GPC-B1* QTL. Background selection was done using polymorphic markers developed by 35 SSRs (distributed on all the 21 wheat chromosomes) and AFLPs. In nine out of 10 BC_3F_1 populations, 2–5 positive plants with the *GPC-B1* QTL showing higher GPC (up to 1.72% higher than the recipient genotypes) and high genomic similarity (up to 100%) with the recipient parental genotype were selected.

In the remaining BC_3F_1 population, plants selected using MAS showed a decrease of 0.93% GPC over the recurrent parent genotype possibly as a result of interaction of high GPC QTL with the genetic background, which needs to be confirmed in future studies. Nevertheless, our results suggested improvement in GPC of the Indian bread wheat cultivars following introgression of *GPC-B1* QTL through MAS. Homozygous BC_3F_2 progenies for the above GPC QTL showing maximum genetic similarity with the recipient parent genotype will be isolated and evaluated in replicated field trials over environments for their agronomic performance.

Molecular marker-assisted selection for pyramiding of leaf rust resistance and PHST. Preharvest sprouting is a major problem word-wide that leads to degradation of grain quality associated with significant losses in yield. In view of this, we earlier identified a major QTL (*QPhs.ccsu-3A.1*) on chromosome 3A that explained >70% phenotypic variation for PHST across a number of environments. The desirable allele of this QTL was introgressed through MAS into the elite, but PHS susceptible, Indian bread wheat cultivar HD2329. HD2329 has the leaf rust-resistance genes *Lr24* + *Lr28*. In each of three backcrosses, foreground selection was performed using flanking markers (GWM155 and WMC153) and background selection was performed using polymorphic markers developed by a set of 35 SSRs (distributed on all the 21 bread wheat chromosome) and AFLPs. During introgression of PHST, the desirable alleles of two leaf rust-resistance genes *Lr24* and *Lr28* also were tracked using linked SCAR markers. In the BC_3F_1 generation, reconstituted plants were selected that exhibited 94.3-97.3% genetic similarity with the recipient bread wheat genotype and contained the QTL allele for PHST. Phenotypically, these plants exhibited a high level of PHS tolerance (PHS scores ranged from 1 to 3; 1= tolerant and 9= susceptible). These results validated the PHST QTL we identified earlier and suggested significant contribution of this QTL in conferring PHS tolerance. The selected plants will be advanced to BC_3F_2 in to obtain homozygous progenies for the PHST QTL. The homozygous and homogeneous progenies with high tolerance to PHS and with maximum genetic similarity with the recipient genotype will be evaluated in replicated field trials over environments.

Analysis of host–pathogen interaction in leaf rust infected bread wheat. Development of leaf rust-resistant cultivars is a major objective of wheat-breeding programs. For the long-term, effective management of resistance against this disease, the molecular basis of disease pathogenicity and the host–pathogen interaction should be known. In collaboration with BITS, Ranchi, and IARI, New Delhi, we have started a DBT-sponsored project in which the host–pathogen interaction in leaf rust-infected bread wheat will be analyzed using cDNA-AFLP display analysis. The cDNA-AFLP experiment will be conducted for the following two genes: (i) seedling-resistance gene *Lr28* (Thatcher NILs) and (ii) adult-plant resistance gene *Lr48* (Agra Local NILs). A single-spore derived 77-5 pathotype of *P. triticina* will be used for infection of wheat stocks. In cDNA-AFLP display analysis, differentially expressed transcripts will be identified and characterized. The above exercise of identification of differentially expressed transcripts will potentially lead to elucidation of specific signal transduction pathways that follow leaf rust-wheat interaction.

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Genetic basis of stripe rust seedling resistance of Cappelle-Desprez and Mega.

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Introduction. Wheat is grown under diverse environments and different agroecological systems. Apart from the inherent yield potential both biotic and abiotic stresses also determine the realized yield of cultivars. Stripe rust or yellow rust of wheat is an important cereal rust disease in many wheat-growing regions of the world, especially in areas with cool and wet environmental conditions (Roelfs et al. 1992). Rust diseases can be managed effectively and economically in a eco-friendly manner through cultivation of resistant cultivars (Line and Chen 1995). Understanding the genetic basis of resistance is of prime importance for their use in breeding program and not only generates information about the nature and number of genes in the donor parents but also helps in formulating efficient strategy for the incorporation of rust resistance. The present investigation was initiated with the objectives of understanding the genetic basis of stripe rust resistance of some the very important winter wheat cultivars. The results of genetic analysis of stripe rust resistance of Cappelle-Desprez and Mega is discussed.

Materials and Methods. The experimental material comprised Cappelle-Desprez, Mega, UP2338, and Agra Local and the F_1s, F_2, and F_3 families of the crosses between Agra Local and Cappelle Desprez and UP2338 and Mega. The F_2 population of the cross 'Cappelle-Desprez/Mega' was studied for an allelism test.

The F_2 and F_3 seedlings were raised in the aluminum bread trays consisting of ten rows; the seventh row of each tray a susceptible check (Agra Local). Inoculations were done as per Nayar et al. (1997). Seedlings were kept in a temperature-controlled glass house at 16°C. Infection types (IT) were recorded 14 days-after-inoculation and plants with zero fleck, fleck, or small pustules with a necrotic area classified as a resistant reaction and large pustules with or without chlorosis were considered susceptible. Pathotype 46S119 (avirulent on *Yr1, 5, 10, 15, 27, SP, Su,* and *CV* and virulent on *Yr2, 3, 4, 6, 7, 8, 9, 22, 23, 25*) was used for inheritance study. A chi square test was used to check the expected ratios in the segregating generations.

Results and Discussion. Seedling infection of the parents and other lines with known resistance genes (McIntosh et al. 1995, 2005; Nayar et al. 2001) are presented in Table 1. The IT of Mega was fleck, whereas Cappelle-Desprez varied from ;1 to ;2. UP2338 and Agra Local were fully susceptible (3+) against pathotype 46S119.

Table 1. Rust response of some *Yr* genes against yellow rust pathotypes. * adult-plant resistance based on terminal disease severity of the flag leaf under controlled condition; R = free from disease symptoms.

		Pathotype				
Cultivar/Line	Genes	47S102	70S69	46S119	78S84	46S119*
UP2338	*Yr9*	0;	0;	3+	3+	100S
Vilmorin23	*Yr3*	3+	3+	3+	3+	100S
Hybrid46	*Yr3, Yr4*	3C	2+3-	3C	;-	80S
Maris Huntsman	*Yr2, Yr3, Yr4, Yr13*	0;	0;	0;	3+	80S
Agra Local	—	3+	3+	3+	3+	100S
Cappelle-Desprez	***Yr3, Yr4, Yr16***	**0;**	**;1–;2**	**;1–;2**	**;-**	**R**
CD-Mara-2D	***Yr3, Yr4***	**0;**	**;1–;2**	**;1–;2**	**0;**	**R**
Mega	*Yr3, Yr4, Yr12*	0;	0;	0;	0;	R

The F_1s from 'UP2338/Mega' were susceptible. Forty-nine seedlings were resistant and 185 were susceptible, which was good fit to a 1 resistant : 3 susceptible ratio (P = 0.14) (Table 2). Among the 112 F_3 families, 61 segregated, 24 were homozygous susceptible, and 27 were homozygous resistant, which was good fit to a 1 resistant : 2 segregating : 1 susceptible ratio (P = 0.59). The F_2 and F_3 data were in compliance with a single recessive gene for resistance against pathotype 46S119.

Table 2. Segregation of the F_2 and F_3 generations in the seedling test against pathotype 46S119.

	Number of seedlings/family					
Cross	Resistant	Segregating	Susceptible	Expected ratio	X^2 value	P value
Agra Local / Cappelle-Desprez						
F_2	12		216	1R:15S	0.54	0.46
F_3	11	105	99	1R:8SEG:7S	0.76	0.68
UP2338 / Mega						
F_2	49		185	1R:3S	2.17	0.14
F_3	27	61	24	1R:2SEG:1S	1.05	0.59
Mega / Cappelle-Desprez						
F_2	158		21	1R:0S	∞	<0.0

The F_1s of the cross between Agra Local and Cappelle-Desprez were susceptible. In the F_2, 12 seedlings were resistant and 216 were susceptible, which fit a 1 resistant : 15 susceptible ratio (P = 0.46) (Table 2). In the F_3 families, 105 segregated, 99 were homozygous susceptible, and 11 were homozygous resistant (Table 2). The F_3 family segrega-

tion was good fit to 1 resistant: 8 segregating : 7 susceptible ratio (P = 0.68). The F_2 and F_3 data indicated presence of two recessive genes for resistance to pathotype 46S119. The F_2 population of the cross 'Cappelle-Desprez/Mega' segregated, which confirmed that different genes were involved in the resistance against pathotype 46S119 in these cultivars.

The F_2 segregation and the F_3 family analysis confirmed presence of a single recessive gene in Mega for stripe rust resistance against the pathotype 46S119. Although the F_2 and F_3 data indicated that two recessive genes governed resistance to pathotype 46S119 in Cappelle-Desprez, we could not be explained why immune-type (seedling reaction 0;) lines were recovered in the F_3 and other advanced generations not only from the cross 'Agra Local/Cappelle-Desprez' but also from 'UP238/Cappelle-Desprez' (data not presented). Cappelle-Desprez may have suppressors of seedling resistance. Furthermore, why the seedlings of Cappelle-Desprez showed a high infection type (;2) and the adult plants were completely devoid of disease symptoms is difficult to explain. Obviously, it is not due to *Yr16,* because the seedling and adult-plant reaction of Cappelle-Desprez and the Cappelle-Desprez-Mara 2D substitution line were identical. Adult-plant resistance genes other than *Yr16* or suppressors of seedling resistance may be present. Either of these possibilities can not be ruled out from this study. The genes governing resistance in Mega and Cappelle-Desprez against pathotype 46S119 are likely to be different from the other documented genes in these cultivars, namely *Yr3a* and *Yr4a* in Cappelle-Desprez and *Yr3, Yr4*, and *Yr12* in Mega (McIntosh et al. 1995), because other cultivars/lines carrying *Yr3a*, *Yr4a,* and *Yr12* were susceptible to pathotype 46S119 (Table 1, p. 64).

In addition to a durable, adult-plant stripe rust-resistance gene (Johnson 1984) and *Yr3a* and *Yr4a*, Cappelle-Desprez also possesses additional seedling-resistance genes against the Indian stripe rust pathotype 46S119. Allelism tests and gene action clearly demonstrated that the resistance genes in Mega and Cappelle-Desprez are different. No reports of effective seedling-resistance genes against virulent pathotypes of stripe rust in Cappelle-Desprez or Mega have been made. Both cultivars have seedling resistance against the highly virulent pathotypes 46S119 (avirulent on *Yr1, 5, 10, 15, 27, SP, Su,* and *CV* and virulent on *Yr2, 3, 4, 6, 7, 8, 9, 22, 23, 25*) and 78S84 (avirulent on *Yr1, 5, 10, 15, 25, SP,* and *CV* and virulent on *Yr2, 3, 4, 6, 7, 8, 9, 22, 23, 27,* and *A*). Particularly for Cappelle-Desprez, the resistance is likely to be short lived, because it has not shown seedling resistance elsewhere in the world and the stripe rust pathotypes distributed in India may not be so virulent. Cappelle-Desprez has been grown every year for last 12 years in an experimental plot, and the pathotypes 46S119 (46E151 + *Yr9*) and 78S84 (78E16) are quite virulent, existing since 1996 and 2002, respectively. Therefore, no evidence exists right now that the seedling resistance gene reported in Cappelle-Desprez will be rendered ineffective very soon. However, the effectiveness of the seedling-resistance gene and the role of a suppressor of resistance is more important. Further studies are required to reach any conclusion about a suppressor gene. We have initiated studies to test whether or not Cappelle-Desprez carries suppressors for seedling resistance against stripe rust. For this purpose, the F_3 lines that were homozygous for a zero fleck reaction at the seedling stage were advanced to the F_4. About 100 seedlings of the F_4 families were tested and the resistance was confirmed to be homozygous. One of the derived zero fleck lines was named FLW-CD. In the next step, segregating populations (F_2 population and F_3 families of 'Agra Local/FLW-CD' and F_2 population of 'Cappelle-Desprez/FLW-CD' are being generated. The results are awaited.

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Evaluation of synthetic hexaploid and indigenous wheat lines for resistance to Karnal bunt.

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The most important phase of any plant-breeding program is to assemble the genetic resources from which breeding populations can be developed. The most elaborate facilities and selection procedures will not compensate for an inadequate germ plasm base. Characterization of germ plasm obtained from different sources for desired breeding traits is particularly instrumental in providing the genetic diversity for breeding programs. The documented genetic base that exists in Indian wheat germ plasm for resistance to Karnal bunt of wheat is extremely narrow. Under the new set-up of IPR regimes, the scope for acquiring germ plasm with desired traits from alien sources are practically eliminated. Therefore, the need for exploration and evaluation of uncharacterized and locally available germ plasm for resistance to Karnal bunt is critical. Thousands of accessions belonging to local wheat strains, old NP series, and introductions from international sources have been preserved in a medium-term storage facility at the germ plasm repository at the Directorate of Wheat Research, Karnal. An attempt has been initiated to evaluate the uncharacterized wheat accessions for resistance to Karnal bunt.

In the crop year 2003–04, local wheat strains, some wheat lines belonging to old NP series, synthetic material developed at CIMMYT, Mexico, and fixed prebreeding lines developed at DWR, Karnal, were evaluated for resistance to Karnal bunt. The susceptible check WL 711 also was planted in the beginning, middle, and end of the test plot. Test materials were subjected to an artificial inoculation procedure described by Aujla et al. (1982). Percent coefficient of infection of each spike was worked out using the formula devised by Aujla et al. (1989), and genotypes were grouped further into response categories (resistant, moderately resistant, etc.). Out of 41 lines (NP series and local strains of the PI and IC series) evaluated, 22 and 6 lines were categorized as resistant or moderately resistant to Karnal bunt, respectively (Table 1). Out of 24 lines (14 CIMMYT synthetic hexaploids and 10 fixed prebreeding lines developed at DWR, Karnal), nine and seven lines were found resistant and moderately resistant, respectively (Table 2, p. 67). The remainder of the lines showed more than a 10.00 % coefficient of infection. The highest coefficient of infection of 42.50% was calculated on the susceptible check WL 711.

Table 1. Response of wheat genotypes (Old NP and local strains) to the Karnal bunt pathogen (*Tilletia indica*) under artificial inoculated conditions.

Lines categorized as resistant (up to 5% coefficient of infection)		
NP 830	VHC 6063	IC 321977
NP 836	IC 321865	IC 321980
NP 839	IC 321924	IC 321981
NP 850	IC 321927	IC 322013
NP 866	IC 321928	IC 322022
NP 884	IC 321932	IC 322026
PI 180967	IC 321939	
PI 180986	IC 321954	
Lines categorized as moderately resistant (5–10% coefficient of infection)		
NP 876	IC 321936	IC 322014
IC 321934	IC 322012	IC 322024

Using the ancestors of modern wheat to introgress genes that have the potential to improve resistance to biotic and abiotic stresses is an international effort. Synthetic hexaploids developed by scientists in Australia, the U.S., and at the International Maize and Wheat Improvement Centre in Mexico (CIMMYT) are the vehicles to introduce these ancient genes into our modern cultivars. Present-day hexaploid wheat originated with involvement of three different wild plant species. In the nature, *T. turgidum* crossed with goat grass, a close relative of modern wheat, and in doing so acquired some useful genes. But this crossing probably occurred only two or three times during the development of our present-day hexaploid wheats, which as a result possess some, but not many, of the 'good' genes from goat grass and durum wheat. Researchers are taking another look to see what else goat grass might have to offer and are finding a wide range of useful genes. To get these genes into our modern wheats, scientists are now 'remaking' wheats by going back to the original goat grass and crossing it with modern durum wheat to make crosses that do not happen in nature, popularly known as synthetic hexaploids. The present set of synthetic wheats was particularly evaluated for resistance to Karnal bunt and, fortunately, some of them did show promising resistance to Karnal bunt.

Karnal bunt had been rated as a minor disease in India before cultivation of Mexican wheats in this country (Joshi et al. 1983). This fact indicates the capability of our old wheat cultivars to resist Karnal bunt under natural conditions. Because of their smaller yield potential compared to Mexican genotypes, cultivation of these genotypes has been completely stopped by Indian farmers. Fortunately, a majority of these genotypes are maintained by Indian wheat

scientists and are safely preserved in germ plasm repository of Directorate of Wheat Research. A few of them were found to be tested for their response to Karnal bunt and those found resistant are listed in Table 2.

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Table 2. Response of synthetic hexaploids and fixed prebreeding lines to the Karnal bunt pathogen (*Tilletia indica*) under artificial inoculated conditions. An * indicates the fixed prebreeding lines developed at the DWR, Karnal, the other lines are CIMMYT synthetic hexaploids.

Pedigrees of wheat lines categorized as resistant (up to 5% coefficient of infection).

DVERD-2 / *Ae. tauschii* (214) / OPATA
YUMAI 13 / 2*KAUZ
BCN / CROC-1 / *Ae. tauschii* (662)
ALTAR 84 / *Ae. tauschii* (219) // 2* LOXIA /3/ KAUZ
*EVD 2-1 1012 / Kauz // WH 542
*FASAN / CROC_1 / *Ae. tauschii* // KAUZ
*HD 2329 / CHOIX // RAJ 3777
*PBW343 / FIOS-1
*AGA / 2*CMH74A.582 / CMH76A.912 / CMH79.681 / BOW // RAJ 3777

Pedigrees of wheat lines categorized as moderately resistant (5–10% coefficient of infection).
XIANG82.2661 / 2*KAUZ
BCN // SORA / *Ae. tauschii* (323)
OPATA // CROC-1 / *Ae. tauschii* (879)
ALTAR 84 / *Ae. tauschii* (219) // SERI
CHEN / *Ae. tauschii* (TAUS) // FCT /3/ STAR
*HD 2329 / CHOIX // RAJ 3777
*PBW 343 // HE1 / 5*CNO79 / BORLAUG 95

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An inheritance study of spot blotch (Bipolaris sorokiniana (Sace) Schoem) resistance in bread wheat.

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Abstract. We studied the inheritance of resistance to spot blotch on six *T. aestivum* cultivars. Artificial epiphytotic conditions in the field were developed in the material, which was evaluated in a six parameter model and consisted of P_1, P_2, F_1, F_2, BC_1, and BC_2 generations. A total of 66 entries were evaluated from the six generation material. Disease scoring was recorded on the flag and penultimate leaf using double-digital rating. The resistance showed its dominance over susceptibility in all the F_1 material. The F_2 segregation ratio of the pathogen in 60% of the crosses involving 'resistant / resistant' and 'resistant / susceptible' cultivars was 15 resistant :1 susceptible. We showed that resistance is conditioned by two dominant genes with duplicate gene interaction. On the other hand, the segregation ratio of 9 resistant :7 susceptible in 40% of the crosses indicated complementary gene action. The BC_1 and BC_2 segregation pattern of 3 resistant : 1 susceptible further supplement the finding of the F_2 results. The genes controlling resistance and susceptibility in these parents are different.

Introduction. India, a major wheat-producing country, occupies second place after China in terms of area and production on global level. Three wheat species, *T. aestivum, T. turgidum* subsp. *durum,* and *T. turgidum* subsp. *dicoccum* are successfully cultivated in different parts of the country. Among the biotic stresses, rusts, smut, and foliar blight are the major diseases damaging the wheat crop at different stages with various intensity. Foliar blight is considered as a complex, because a number of pathogens causing blight, blotch, and spot are associated with wheat in India (Misra 1973; Joshi et al. 1978). *Drechslera sorokiniana* (Syn. *Helminthosporium sativum*; perfect stage *Cochliobolus sativus*) appears to be the major pathogen, along with *D. tritici repentis* and *D. tetramera* and *Alternaria triticina* and *A. alternata* (Joshi

et al. 1974). The chief fungus causing blight or blotch is *B. sorokiniana* (Singh et al. 1980; Meena Kumari 1985). *Bipolaris sorokiniana* has been found to infect barley, oats, rice, and 12 other grasses (Misra 1973). Foliar blight is a problem in North Western Plains (Singh et al. 1993), the North Eastern Plains (Nagarajan and Kumar 1997; Chattopadhyay and Chakarabarty 1968; Narain et al. 1973), the Peninsular zone, and Nepal (Singh et al. 1998). A thick canopy and the profuse tillering of high-yielding cultivars favours the build up of a congenial microclimate for the development of this fungus (Joshi et al. 1983; Singh et al. 1986). The distribution of *A. triticina* is comparatively less than that of spot blotch. *Bipolaris sorokiniana* affects the wheat crop more occasionally than *A. trticiana* (Singh et al. 1993). More humid conditions during the growing period are conducive for establishment and subsequent spread of this disease. *Bipolaris sorokiniana* is a dominant species and is fast emerging as one of the major disease on national level (Singh et al. 1995).

Most of the present day wheat cultivars are susceptible to one or the other pathogen of this disease. Information on the inheritance of resistance to spot blotch is still scanty. A systematic program to breed spot blotch-resistant cultivars is needed and could be effectively undertaken if the donors imparting resistance to this pathogen and inheritance to this pathogen are studied on a sound footing. In the present study, *T. aestivum* material selected on the basis of multilocation screening against spot blotch was used to study the inheritance of resistance to this pathogen.

Materials and Methods. The present study was conducted with six wheat cultivars/ breeding lines of diverse origin (Table 1). Among them, HD 2733, HD 2881, and DW 1293 were the resistant parents and Sonalika, DW 1277, and DW 1282 were highly susceptible to spot blotch. These parents were selected from Plant Pathological Screening Nursery (PPSN), which evaluates material on multilocation testing that are spread out through the hot spot. These six wheat lines were crossed in a half diallel to develop F_1, F_2, BC_1, and BC_2 generations. Three crop season were needed to develop the experimental material. The summer nursery facility at the IARI Regional Station, Wellington, Nilgiri, Tamilnadu, India, was utilized to advance the breeding material. The genetics of resistance to spot blotch was determined from breeding material comprised of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations.

Table 1. Parental lines and pedigrees used in this study.

Parent	Pedigree
HD 2733	ATTILA /3/ TU1 / CARC // CHEN / CHTO /4/ ATTILA
HD 2881	KS / *T. turgidum* // HD 1999 // SKA*3 / *T. turgidum* subsp. *carthilicum* // HD 2204
DW 1293	HD 2402 // ALDAN / PF70534 // 2*Kauz /3/ HD 2657 / CPAN 2009
DW 1277	Kauz /3/ Tob / BAU / Bb /4/ ALD'S" /5/ Opata /6/ ToB /7/ HD2631
DW 1282	J-155 / HD 2007 // TRAP /3/ HD 2329N
Sonalika	II54.388 / AN /3/ Yt-54 / NIOB / LR64

The experimental material consisted of 66 entries (six parents, 15 F_1s, 15 F_2s, 15 BC_1, and 15 BC_2s). These lines were planted in three replications using a randomized block design at the research farm of the Indian Agricultural Research Institute, New Delhi, India, during crop seasons rabi 2003–04. Two rows of the parental lines, four rows each of the F_1s; six rows each of the BC_1 and BC_2, and ten rows each of the F_2 generations were grown with a row-to-row distance of 23 cm and 10 cm plant-to-plant. Recommended agronomic practices were followed to raise a good crop.

For effective screening against spot blotch, inoculum spraying was according to the standard techniques at 60 DAS to create sufficient disease pressure. Scoring of disease symptoms was on the flag and penultimate leaves using a double-digit rating system at the seventh day of growth stage 59 (Zadock scale) as proposed by Kumar et.al. (1998), which rated both severity and response and an improved field scale over the 0–9 scale suggested by Sarri and Prescot (1975). Plant were scored based on percent leaf area covered on flag and penultimate leaf as 0 (immune); 01–13, very resistant (VR); 14–35, resistant (R); 36–57, moderately susceptible (MS); 58–78, susceptible; and 79–99, highly susceptible (HS). In the experimental population, plants showing either of the categories (reactions) were the basis to proceed further. All the plants in different generations were observed carefully, counted, and a probable genetic ratio was fit for each cross. A chi-square test, as outlined by Stansfield (1969), was used to test the goodness-of-fit for the appropriate genetic ratio in all 15 crosses.

Results and Discussion. A half diallel between spot blotch resistant and susceptible lines comprised of 15 crosses was evaluated in the F_1, F_2, BC_1, and BC_2 in a randomized block design to study the inheritance (Table 2, p. 69). Disease attained full severity in these lines at the late milky stage and disease severity recorded. These parents were selected on basis of their diverse origin, distinct parentage, and distinct response to leaf blight.

The segregation ratio with respect to crosses involving the resistant parent HD 2733 and the remaining five parents (HD 2881, DW 1293, Sonalika, HD 1277, and DW 1282); HD 2881/DW 1293; HD 2881/DW 1277; and HD 2881/DW 1282 were 15:1. The calculated X^2 values in these crosses varied from 0.02 to 1.82 (Table 3, p. 70). The X^2 analysis revealed that the observed ratios were in agreement with the expected ones with a high degree of confidence (P value ranges from 0.016 to 2.71), indicating that resistance in these crosses is controlled by two genes with a duplicate type of gene interaction. This finding is in accordance with Adlakha (1984) who found that the inheritance of resistance to spot blotch is simple and is governed by one or two dominant factors. Three crosses involving 'susceptible / susceptible' parents, i.e., 'Sonalika/DW 1277', 'Sonalika/DW 1282', and 'DW 1277/DW 1282' show the segregation ratio as 9:7 suggesting that either of the parents contributed a dominant resistance factor in the F_1s. In earlier studies, the resistance to spot blotch in Sharbati Sonora and E 4858 was established as two complimentary genes. Two pairs of dominant, complimentary genes for susceptibility to *A. triticina* in NP 891 and one pair of dominant independent genes were reported by Kulshreshtra and Rao (1976). Three cross combinations were made with one susceptible parent, namely 'HD 2281/ Sonalika', 'DW 1293/Sonalika', and 'DW 1293/DW 1277'. The segregation pattern/ratio was 9:7 (R:S). In these crosses, the calculated X^2 value ranges from 0.11 to 1.84, which fits with the table value ranges from 0.15 to 2.71 at one degree of freedom (Table 3, p. 70) indicating complementary gene interaction.

Table 2. Half-diallel cross combinations, parents, and segregation ratio for spot blotch resistance in the F_2 populations (R = resistant, S = suceptible parent).

Cross	Type of cross	Segregation ratio (F_2)
HD 2733 / HD 2887	R / R	15:1
HD 2733 / DW 1293	R / R	15:1
HD 2733 / Sonalika	R / S	15:1
HD 2733 / DW 1277	R / S	15:1
HD 2733 / DW 1282	R / S	15:1
HD 2881 / DW 1293	R / R	15:1
HD 2881 / Sonalika	R / R	9:7
HD 2881 / DW 1277	R / R	15:1
HD 2881 / DW 1282	R / S	15:1
DW 1293 / Sonalika	R / S	9:7
DW 1293 / DW1277	R / S	9:7
DW 1293 / DW 1282	R / S	15:1
R X S		
Sonalika / DW 1279	S / S	9:7
Sonalika / DW 1282	S / S	9:7
DW 1277 / DW 1282	S / S	9:7

Furthermore, the appearance of resistance in F_1 material indicated that resistance is dominant over susceptibility. The segregation pattern of spot blotch in 'resistant/resistant' parents and 'resistant/susceptible' crosses is observed as 15:1 (resistant : susceptible) in 60% of the cases, an indication that resistance is conditioned by two dominant genes with duplicate gene interaction. These results agree with the findings of Gopalakrishnan et al. (2003) showing interaction of two dominant genes modifying the Mendelian ratio. On the other hand, a 9:7 (R:S) ratio in 40% of the crosses indicated complementary gene action. The fact that the BC_1 and BC_2 generations were 3R:1S further support the results obtained from the F_2 generation. Finally, it is worth noting that the gene/s conditioning resistance and susceptibility in the parents used in this study were different showing variation in the expression.

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Table 3. Reaction to spot blotch in of F_2 and BC_1 populations of the different crosses. For the frequency distribution, 0, 1–13, and 14–35 are resistant classes and 36-57 and 58-78 and greater are susceptible reactions.

Cross	Generation	Frequency distribution					Observed frequency (R:S)	Total plants observed	Expected frequency (R:S)	Expected segregation ratio	X^2 value	Table X^2 value	Probability (P)
		0	01-13	14-35	36-57	58-78 and >							
HD 2733/HD 2887	F_2	—	84	20	9	—	104:9	113	105.95:7.06	15:1	0.93	0.46-1.07	0.30-0.50
	BC_1	—	40	18	16	—	58:16	74	55.50:18.50	3:1	0.45	0.15-0.46	0.50-0.70
HD 2733/DW 1293	F2	—	90	13	5	—	103:5	108	101.25:6.75	15:1	0.48	0.46-1.07	0.30-0.50
	BC1	—	39	5	17	—	54:17	71	53.25:17.70	3:1	0.04	0.016-0.15	0.70-0.90
HD 2733/Sonalika	F_2	—	50	40	7	—	90:7	97	90.94:6.06	15:1	0.16	0.016-0.15	0.70-0.90
	BC_1	—	7	74	14	2	51:16	67	50.25:16.75	3:1	0.04	0.016-0.15	0.70-0.90
HD 2733/DW 1277	F_2	—	42	54	10	—	96:10	106	99.38:6.63	15:1	1.82	1.64-2.71	0.10-0.20
	BC_1	—	18	30	13	5	48:18	66	49.50:16.50	3:1	0.18	0.15-0.46	0.50-0.70
HD 2733/DW1282	F_2	—	45	40	7	—	85:7	92	86.25:5.75	15:1	0.29	0.15-0.46	0.50-0.70
	BC_1	—	15	30	18	—	45:18	63	47.25:15.75	3:1	0.43	0.15-0.46	0.50-0.70
HD 2881/DW1293	F_2	—	80	20	5	2	100:7	107	100.31:6.69	15:1	0.02	0.004	0.95
	BC_1	—	36	22	15	—	58:15	73	54.75:18.25	3:1	0.77	0.46-1.07	0.30-0.50
HD 2881/Sonalika	F_2	—	60	9	45	3	69:48	117	65.80:51.19	9:7	0.20	0.15-0.46	0.50-0.70
	BC_1	—	29	20	18	—	49:18	67	50.25:16.75	3:1	0.12	0.016-0.15	0.70-0.90
HD 2881/DW1277	F_2	—	61	46	8	—	107:8	115	107.80:7.19	15:1	0.11	0.016-0.15	0.90-0.70
	BC_1	—	36	20	18	4	56:22	78	58.50;19.50	3:1	2.34	1.64-2.71	0.10-0.20
HD 2881/SW 1282	F_2	—	49	42	6	2	91;8	99	92.80;6.19	15:1	0.55	0.46-1.07	0.30-0.50
	BC_1	—	8	35	18	—	43:18	61	45.75;15.25	3:1	0.66	0.46-1.07	0.30-0.50
DW 1293/Sonalika	F_2	—	45	21	41	5	66;46	112	63.00:49.00	9:7	0.32	0.15-0.46	0.50-0.70
	BC_1	—	18	31	14	6	49:20	69	51.75:17.25	3:1	0.58	0.46-1.07	0.30-0.50
DW 1293/DW 1277	F_2	—	60	7	45	1	67:46	113	63.56:49.44	9:7	0.43	0.15-0.46	0.50-0.70
	BC_1	—	26	18	19	—	44:19	63	47.25:15.75	3:1	0.89	0.46-1.07	0.30-0.50
DW 1293/DW1282	F_2	—	47	55	9	—	102:9	111	104.6:6.94	15:1	0.65	0.46-1.07	0.30-0.50
	BC_1	—	17	33	16	7	50:23	73	54.75:18.25	3:1	1.65	1.64-2.71	0.10-0.20
Sonalika/DW 1279	F_2	—	7	41	10	30	48:40	88	49.50:38.50	9:7	0.11	0.016-0.15	0.70-0.90
	BC_1	—	5	37	9	13	42:22	64	48.00:16.00	3:1	3.0	2.71-3.84	0.05-0.10
Sonalika/DW 1282	F_2	—	2	43	19	24	45;43	88	49.50:38.50	9:7	0.94	0.46-1.07	0.30-0.50
	BC_1	—	6	40	6	15	46:21	67	50.25:16.75	3:1	1.44	1.07-1.64	0.20-0.30
DW 1277/DW 1282	F_2	—	7	41	8	36	48:44	92	40.25:40.25	9:7	1.84	1.64-2.71	0.10-0.20
	BC_1	—	8	36	3	16	44:19	63	47.25:15.75	3:1	0.89	0.46-1.07	0.30-0.50

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Development of a genetic stock carrying multiple rust and powdery mildew resistance genes.

M. Sivasamy (IARI Wellington) and Vinod and S.M.S. Tomar (IARI, New Delhi).

Yellow or stripe rust is one of the important rust diseases causing considerable yield loss in India, particularly in the North Western Plains and the Northern and Southern Hill regions. The *T. turgidum* subsp. *dicocoides*-derived yellow rust-resistance gene *Yr15*, present in the Israeli stock V763-2312, confers high degree of resistance against widely prevalent races in India, especially races 78S84 (virulent on *Yr9*), 46S119 (virulent on PBW 343), and I (Southern Hills) (Vinod et al. 2006). The line V 763-2312 is used widely as donor for the development of resistance lines at IARI, Regional Station, Wellington, India. The Australian stock Cook, carrying the *Th. ponticum*-derived, linked genes *Lr19 + Sr25* and *T. timopheevii*-derived, linked genes *Sr25 + Pm6*, confers a high degree of resistance against most prevalent races of the leaf and stem rust and powdery mildew pathotypes in India, although a new pathotype is reported virulent on *Lr19*. This stock is used effectively in developing several NILs of popular Indian bread wheat cultivars at the IARI, Regional Station, Wellington.

The availability of stocks carrying these genes in a spring wheat background will immensely help the breeders develop lines resistant to these pests. V763-2312 was crossed to Cook and the line HW 6001, which is resistant to leaf, stem, and yellow rust and powdery mildew, was obtained at the BC_3F_4 stage. The gene *Sr36* confers a very high degree of resistance against the widely occurring stem rust pathotypes in India and also to race Ug99, which is virulent on *Sr31* and becoming a threat to wheat production worldwide. Therefore, this stock with resistance genes *Lr19 + Sr25*, *Sr36 + Pm6*, and *Yr15* developed at Wellington will be very useful for the breeders in wheat-improvement programs for developing resistant wheat cultivars (Table 1).

Table 1. Characteristics of parental lines and HW 6001, a genetic stock with multiple rust and powdery mildew resistance genes.

Line/Cultivar	Black rust	Brown rust	Yellow rust	Powdery mildew
V763-2312	R	80S	R	2 (0–4 scale)
Cook	R	R	F (undesignated)	R
New line HW 6001 with *Lr19+Sr25*, *Sr36+Pm6,* and *Yr15*	R	R	R	R

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ITEMS FROM ITALY

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Molecular characterization of Italian soilborne cereal mosaic virus isolates.

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A mosaic disease of winter wheat was first described in the USA by McKinney in 1925 and subsequently in many other wheat-growing countries. Until recently, the disease was associated worldwide to wheat soil-borne mosaic virus (WSBMV). Results of sequence analysis by German and Chinese researchers, however, have prompted the International Committee on Taxonomy of Viruses to approve a taxonomic proposal to divide American, European, and Chinese isolates into different species within the genus *Furovirus*. The novel species have been denominated wheat soil-borne mosaic virus, cereal soilborne mosaic virus (CSBMV), and wheat Chinese mosaic virus (WCMV). On the basis of the new classification, the wheat mosaic disease is believed to be generally caused by WSBMV in United States, Brazil, and Canada; by CSBMV in Europe; and by WCMV in Asia. Twenty-four wheat samples showing typical Furovirus symptoms were collected from farmers in fields northern, central, and southern Italy to study their degree of genetic diversity. SsRNA was extracted, and the nucleotide sequence of a viral coat protein gene was determined for each sample. Nucleotide and amino-acid sequences alignment between the sequences obtained and the published RNA2 CP sequences of CSBMV, WSBMV, and WCMV isolates was generated applying the Clustal V method, and phylogenetic distance trees were constructed. Branching orders identified three major phylogenetic groups. In the first group, all the Italian isolates clustered closely together along with French, English, and German isolates (SBCMV species), whereas the second group included the American isolates, and the third ascribed the Asian isolates. Sequence data analysis revealed a high degree of genetic identity among Italian isolates (96.6 to 100.0 %) and between Italian isolates and SBCMV accessions from the United Kingdom, France, and Germany (88.7 to 99.6 %). Sequence divergences from 29.6 to 45.9 % were observed between Italian SBCMV isolates and SBWMV or CWMV isolates. Amino-acid sequence analysis of CP cistron revealed few nonspecific exchanges as well as a high degree of sequence identity (97.7 to 100%) among CSBMV isolates from Italy and other European countries. Amino-acid sequence similarity between Italian and Asian or American isolates ranged from 71.0 to 81.2 %. Eventhough all the Italian isolates so far analyzed belong to the novel CSBMV species, the presence of SBWMV in this country cannot be excluded.

Reaction of 34 durum wheat cultivars to cereal soilborne mosaic virus.

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Cereal soilborne mosaic virus (CSBMV) in Italy was first detected in the Po Valley in 1960 and is now known be widespread throughout most of the country, particularly in the northern and central regions. Thirty-four durum wheat cultivars were grown during 2006–07 in a field with SBCMV at Cadriano, near Bologna, and evaluated for resistance to CSBMV on the basis of symptom severity, DAS-ELISA readings, and agronomic performance. Seventeen of these cultivars (marked with asterisks in Table 1, p. 72) had never been tested for CSBMV resistance. The cultivars, planted 6 November, 2006, were grown in 10-m^2, solid-seeded plots distributed in the field according to a randomized block design

Table 1. Mean symptom severity, mean ELISA value, and agronomic performance of 34 cultivars of durum wheat grown in a field with cereal soilborne mosaic virus near Bologna, Italy, during the 2006–07 season. Cultivars marked with asterisks (*) have never been tested for CSBMV resistance previously.

Cultivar	Mean symptom severity (0–4)	Mean ELISA value	Heading (Number of days from 1 April)	Plant height (cm)	1,000-kernel weight (g)	Test weight (g)	Grain yield (13% humidity)
Achille *	3.3 a	1.516 af	38.7 ac	61.7 op	32.6 fh	71.1 ad	1.24 ij
Anco Marzio	3.0 ab	1.631 ad	32.7 gl	70.0 kn	33.3 eh	67.8 bj	1.42 hj
Ariosto *	0.8 lp	1.444 af	35.0 dh	87.0 ae	40.6 ab	70.2 af	2.43 ch
Asdrubal *	1.2 hm	0.612 hj	28.0 no	88.7 ac	34.7 dg	72.8 a	4.47 a
Capri *	3.1 ab	1.653 ad	39.0 ab	72.3 in	31.1 gi	68.2 ai	1.62 gj
Casanova *	1.8 eh	1.777 ab	31.3 in	80.7 ci	39.5 ac	67.9 bi	2.36 dh
Catervo *	1.4 gm	1.368 bf	35.0 dh	78.3 ek	36.2 bf	64.4 hj	1.84 fj
Chiara *	1.4 gm	1.406 af	34.7 di	73.3 hn	37.9 bd	67.6 bj	2.91 cf
Claudio	2.5 bd	1.736 ac	34.0 ej	85.0 bf	36.6 bf	72.6 a	2.45 ch
Creso	1.6 ej	1.114 eg	36.3 bf	74.7 gn	39.2 ad	70.6 ae	2.39 dh
Dario *	0.3 oq	0.389 ik	30.7 jo	94.0 a	35.4 cg	69.8 af	2.75 cf
Duilio	1.0 in	1.226 df	34.0 ej	81.7 ch	40.6 ab	69.7 af	3.29 bd
Dylan	0.4 nq	0.305 jk	34.7 di	92.7 ab	37.4 be	71.5 ac	4.18 ab
Grazia	3.2 a	1.685 ad	37.0 ae	66.7 no	29.2 hi	69.5 af	1.07 j
Hathor *	0.1 pq	0.086 k	38.7 ac	71.3 jn	38.3 ad	67.1 cj	1.89 fj
Iride	0.7 mq	1.045 fh	29.0 mo	81.0 ci	35.0 cg	68.9 ah	3.47 bc
Isildur *	3.0 ab	1.732 ac	40.0 a	56.7 p	27.2 i	66.5 dj	1.57 gj
K26 *	1.5 fl	1.551 ae	35.7 bg	72.3 in	36.3 bf	68.9 ah	1.86 fj
Latinur *	1.7 ei	1.433 af	34.0 ej	69.3 lo	39.2 ad	67.3 bj	2.78 cf
Levante	1.2 hm	1.036 fh	34.0 ej	87.3 ad	34.8 dg	69.4 af	3.18 be
Meridiano	1.1 hm	1.095 eg	31.7 hm	85.7 af	35.3 cg	70.5 ae	4.15 ab
Neodur	0.9 ko	1.607 ad	35.3 cg	82.0 ch	38.5 ad	71.7 ac	3.33 bd
Neolatino *	1.1 hm	1.382 bf	29.3 lo	83.3 cg	38.6 ad	71.9 ab	3.28 bd
Normanno	1.3 hm	1.245 cf	34.0 ej	81.3 ch	39.3 ad	69.1 ag	2.57 cg
Orfeo *	1.5 ek	0.757 gi	36.3 bf	78.3 ek	42.7 a	63.3 j	1.21 ij
Orobel	3.0 ab	1.728 ac	39.0 ab	76.7 fm	32.3 fh	65.5 fj	1.4 hj
Pr22d40	3.3 a	1.779 ab	38.0 ad	58.3 p	29.6 hi	68.1 ai	1.55 gj
Pr22d89 *	2.2 ce	1.699 ad	34.7 di	75.3 gn	34.9 cg	71.7 ac	2.30 dh
Saragolla *	0.0 q	0.187 jk	30.3 ko	79.7 dj	34.9 cg	69.7 af	4.78 a
Sfinge *	1.2 hm	1.295 bf	27.7 o	78.0 el	37.9 bd	66.2 ej	3.12 ce
Simeto	2.8 ac	1.892 a	33.3 fk	68.3 mo	37.7 be	64.6 gj	1.97 fj
Solex	1.0 jn	1.060 fg	33.3 fk	81.7 ch	39.5 ac	70.1 af	2.70 cf
Vendetta	2.1 df	1.617 ad	32.7 gl	74.3 gn	37.1 be	63.7 ij	2.13 ei
Virgilio	2.0 dg	1.571 ae	33.3 fk	82.7 cg	36.0 bf	67.4 bj	2.35 dh
MEAN	1.7	1.284	34.2	77.4	36.2	68.7	2.53

with three replicates. Symptom severity was evaluated on two dates using a 0–4 scale. DAS-ELISA was performed on extracts from a bulk of the apical half of the second and third youngest leaves of ten randomly chosen plants/plot collected 21 February and 12 March, 2007. The cultivar Saragolla remained symptomless throughout the entire season, showed the second lowest mean ELISA value and produced the highest grain yields. The cultivars Dylan, Dario, and Hathor also had very low mean ELISA values (≤ 0.389) and very low symptom scores (≤ 0.4); the latter two cultivars, however, produced decidedly low yields as did other relatively CSBMV-resistant wheats (i.e., Orfeo, Catervo, and K26), possibly due to adverse factors different from CSBMV. In the cultivars Meridiano and Neodur, mild symptoms and high grain yields were accompanied by high ELISA values, which was not expected because foliar extracts from these two cultivars had given ELISA values close to zero, even under severe disease pressure, in nine previous experiments carried out at a different site near Bologna. Cultivars Duilio and Iride, showing mild symptoms and previously classified as moderately resistant, also showed unexpectedly high ELISA values. The correlation between mean ELISA value and

Table 2. Estimated mean effects of cereal soil-borne mosaic virus on 34 durum wheat cultivars with different disease severity grown in a field near Bologna, Italy, during 2006–07.

Disease severity score	Number of cultivars	Grain yield loss		Plant height reduction		Kernel weight reduction		Heading delay days
		t/ha	%	cm	%	g	%	
0.00–1.00	9	3.20	14	83.5	5	37.8	5	2.1
1.01–2.00	14	2.75	26	79.6	10	37.7	5	1.6
2.01–3.00	7	1.89	49	72.3	18	34.2	14	3.8
3.01–3.30	4	1.37	63	64.8	26	30.6	23	6.8

Table 3. DAS-ELISA values for durum wheat cultivars to wheat spindle streak mosaic virus in central Italy.

Cultivar	Mean ELISA 1999 (44 cvs)	Mean ELISA 2004 (44 cvs)	Mean ELISA 2007 (20 cvs)	ELISA index 1999 (%)	ELISA index 2004 (%)	ELISA index 2007 (%)	ELISA index Mean (%)
Arcobaleno	0.046 df	0.106 ac		6	23		14.6
Avispa		0.118 ac		26			25.6
Baio	0.420 af	0.148 ac		58	32		44.9
Bronte	0.351 af			48			48.2
Cannizzo		0.159 ac			34		34.5
Canyon		0.295 ac	0.021 c		64	1	32.6
Cappelli			0.959 ac			49	48.8
Ceedur	0.270 af			37			37.0
Ciccio	0.729 a	0.443 ab	1.967 a	100	96	100	98.7
Cirillo	0.594 ab			82			81.6
Claudio	0.004 f	0.000 c	0.018 c	1	0	1	0.5
Colorado	0.114 bf	0.031 bc		16	7		11.2
Colosseo	0.418 af	0.362 ac	1.348 ab	57	79	69	68.2
Creso	0.110 bf	0.190 ac	0.598 bc	15	41	30	28.9
Derrick		0.277 ac			60		60.2
Duilio	0.272 af	0.116 ac	0.979 ac	37	25	50	37.4
Dupri	0.039 df			5			5.4
Dylan			1.116 ac			57	56.7
Elios	0.210 bf			29			28.8
Flaminio	0.272 af			37			37.4
Fortore	0.221 bf			30			30.3
Gargano	0.348 af	0.188 ac		48	41		44.3
Gianni	0.114 bf	0.393 ac		16	85		50.5
Giemme	0.267 af			37			36.7
Giotto		0.359 ac			78		77.9
Grazia	0.344 af	0.279 ac	0.023 c	47	61	1	36.3
Ionio = Ares	0.471 af	0.247 ac		65	54		59.1
Iride	0.000 f	0.185 ac	0.677 bc	0	40	34	24.9
Italo	0.010 f			1			1.3
Ixos	0.227 bf			31			31.2
Karalis			1.357 ab			69	69.0
Lesina		0.193 ac			42		41.9
Lloyd	0.526 ad			72			72.1
Marco		0.162 ac			35		35.3

mean symptom score was highly significant (0.772**), and the same was found for the relationships between mean symptom score and heading date (0.504**), plant height (-0.704**), 1,000-kernel weight (-0.614**), and grain yield (-0.719). Regression analysis indicated that the effects of CSBMV on grain yield, kernel weight, plant height, and heading date (Table 2) were ruinous on the most susceptible cultivars and quite substantial also for the resistant ones.

Reaction of 72 durum wheat cultivars to wheat spindle streak mosaic virus in central Italy.

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In Italy, wheat spindle streak mosaic was first detected in a field near Rome in 1985. Subsequently, WSSMV has been identified, either alone or in mixed infection with CSBMV, in approximately 20 other sites throughout the northern and central and regions of the country. Field trials in 1998–99, 2003–04, and 2006–07 at the Experimental Farm of the Cereals Research Institute near Rome in a field with natural inoculum sources of both WSSMV and CSBMV evaluated the reaction to WSSMV using DAS-ELISA of 72 durum wheat cultivars marketed in Italy. Nine of these cultivars were grown over three seasons, 17 over two seasons, and 46 in one season only. The cultivars were grown in 10-m^2, solid-seeded plots, distributed in the field according to a randomized

block design with either two (1999) or three replicates (2004 and 2007). Virus concentration was determined on extracts from a bulk of the apical half of the second and third youngest leaves of ten randomly chosen plants/plot collected 18 March, 1999, 16 March, 2003, and 27 February, 2007. Simple correlation coefficients between ELISA values in different seasons were relatively low (r = 0.482* for 22 cultivars tested both in 1999 and 2004; r = 0.710* for the 10 tested both in 1999 and 2007; and r = 0.482 n.s. for the 12 tested both in 2004 and 2007). The DAS-ELISA readings obtained for each cultivar in different years are presented in Table 3 (pp. 74-75), where they are given also as percentage of the highest reading obtained in each season (ELISA index).

Among the nine cultivars assayed for three seasons, the lowest mean ELISA index was observed for Claudio (0.5%), which seems, at present, the best choice for soils with WSSMV in Italy. Among the 17 cultivars tested for two seasons, the lowest mean ELISA index were observed for Colorado (11.2%), Rusticano (11.4%), and Provenzal (11.9%). Cultivars Tiziana (0.1%), Italo (1.3%), Ofanto (4.4%), and Dupri (5.4%), assayed for only one season, also had relatively low ELISA values. Colorado, Provenzal, Tiziana, and Dupri appear of particular interest because they have shown a high degree of resistance towards CSBMV in Italy. Given the consistently high ELISA values recorded for Ciccio throughout three seasons (mean ELISA index = 98.7%), this cultivar will be used as the susceptible control in future assays.

Table 3 (continued). DAS-ELISA values for durum wheat cultivars to wheat spindle streak mosaic virus in central Italy.

	Mean ELISA			ELISA index			
Cultivar	1999 (44 cvs)	2004 (44 cvs)	2007 (20 cvs)	1999 (%)	2004 (%)	2007 (%)	Mean (%)
Meridiano		0.261 ac	0.810 ac		57	41	48.9
Mongibello	0.295 af			40			40.4
Nefer	0.150 bf	0.275 ac		21	60		40.1
Neodur	0.523 ad	0.166 ac		72	36		54.0
Nerone	0.544 ac			75			74.6
Normanno			1.193 ac			61	60.7
Ofanto	0.032 ef			4			4.4
Orobel		0.243 ac	0.689 bc		53	35	43.9
Platani		0.262 ac			57		56.9
Parsifal	0.409 af			56			56.1
Pietrafitta		0.146 ac			32		31.7
Platani	0.285 af			39			39.1
Poggio	0.406 af			56			55.7
Portorico		0.275 ac			60		59.7
Preco		0.204 ac			44		44.3
Provenzal	0.054 df	0.075 ac		7	16		11.9
Quadrato		0.165 ac			36		35.8
Rusticano	0.037 df	0.081 ac		5	18		11.4
Saadi'	0.444 af			61			61.0
San Carlo	0.000 f		0.690 bc	0		35	17.5
Saragolla			1.913 a			97	97.3
Settedue		0.168 ac			36		36.5
Simeto	0.053 def	0.379 ac	0.683 bc	7	82	35	41.5
Solex	0.091 cf	0.154 ac		12	33		22.9
Svevo	0.039 df	0.124 ac	0.674 bc	5	27	34	22.2
Tiziana		0.001 c			0		0.1
Torrebianca		0.310 ac			67		67.4
Tresor	0.134 bf			18			18.4
Valbelice	0.509 ae	0.208 ac		70	45		57.5
Valnova	0.478 af	0.278 ac		66	60		63.1
Valsalso		0.353 ac			77		76.7
Varano	0.522 ae			72			71.6
Vendetta			1.333 ab			68	67.8
Verdi		0.331 ac			72		72.0
Vesuvio		0.264 ac			57		57.4
Vetrodur		0.128 ac			28		27.7
Vinci			0.464 bc			24	23.6
Vitromax		0.460 a			100		100.0
MEAN	0.265		0.217		0.876		
Minimum	0.000		0.000		0.018		
Maximum	0.729		0.460		1.967		

Inheritance of resistance to cereal soil-borne mosaic virus in a durum wheat population of lines derived from the cross 'Meridiano / Claudio'.

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According to the literature, in hexaploid wheat resistance to CSBMV is controlled by a few major genes. In field trials carried out for many years in Italy, most of the cultivars of hexaploid and durum wheat marketed in this country exhibited a consistent array of intermediate reactions to the virus, suggesting that, in these wheats, resistance to CSBMV is governed by numerous genes. A population consisting of 184 RILs (at the F_7 generation) obtained by Produttori Sementi Bologna Spa, Italy, from a cross between the durum wheat cultivars Meridiano (classed as either resistant or moderately resistant to CSBMV in various seasons) and Claudio (repeatedly classed as moderately susceptible) was grown during the 2006–07 season in a field near Cadriano (Bologna) with natural inoculum sources of CSBMV and evaluated for resistance on the basis of both symptomatology (on a 0–4 scale) and virus concentration (by ELISA). Disease pressure at the experimental site was severe, as testified by the relatively high percentage of lines (6%) with symptom severity scores equal or above 3.5. The results obtained showed that in the 'Meridiano / Claudio' cross, resistance to CSBMV is controlled by no less than four genes and that genotypes expressing more extreme reactions than either parent may be recovered (Tables 4 and 5). Our results also strongly suggested the presence of a further gene that, regardless of the symptomatology and virus concentration displayed on the first observation date, has a marked impact on the subsequent reaction to CSBMV of each line, i.e., a plus or minus effect of about 0.250 in terms of ELISA value and of about 0.2 in terms of symptom severity expression. The 'Meridiano / Claudio' population will be evaluated again for CSBMV-resistance in the same field during the 2007–08 season. Presently, the population is being profiled with SSR and DArT markers. Analysis of phenotypic and molecular data will allow us to identify the QTL involved in the control of CSBMV resistance.

Table 4. Symptom severity score frequency (%) distribution at three sampling dates for 184 lines from a 'Meridiano / Claudio' population.

Symtom severity interval	14 Feb	21 Feb	2 Apr
0.00–0.10	17.4	16.8	21.2
0.11–0.20	3.8	7.6	7.6
0.21–0.30	9.2	7.6	3.8
0.31–0.40	3.8	4.3	2.7
0.41–0.50	0.0	2.2	4.3
0.51–0.60	4.3	0.0	1.1
0.61–0.70	1.6	2.7	2.7
0.71–0.80	1.1	1.6	2.7
0.81–0.90	3.3	3.3	1.1
0.91–1.00	3.3	1.6	2.7
1.01–1.10	0.0	0.0	0.0
1.11–1.20	1.6	2.7	0.5
1.21–1.30	2.2	1.1	0.5
1.31–1.40	3.8	0.5	0.0
1.41–1.50	1.1	1.6	0.5
1.51–1.60	0.0	0.0	0.0
1.61–1.70	3.3	2.2	1.1
1.71–1.80	3.3	2.7	0.5
1.81–1.90	1.6	1.1	0.5
1.91–2.00	1.6	1.6	1.1
2.01–2.10	0.0	0.0	0.5
2.11–2.20	2.2	2.2	0.0
2.21–2.30	6.5	2.2	0.0
2.31–2.40	3.8	3.3	2.2
2.41–2.50	4.3	2.2	1.1
2.51–2.60	0.0	0.0	0.0
2.61–2.70	6.0	4.3	2.7
2.71–2.80	3.3	7.6	2.7
2.81–2.90	3.8	6.5	3.8
2.91–3.00	3.3	5.4	7.1
3.01–3.10	0.0	0.0	0.0
3.11–3.20	0.0	3.3	3.8
3.21–3.30	0.5	0.5	6.5
3.31–3.40	0.0	1.1	5.4
3.41–3.50	0.0	0.0	3.3
3.51–3.60	0.0	0.0	0.0
3.61–3.70	0.0	0.0	2.2
3.71–3.80	0.0	0.0	2.2
3.81–3.90	0.0	0.0	0.5
3.91–4.00	0.0	0.0	1.1

Table 5. ELISA value frequency (%) distribution at two sampling dates for 184 lines from the 'Meridiano / Claudio' population.

ELISA value intervals	14 Feb	12 Mar
0.000–0.050	0.0	0.0
0.051–0.100	1.1	1.6
0.101–0.150	1.6	1.1
0.151–0.200	1.1	1.1
0.201–0.250	1.1	0.0
0.251–0.300	1.6	0.5
0.301–0.350	0.5	0.0
0.351–0.400	1.1	1.6
0.401–0.450	3.3	0.5
0.451–0.500	4.3	1.1
0.501–0.550	2.7	2.2
0.551–0.600	2.2	1.6
0.601–0.650	3.8	2.7
0.651–0.700	0.5	1.1
0.701–0.750	3.8	0.0
0.751–0.800	3.3	2.7
0.801–0.850	4.3	3.3
0.851–0.900	1.6	2.7
0.901–0.950	2.7	3.3
0.951–1.000	5.4	2.2
1.001–1.050	2.2	1.1
1.051–1.100	3.3	2.2
1.101–1.150	2.7	1.1
1.151–1.200	3.8	1.6
1.201–1.250	4.3	1.6
1.251–1.300	6.5	1.1
1.301–1.350	5.4	4.3
1.351–1.400	4.3	2.2
1.401–1.450	3.8	3.8
1.451–1.500	3.3	1.1
1.501–1.550	2.2	1.6
1.551–1.600	3.8	2.2
1.601–1.650	3.8	2.7
1.651–1.700	2.7	4.3
1.701–1.750	0.0	6.0
1.751–1.800	1.1	6.5
1.801–1.850	0.0	8.2
1.851–1.900	0.0	10.3
1.901–1.950	0.5	6.0
1.951–2.000	0.0	2.7

Application of DMI fungicides against Fusarium head blight at two growth stages in bread and durum wheats.

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Fusarium head blight is one of the most important wheat disease in Italy and causes partial or total premature ear necrosis or emptiness of the mature ears and, in the presence of severe attacks, grain losses from 30% to 70%. Disease incidence and severity can be reduced by adopting correct agronomic practices, including the use of healthy seed, treating seed with fungicides against *Fusarium* species, and applying fungicides at the beginning of anthesis. In Italy, many tend to anticipate the application of fungicides to the stage of complete inflorescence emergence. We examined the effectiveness of fungicide active ingredients against FHB applied at two different growth stages, i.e., at complete inflorescence emergence (Zadoks' Growth Stage (GS) 58-59) and at the beginning of anthesis (GS 60-61) on five bread and five durum wheat cultivars. The fungicides tested were bromuconazole (Granit®) at 250g/ha, prochloraz (Sportak®45 EW) at 585g/ha, and tebuconazole (Horizon®) at 250g/ha. All three fungicides are registered in Italy for FHB control. Product activity was evaluated at the milk stage (GS 77) by comparing disease incidence (percentage of infected heads) and severity (infected area of the heads) in fields located in the region of Emilia-Romagna (northern Italy). Results showed that at the sites considered FHB disease was mainly caused by *F. graminearum* and *F. culmorum*. Bromuconazole, prochloraz, and tebuconazole proved efficient in reducing disease incidence and severity in all the cultivars examined. Their application at GS 60-61 stage, when the sensitivity of the plant to the disease is highest, furnished a better control than application at GS 58-59 in most of the wheat cultivars investigated.

Effects of three DMI fungicides on Fusarium head blight in durum wheat cultivars and their influence on DON content in kernels.

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In Italy, the main causative agents of FHB, a disease complex caused by *Fusarium* and *Microdochium* genera, are *F. graminearum*, *F. culmorum*, *F. avenaceum,* and *F. poae*. FHB-infected kernels may be harmful to human and other mammals because of an associated mycotoxin accumulation. *Fusarium graminearum* and *F. culmorum*, in fact, produce deoxynivalenol (DON), a mycotoxin having neurotoxic and immunotoxic effects. The purpose of our study was to evaluate the effect of three commercial fungicides registered in Italy for FHB control, bromuconazole (Granit®) at 250g/ha, prochloraz (Sportak®45 EW) at 585g/ha, and tebuconazole (Horizon®) at 250g/ha, on the development of FHB and the percentage of Fusaria-infected kernels and on the accumulation of DON. The trial was carried out on three durum wheat cultivars (Gianni, Neodur, and Orobel) commonly cultivated in the Emilia-Romagna region (northern of Italy) inoculated with a $2.5x10^4$ conidia/ml mixture of toxigenic isolates of *F. culmorum* and *F. graminearum*. A single application of either bromuconazole, prochloraz, or tebuconazole applied at the beginning of anthesis (Zadoks' Growth Stage 60-61) reduced either incidence and severity of FHB by about 60% compared with the untreated control. Application of these fungicides, moreover, was found to decrease the percentage of kernels infected by *F. graminearum* and *F. culmorum* by about 60% and to reduce the quantity of DON by about 53% in kernels, 55% in semolina, and 66% in the bran.

Fungal population in wheat cultivars with different degrees of susceptibility to cereal soil-borne mosaic virus.

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Cereal soil-borne mosaic virus is widespread in Italy, especially in the northern and central regions, where it is known to cause grain yield reductions of up to 70% on the most susceptible cultivars of hexaploid wheat and durum wheat. Following reports indicating that the spread of FHB is greater in plants infected by barley yellow dwarf virus (BYDV) than in BYDV-free ones, we investigated the possibility of an analogous correlation between CSBMV and fungi having antag-

onistic and/or toxigenic activity. Four cultivars of bread wheat (Artico, Trofeo, Agadir, and Isengrain) and four of durum wheat (Neodur, Provenzal, Claudio, and Orobel), exhibiting a wide range of reactions to CSBMV, were grown in a in field near Cadriano (northern Italy) with natural inoculum sources of this virus. Mycoflora composition was investigated (CFU/g) in the rhizosphere soil and, towards the end of the wheat growth cycle, also in roots, stems, and seeds. Fusaria species were identified molecularly. The fungi isolated from the soil were mostly saprophytes. *Penicillium* was found mainly in May, whereas *Fusaria* were most abundant in July; the antagonistic *Trichoderma* was not detected. *Fusaria* were detected in the seeds of all cultivars and were most abundant in durum wheat cultivars Orobel (17%), susceptible to CSBMV, and Provenzal (12%), resistant to the virus. Several *Fusarium* species were identified: *F. culmorum* prevailed in durum wheat and *F. poae* in bread wheat. Preliminary data suggest that there is no correlation between fungal colonization and susceptibility to CSBMV of the withering plants. Further studies are in progress.

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ITEMS FROM JAPAN

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Cytological and microsatellite mapping of mutant genes for spherical grain and compact spikes in durum wheat.

Two mutants for sphaerococcoid seed (MA 16219) and compact spike (MA 17648) were isolated from the M_3 progeny of the durum wheat cultivar,Altaiskaya Niva mutagenized with chemical mutagens. The chromosomal locations of the genes involved were determined by the use of a complete set of D-genome disomic substitutions in durum cultivar Langdon. The gene for sphaerococcoid grain, s^{16219}, was allelic to *S2*, located in the centromeric region of chromosome 3B in hexaploid wheat. The gene for compact spike, C^{17648}, was located on chromosome 5AL distal to the *Q* locus. Using microsatellite markers, C^{17648} and the awn inhibitor gene *B1* were located in the F_2 of 'LD222 / MA17648'. The gene order was *Xbarc319* – C^{17648} – *Xgwm179* – *Xgwm126* – *Xgwm291* – *B1*.

Exploration of genetic diversity among Xinjiang Triticum and Triticum polonicum by AFLP markers.

Seventy-two Xinjiang *Triticum* and *T. turgidum* subsp. *polonicum* accessions were subjected to AFLP analyses to discuss the origin of *T. petropavlovskyi*. A total of 91 putative loci were produced by four primer combinations; 56 loci were polymorphic, which is equivalent to 61.53% of the total number of putative loci. Genetic diversity among 11 *T. petropavlovskyi* accessions was narrow due to the lowest number (32) of polymorphic loci among the wheat species. Forty-four polymorphic loci were found in *T. aestivum* subsp. *aestivum* and *T. aestivum* subps. *compactum*, whereas the highest polymorphism was observed in *T. turgidum* subsp. *polonicum*. On the basis of the UPGMA clustering and PCO grouping and genetic similarity estimates from the AFLPs, we noted that *T. petropavlovskyi* was more closely related to the Chinese accessions of *T. turgidum* subsp. *polonicum* than to accessions from other countries. Two accessions of *T. aestivum* subsp. *aestivum* were grouped with *T. petropavlovskyi* in the UPGMA clustering; both were similar to *T. petropavlovskyi* in respect of spike structure, i.e., presence of awn, glume awn, and leaf pubescence. Six loci, which were commonly absent in Chinese *T. turgidum* subsp. *polonicum*, also were absent in nearly all of the *T. petropavlovskyi* accessions. The findings of this study reduced the probability of an independent allopolyploidization event in the origin of *T. petropavlovskyi* and indicated a greater degree of gene flow between *T. aestivum* subsp. *aestivum* and *T. turgidum* subsp. *polonicum* leading to *T. petropavlovskyi*. Most likely, the *P* gene of *T. petropavlovskyi* hexaploid wheat was introduced from *T. turgidum* subsp. *polonicum* to *T. aestivum* subsp. *aestivum* via a spontaneous introgression or breeding effort.

Comparative genetic diversity of T. aestivum subsp. aestivum–T. turgidum subsp. polonicum introgression lines with long glume and T. petropavlovskyi by AFLP-based assessment

Genetic diversity of a set of introgression lines of *T. aestivum* subsp. *aestivum* L./*T. turgidum* subsp. *polonicum* with long glume and *T. petropavlovskyi* were analyzed by AFLP. Small-scale, bulk-breeding method was used throughout until the F_6 generation to develop the introgression lines. Thirty-eight hexaploid F_7 plants with long glume phenotype and their parents were subjected to AFLP analysis by four primer combinations. A total of 47 polymorphic loci were detected between the parents and 15 were introgressed across the 38 lines. We hypothesized that approximately 50% of A or B genomes associated polymorphic loci were introgressed. The variation of introgression lines was limited within the diversity between their parents, *T. aestivum* subps. *aestivum* cv. Novosibirskaya 67 (N67) and *T. turgidum* subsp. *polonicum* cv. IC12196. N67 was closer to 38 introgression lines than that of IC12196. The UPGMA cluster and principal coordinate analysis (PCO) grouping showed 0.84 to 0.98 similarity values between N67 and the introgression lines. Eleven *T. petropavlovskyi* accessions were distinguished from introgression lines with UPGMA clusters and PCO groupings, and *T. petropavlovskyi* was located between the introgressions lines and IC12196. Several introgression lines

Table 1. Near-isogenic lines of durum wheat cultivar LD222.

Code	Character	Allele	Donor
Chromosome 1A			
ANW 1A	Black glume	*Bg*	*T. turgidum* subsp. *durum* var. *reichenbachii*
ANW 1B	Black glume, hairy glume	*Bg, Hg*	*T. turgidum* subsp. *carthlicum #521*
ANW 2A	Hairy Glume	*Hg*	*T. turgidum* subsp. *durum* var. *melanopus*
Chromosome 3A			
ANW 9A	Red grain	*R-A1b*	DS LDN (DIC 3A)
ANW 10A	Brittle rachis	*Br2*	DS LDN (DIC 3A)
ANW 11B	Sphaerococcoid	*S3*	MS 1453, a mutant of Saratovskaya 29 (2n=42)
Chromosome 5A			
ANW 16C	Reduced height	*Rht 12*	Mv 17 (Karcagi 522 5A, 2n=42)
ANW 22A	Compact spike	C^{17648}	MA17648, a mutant of Altaiskaya Niva
Chromosome 7A			
ANW 5A	Long glume	*P1*	*T. turgidum* subsp. *polonicum* var. *vestitum*
ANW 5C	Long glume	*P1*	*T. petropavlovskyi* Maystrenko's line (2n=42)
ANW 5D	Long glume	*P1*	*T. turgidum* subsp. *polonicum* var. *abyssinicum*
ANW 5E	Long glume	*P1*	*T. petropavlovskyi* k44126
ANW 5F	Long glume	*P1*	*T. aestivum* subsp. *aestivum* PI 191834
ANW 5G	Long glume	*P1*	*T. aestivum* subsp. *aestivum* AUS 20561 (2n=42)
ANW 7A	Chlorina	*cn-A1d*	CDd6, a mutant of Langdon
Chromosome 2B			
ANW 3A	Nonglaucousness	*WI1*	*T. turgidum* subsp. *durum* var. *pyramidale*
ANW 3B	Nonglaucousness	*w1*	AUS 2499
ANW 12A	Ligulelessness	*lg1*	A variant of Marvroullos
Chromosome 3B			
ANW 9B	Red grain	*R-B1b*	DS LDN–TDIC (3B)
ANW 10B	Brittle rachis	*Br3*	DS LDN–TDIC (3B)
ANW 11C	Sphaerococcoid	*S2*	MSK 2454, a mutant of Skala (2n=42)
ANW 11D	Sphaerococcoid	S^{16219}	M-16219, a mutant of Altaiskaya Niva
Chromosome 4B			
ANW 4A	Reduced height	*Rht-B1b*	*T. turgidum* subsp. *durum* cv. Cando
ANW 4B	Reduced height	*Rht-B1c*	Maringa NIL (2n=42)
ANW 4C	Reduced height	*Rht-B1d*	*T. aestivum* subsp. *aestivum* cv. Saitama 27 (2n=42)
ANW 4D	Reduced height	*Rht-B1e*	*T. aestivum* subsp. *aestivum* cv. Krasnodari 1 (2n=42)
ANW 4E	Reduced height	*Rht-B1f*	*T. aethiopicum* W6824D
ANW 4F	Reduced height	*Rht-B1h*	*T. turgidum* subsp. *polonicum* IC 12196
ANW 4G	Reduced height	*Rht-B1f*	*T. aethiopicum* W6807C
ANW 14A	Hairy peduncle	*Hp*	Hp-S615, an S615 NIL (2n=42)
ANW 20A	Blue grain	*Ba2*	UC66049
Chromosome 7B			
ANW 5B	Long glume	*P2*	*T. ispahanicum*
ANW 7B	Chlorina	*cn-B1b*	CDd2, a mutant of Langdon
ANW 6A	Purple culm	*Pc*	DS CS–Hope (7B)
ANW 13A	Chocolate black chaff	*cc*	Vic CBC mutant
Location unknown			
ANW 8A	Yellow leaf	digenic	Yellow mutant (15:1)
ANW 11A	Sphaerococcoid	digenic	Sphaerococcoid mutant
ANW 16D	Reduced height	*Rht 14*	Castelporziano
ANW 16F	Reduced height	*Rht 16*	Edmore M1
ANW 16G	Reduced height	*Rht 18*	Icaro
ANW 16H	Reduced height	*Rht 19*	Vic SD1 line b

resembled with *T. petropavlovskyi* for awning and glume length. The genetic variation among 38 introgression lines was much wider than that of *T. petropavlovskyi*. We concluded that *T. petropavlovskyi* was established by intensive selection of hybrid between *T. aestivum* subsp. *aestivum*/*T. turgidum* subsp. *polonicum*.

Quantitative trait loci for soil-penetration ability of roots in durum wheat.

Increasing the ability of root penetration (RP) into hard soil is important to improve drought resistance in durum wheat. Traits related to RP ability were evaluated in 110 RILs derived from the cross 'Jennah Khetifa /Cham1' using paraffin-Vaseline (PV) discs. QTL analyses were made for the number of roots penetrating the PV disc (PVRN), total number of seminal and crown roots (TRN), RP index (PVRN/TRN), and root dry weight (DW). Jennah Khetifa had higher PVRN, RP index, and root DW values than those of Cham1, and the RILs showed significant differences for these traits. Two closely-linked markers, *Xgwm617a* and *Xgwm427b*, on the long arm of chromosome 6A were associated with PVRN and RP index. For root DW, a QTL was linked to marker *Xgwm11* on chromosome 1B. Alleles of Jennah Khetifa were associated with increased PVRN, RP index, and root DW. No QTL was detected for TRN in this mapping population. The absence of co-located QTL suggested that RP ability was controlled separately from TRN and root DW. Although the population size and number of replications were small, this study helps in understanding the complexity of root growth and the potential of marker-assisted selection for selecting genotypes with high RP ability in durum wheat populations.

Development of near-isogenic lines in durum wheat.

The NILs for sphaerococcoid seed and compact spike were established as ANW 22A and ANW 11D. Multiple alleles at the *Rht-B1* locus were introduced into the genetic background of cultivar LD222. *Triticum turgidum* subsp. *polonicum* IC 12196 may be considered as new source of *Rht* gene. The NILs for GA-sensitive *Rht* genes (*Rht14*, *Rht16*, *Rht18,* and *Rht19*) were developed, although their chromosomal locations have not been determined. The effort to develop NILs was extended to introduce taxonomy-related traits such as spelt, squarehead, and glume awns. Table 1 (p. 80) summarizes presently developed near-isogenic lines of durum wheat cultivar LD222. Several NILs are available upon request. The information is also available at the website: http://seimei.agr.ibaraki.ac.jp/ibaraki_public_html/catalogue.htm.

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NATIONAL INSTITUTE OF CROP SCIENCE (NICS)
Tsukuba, Ibaraki 305-8518, Japan.

Flour particle size selection for high flour yield lines of hexaploid wheats in CIMMYT ~ A collaboration work between the Japan International Research Center for Agricultural Sciences (JIRCAS) and CIMMYT wheat-breeding programs.

Hiro Nakamura (NICS, JIRCAS) and Richard Trethowan (University of Sydney, CIMMYT).

Introduction. In order to strengthen the international competitiveness of Japanese domestically produced common wheat, improving flour-milling quality is essential. Also necessary is developing a high-quality product that will satisfy the demands of domestic consumers in many developing countries. To achieve these goals, high flour milling and high-yielding wheat cultivars must be developed. Hiro Nakamura (JIRCAS, now at NICS) hoped to breed high flour-milling quality and high-yielding wheat cultivars at CIMMYT for many developing countries and proposed this wheat-breeding project to CIMMYT in 2005. Improving both the international competitiveness of common wheat grown in developing countries and its grain quality to satisfy the demands of local milling companies is important, but the most important aspect of wheat quality is grain hardness, which is related to flour yield.

In the U.S., the particle size parameters of wheat flour have been analyzed by laser-beam diffractometry since the late 1980s, and the American Association of Cereal Chemists (AACC) technical committee on quality tests for wheat and flour reported the results of a study to determine wheat flour particle size parameters using this method (Gaines 1985; McDonald 1994). Wu et al (1990) measured flour particle size distributions by sieving and air classification. Additionally, it was reported that detailed particle size distributions could be easily determined using laser light apparatus (Devaux et al 1998). Flour yield also has a major affect on the quality of wheat-based bread and noodle products in Japan (Yamashita 1994). A previous report showed that the particle size index of soft cultivars of common wheat was significantly associated with the flour yield obtained by milling (Yamazaki and Donelson 1983). The particle size of wheat flour is known to be related to the hardness of the wheat kernel, which is an important factor in determining the functionality of wheat-based food products (Obuchowski and Bushuk 1980). Therefore, determining the relationship between flour yield after milling and flour particle size distribution using the laser light-diffraction apparatus is important.

Wheat that is used to produce breads and/or noodle must meet certain minimum requirements in terms of flour yield and protein content. The Wheat Breeding Institute is making great efforts to improve protein quality as part of Japanese wheat-breeding programs (Nakamura 1999, 2000). Flour yield is the most important technical and economic factor in milling and has a major influence on grain marketing. Improving the flour yield of commercial wheat cultivars will, thus, be of great importance in wheat-breeding programs all over the world. In addition to its nutritional importance, flour hardness has a significant effect on food processing during the manufacture of breads, biscuits, breakfast cereals, pasta, and udon products. The aim of the current study was to identify lines in CIMMYT wheat-breeding program with high flour yield using the flour particle size and/or the flour particle size distribution as an index of flour yield; as done previously in Japanese wheat-breeding programs (Nakamura 2005, 2006).

JIRCAS-CIMMYT research in wheat breeding at CIMMYT (JIRCAS proposal in 2005).
The activities in this project are as follows:

Develop high flour-milling and high-yielding wheat lines through breeding.

1. Screen wheat germ plasm with high flour-milling quality using the flour particle size distribution method.
   1) Evaluate CIMMYT wheat germ plasm by applying the flour-milling quality evaluation method.
   2) Screen and identify gene pools for high flour-milling quality using the CIMMYT gene-bank collections.
2. Select improved wheat lines with high flour-milling quality and high-yield.
   3) Accumulate high flour-milling quality genes in CIMMYT high-yielding cultivars by crossing (higher-yielding wheat lines × high flour-milling quality wheat lines).
   4) Evaluate and select improved wheat lines with high flour-milling quality and high yield (higher-yielding wheat lines × high flour-milling quality wheat lines) under field conditions in Mexico.

Expected results.

1. Identify wheat germ plasm with high flour-milling quality.
2. Develop wheat lines with high flour-milling yield and high grain yield at CIMMYT.

Materials and Methods. In total, 154 lines and cultivars of hard and soft, CIMMYT hexaploid wheat were examined in this study. The 154 wheat lines and cultivars were used in crossing at CIMMYT by Richard Trethowan; wheat breeding leader for rain-fed environments. The samples were cultivated during the same growing season in a wheat-breeding field. The wheat samples were passed through a Brabender Quadrumat wheat flour laboratory mill under constant temperature. The Brabender Quadrumat laboratory milling procedures are standardized in the CIMMYT wheat-breeding programs. The resulting flour samples were subjected to wheat quality analysis. In Japan, an air classifier was used to separate the flour samples. A standard-range laser instrument was used to measure particles, ranging in diameter from 0.9 to 209.7 μm, suspended in gas using low-angle light scattering from a helium-neon laser. For the laser measurements, 2-g samples were separated from 50–100-g flour with a spinning riffler and placed in air-tight vials.

Results and Discussion. In the previous study, flour yield was associated with the median particle size (μm), and the hard wheat cultivars with flour particle size distribution pattern III with one peak had a greater flour yield than those showing patterns II and I (Nakamura 2006). Therefore, the flour particle size of 154 lines and cultivars of hexaploid wheat from CIMMYT was investigated in relation to the median flour particle size, and the flour particle-size distribution pattern (I–III) as determined by laser diffraction. Hard and soft wheat cultivars are known to differ in flour yield after milling. This study demonstrated that hard and soft wheat cultivars also differed in median flour particle size and flour particle-size distribution patterns based on the results of air classification. The hard wheat samples differed from the soft wheat samples in terms of the median flour particle size based on the air classification results. The hard and soft wheat cultivars also showed different flour particle size according to the air classification.

By using wheat flour particle size distribution measurement (median particle size, mainly), high flour-yielding materials were selected among the 154 wheat lines and cultivars. The results indicate that median particle size is widely distributed in CIMMYT hexaploid hard wheats (Fig. 1). In total, 24 lines and cultivars possessed a median particle size of more than 100 μm, which was associated with high flour-yield (Fig. 1). Considering wheat cultivation, disease resistance and other quality items such as bread-making quality, 12 lines were selected for crossing and selection in the CIMMYT wheat-breeding program to develop high yielding wheat with superior milling quality. The 12 parents were crossed with high yielding materials producing 65 combinations at CIMMYTs Ciudad Obregon wheat breeding station in Sonora in February 2006. The particle size distribution analysis method could be used to identify lines with high flour-yield in early generation testing, as has been revealed in a previous study (Nakamura 2005, 2006). In this study, we could simply and quickly identify wheat genetic resources with high flour milling yield in a systematic evaluation of CIMMYT materials and crosses to high grain yielding lines were subsequently made the CIMMYT shuttle breeding system, which allows two generations per year, by growing nurseries at Obregon in northwestern Mexico and at Toluca in central Mexico, will allow these materials to be rapidly developed (Braun et al. 1996, Trethowan et al. 2007, Ortiz et al. 2007).

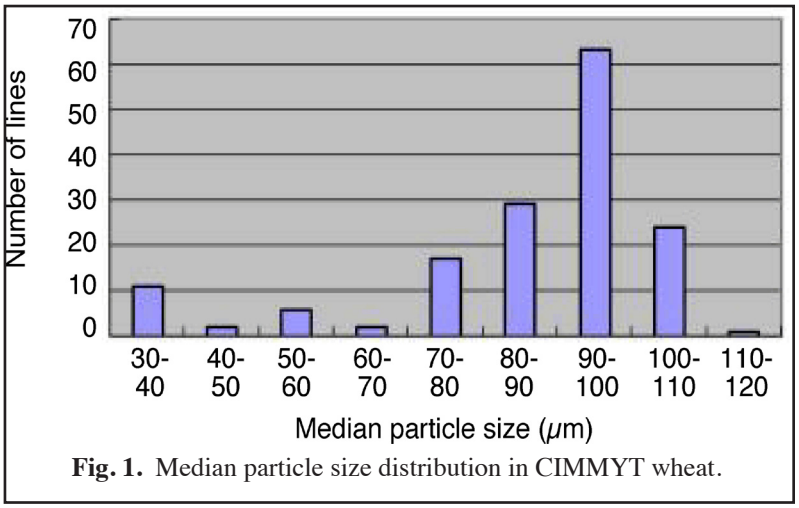

Fig. 1. Median particle size distribution in CIMMYT wheat.

Flour yield is a critical technical and economic factor in milling. The flour particle size distribution is another significant parameter that must be considered in the design, adjustment, and operation of a mill. In addition, particle size is an important indicator of the quality of high-ratio flour (Posner and Hibbs 1997). This new technique for the selection of cultivars suitable for bread production in the CIMMYT wheat breeding and quality evaluation program is easy to perform and does not require expensive equipment. The median flour particle size comprises a genotypic fingerprint that can be used for many purposes, including hard and/or soft wheat variety protection, registration, certification, and crossing, as well as functioning as a tool in wheat breeding. Although, the median flour particle size might not be the primary factors determining bread-making quality, they might be linked to other parameters that contribute to wheat quality and yield.

Acknowledgements. The authors gratefully acknowledge Javier Penaa and Yann Manes at the CIMMYT wheat program and the staff of the Field and Quality Management Section of CIMMYT for help with providing wheat flour samples and with growing the crops. We also thank JIRCAS for financial support at this collaboration work at CIMMYT.

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Personnel.

Hiro Nakamura is now a senior scientist at National Institute of Crop Science in Japan since April 2007. Richard Trethowan is now a professor at University of Sydney in Australia since July 2007.

ITEMS FROM KAZAKHSTAN

KOKSHETAU STATE UNIVERSITY AFTER SH. UALIKHANOV
Institute of Biological and Biotechnology of Plants SCB Republic of Kazakhstan, Almaty, and Abay, 76. Kokshetau 020000, Kazakhstan.

Influence of arsenic on the content of some macroelements in the roots and shoots of spring wheat.

A.S. Kurmanbaeva, N.M. Safronova, and B.A. Sarsenbaev.

This study examined the effect of arsenic on the distribution of nitrogen, phosphorous, and potassium in plant roots and shoots. Seeds of the spring wheat cultivar Omskaya-17 were germinated and then transferred to Knop's solution. In the experimental variants, arsenic was adding to the incubation solution as the salt Na_3AsO_3 in concentrations 12.5 and 25 mg/L. Based on previous experiments, concentrations of arsenic from 25 to 100 mg/l are toxic to the growth of wheat seedlings. The contents of organic and inorganic nitrogen, phosphorous, and potassium in organs of 11-day-old seedlings were determined by the standard methods in dry material (Pleshkov 1976).

An increase in the arsenic concentration to 25 mg/l in the growing solution corresponded with a higher content of mineral nitrogen in the roots and shoots of wheat plants. In the control seedlings, inorganic nitrogen was 29% of the general nitrogen, whereas this index increased to 43% with 25 mg As/l. On the other hand, the level of organic nitrogen in seedlings was reduced. The decrease of organic nitrogen caused by arsenic was observed in the shoots, from 20.5% (12.5 mg As/l) to 46.1% (25 mg As/l), whereas in the roots, no significant change was observed. Based on this data, it appears that the arsenic delayed the transport of nitrogen to shoots and stopped the synthesis of organic substances with nitrogen in wheat seedlings.

The control plants contained more potassium than ones grown on the solution with arsenic (Table 1). Potassium concentration especially decreased under higher levels of arsenic, 50% in the roots and 75 % in the shoots. A potassium deficiency in seedlings was noted in the presence of arsenic. The concentration of phosphorous in wheat shoots also decreased. The reduction was 17% with 12.5 mg As/l and 19% with 25 mg As/l. Changes were insignificant in the roots. The reduction in phosphorous was 3-4%. These results showed that arsenic inhibited the transport of phosphorous from roots to above ground organs but did not influence on the absorption of phosphorous by roots.

Arsenic suppressed the transport of nitrogen, potassium, and phosphorous from root to shoot, the uptake of potassium, and the inclusion of nitrogen into organic synthesis in wheat seedlings. The toxic effect of arsenic upon the plants could be related with the difficulty of transport of general nutritional elements to metabolically active areas.

Table 1. The content of macroelements in the roots and shoots of wheat seedlings (mg/g dry matter) under arsenic in the substrate.

	Control		12.5 mg As/l		25 mg As/l	
	shoots	roots	shoots	roots	shoots	roots
organic nitrogen	39.0 ±1.5	16.0±1.2	31.0±1.4	17.0±1.3	21.0±1.2	18.0±0.1
inorganic nitrogen	9.0±0.9	13.0±1.2	9.0±0.8	10.0 ±1.3	16.0±0.8	12.0±0.3
phosphorous	6.9±0.2	6.4±0.2	5.7±0.3	6.2±0.2	5.6±0.1	6.0±0.3
potassium	0.27±0.03	0.04±0.01	0.12±0.02	0.02 ±0.01	0.09±0,02	0.02±0.01

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ITEMS FROM MEXICO

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

Hans-Joachim Braun and Tom Payne.

During the past few years a number of changes have occurred within CIMMYT and CIMMYT's wheat research group. The challenges wheat research faces today are as daunting as ever, with high commodity prices (approaching US$12.00/bu), rapid changes and migrations in wheat pathogen virulences, and customers' increasing awareness of our intertwined relationship between food, agriculture and climate.

CIMMYT Director General.

Dr. Thomas Lumpkin, a well respected scientist and science administrator, will succeed Dr. Masa Iwanaga as the new Director General of CIMMYT. Dr. Lumpkin, a U.S. national, is currently Director General of AVRDC, the World Vegetable Center, headquartered in Taiwan. Under his leadership, the center has expanded significantly, reaching beyond its roots in Asia to apply its expertise and strengthen its presence in parts of the world where vegetables could make a significant difference in the lives of the rural poor.

Dr. Lumpkin will assume his post at CIMMYT on 15 March, 2008. Prior to his appointment at the World Vegetable Center, he chaired the Department of Crop and Soil Sciences at Washington State University. Dr. Lumpkin holds a BSc in Agronomy from Washington State University and MSc and PhD degrees in Agronomy from the University of Hawaii. He is widely known in agriculture and development circles for his books and publications on global horticultural needs and approaches to poverty alleviation in the developing world.

International wheat nurseries.

CIMMYT annually distributes nearly 6 t of seed of thousands of experimental lines. Our international nurseries are targeted to specific wheat mega-environments and grain-color types. In addition, CIMMYT holds in-trust approximately 144,000 wheat, triticale, and barley accessions, which are freely available. All germ plasm is distributed under the standard material transfer agreement (SMTA). Further information can be obtained at:

CIMMYT International Nurseries: http://www.cimmyt.org/english/wps/obtain_seed/sidu.htm.

CIMMYT International Wheat Nursery data: http://www.cimmyt.org/ wpgd/index.htm.

CIMMYT International Nursery field books: http://www.cimmyt.org/ iwin/index.htm.

Standard Material Transfer Agreement (SMTA), for seed and germ plasm distribution: http://www.cimmyt.org/ english/wps/obtain_seed/smtainformation-en.htm.

Frequently asked questions (FAQ) regarding the SMTA: http://www.cimmyt.org/english/wps/obtain_seed/smtafaq-en.htm.

Spot blotch screening in Mexico.

Etienne Duveiller.

Although a lot of progress has been achieved toward understanding the epidemiology and factors modulating the expression of field resistance of wheat to spot blotch caused by *C. sativus*, sources of genetic resistance to this disease remain limited. The Eastern Gangetic Plains Screening and Yield Trial nurseries (EGPSN and EGPYT) have contributed to the dissemination of high-yielding, heat stress-tolerant materials harboring spot blotch resistance with local adaptation to the warmer areas in the Indian Subcontinent. However, when sources of genetic resistance and genotypes cited during the last 10 years to harbor genetic resistance are analyzed, most materials appear to result largely from the direct use of resistant sources identified through CIMMYT screening in the lowlands of Mexico. Thus, if the base of genetic resistance has to be expanded including through the use of new interspecific crosses or synthetic derivatives, field screening against spot blotch in Mexico should not be overlooked. This was confirmed during a visit to Agua Fria, a CIMMYT Maize station at the limit of Puebla and Veracruz, where several hundreds advanced lines were tested. Typical spot blotch symptoms could be observed, and scoring was easily conducted in second half of February. The disease, however, must be induced by spreading in the rows infected sorghum grains around the first two weeks of January. The wheat pathology laboratory produced about 70 kg of a grain-based sorghum inoculum that had been incubated for approximately 6 weeks at room temperature after being inoculated with three local *C. sativus* strains. A list of resistant sources to spot blotch cited or identified in the last 10 years is included.

Septoria tritici blotch research.

Etienne Duveiller.

Field Testing of 30 genotypes against ten *M. graminicola* isolates. For the second year, 30 bread wheat genotypes were tested in Toluca against ten strains of *M. graminicola* originating from the state of Mexico. These strains had previously been characterized (2006) in the laboratory for their virulence against a set of differential lines and genotypes using a detached leaf technique. Preliminary results confirmed that excellent sources of resistance to Septoria tritici blotch are available in CIMMYT materials. Resistance in the most resistant genotypes does not seem to be isolate-specific, but a more comprehensive analysis with all stains needs to be conducted on 2006 and 2007 results. Several genotypes such as Tinamou, 'Milan/S87230//Babax', and 'Milan/OTUS//Attila/3*BCN' are moderately resistant to strain 26 and 32 but significantly more susceptible to the more aggressive strain 86. In contrast, 'KAUZ/Pastor//PBW343' and 'PBW343*2/Kukuna' seem moderately susceptible to the three strains.

In the *M. graminicola*–wheat pathosystem, we recognize that a high diversity exists among isolates within a field as a result of sexual recombination. There might be not less variability within a field than between distant locations. During a visit at ETH, Zurich, in January 2007, we discussed earlier results related to isolates sent from Patzcuaro, Mexico, for a population diversity research. Against expectations, these isolates were found to be clonal, which suggests that they might originate form a single source. Because the Patzcuaro fields had not been inoculated, one hypothesis could be the absence of sexual recombination, which would imply that both mating types were not found. A series of strains isolated from farmers' fields and used at CIMMYT were sent to Belgium, UCL, Unit of Phytopathology, to determine the mating type with PCR. Results showed that both mating types were found in equal amount, suggesting that sexual recombination does occur and that isolate diversity can be found as in other parts of the world. However, the situation in Mexico differs for instance from Tunisia where the *S. tritici* disease severity observed is much more severe in durum wheat than bread wheat. Samples collected on durum and bread wheat in Tunisia were sent to Wageningen for isolation and characterization.

Screening for tan spot resistance in El Batan and Oaxaca. Tan spot, caused by *P. tritici-repentis*, is considered to be the most important foliar wheat disease associated with zero tillage because the fungus can over-wintering on stubble. Screening for resistance in the field is cumbersome and difficult: the production of inoculum in sufficient quantity is complicate and slow because conidia are important for the disease development but are only induced under specific light requirements. Also, tan spot development in El Batan is relatively slow and symptoms are difficult to assess because plants are submitted to earlier attacks by other foliar pathogens such as rusts. In Mexico, two races (1 and 2) at least (based on host specific toxins) are known to exist. In 2007, systematic field screening in pathology plots resumed at El Batan using race 1, the most commonly found race globally. A range of approximately 120 wheat entries known to show

differences in resistance were field-tested from June to late September. The inoculum production protocol was revised and the rate of conidia production in the laboratory was dramatically improved. However, we confirmed the difficulty to establish the tan spot epidemics at El Batan; plots had to be inoculated about twice a week during a month, which required some 2,000 petri dishes of fungal culture. Because of slow disease progress in spite of having set-up the trial in an area under fine misting system, tan spot evaluation could not start before the end of Aug. when attacks of yellow and leaf rust had already killed various entries. Clear-cut differences for tan spot among various genotypes, including known differentials, were eventually observed and results were relatively encouraging. Some known resistant genotypes such as Milan, 'Milan/Sha-7', or 'Gisuz/Sabuf' appeared much more resistant than Ciano-79 or 'Irena/Kauz'. These observations were confirmed by results obtained in Oaxaca (Yanhuitlan) a location where CIMMYT used to screen efficiently for tan spot resistance under natural conditions until 1997 and where we resumed our collaboration with INIFAP pathologist L. Osorio in 2007. In Yanhuitlan, although tan spot severity was low, due probably to an area reduction in wheat grown in monoculture in the area, tan spot symptoms were typical and easier to recognize than in El Batan. In Oaxaca area, we collected leaf samples from farmer fields to enrich the *P. tritici-repentis* collection at CIMMYT with new isolates.

Fusarium head blight.

Etienne Duveiller.

CIMMYT started a breeding program for FHB resistance approximately 20 years ago. FHB of wheat is now recognized as a very important disease, which should be controlled in order to attain sustainable production of wheat crops in both developing and developed countries. For its role and contribution to FHB research, CIMMYT is considered a very suitable institute to organize a FHB network in partnership with national and international institutions throughout the world. The present research program aims to identify new FHB-resistance gene sources by screening germ plasm accessions maintained at CIMMYT and to use them in the development of resistant wheat lines employing the latest biotechnology approaches. Although the field screening of up to 9,500 wheat and barley materials under inoculation and a fine misting system consists in the core activity, attention is increasingly given to the detection of low toxin content in field resistant materials.

In 2007, for the second year we used our FHB-screening system at El Batan, which gives greater screening capabilities, accuracy, and precision. We use an automated, programmable misting system and precision CO_2 sprayers for liquid inoculum application. Over 9,000 plots were planted in El Batan, Mexico, under artificial inoculation and misting for FHB evaluation in 2007. The isolates are *F. graminearum* from El Batan for which DON chemotype had been confirmed and aggressiveness has been tested in the greenhouse on a resistant and susceptible checks. In the field, ten spikes were tagged at anthesis (wheat) or heading (barley) and spray inoculated. Wheat plots were rated at 31 days after the first spray inoculation. Careful notes were taken on a sample of ten spikes (number of spikelets infected and the total number of spikelets). For wheat, preliminary screening materials, FHB index (a disease statistic reflecting a combination of the severity and incidence of disease) ranged from <1% to 100%.

Identification of isolates for 2007 field screening season. To keep our pathogen isolate collection valid and fresh for the field inoculations for the 2007 FHB nursery, 13 isolates from various origins identified as *F. graminearum* according to PCR evaluation were screened for aggressiveness by single-floret inoculation of five different genotypes in the greenhouse in the spring of 2007. Spikes were inoculated by point inoculation using 10 μl or inoculum at 100,000 spores/ml. Following inoculation, spikes were misted in a misting chamber for approximately 2 days to ensure infection, after which they were returned to normal greenhouse benches for evaluation. Spikes were evaluated for visual symptoms of disease in the spikelets as well as the rachis at 7, 14, and 21 dpi.

The line HEILO, CMSS93Y02492S-2Y-010M-010Y-010M-10Y-1M-0Y-3SJ-0Y, was identified with similar levels of resistance to FHB as that of Sumai #3.

Research on toxins and DON evaluation in field selected wheat materials. We are placing a high priority on toxin evaluation of selected trials/entries from the FHB-screening nurseries. We realize that the correlation between field symptoms and DON assessment may not be strong since the toxin production depends on gene expression of the fungus and because the DON production itself might depend on the resistance level of the host. In other words, depending on the resistance mechanism, the level of stress caused to the pathogen may affect the DON production. The toxin content

in grain depends on the Fusarium species involved, their ability to produce one or another toxin, and the environment and the level of scabby kernels. Also, a situation where grain samples are collected in an inoculated plot may largely differ from a field under natural infection. In principle, because *F. graminearum* has been used in field trials, DON is the major toxin of concern.

In 2006, we started to actively place a high priority on toxin evaluation of selected trials/entries from the FHB screening nurseries. The first approach was to use the RIDASCREEN® FAST DON ELISA kit and quantitative PCR (qPCR) to evaluate the amount of DON based on serology and on the amount of fungal DNA (TRI5 gene). Additional evaluation methods also are being used for examining the correlation between toxin evaluation using other possible methods such as the Fluoroquant method (in collaboration with colleagues in the Southern Cone, South America), or a new immunoassay under development at Ghent University, Belgium, and tested at CIMMYT in 2007. Other approaches to investigate these correlations included spike point inoculation in the greenhouse, fungal biomass accumulation and visually scabby kernels.

The 11th CIMMYT Scab Resistance Screening nursery. CIMMYT has regularly developed and distributed a Scab Resistant Screening Nursery (SRSN) over the past decade. These nurseries have consisted of the best scab resistant material identified through CIMMYT's FHB-screening trials and have been distributed to interested programs around the world upon request. The most recent nursery distributed was the 10th SRSN, which was made available in 2006. Since that time, CIMMYT's method for screening FHB has been modified for more effective identification of FHB resistant germ plasm. These changes have included modifications in the location of the screening nursery, isolates used for inoculation, inoculation technique, and misting technology. After two years of screening a range of materials using the modified methodologies, entries for the 11th SRSN have been identified. This nursery primarily includes the best FHB-resistant, advanced lines developed by the CIMMYT wheat breeding programs. The 11th SRSN will be available for distribution in 2008.

Selection of lines for the 11th scab resistant screening nursery (SRSN). ***El Batan field screening 2006 and 2007.*** In 2006 we made changes to our FHB-screening methods. Given the importance of these changes, we decided to have two years of screening under the new screening methods before selecting entries to distribute in the internationally distributed Scab Resistant Screening Nursery. Plants were planted in 1-m single replication or 1.5-m replicated double-row plots. At 50% anthesis, ten spikes in each plot were tagged. At anthesis and 2–3 days post anthesis, the plot was sprayed with 33 ml of *F. graminearum* conidia (100,000 spores/ml in 2006, 80,000 spores/ml in 2007). The programmed misting system was used to create wet/humid conditions conducive to disease throughout anthesis and grain fill. Thirty-one dpi, the ten marked spikes in each plot were scored for the total number of spikelets and the number of infected spikelets on each spike. These numbers were used to calculate the % incidence and % severity. From these data, the FHB Index was calculated (FHB Index = % Incidence x % Severity / 100).

Selections and post-harvest processing in 2006 and 2007. In 2006, over 3,700 entries were screened in 1-m, single replication plots for preliminary screening (though some of these had been screened once before in Toluca, Mexico), and nearly 300 were screened in 1.5-m replicated plots for possible inclusion in the SRSN. Those that performed very well for visual field symptoms, and for which we had an appropriate seed source for increasing in Mexicali Mexico (our Karnal Bunt free-site), were sent to Mexicali for increase in 2006–07 winter season.

FDK and ELISA from 2006 harvest. Lines that were selected according to visual field symptoms in 2006 were further processed for *Fusarium* damaged kernels (FDK) and contamination with DON via ELISA. FDK was examined from a 40-g sample of seed cleaned of chaff. These samples were quantified for DON used for ELISA using the RIDASCREEN ® FAST DON kit with the following modifications:

- For preliminary screening materials (single replication), a gravity divider was used to separate the original 40-g sample into two 20-g samples. One of these 2-0g samples was ground, from which a 2-g sample was taken.
- For advanced FHB-screening materials (replicated), the entire 40-g sample was ground, from which a 2-g sample was taken. The appropriate proportion of water was added to each 2-gram subsample and shaken. A 1-ml aliquot of the resulting liquid was centrifuged at 14,000 rpm for 15 minutes, from which 50 μl of the supernatant was used for ELISA.

2007 selection. In 2007, two 4-replicate, incomplete-block design trials were created, one from lines that had been selected from a single replication in 2006 (31 entries plus four checks), and one from lines that were selected from repli-

cated trials in 2006 (38 entries plus four checks, four replications). These trials were evaluated for FHB using the same procedure outline above for 2006. Lines that again performed very well for visual symptoms in the field in 2007 were selected for inclusion in the 11th SRSN. Many of the lines are in elite backgrounds as selected by CIMMYT's bread wheat breeders. One resistant (Sumai 3) and two susceptible checks are included. Eleven lines with consistently high levels of resistance have been repeated from the 10th SRSN to ensure their distribution to FHB researchers. The 2006 FHB Index, DON, and FDK values shown are just for a general guide and must not be interpreted strictly, because these data are from multiple trials within 2006 (some replicated, others not), and more than one person was involved in taking notes (a single person/trial).

Facilitation of new international Fusarium nurseries. In March 2006, CIMMYT organized the 'CIMMYT Workshop on the Global Fusarium Initiative for International Collaboration' to provide a platform for international collaboration on Fusarium research projects. This workshop concluded and endorsed two new international spring wheat nurseries that were needed for better facilitation of international exchange and evaluation of Fusarium-relevant, spring wheat materials and the exchange of knowledge generated through the evaluation of these materials. These two nurseries include

1. the Fusarium Elite Spring Wheat Nursery (FESWN). The specific objective of this nursery is to enable contributors to know the performance of their entries across environments, and allow participants to identify useful sources of resistance in entries from other programs. The nursery will include two types of entries:
   - Elite FHB/FCR resistant spring wheat (registered or near-registered resistant cultivars) that have performed well in regional FHB/FCR nurseries.
   - Regional FHB/FCR resistant and susceptible reference/standard checks.
2. Fusarium Preliminary Spring Wheat Nursery (FPSWN). The purposes of this nursery include identification of new sources of resistance; examination of stability of QTL for FHB/FCR resistance; surveillance for new and/or problematic pathogen strains; and development of knowledge or solutions in regard to other issues such as negative correlations between resistance QTL and other traits. The nursery may include
   - Any materials which address the objectives listed above including Near Isogenic Lines (NILs) of FHB/FCR QTL; Parents of mapping populations;

The overall objective of these two nurseries is to make useful materials for FHB and Fusarium Crown Rot available throughout the world. CIMMYT is serving as the coordinator of these two nurseries. CIMMYT routinely develops internationally distributed nurseries. The first nurseries will be distributed in 2008.

Launching of Global Fusarium Initiative Website. The new website of the Global Fusarium Initiative (GFI) was launched in early 2007. The site includes a message board that offers possibilities to exchange actively new information between scientists. One of the first outcomes is the presentation of the full proceedings of the GFI workshop held at CIMMYT in Mexico in March 2006 and a calendar of important events related to FHB activities, including field screening, international nurseries, and research on mycotoxins. The website is located at http://www.globalfusarium.org

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Performance of advanced wheat lines that will form 30th Elite Selection Wheat Yield Trial (ESWYT) and 42nd International Bread Wheat Screening Nursery (IBWSN).

Ravi Singh and Julio Huerta.

A total of 1,540 new entries were tested for first-year, grain yield performance at Obregon during 2006–07 on raised beds. The season was good for the expression of yield potential with an average yield over 55 yield trials (Alpha-Lattice-Latinized design with three replications, two checks, and 28 entries in each trial) of 8.182 (ranging between 9.160–7.537) and 7.472 (ranging between 8.530–5.292) t/ha for the checks Roelfs 2007 and Waxwing, respectively. On average, Roelfs 2007 yielded 9.5% over Waxwing.

Progress was made in kernel weight, and a large portion of lines now has medium to large grain. For reference, the grain weight of Waxwing, Roelfs 2007, Kronstad, and Tarachi is 43.8, 47.2, 40.6, and 41.0 mg, respectively. Kernel weight was smaller than in the 2005–06 season. Small-grained (Kauz type) lines remain absent. The largest 1,000-kernel weight was 62.85 g for the line 'CNDO/R143//ENTE/MEXI_2/3/AE.SQ.(TAUS)/4/ Weaver/5/2*KAUZ/6/ PRL/2*Pastor', which is derived from a cross involving synthetic wheat. Because the 'PRL*2/Pastor' parent had a 1,000-kernel weight of 50.7 g, the synthetic wheat must have contributed to a further increase in kernel weight.

Data for leaf rust (El Batan, 2 yrs, and Obregon,1 yr), yellow rust (Toluca, 2 yrs, and Ecuador, 1 yr), and stem rust (Kenya, 2 yrs) were obtained and used in selecting lines for further testing. *Septoria* and *Fusarium* data were also obtained and considered.

Quality analysis indicated that 15.4% of lines included in the second year yield trial during 2007–08 had excellent industrial bread-making quality characteristics, and another 23.9% would make good flat breads and chapatti; a major change in the last few years in irrigated bread wheat improvement materials. These lines are being tested for the second year during the Cd. Obregon 2007–08 season under five environments: raised-bed, full irrigation; flat (melga)-full irrigation; raised-bed reduced irrigation; raised-bed drip-based water stress; and raised-bed late sown.

Performance of advanced lines that formed 29th ESWYT and 41st IBWSN. The 29th ESWYT and 41st IBWSN were formed using two years of yield data from Obregon where 448 lines and checks (16 yield trials, 28 entries, and two checks, each trial with three replicates) were tested in Obregon 2006–07 under three environments: raised-bed four supplementary irrigations; flat (melga), four supplementary irrigations; and raised-bed, one supplementary irrigation. Compared to the check Roelfs F2007, 16.0%, 34.4%, 30.0%, and 20.5% lines displayed grain yield at 100% or greater in raised-bed, four supplemental irrigations; flat, four supplemental irrigations; raised-bed, one supplemental irrigation; and for the mean of the three environments, respectively. Correlation coefficients (r) for grain yields (expressed as % of Roelfs F2007) for 476 lines in raised-bed, four supplementary irrigations for two seasons (2005–06 and 2006–07); flat,

four supplementary irrigations (2006–07), and raised-bed, one supplementary irrigation (2006–07) were calculated. Correlation coefficient (r) of about 0.4 under irrigated conditions is not too bad, however, there was practically no relationship between well-watered and reduced irrigation scenario. Despite this, noteworthy is that several lines maintained their performance irrespective of the planting method or irrigation regimes.

Performance of early maturing lines in northeastern India. One of the breeding strategies at CIMMYT in recent years has been to select early maturing wheats with increased yield potential to escape from late heat stress. Eight early maturing lines that have shown superior yield potential in Mexico were chosen to establish yield trials at experimental station of BHU, Varanasi, and eight farmers' fields together with two released varieties HUW234 and HUW468 and Baz, a line that performed well during 2005–06 in a similar trial. The two best lines showed an average yield advantage of 22 and 18% over the HUW234 check. All eight lines were statistically superior to HUW234 and HUW468 with 6–16% higher yields. 'Waxwing*2/Vivitsi' and 'Kiritait//HUW234+Lr34/Prinia' are resistant to Ug99 and are being evaluated and promoted during the 2007–08 crop season by Dr. A.K. Joshi.

Performance of entries in 2nd Elite Bread Wheat Yield Trial (EBWYT). The 2nd EBWYT was distributed to 28 sites in 11 countries (Mexico, India, Nepal, Pakistan, Iran, Afghanistan, Egypt, Turkey, Sudan, Syria, and Ethiopia) and data has been obtained from 25 sites. The trial is being grown in Ethiopia and Turkey at present. Seed multiplication in El Batan allowed us to disseminate and test these new materials two years earlier, especially considering the threat from Ug99 has increased. Fifteen entries were characterized to carry stem rust resistance based on two years of evaluations, including with the *Sr24* virulent variant. Resistance categories are R (15–20%), MR (30%), and MR–MS (40%) and were given based on two years of evaluation when susceptible lines were dead because of heavy high stem rust pressure. Resistance up to MR is considered adequate, but MR–MS lines also are expected to survive in areas where stem rust is not endemic causing epidemic to start late. Of note is gene *SrTmp*, which only gave an MR–MS level of resistance. For each country, resistant lines with superior yields over the check could be identified. Five entries on the average of 25 sites gave 6 to 10% higher yields over the check. At the individual country level, we see the yield advantage of new lines is much higher. For example, in India the best lines were 'Waxwing*2/Kiritati' (entry 521) and 'Babax/*Lr42*//Babax*2/3/Vivitsi' (entry 519) with yield advantages of 17 and 16%, respectively. Both of these lines are resistant to Ug99. Interestingly, even in the heat-stressed sites of Sudan, five entries had between 10–17% superior yields over the check. We succeeded in identifying lines that are not only resistant to all three rusts but also will increase productivity in each country by a significant margin of at least over 10%. Recuperation of data was 100%.

Grain yield performance of lines with *Gpc-B1* at Obregon 2006–07. A small project was initiated in 2002 to incorporate the *Gpc-B1* gene from ND643, a genetic stock from North Dakota, into selected CIMMYT wheats. We made 13 crosses and single-backcrosses with CIMMYT wheats and selection was carried out until the advanced lines with good agronomic features were developed. Marker analysis of 109 of these lines indicated that we succeeded in obtaining 55 lines from seven crosses that carry this gene. The seven genetic backgrounds are two different selections of Weebill1, 'PRL/2*Pastor', 'Attila/2*Pastor', and 'Seri/Rayon' and 'Seri 1B*2/3/KAUZ*2/BOW//KAUZ' and 'Seri 1B/KAUZ/HEVO/3/AMAD'. We failed to recover any line that had recovered the yield potential if it had the *Gpc-B1* gene. In contrast, some of the lines that inherited a gene for stem rust resistance from ND643 had recovered the yield potential; indicating that the early senescence associated with *Gpc-B1* may have negative effect on grain yield. New crosses have been made to see if this negative association can be overcome by manipulating the genetic background.

Shuttle breeding for stem rust resistance between Mexico and Kenya. About 1,000 seeds of 231 F_3 stem rust, 125 F_4 stem rust, and 28 F_5 stem rust populations (populations from crosses having at least one parent resistant to Ug99 race of stem rust) were also grown in two-row, 5-m plots/population in Kenya under high stem and yellow rust pressure during the 2006–07 off-season. A bulk selection was carried out after removing the tall plants from the populations. About 800 plump seeds were selected and grown again during the main season under high stem and yellow rust pressure and also sent to Mexico. Resistant plants with good agronomic features were selected in Kenya, and seed has been sent to Mexico for planting in Obregon most likely during the last week of November. However, a total of 203 F_4 and F_5 populations with plump grain sent earlier from one season of selection in Kenya were planted in Obregon during November 2007 for individual plant selections. We eventually will have parallel populations from the same crosses with no selection in Kenya in segregating generations, with one round of selection in Kenya, and with two rounds of selections in Kenya. These populations will allow us to determine the best strategy to obtain stem rust resistant lines that also have high yield potential. We have sent 406 new F_3 stem rust and 222 F_4 stem rust populations to Kenya, which were planted during the last week of November 2007 at Njoro.

Stem rust resistance in ESWYT and IBWSN. During the 2006–07 off-season in Kenya, we screened 1,650 new CIMMYT advanced lines entering in the first year of yield trials in Mexico and an additional 319 lines entering in the second year of yield trials and seed multiplication for forming international nurseries 29th ESWYT or 41st IBWSN during 2006–07 off-season. All 319 lines and 359 lines selected out of the 1,650, based on grain yield performance and resistance to three rusts, were retested in Kenya during he 2007 main season. During 2007, these materials were evaluated three times; 24 September, 1 October, and 11 October. The first stem rust notes were recorded when several susceptible lines already had 80% severity and a susceptible reaction. By the third notes, the susceptible entries had dried out from the high stem rust infection. A total of 26.3% and 30.1% entries in the two groups of nurseries displayed adequate adult-plant resistance (R, R–MR, and MR categories) under severe stem rust pressure in both years that is expected to be durable because race-specific resistance is not involved. The 7.4% and 19.6% of the entries in the MR–MS category in the two groups of materials also can confer a useful level of resistance or can be used as parents to build additional adult-plant resistance. An additional 9% and 11.6% of the entries carried effective known and unknown race-specific resistance genes. The *Sr25* resistance gene source in the lines being multiplied for inclusion in 30th ESWYT and 41st IBWSN is located in the translocation where a yellow-pigment gene has been eliminated through mutation.

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The global strategy for ex situ conservation with enhanced access to wheat, rye, and triticale genetic resources.

Hans Braun.

The Global Strategy for *ex situ* Conservation with Enhanced Access to Wheat, Rye, and Triticale Genetic Resources was the result of consultations involving genetic resource specialists and crop researchers. The authors, a Strategic Advisory Group (SAG), foresee a strategy that will serve as a dynamic work-in-progress, ever evolving as the client base of collections broaden and vary, as the collections themselves change, and as the world community becomes more aware of the incalculable value of crop genetic diversity. The SAG strongly endorses the support of conservation networks, involving diverse stakeholders oriented towards regional demands, and even involving crops beyond those discussed directly in this report. Bridging diverse cultures, philosophies, and approaches to research, development, and business, to achieve greater and more sustainable food and agricultural development in light of increased awareness of our changing climate are goals we can only fully achieve together.

The SAG was composed of a small group of experts with global experience in all aspects of the conservation and use of the genetic resources of wheat, rye, and triticale. The major global germ plasm collections of wheat, rye, and triticale were identified from existing public databases including those held by the Food and Agricultural Organization of the United Nations (FAO), Bioversity International (formerly the International Plant Genetic Resources Institute, IPGRI), and the European Cooperative Programme for Plant Genetic Resources (ECPGR). Particular emphasis was given to identification of collections holding unique accessions of wild relatives and genetic stocks of wheat. The wild relatives of wheat have proved to be highly useful sources of resistance to biotic and abiotic stresses in wheat breeding over the last two decades, and this trend is expected to accelerate in the future. Similarly, genetic stocks are finding increasing use as tools in the sophisticated application of modern biotechnologies in wheat improvement. Surveys were conducted of genebank managers and users (primarily wheat breeders). Catalogues of collections of precise genetic stocks and wild relatives of wheat also were compiled. Using information gleaned from the surveys and the SAG, a list of key collections that should be targeted for inclusion in global networks of wheat, rye, and triticale genetic resources was developed. Identification of gaps in the existing collections, establishment of priorities to fill those gaps, and plans to meet the most urgent priorities is a high priority. The evaluation of options for the development of integrated information management systems for the global networks of collections of each of the crops and how these fit with both current developments by strong existing networks as well as broad developments in the field of information technology was roundly endorsed.

The full strategy document can be found at http://www.croptrust.org/main/strategies.php?itemid=37.

ITEMS FROM NEPAL

CIMMYT
Ramput, Nepal.

Development and identification of HLB and heat tolerant wheat germplasm for the Eastern Gangetic Plains (EGP) of South Asia.

G. Ortiz Ferrara, M.R. Bhatta, R.C. Sharma, D. Thapa, A.K. Joshi, and M.A. Sufian.

Close research collaboration was maintained with the National Wheat Research Program (NWRP) of NARC-Nepal.

About 200 new crosses were made in Bhairahawa, Khumaltar, and at the IAAS, Rampur, Nepal, during 2006–07. One hundred seventy-five new lines selected for resistance to Helminthosporium leaf blight and leaf rust, earliness, and heat-stress tolerance and with bold, white grain were incorporated and distributed in the EGPSN and EGPYT regional trials. During 2007, 12 sets of the 11th EGPSN and 10 sets of the 9th EGPYT were distributed to coöperators in Bangladesh, Nepal, and eastern and far-eastern India. The EGPSN and EGPYT material was distributed within the Eastern Gangetic Plains from 1997–2007. About 1,820 improved lines were distributed to 266 locations/years during that period.

Two wheat cultivars, **Bijoy** (= BAW-1006 = NL-297*2/Lr25; NC 1815-6B-020B-020B- 010N-1B-0B) and **Prodip** (= BAW 1008 = G162/BL 1316//NL 297), were distributed through these regional nurseries and released in Bangladesh in 2005. These two cultivars are under extensive seed multiplication with the aim to diversify the area under the popular wheat cultivar Kanchan. Another line, **WK-1204** (SW89-3064/Star, CMBW91Y016275-13Y-010M-010Y-010M- 3Y-0M) was released for commercial production in Nepal during 2007. Many promising lines distributed through these nurseries have been used in the crossing/breeding programs of Bangladesh, Nepal, and eastern India.

Yield stability and adaptation studies, using the EGPSN/EGPYT data, were conducted jointly with IAAS-Rampur, Nepal, and with BHU-Varanasi, India. The results of the 10th EGPSN and 8th EGPYT were analyzed and distributed electronically to cooperators in the region. Several lines in these two nurseries were identified with stability, HLB tolerance, early maturity, and sterility resistance. This material also is in national crossing programs.

Genotype-by-environment interaction of the 8th EGPYT. A combined ANOVA of the 25 entries in the EGPYT across the six sites revealed a significant 'genotype X environment' effect for grain yield, 1,000-kernel weight, days-to-heading and maturity, plant height, and HLB severity. The data were subject to biplot analysis (Yan and Kang 2002) to determine stability of the 25 genotypes for grain yield. Genotypes #10 (BL 3218, NC98B3060-13B-020B-020B-5B-0B) and #20 (SW89-5124*2/Fasan, CMBW91Y03050F-030TOPM-2Y-010M-010Y-010M) were the most stable among those lines with the highest yield as shown by their position close to the ideal cultivar. Bhrikuti (Entry #23), a commercial cultivar in Nepal, was the most stable among the four checks.

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ITEMS FROM PAKISTAN

COMSATS INSTITUTE OF INFORMATION TECHNOLOGY
Department of Environmental Sciences, CIIT, Abbottabad, Pakistan.

Wheat-improvement program: Overall goals.

M. Maroof Shah, Mustafa S. Nawaz, A. Hassan, I. A. Raja, B. Nawab, A. Pervez, K. Maqbool, and S. Khan.

One of the major areas of concentration in research and development in the department of Environmental Sciences at COMSATS, Abbottabad, is the application of biotechnology in plants and environment. Work is in progress to manipulate genetic mechanisms underpinning biotic and abiotic environmental stresses, quality traits, and energy potential in a number of important plant species. Wheat, among the prime crops of Pakistan nourishing millions every day, is facing serious problems of low yield, poor adaptation, disease susceptibility, and abiotic stress. A lack of genetic understanding and complexity of the genome are the most important factors. The main objectives of our wheat-improvement program at COMSATS, Abbottabad, are to target the genetic basis of each problem using conventional and advanced techniques. Our immediate objectives are to explore the genetic diversity in the available germ plasm using conventional and molecular markers. Comparative genomics and association mapping were considered bigger potential tools for understanding and underpinning biotic and abiotic environmental stresses, quality, bio-fuels, and yield-related traits. Introducing and introgressing genes from wild relatives by understanding chromosome-pairing mechanisms, targeting specific homoeologous groups and chromosome bins or gene-rich regions, and transformation are some of the focus areas.

Targeting the Ph1 gene for wheat improvement.

M. Maroof Shah, A. Pervez, and Ummara W. Khan.

Pakistan has unique wealth of wild wheat germ plasm that can be used to transfer useful genes into cultivated wheat to broaden its gene pool. However, the genetic activity of the gene 'pairing homoeologous' (*Ph1)*, the chromosomes of wild relatives either do not pair or very poorly recombine with wheat, resulting in either no transfer or transferring of large segments of chromosomes with undesirable blocks of genes from the alien species. One option is to utilize deletion based mutant lines for *Ph1* locus available in Chinese spring wheat for transferring the alien genes into cultivated wheat. The main difficulties during such alien gene transfer experiments are scoring of the plants for the presence or absence of

Ph1 gene segment. With the advent of molecular marker techniques, the chromosomal region containing *Ph1* gene may be enriched and the identified linked markers will provide a direct and swift mean to score the gene where alien transfer will be employed. Saturation mapping in the *Ph1* gene region will lead to eventually clone the gene which will have tremendous impact on all of the biological systems in living species. In current study we aimed to identify molecular markers using comparative genomic approaches to enrich the *Ph1* gene region. We have used genetic linkage maps and physical maps in wheat and other cereals and have identified more than 30 markers potentially lying in 0.5L region that contains the *Ph1* gene region. Among these 18 seems to be specific for *Ph1* region (Fig. 1). The *Ph1* gene region markers identified by this approach were observed for their genetic position on the chromosome of cereal crops collinear to wheat. The markers will be tested either using restriction based DNA analyses or amplification based techniques by generating site specific primers. This study will have global impact in wheat genetics and breeding where the geneticists and breeders will be able to transfer a wealth of genes from the alien sources expanding the wheat gene pool for yield and quality traits.

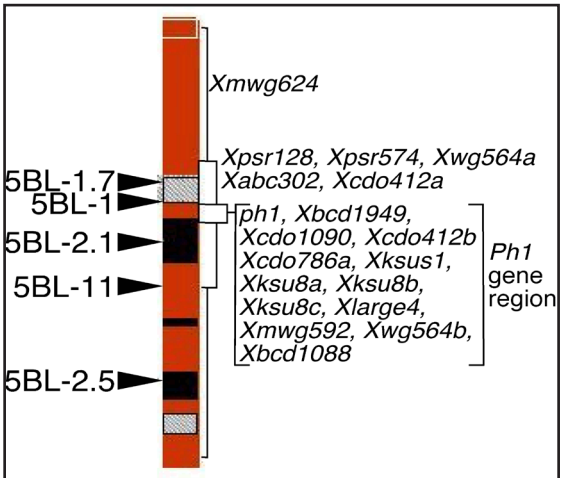

Fig. 1. Physical map of the 5L0.5 gene-rich region containing the *Ph1* locus.

Fine manipulation of the gene even without its cloning may assist in transferring alien genes into wheat. The greater challenges are to score the gene in the lines and populations that carries its null alleles. The phenotypes of the chromosomal genotypes are not manifested in the observable traits in the greenhouse or the field. The known phenotype, in this case, is chromosome-pairing (multivalent), which is a long and laborious task. The current study may serve as a means to score the gene by identifying closely linked molecular marker (s) to the gene region. The information will be utilized to improve wheat cultivars in Pakistan by transferring useful genes from its wild relatives using the *Ph1* gene systems and the linked markers.

Recombinant chromosome lines (RCLs) of wheat chromosome 3A.

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Recombinant chromosome lines for wheat chromosome 3A were developed between winter wheat cultivar Cheyenne (CNN) and a chromosome substitution line DS CNN–WI (3A) at the University of Nebraska, Lincoln, USA (Morris et al. 1960-84) and characterized for QTL mapping and gene identification (Shah et al. 1999). This material is extremely unique; taking more than 30 years of research at the University of Nebraska-Lincoln, U.S. This material is strictly winter habit and needs at least 6 weeks of vernalization to flower and set seed. The number and linkage relationship of the gene(s) or QTL controlling important agronomic traits on chromosome 3A were estimated using DNA markers on RCLs in diverse environments (Shah et al. 1999). The RFLP map developed for chromosome 3A was used to identify and map genes controlling important traits including earliness per se and yield (Shah et al. 1999). The map was reproduced and placed as the first interactive QTL map of wheat chromosomes on the GrainGenes web site by the USDA under 'gene mapathon' http://wheat.pw.usda.gov/ggpages/ggmapathon.html.

The genetic material, including 50 RCLs of chromosome 3A with four winter wheat parental lines, were kindly provided by Dr. P.S. Baenziger, University of Nebraska-Lincoln. The aim of current study was to identify and map QTL responsible for growth habit and plant morphology, because these traits play important role in contributing toward biomass and the final yield. Another important objective was to increase pure seed in a different environment from this precious material, which will be needed for future studies. Confirming early maturity (action of possibly *Eps* gene) was also an interest so that the material can be multiplied and be introduced in the winter and may be semiwinter growing areas of Pakistan where a wheat–maize overlap causes the sacrifice of the grain of one of the crops. Interesting findings were obtained. Without giving the required vernalization treatment, a large amount of seed from a single seed of each of the 50 lines and parental cultivars was obtained. The seed was threshed by hand and carefully stored in the laboratory. Complete data on all the relevant traits were collected and is being analyzed. The means of some of the traits are

Table 1. Means of various qualitative and quantitative traits for 50 recombinant chromosome lines and their winter wheat parental lines grown in Peshawar and Abbottabad, Pakistan, during 2006–07.

Line	Crown morphology	Tiller number	Plant height (cm)	Awn length (cm)	Spike length (cm)	Florets/ spike	Glume length (cm)	Lemma (cm)	Palea (xm)	Spikes/ plant	Seed/ spike
CNN	4	16	86	6.00	10.00	12.33	0.7	0.5	1	10	70
WI	5	24	78	6.33	7.33	15.67	0.6	0.8	0.6	9	97
CNN(WI3A)	7	25	75	8.33	7.33	19.67	1.0	0.7	0.6	14	103
CCWI3A01	4	21	85	6.67	6.67	17.00	0.9	0.8	0.9	8	87
CCWI3A02	4	17	80	7.83	9.00	15.67	0.8	0.9	0.8	9	67
CCWI3A03	7	25	74	6.00	8.33	11.33	0.7	1.0	0.7	9	98
CCWI3A04	5	16	85	8.17	6.17	17.33	0.5	1.0	0.6	10	100
CCWI3A05	5	16	78	6.83	6.33	20.67	0.7	1.0	0.6	6	58
CCWI3A06	8	19	75	5.67	9.33	13.67	0.9	0.6	0.7	8	88
CCWI3A07	5	25	85	5.5	7.00	14.67	1.0	0.8	0.8	9	101
CCWI3A08	6	25	80	8.33	8.83	20.00	0.5	0.9	0.9	6	57
CCWI3A09	9	27	79	7.33	8.33	11.67	0.8	0.7	0.8	6	78
CCWI3A10	7	25	70	7.00	8.50	16.67	1.0	1.0	1.0	10	115
CCWI3A12	4	18	74	6.50	9.00	15.33	0.9	0.6	0.5	8	27
CCWI3A13	6	17	80	7.83	7.17	15.00	0.5	0.8	0.6	10	100
CCWI3A17	5	24	78	8.00	10.33	20.67	0.7	0.8	0.9	8	97
CCWI3A18	5	18	78	8.50	7.33	13.00	0.6	0.8	0.7	14	108
CCWI3A19	8	22	85	8.00	7.50	13.67	0.5	0.7	0.8	14	89
CCWI3A20	3	22	90	7.00	7.50	17.33	0.9	0.8	0.7	12	163
CCWI3A21	7	19	75	5.67	8.33	15.67	0.8	0.8	1.0	17	243
CCWI3A22	3	18	74	6.17	10.17	17.33	0.6	0.6	0.7	16	289
CCWI3A23	8	22	77	5.50	8.67	15.33	0.8	0.8	0.7	10	110
CCWI3A24	4	24	85	8.33	9.33	19.67	1.0	0.6	0.8	12	98
CCWI3A25	8	21	88	8.67	7.83	17.00	0.9	1.0	1.0	17	346
CCWI3A26	3	20	90	8.33	8.50	15.33	0.9	0.5	0.5	13	170
CCWI3A27	4	16	80	6.17	8.50	19.67	0.5	0.8	0.5	9	167
CCWI3A28	9	19	74	5.50	8.50	17.00	0.7	0.9	0.6	12	200
CCWI3A29	7	19	85	6.67	7.83	16.00	0.8	1.0	0.9	17	256
CCWI3A30	9	14	78	8.17	7.33	15.67	1.0	0.9	0.7	19	332
CCWI3A31	7	22	80	6.50	8.00	20.33	0.9	0.5	0.8	7	66
CCWI3A32	4	15	90	8.33	8.33	18.67	0.6	0.7	0.6	7	140
CCWI3A33	6	22	74	5.67	8.50	17.33	0.6	0.8	0.5	15	220
CCWI3A34	4	14	90	7.50	8.50	15.67	0.7	0.9	0.8	8	172
CCWI3A35	4	15	75	8.17	7.33	15.00	0.9	1.0	0.8	15	229
CCWI3A36	7	25	78	7.33	7.33	17.67	0.5	0.8	0.6	7	113
CCWI3A37	8	21	80	7.17	9.50	20.00	0.8	0.8	0.5	11	273
CCWI3A38	9	18	85	5.50	10.17	19.67	0.9	0.6	0.8	20	182
CCWI3A39	9	19	74	6.67	8.67	13.00	1.0	0.7	0.9	17	220
CCWI3A40	8	15	80	8.00	7.67	15.00	0.9	0.8	0.9	11	266
CCWI3A41	7	23	75	8.50	8.17	15.67	0.5	0.8	1.0	17	77
CCWI3A42	8	15	80	6.50	8.00	14.00	0.6	0.7	0.7	9	215
CCWI3A43	9	22	85	7.67	9.00	15.67	0.9	1.0	1.0	10	165
CCWI3A44	6	19	80	7.50	8.17	18.67	0.6	0.7	0.6	11	265
CCWI3A45	8	15	84	7.00	8.50	18.33	1.0	1.0	0.9	17	185
CCWI3A46	3	26	78	8.17	8.17	20.00	0.6	1.0	0.5	13	201
CCWI3A47	7	21	75	7.50	7.00	14.67	0.6	0.6	0.7	10	88
CCWI3A48	8	17	80	8.67	9.50	15.00	0.6	0.6	0.8	12	63
CCWI3A49	8	23	74	6.17	6.67	10.67	0.7	0.7	0.7	14	153
CCWI3A50	9	22	90	7.33	9.00	19.00	0.9	1.0	1.0	14	242
Aapahoe	8	27	78	8.67	7.50	19.00	0.7	1.0	1.0	6	57
Pronghorn	3	15	80	7.83	7.33	19.67	0.7	0.5	1.0	17	300
Millenium	6	19	90	6.33	10.00	15.33	0.9	0.7	0.5	13	162
Alliance	5	27	75	7.17	7.00	12.67	0.9	0.6	0.9	9	176

presented in Table 1 (p. 98). The traits include crown morphology, tiller number, plant height, awn length, spike length, florets/spike, glumes length, seed/plant, spikes/plant, palea, and lemma.

A future goal of this research is to screen the germ plasm for the same traits in different environments and use polymorphic molecular markers on the 3A. Using bin-mapping information and ESTs on physical maps, we may be able to target specific genes in Pakistani wheat germ plasm that will be useful for this crop improvement. Indigenous and overseas collaborations will be sought out. Dr. P. S. Baenziger's wheat program and the John Innes Center, UK, are the potential overseas collaborators in these efforts.

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Wheat regeneration, transformation, and tissue-culture studies.

A. Hassan, S.H. Shah, U.W. Khan, H. Kiran, and M.M. Shah.

Successful callus culture and regeneration is fundamental to transformation of genes across species using genetic-engineering tools. A number of genes were identified and cloned in the cereals and Poaceae that need to be transformed into cultivated wheat. Wheat, being a monocot species, is notorious in regeneration through tissue culture, thus buffering the possibilities of quick gene transformation that may help in its improvement. Although wheat has a poor response to callus production and organogenesis, sustained efforts should continue to tap the benefits of genetic engineering. Pakistan has a wealth of indigenous wheat germ plasm including improved cultivars and land races. Several diploid and tetraploid wheat relatives are spread all over northern Pakistan. After successful establishment of tissue culture facilities in the Department of Environmental sciences, COMSATS University, Abbottabad, a team of scientists has developed an effort on wheat and potato transformation. The key goals for wheat transformation will be disease and stress (mainly drought and salinity) resistance. As part of this effort, plant pathologist Dr. Amjad Hassan, with a team of dedicated students and researchers will lead the work on wheat transformation protocols after optimizing potato tissue culture work. Initially, we will look at optimizing the culture conditions for the regeneration of Bobwhite or Pavon, the main wheat cultivars used in transformation. We have plans to survey our spring and winter wheat germ plasm to find better candidate(s) with maximum regeneration. We also will screen winter wheat substitution lines or CS nulli-tetrasomic lines to identify chromosomal locations of gene(s) responsible for tissue culture response, as well. A majority of the local germ plasm (about 100) and winter wheat cultivars along with chromosomes substitution lines have been collected and screening using different media are underway.

Personnel.

Dr. Mustafa N. Shafqat, a graduate of Kansas State University and researcher in soil sciences and wheat genetics at the University of Washington, Pullman, joined COMSATS University under the Higher Education Commission of Pakistan as Assistant Professor. He joined the wheat project and will work on association mapping of stress-related genes. Dr. Amjad Hassan, a graduate and then Assistant Professor at Niigata University, Japan, in Biosphere Sciences and Molecular Plant Pathology, joined COMSATS University under the Higher Education Commission of Pakistan as Assistant Professor. He will lead wheat tissue culture, transformation, and disease related gene studies. Ms. Ummara W. Khan joined the project as a Research Associate (also began her MSc program) and will work on the *Ph1* gene and wheat transformation.

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

Karim Dino Jamali.

Breeding for semidwarf habit and high grain yield in hexaploid wheat.

Wheat is an excellent crop for Pakistan and serves as staple food crop. To achieve high yield, raising productivity per unit area by adapting modern technologies such as high-yielding cultivars, improved cultural practices, and proper management of crop are needed. In 2006–07, an overall production of 23,520 x 10^6 t was achieved from an area of 8,493.9 x 10^6 ha (Table 1).

Table 1. Wheat area and production in Pakistan for the year 2006–07 (Source: Ministry of Food, Agriculture and Livestock, Islamabad Pakistan).

Province	Area (x 10^3 ha)	Production (x 10^3 tons)	Yield (kg/ha)
Punjab	6,393.1	17,850.0	2,792
Sindh	937.1	3,409.0	3,638
NWFP	754.8	1,390.0	1,842
Balochistan	408.9	871.0	2,130
Total	**8,493.9**	**23,520.0**	**2,769**

Wheat breeding at NIA, Tando Jam. Wheat breeding at the NIA is being pursued with the objectives of developing new cultivars endowed with high yield and good quality characters with tolerance to biotic and abiotic stresses. Currently, our breeding material is at different stages of evolution and is summarized below.

Performance of candidate cultivar 7-03. The candidate cultivar 7-03 has completed two years of National trials. The line tested in farmers' fields in performance trials. The candidate was tested in the Hyderabad, Matyari, Sanghar, and Khairpur districts. The line is resistant to both rusts according to CDRI (Cereal Disease Research Institute), Islamabad, in screening during 2006–07.

Performance of candidate cultivar 15-10. Another candidate line, 15-10, has completed one year of testing in national trials. Seed for the second year was sent to national trial; the results are still awaited. The candidate line has the best quality characters as analyzed by NARC (National Agriculture Research Council), Islamabad. The line has the highest grain ash (2.02%) with the exception of line V-022668 (2.112%). Line 15-10 also has the highest grain protein (15.81% d.b) of all lines and check cultivars in the national trial (20 genotypes). The line has the higher wet gluten (40.04%) and the dry gluten (12.34%) than all the check cultivars and lines in National trials in 2005–06. Line 15-10 has a comparatively higher combined grain yield (normal and late sowing) over ten locations of national trials than do the various check cultivars of the respective area. Line 15-10 was resistant to leaf rust during 2006–07 according to CDRI screening.

Zonal Trial Studies. Two candidate lines, 54-03 and 22-03, have completed two years of zonal trials in the Sindh province. Both lines are resistant to leaf rust according to CDRI, Islamabad, screening during the year 2006-07.

Advance Station Trials. Six trials were conducted for yield and yield components studies. Trial I, Trial II, Trial III, and Trial V all have 16 genotypes, including two check cultivars Sarsabz and Kiran-95. Trial IV consisted of 36 genotypes and two check cultivars (Sarsabaz and Anmol), and Trial VI consisted of 11 genotypes with two checks (Sarsabz and Kiran). All the trials consisted of three replicates of six, 4-m rows, except for Trial VI, which was 4.7-m long.

Trial I. In this yield comparison, line 11 (1.850 kg/plot) had the highest grain yield, more than any other line or cultivar. Subsequent lines that had high grain yields were 14 (1.383 kg), 10 (1.367 kg), and 13 (1.350 kg). Possible reasons for the higher grain yield in line 11 could be due to its tall, dwarf plant height and a higher number of grains/spikelet. The higher gain yield in line 14 could be due to its late heading and high number of spikelets/spike. The higher grain yield in line 10 could be due to a very early heading date, even earlier than the check cultivar Sarsabz, a tall, dwarf plant height, and a higher number of spikelets/spike. The higher grain yield in line 13 could be due to the tall, dwarf plant height. Line 06 had the lowest grain yield/plot.

Trial II. In this yield comparison, line 14 (1.083 kg/plot) had the highest grain yield per plot. The high grain yield in line 14 could be due to late heading date; it also had the highest number of spikelets/spike. Subsequent lines that had high grain yields were 10 (1.017 kg), 8 (0.867 kg), and 9 (0.850 kg). Line 7 had the lowest grain yield per plot. In this comparison, the check cultivar Kiran-95 (0.817 kg) had a higher grain yield than Sarsabz (0.783 kg).

Trial III. In this yield comparison, line 04 (1.317 kg/plot) had the highest grain yield/plot when compared to all other genotypes. Subsequent lines with higher grain yields were 8 (1.100 kg), 1 and 10 (1.083 kg), and 11 (0.933 kg). Line 7 (0.667 kg) had the lowest grain yield per plot. The check cultivars had comparatively lower grain yields compared to most of the lines. Kiran-95 (0.817 kg) had higher grain yield than Sarsabz (0.737 kg/plot).

Trial IV (isoline studies). In this trial, line 32 (1.567 kg) had the highest grain yield/plot. Subsequent lines with higher grain yields were 1 (1.350 kg/plot), 29 (1.300 kg), and lines 3, 23, and 33 (1.233 kg). Possible reasons for the high grain yield in line 32 include its early maturity, increased plant height, higher main spike grain yield, and increased number of grains/spikelet. The higher grain yield in line 1 could be due to a mid-maturity date, a higher number of spikelets, an increased number of grains, and a better main spike grain yield. The grain yield in line 29 could be due to a double dwarf plant height. Earliness in days-to-heading and an increased number of grains/spikelet could contribute to the high grain yield in line 3. The higher yield in line 23 could be due to a medium length in days-to-heading and an increased number of grains/spikelet. Line 33 is early in days-to-heading, has a higher number of spikelets, and an increased number of grains/spike and grains/spikelet. The check cultivar Anmol (1.300 kg) had comparatively higher grain yield/plot than Sarsabz (0.750 kg).

Trial V (CIMMYT Coordinated Trial). In this trial, line 6 (2.183 kg) had the highest grain yield/plot, followed by lines 4 (2.167 kg), 1 (2.00 kg), 13 (1.933 kg), and 2 (1.916 kg). The high grain yield in line 6 could be due to its tall, dwarf plant height, longer spikes, higher number of spikelets, and higher number of grains/main spike. The high grain yield in line 4 could be due to its mid-maturity. The high yield in line 1 could be due to its tall, dwarf plant height, higher number of grains/spike, and increased main spike grain yield. A medium maturity and tall, dwarf plant height may contribute to the high grain yield in line 13. Line 2 has long spikes, a higher main spike grain yield, and a larger number of grains/spikelet. The check cultivars Sarsabz and Kiran-95 had grain yields of 1.233 and 1.083 kg/plot, respectively.

Trial VI (double dwarf trial). In this yield comparison, line 08 (1.267 kg) had the highest grain yield/plot. Subsequent lines with high grain yields/plot were 06 (1.167 kg), 01 (1.067 kg), 02 (1.017 kg), and 03 (1.017 kg). The check cultivars Sarsabz (0. 983 kg) and Kiran-95 (0.833 kg) had comparatively lower grain yields than all other lines.

Coleoptile length studies.

Eleven genotypes (seven cultivars and four lines) were studied for coleoptile length in three replicates. Genotypes with Rht_1, Rht_2, Rht_1Rht_2, Rht_8Rht_9, and *rht* were compared for their coleoptile length under controlled environmental conditions. The results suggested that the traditionally tall cultivar C-591 (*rht*) had a longer coleoptile than all other cultivars and genotypes. Subsequent genotypes with long coleoptile lengths were Chinese Spring (*rht*) and Rht8-01 (Rht_8). The cultivars Mara (Rht_8Rht_9), Sarsabz (Rht_1), and Soghat-90 (Rht_2) were not significantly different. Line Rht8-02 has the Rht_8 dwarfing genes but was not significantly different than the double-dwarf cultivar Yeccora (Rht_1Rht_2). These results suggest that dwarfing genes probably do not affect the coleoptile length. The genetic background may affect the coleoptile length of individual cultivars.

Participation in an international meeting.

K.D. Jamali participated in an international project planning meeting and presented country report of the IAEA project No. RAS/05/045 held from 25–30 June, 2007, in Kuala Lumpur, Malaysia.

PEOPLES REPUBLIC OF CHINA

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Allelic variation of polyphenol oxidase genes located on chromosomes 2A and 2D and development of functional markers for the PPO genes in common wheat.

Polyphenol oxidase (PPO) activity is highly related to the undesirable browning of wheat-based end products, especially Asian noodles. Characterization of PPO genes and the development of their functional markers are of great importance for marker-assisted selection in wheat breeding. In the present study, complete genomic DNA sequences of two PPO genes, one each located on chromosomes 2A and 2D and their allelic variants were characterized by means of *in silico* cloning and experimental validation. Sequences were aligned at both DNA and protein levels. Two haplotypes on chromosome 2D showed 95.2% sequence identity at the DNA level, indicating much more sequence diversity than those on chromosome 2A with 99.6% sequence identity. Both of the PPO genes on chromosomes 2A and 2D contain an ORF of 1,731 bp, encoding a PPO precursor peptide of 577 amino acids with a predicted molecular mass of ~64 kD. Two complementary dominant STS markers, *PPO16* and *PPO29*, were developed based on the PPO gene haplotypes located on chromosome 2D; they amplify a 713-bp fragment in cultivars with low PPO activity and a 490-bp fragment in those with high PPO activity, respectively. The two markers were mapped on chromosome 2DL using a DH population derived from the cross 'Zhongyou 9507/CA9632', and a set of NT and Dt lines 2DS of Chinese Spring. QTL analysis indicated that the PPO gene cosegregated with the two STS markers and was closely linked to SSR marker *Xwmc41* on chromosome 2DL, explaining from 9.6% to 24.4% of the phenotypic variance for PPO activity across three environments. In order to simultaneously detect PPO loci on chromosomes 2A and 2D, a multiplexed marker combination *PPO33*/*PPO16* was developed and yielded distinguishable DNA patterns in a number of cultivars**.** The STS marker *PPO33* for the PPO gene on chromosome 2A is homologous with *PPO18* that we reported previously, and can amplify a 481-bp and a

290-bp fragment from cultivars with low and high PPO activity, respectively. A total of 217 Chinese wheat cultivars and advanced lines were used to validate the association between the polymorphic fragments and grain PPO activity. The results showed that the marker combination *PPO33*/*PPO16* is efficient and reliable for evaluating PPO activity and can be used in wheat-breeding programs aimed for noodle and other end product quality improvement.

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

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

QTL mapping for flour color components, yellow pigment content and polyphenol oxidase activity in common wheat.

Improvement of flour color is an important breeding objective for various wheat-based end-products. The objectives of this study were to genetically dissect the QTL for flour color components, yellow-pigment content (YPC), and PPO activity, using 240 RILs derived from the cross between the Chinese wheat cultivars PH82-2 and Neixiang188. Field trials were performed in a Latinized α-lattice design in Anyang and Jiaozuo of Henan Province and Taian of Shandong Province in 2005–06 and 2006–07 cropping seasons. One hundred and eighty-eight polymorphic SSR markers, one rye secalin marker *Sec1*, one STS marker *YP7A* for phytoene synthase gene (*Psy-A1*), and four glutenin subunit markers, were employed to genotype the population and construct the linkage map for subsequent QTL analysis. The results indicated that 27 QTL were detected for color components, YPC, and PPO activity, mainly in two clusters on chromosomes T1B·1R and 7AL, respectively. The T1B·1R translocation and phytoene synthase (*Psy*) gene on chromosome 7AL showed great influence on YPC and different color parameters of flour and noodle, explaining 31.9 and 33.9% of phenotypic variance for YPC, respectively. PPO activity was primarily conditioned by the QTL *QPpo-2A* that was closely linked to the SSR marker *Xwmc170* on chromosome 2A and explained 18.3–23.3% of phenotypic variance across three environments. Among different color parameters, flour yellowness index exhibited the highest correlation with YPC (r=0.96, P<0.0001) and very significant correlation with white salted noodle color b* (Nb*) (r=0.76, P<0.0001) and is, thus, a most desirable indicator for yellowness of flour and noodle. The markers *Sec1* and *YP7A* were very closely linked to the QTL for YPC and flour-color components and, therefore, could be used as efficient molecular markers targeting for the selection of YPC and flour-color parameters in wheat breeding programs.

Isolation and expression of novel Viviparous-1 genes in common wheat.

Preharvest sprouting (PHS) of wheat reduces the quality and economic value of grain and increasing PHS tolerance is one of the most important traits in wheat breeding. Two new *Vp-1B* alleles related to PHS tolerance were identified on the B genome of bread wheat and designated as *Vp-1Bb* and *Vp-1Bc*. Sequence analysis showed that *Vp-1Bb* and *Vp-1Bc* had an insertion of 193 bp and a deletion of 83 bp located in the third intron region of the *Vp-1B* gene, and shared 95.43% and 97.89%, respectively, similar to the sequence of AJ400713 (*Vp-1Ba*) at the nucleotide level. Their sequences are deposited in the GenBank under the accession numbers of DQ517493 (*Vp-1Bb*) and DQ517494 (*Vp-1Bc*). Semiquantitative RT-PCR analysis showed that alternatively spliced transcripts of the *Vp-1A*, *Vp-1B*, and *Vp-1D* homologues were present and there were no differences in the splicing patterns or abundances of *Vp-1A* and *Vp-1D* from 35

DAP embryos between PHS-tolerant and susceptible cultivars. *Vp-1Ba, Vp-1Bb*, and *Vp-1Bc* each could produce a set of transcripts, only one of which was correctly spliced and had the capacity to encode the full length VP1 protein. The protein was more highly expressed in genotypes with *Vp-1Bb* and *Vp-1Bc* than in those with *Vp-1Ba*. Comparison of the expression patterns of *Vp-1Ba, Vp-1Bb*, and *Vp-1Bc* at different times after pollination also revealed that the expression of these genes was developmentally regulated. Furthermore, genotypes with different levels of tolerance to PHS showed different responsiveness to ABA exposure and differences in transcript levels of *Vp-1Ba, Vp-1Bb*, and *Vp-1Bc* were observed after ABA treatment. The results indicated that insertion or deletion in the third intron region may affect the expression of the *Vp-1B* gene and its sensitivity to ABA and, thus, resistance to PHS.

Development and validation of a Viviparous-1 STS marker for preharvest sprouting tolerance.

Preharvest sprouting of wheat reduces the quality of wheat grain, and improving PHS tolerance is a priority in certain wheat growing regions where environments favor happens of PHS. Two new *Viviparous-1* allelic variants related to PHS tolerance were explored on B genome of bread wheat and designated as *Vp-1Bb* and *Vp-1Bc*. Sequence analysis showed that *Vp-1Bb* and *Vp-1Bc* had an insertion of 193 bp and a deletion of a 83-bp fragment, respectively, which are located in the third intron region of the *Vp-1B* gene. The insertion and deletion affected the expression level of Vp1 at the mature seed stage. More correctly spliced transcripts were observed from the genotypes with either insertion or deletion than that of the wild type. Based on these insertions and deletions, a codominant STS marker of *Vp-1B* gene was developed and designated as Vp1B3, which in most cases could amplify an 845-bp or a 569-bp fragment from the tolerant cultivars and 652 bp from the susceptible ones. This Vp1B3 marker was mapped to chromosome 3BL using a set of Chinese Spring NT and Dt lines. A total of 89 white-grained, Chinese wheat cultivars and advanced lines were used to validate the relationship between the polymorphic fragments of Vp1B3 and PHS tolerance. Statistical analysis indicated that Vp1B3 was strongly associated with PHS tolerance in this set of Chinese germ plasm, suggesting that Vp1B3 could be used as an efficient and reliable codominant marker in the evaluation of wheat germ plasm for PHS tolerance and marker-assisted breeding for PHS tolerant cultivars.

Characterization of CIMMYT bread wheats for high- and low-molecular-weight glutenin subunits and other quality-related genes with SDS-PAGE, RP-HPLC, and molecular markers.

Two hundred seventy-three CIMMYT bread wheat cultivars and advanced lines were investigated with gene-specific markers for PPO, phytoene synthase (Psy), and waxy genes. We tested 142 lines with SDS-PAGE, RP-HPLC, and molecular markers for the characterization of HMW-glutenin and LMW-glutenin subunits. The over-expression of Bx7 (Bx7OE) and subunit By8* were detected by RP-HPLC. Quality parameters for SDS-sedimentation volume (SDS-SV), flour protein content, mixing time, and Alveograph parameters, such as W and P/L, were investigated in the quality laboratory at CIMMYT. Results showed that in the 273 lines tested by marker PPO18 the frequencies of alleles *PPO-A1a* and *PPO-A1b* were 79.1% and 20.2%, respectively, and no PCR fragment was amplified in two lines (3.5%), whereas 227 lines (83.2%) contained the allele *Ppo-D1a* and 46 lines (16.8%) had *Ppo-D1b* detected by markers PPO16 and PPO29, respectively. In the test with the marker YP7A, 142 lines (52.0%) were assumed to have the allele *Psy-A1a* and 131 lines (48.0%) contained the allele *Psy-A1b*. Using the marker YP7B for the gene *Psy-B1*, the alleles *Psy-B1a* and *Psy-B1b* were detected in 55 (56.8%) and 43 (15.8%) lines, respectively, and 75 (27.5%) lines possessed the allele *Psy-B1d* detected by the marker YP7B-3. All of 273 lines contained the alleles *Wx-A1a* and *Wx-D1a* tested by the markers MAG264 and MAG269, respectively. Using the marker Wx-B1, 204 lines (74.7%) were assumed to have the *Wx-B1a* allele and 69 (25.3%) possessed the allele *Wx-B1b*. The lines with subunits Ax2*, By8, By9, Bx17, Bx20, Dx5, and Glu-B3j were 90, 16, 57, 5, 46, 118, and 33, respectively, in the 142 lines detected by molecular markers. They were consistent with the results tested with SDS-PAGE, except that one line with the T1A·1R translocation and SDS-PAGE could not discriminate the subunits By8 and By8*. Eight lines with Bx7OE were determined by RP-HPLC. Subunits Ax1 and Ax2* at the *Glu-A1* locus showed significantly better effect on all quality parameters than the subunit Null. The possession of subunits 17+18 and 7+8 at the *Glu-B1* locus showed superior value than subunits 7 and 20 on SDS-SV and Alveograph W. Subunits 5+10 represented significantly better effects for all parameters. Subunit Glu-A3b showed more positive effects than its counterpart allelic variation on SDS-SV and SDS-sedimentation volume/protein content index (SPI) at the *Glu-A3* locus. The allele *Glu-B3g* showed the best effect on quality parameters SDS-SV and Alveograph W, whereas *Glu-B3j*, associated with T1B·1R translation, exhibited a strongly negative effect on all quality parameters.

Development of two multiplex PCR assays targeting improvement of bread-making and noodle qualities in common wheat.

Wheat quality properties are genetically determined by the compositions of high- and low-molecular-weight glutenin subunits, grain hardness, PPO activity, and starch viscosity. Two multiplex PCR assays were developed and validated using 70 cultivars and advanced lines from Chinese autumn-sown wheat regions. Multiplex PCR I includes molecular markers for genes/loci α-secalin, *Glu-B1-2a* (By8), *Glu-D1-1d* (Dx5), *Glu-A3d*, *Glu-B3* (for non T1B·1R type), and *Pinb-D1b* targeting improved gluten parameters and pan bread quality. Multiplex PCR II comprises markers for genes/loci *Ppo-A1*, *Ppo-D1*, and *Wx-B1b* targeting improved noodle quality. The results were consistent with those achieved by SDS-PAGE and RP-HPLC, indicating that the two multiplex assays were highly effective, with good repeatability and low costs enabling their use in wheat-breeding programs. In total, nine alleles (subunits) at locus *Glu-B1*, four at *Glu-D1*, and five at *Glu-A3* locus were identified, and the alleles (subunits) *Glu-B1b* (7+8), *Glu-B1c* (7+9), *Glu-D1a* (2+12), *Glu-D1d* (5+10), *Glu-A3a*, *Glu-A3c*, and *Glu-A3d* were most frequently present in the cultivars and lines tested. The T1B·1R translocation was present in 28 (40.0%) lines, whereas the *Wx-B1* null allele for better noodle quality was present in only seven (10.0%) cultivars and advanced lines, and 37 (52.9%) lines had *Pinb-D1b* associated with hard grains. The allele *Ppo-A1b* on chromosome 2AL associated with lower PPO activity was present in 38 (54.3%) genotypes, whereas the less effective allele *Ppo-D1a* on chromosome 2DL, also associated with low PPO activity was present in 45 (64.3%) of genotypes. These two multiplex PCR assays should be effective in marker assisted selection targeting improved pan bread making and noodle qualities.

Allelic variation at the vernalization genes Vrn-A1, Vrn-B1, Vrn-D1, and Vrn-B3 in Chinese wheat cultivars and their association with growth habit.

Information on the distribution of vernalization genes and their association with growth habit is crucial to understand the adaptability of wheat cultivars to different environments. In this study, 278 Chinese wheat cultivars were characterized with molecular markers for the vernalization genes *Vrn-A1*, *Vrn-B1*, *Vrn-D1*, and *Vrn-B3*. Heading time of the cultivars was evaluated in a greenhouse under long days without vernalization. The dominant *Vrn-D1* allele showed the highest frequency in the Chinese wheat cultivars (37.8%), followed by the dominant *Vrn-A1*, *Vrn-B1*, and *Vrn -B3* alleles. Ninety-two winter cultivars carried recessive alleles of all four vernalization loci, whereas 172 spring genotypes contained at least one dominant *Vrn* allele. All cultivars released in the North China Plain Winter Wheat Zone were winter type. Winter (53.0%), spring (36.1%), and early heading (10.9%) cultivars were grown in the Yellow and Huai River Valley Winter Zone. Most of the spring genotypes from this zone carried only the dominant *Vrn-D1* allele, which was also predominant (64.1%) in the Middle and Lower Yangtze Valley Winter Zone and Southwestern Winter Wheat Zone. In three spring-sown wheat zones, all cultivars were early heading spring types that frequently possessed the strongest dominant *Vrn-A1a* allele, and combinations with other dominant *Vrn* gene (s). The *Vrn-D1* allele is associated to the latest heading time, *Vrn-A1* the earliest and *Vrn-B1* intermediate values. The information is useful for understanding the adaptation of Chinese wheat cultivars, and also important for breeding programs in other countries with an interest in using Chinese wheats.

Development of a STS marker specific to Yr26 conferring resistance to wheat stripe rust using the resistance gene-analog polymorphism (RGAP) technique.

The gene *Yr26* confers resistance to all races of *P. striiformis* f. sp. *tritici*. Here, we report development of the molecular markers specific to *Yr26* using a resistance gene-analog polymorphism (RGAP) technique. A total of 787 F_2 plants derived from the cross between resistant cultivar Chuanmai 42 and susceptible line Taichang 29 were used for linkage analysis. Eighteen NILs, 18 Chinese wheat cultivars, and advanced lines with different stripe rust-resistance genes were employed for the validation of the STS markers. In all, 1,711 RGAP primer combinations were chosen to test two parents and the resistant and susceptible bulks. Five polymorphic RGAP markers were used for genotyping the F_2 plants. Linkage analysis showed that the five RGAP markers were closely linked to *Yr26* with genetic distances ranging from 0.5 to 2.9 cM. These markers were then successfully converted into STS markers, of which CYS-5, with the genetic distance of 0.5 cM distal to *Yr26*, was specific to the resistance gene in the validation of 18 NILs and 18 Chinese wheat cultivars and lines. The results indicated that CYS-5 can be used in a MAS program targeting for the pyramiding of *Yr26* with other resistance genes to wheat stripe rust.

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ITEMS FROM THE RUSSIAN FEDERATION

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Amphimixis in soft wheat and apomixis in rye after mutual pollination of flowers.

V.G. Kyzlasov.

Pseudogamy of metasperms is a type of apomixis where the ovocyte of the fetal sac in the pistil grows parthenogenetically, and the endosperm originates from the fertilized central cell (Shishinskaya 2005). Kandelaki (1970) managed to induce pseudogamy in soft wheat by means of pollinating the flowers with pollen from other species. Apomictic development of soft wheat seed does not occur in practice. In experiments previously conducted by Kyzlasov (2005), matromorphic development of the germ was discovered in soft wheat, rye, and triticale after pollination with pollen from related species. The percentage of seeds formed in these experiments varied from 6.9% to 7.9% of the total number of pollinated flowers. R-1 winter rye, Nemchinovskaya 24 winter wheat, and Victor triticale were used as the initial material in these experiments. The technology for obtaining matromorphic plants has found practical application in creating lines of Nemchinovskaya 24, a SWWW with consistent stem length (Kyzlasov 2007). Initially, for unknown reasons, this cultivar always segregates for stem length. However, matromorphic families of this wheat obtained after pollinating with pollen from R-1 winter rye were found to have similar stem length.

Table 1. Productivity indices of the spike and percentage of seed set for parental lines and their crosses.

Parent lines and crosses	Number of polllinated flowers/ spike	Number of grain/ spike	% seed set (mg)	Caryopsis weight (g)	Spike productivity
A-1 spring wheat	39	37	95	31	1.16
R-2 spring rye	28	26	93	31	0.80
F_0 A-1 / R-2	36	22	61	10	0.21
F_0 R-2 / A-1	24	21	88	27	0.58

The soft spring wheat line A-1 and R-2 spring rye were used for crosses (Table 1). R-2 spring rye was created by hybridizing R-1 winter rye and spring rye. A-1 spring wheat was pollinated with R-2 spring rye and R-2 spring rye was pollinated with A-1 spring wheat in the field. We observed that the percent seed set was extraordinarily high. The percentage for the 'A-1/R-2' combination was 61%, whereas that for the 'R-2/A-1' cross was 88%. For the 'A-1/R-2' combination, F_0 caryopses were small (10 mg), the germ was missing in the majority of the caryopses and, thus, seed germination was low. Slow sprouting of seed was observed after sowing. Productivity also was low (0.21 g). The influence of pollinating R-1 rye with A-1 soft wheat on the size of the caryopses formed and the productivity of the spike was insignificant.

For the 'A-1/R-2' hybridization combination, all 153 grown plants were common hybrids of wheat and rye. Examination of F_1 obtained in the greenhouse after self-pollination showed numerous flowers in the spike (Table 2, p. 108), but a very low seed set because of the lack of pollen. More than 100 caryopses similar to triticale were obtained without paternal pollination. All of these caryopses are distinguished from other wheat and rye cultivars by their large grain size (44 mg). We are interested in tracing the inheritance of the features of productivity and ability for matromor-

Table 2. Productivity indices of the spike and percentage of seed set for self-pollinated parental lines and their crosses.

Parent lines and crosses	Number of polllinated flowers/ spike	Number of grain/ spike	% seed set (mg)	Caryopsis weight (g)	Spike productivity
A-1 spring wheat	39	36	92	25	0.90
R-2 spring rye	40	4	10	15	0.06
F_1 A-1 / R-2	100	1	1	44	0.04
F_1 R-2 / A-1	37	7	19	20	0.14

phic development in the lines of these caryopses. For all the other F_1 wheat/rye hybridization combinations, no caryopses formed.

For the 'R-2 rye/A-1 wheat' hybrids, all 127 F_1 plants were completely identical to the maternal R-2 rye. No significant inbreeding depression was observed in these plants. Seed set after self-pollination was 19%, almost twice that of R-2 rye. Caryopsis size and productivity of the spike in these slightly surpassed R-2 rye. The absence of wheat protein fractions in the endosperm of the F_0 'R-2 / A-1' caryopses means that the obtained plants were true apomicts. Pseudogamy is not present in this case. Meister and Tyumyakov (1926) were the first in Russia to report matromorphic development of rye caryopses after pollination with wheat pollen.

While creating the A-1 soft spring wheat cultivar, seed formation without participation of the paternal parent was discovered. Initially, the flowers of soft wheat with light-colored grains and polygynous flowers were pollinated with plants with dark-colored grains and xenia-colored caryopses. Creation of the line with polygynous flowers and dark-colored grains with xenia-colored caryopses has been described in previously (Kyzlasov 1991, 2001). All hybrid F_0 grains of 'light-grained wheat/dark-grained wheat' grown as with the maternal plants with light-colored grains were found to have dark-colored grains and xenia color. For 441 F_1 plants, segregation by caryopsis color within separate spikes was observed (9 pigmented caryopses : 7 colorless caryopses). At the same time, in nine F_1 plants, all the caryopses were colorless. They were completely similar to the maternal line. No plants with polygynous flowers were discovered. The formation of seed with light-colored grains similar to the maternal line among the F_1 plants after crossing light-colored grains with dark-colored grains was a surprise. The pigmentation of the aleuron layer, which appeared in hybrid F_0 caryopses did not disappear. Perhaps these plants appeared as a result of pseudogamy.

In the next generation, seeds of each of nine F_1 plants with light-colored grain were sown separately. Stamens were removed from 108 spikes during the spike formation. Approximately 5,400 flowers were sterilized. No grain formed in unpollinated flowers of eight families. In one family, 22 caryopses appeared in six spikes without any paternal parent pollen (Table 3). The letter 'A' in Table 3 denotes apomictic development of caryopses in three generations. On average, 3.7 caryopses/spike formed in the A_1. Two spikes had nine caryopses/spike, and four spikes had one caryopsis/spike. The caryopses were very small, light-colored, with an average weight of one caryopsis equal to 7 mg.

Table 3. Apomictic development of caryopses in unpollinated flowers of soft wheat.

Apomictic generation	Number of sterilized flowers	Number of formed caryopses		
		Total	Per spike	% seed set
A_1	300	22	3.7	7.3
A_2	350	35	5.0	10.0
A_3	400	52	6.5	13.0

Twenty-two A_2 caryopses formed in the A_1 plants without participation of paternal parent were sown. Nine plants sprouted and formed spikes. Stamens were removed from 350 flowers in these plants, and 35 caryopses appeared in the flowers without pollination. On average, five caryopses/spike formed without pollination. The percent seed set, compared with the number of sterilized flowers, was 10%. Seeds in plants of the A_2 apomictic generation after self-pollination were found to be substantially larger than those in unpollinated flowers. The weight of one caryopsis for self-pollinated plants was 28.0 ± 3.6 mg and, for apomictic seed, almost three times less (11.6 ± 2.1 mg). Formation of apomictic caryopses in sterilized flowers took 5 to 8 days longer compared with those from self-pollination in the same plants. In the apomictic A_3 generation, stamens were removed from 400 flowers and 52 caryopses were set in unpollinated flowers. An average of 6.5 caryopses/spike formed. The percent seed set, compared to the number of sterilized flowers, was 13%. Many other spikes where no grains were formed after removal of stamen were not taken into consideration in this calculation.

Line A-1 was selected in an F_3 hybrid population (wheat with light-colored grains and polygynous flowers/ wheat with dark-colored grains and xenia-colored caryopses) is similar to common wheat cultivars with regard to morphological features. Erythrospermum has an aristate, white spike and red grain. Stems of the plants are thin and long (100–120 cm). The spike contains 18–20 spikelets and the grains are small (1,000-kernel weight < 30 g). Under favorable cultivation, up to 80 caryopses/spike form; the fertility of flowers is high. Glumes of the spike are gentle and thin. The plants tiller intensely and produce many stems. The stems show tendency to branch. The tillering period is longer than for other wheat cultivars. The source maternal line with polygynous flowers has a high shade tolerance. When cultivated under low-light conditions in the greenhouse in the winter, substantially more caryopses in the spikes are formed than in the standard cultivars. Due to this advantage over other lines, erythrospermum was selected for hybridization, and the A-1 line was selected among the offspring. In some sister lines of A-1 (Table 3), the seeds are formed without pollination. Under usual conditions, these lines reproduce by way of gamogenesis. Pollen of the A-1 line can induce large-scale apomictic development of caryopses in R-2 rye.

Until now, no wheat with apomictic type reproduction is known in the world collection and no one managed to create such a cultivar artificially. Among wheats, apomixis occurs *Ag. scabrum* (Hair 1956). This species can hybridize with wheat and the resulting hybrids are fertile. During our research, the occurrence of apomictic lines of soft wheat having haploid (n = 21) chromosome number and germ-less seeds was observed. The formation of such plants also has been observed in case of pollinating wheat flowers with wild species such as *Ag. glaucum* and *Ae. speltoides*. The search for apomicts has taken a very long time, however with no positive results. We have found a line of soft spring wheat that can be satisfactorily hybridized with the diploid (2n = 14) species *T. sinskajae* (Kyzlasov 1997). The existing diploid species of wheat can hybridize with hexaploid species with great difficulty. A soft wheat has been created in which the flower stamens transform into pistils (Kyzlasov 1998). A hexaploid line has been selected having three stamens and from two to five pistils formed in each normally developed flower (Kyzlasov 1996). The number of caryopses formed in polygynous flowers corresponds to the number of pollinated pistils. Kyzlasov (2006) discovered that the additional pistils in the flowers of soft wheat are formed from lodicules. From two to four lodicules-pistils are formed in the flowers of this wheat and up to five caryopses formed in a flower. Apomictic development of soft wheat seed has been induced by pollinating wheat with rye (Kyzlasov 2005).

More than 17 species of Gramineous plants have the capability of apomictic reproduction. The gametophytic type of apomixis was discovered in the family of Gramineous plants (Khokhlov 1970). The germ may develop from the cells of the archesporium, nucellus, unfertilized ovule, synergid, or antipode. According to Kandelaki (1970), the occurrence of apomictic plants may be linked with diploidization of ovule nucleus. The mechanism of embryogeny in unpollinated flowers of apomictic soft wheats is still unknown. The genetic structure of the caryopses apomictic development is also unclear. Some features of organisms are known to appear as a result of gene interaction. If such genes are localized in nonhomologous chromosomes, the feature is inherited stably by double or triple homozygotes, for example, the xenia color of wheat caryopses, absence of stamens in the flowers, or polygynous flowers (Kyzlasov 2005). If such genes are allelic or if they are localized in homologous chromosomes, obtaining homozygous lines is not possible. Preserving such features by inbreeding also is impossible. This fact was discovered while investigating caryopsis apomictic development of the described soft wheat cultivars. All lines that appeared without participation of a paternal parent did not inherit this feature (Table 3). For this reason, an obligate soft wheat apomict could not be created. The main element of detecting apomicts in plant populations is the selection of matromorphic breeds. Apomictic wheat plants described here were discovered as the result of formation of seeds of maternal type in unpollinated flowers and xenia-colored caryopses served as an indicating attribute for identifying these plants.

In summary, a high percentage of hybrid F_0 caryopses was detected after hybridizing A-1 soft spring wheat with R-2 spring rye. Numerous, apomictic rye caryopses were formed as a result of pollinating flowers of R-2 rye with A-1 soft wheat. Protein fractions of wheat are absent in the endosperm of such caryopses. Matromorphic breeds of the F_1 hybrid (wheat with polygynous flowers/wheat with xenia-colored caryopses) obtained without pollination do not inherit this feature. The investigation of large-grained, F_1 hybrids (A-1 wheat/R-2 rye) obtained without participation of paternal parent are continuing.

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Laboratory of Winter Bread Wheat Breeding: New winter wheat cultivar Zhemchuzhina Povolzhjya.

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Winter wheat is a priority for grain production in the Saratov Region of the Russian Federation. Since the mid-1990s, a number of the Saratov winter wheat cultivars were established, including Saratovskaya 90, Victoria 95, and Gubernia. These cultivars are high-yielding with adaptability to the steppe conditions of the region. In addition, the cultivars have a wide range of individual characteristics that allow them to compete in the climatic conditions of Volga region.

To further enhance the yield of winter wheat, we have released the cultivar **Zhemchuzhina Povolzhjya**, which has a higher yield potential compared with the existing popular cultivars. The description of this new cultivar is presented in Table 1. According to winter hardiness, this cultivar belongs to the Saratovskaya 90 group, which is the most resistant to stable cold temperatures. Zhemchuzhina Povolzhjya also is resistant to leaf rust and has high grain quality.

Table 1. Grain yield, 1,000-kernel weight, test weight, protein content, and SDS-sedimentation test of winter wheat in the ecological test. All data is the mean from plants grown at Saratov in 2000–07.

Cultivar	Yield (t/ha)	1,000-kernel weight (g)	Test weight (g/l)	Protein content (%)	SDS sedimentation (mm)
Mironovskaya 808 (check)	3.47	43.0	753	13.88	53
Donskaya bezostaya (check)	2.72	39.6	746	15.58	67
Saratovskaya 90	3.35	43.7	747	14.42	59
Victoria 95	3.42	41.9	738	14.68	50

Laboratory of Spring Bread Wheat Breeding: A new spring bread wheat cultivar for the Volga River region.

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A new cultivar of spring bread wheat Saratovskaya 73 for Volga river region was introduced in 2008. The new cultivar was breed at the Agricultural Research Institute for South-East Regions of Russia (Saratov). In the last five years (2003–07), the grain yield of Saratovskaya 73 was higher than those of the standards from mean 0.4 t/ha (≥ 27%; Table 2), although environmental conditions varied greatly between the years. Saratovskaya 73 is characterized by higher 1,000-kernel weight and resistance to leaf rust than those of the check cultivars. Saratovskaya 73 had higher baking properties than those of the other best cultivar Povolgye.

Table 2. Grain yield, quality of grain and phytopatogenes test of spring bread wheat cultivars (means from 2003–07). Items with an * are significant at the 5% level.

Traits	Saratovskaya 55 (new cultivar)	Saratovskaya 70 (standard)	Saratovskaya 73 (standard)
Grain yield (t/ha)	15.8	15.2	20.1*
1,000-kernel weight (g)	34.9	35.6	37.5
Test weight (g/l)	769	772	767
Protein content (%)	13.4	14.5	14.3
Bread volume (sm^3)	638	732	748
Strength of flour, W e.a.	488	279	381
Loose smut severity (%)	0.28	0.03	0.04
Leaf rust severity (%)	75	85	17*

Laboratory of Spring Durum Wheat Breeding: New spring durum wheat cultivars for the Volga River region of Russia.

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The durum wheat-breeding program was begun in 1910 in Saratov with the main goal to develop new cultivars for resistance to heat and drought, the main diseases and pests that are wide-spread in this region, and high grain quality. The description of two newly developed cultivars are presented here.

Yelizavetinskaya. The early, strong gluten cultivar Yelizavetinskaya is recommended for the dry conditions of the Volga River region of Russia (vast steppe area). This cultivar was derived from the cross 'Saratovskaya zolotistaya (Saratov zolotistaya)/Svetlana'. Saratovskaya zolotistaya is the well-known local cultivar that has a very high yellow pigment content, and Svetlana is resistant to loose smut.

Compared to the check Saratovskaya zolotistaya, Yelizavetinskaya has a more compact plant habit. The color of that plant before heading is bright-green. After heading, the waxiness of the plant is expressed, but less than that of the check. Yelizavetinskaya is characterized by high gluten strength, higher than that of Krasnokoutka 10 and Saratovskaya zolotistaya. Yellow pigment content is similar to that of Saratovskaya zolotistaya and falling number is equal to that of Krasnokoutka 10 (Table 3, p. 112). This cultivar has s higher grain yield when compared with the check cultivars, but 1,000-kernel weight and test weight are lower than those of the check (Table 3, p. 112).

Annoushka. In 2007, the very strong gluten cultivar Annoushka was included in the state list of the cultivars permitted for use in vast steppe area of the dry south-east regions of Russia. This cultivar was derived from the cross 'Saratovskaya 53/Medora//D-1995/3/Leucurum 5594'. Annoushka is high yielding, drought resistant, and a well-adapted cultivar for the Volga River region of Russia, which can provide to farmers a wide area of for durum wheat cultivation. Potential productivity of the cultivar under dry conditions is about 3 t/ha. Annoushka is resistant to loose smut and moderately tolerant to tan spot.

The yield and micro-SDS-sedimentation test parameters of Annoushka are higher than those of the check cultivars. The micro-SDS-sedimentation test parameter was approximately 59 mm compared to 49 mm in Saratovskaya zolotistaya and 30 mm in Krasnokoutka 10 (Table 3, p. 112). Falling number is close to that of Saratovskaya zolotistaya, the check cultivar. The carotenoid content in the grain of Annoushka is higher than that of Krasnokoutka 10 and less

Table 3. Yield, 1,000-kernel weight, test weight, falling number, protein content, micro-SDS-sedimentation test, and carotinoid pigment content of Yelizavetinskaya and Annushka, new cultivars for the South-East Region of Russia in comparison with check cultivars. All data are means from the ARISER main yield trial grown at Saratov in 2003–07.

Cultivar	Yield (t/ha)	1,000-kernel weight (g)	Test weight (g/l)	Falling number (sec)	Protein content (%)	Micro-SDS-sedimentation (mm)	Carotinoid pigment content (mg/kg)
Krasnokoutka 10 (check)	1.88	44.8	808	458	13.9	30	4.4
Saratovskaya zolotistaya (check)	1.82	44.4	785	438	14.5	49	7.5
Yelizavetinskaya	1.97	42.5	773	456	14.4	54	7.1
Annoushka	2.09	43.2	777	432	14.2	59	6.0
LSD (5%)	0.13	1.3	8	36	0.6	5	0.6

only when compared with Saratovskaya zolotistaya. Annoushka is recommended for cultivation on agrotechnologies accepted in the given zone for durum wheat.

Laboratory of Plant Cell Breeding: Characterization of primary triticales for storage protein spectra and peculiarities of the meiosis in the mother pollen cells.

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The primary hexaploid and octoploid triticale (AABBRR and AABBDDRR, respectively) were developed with the participation of Saratov-bred cultivars of winter bread wheat and rye using of embryo rescue followed by colchicine treatment of plants.

Cytology of meiosis in the pollen mother cells showed that all amphidiploids studied have a significantly higher percentage of irregular metaphase I that of the standard cultivar Student. The frequency of PMCs with univalent chromosomes ranged from 73.4 to 86.1%. The frequency of univalent chromosomes in the PMCs of standard cultivar is rather high, above 40%. Interploid hybrids between hexaploid and octoploid triticales did not have an advantage compared to the primary triticales.

Protein markers are used in the genetic analysis of triticale, because they permit the study of the peculiarities of chromosomal fragments in amphiploids and control substitutions in recombinant breeding. The amphidiploids studied have 2–4 biotypes of gliadin spectra. These biotypes differ from one another in gliadin components that are controlled by genes on chromosomes 1A, 6A, and 1B. AD 460/08 (Novinka/Saratovskaya 6) has three biotypes with differences in 1A, 6A, and 1B chromosomes. AD 459/08 (Leucurum 921h21/Saratovskaya 6) has four biotypes with differences on chromosomes 1A and 6A. The electrophoretic spectra of the emergency proteins of AD 458/08 (Leucurum 170h389/ Saratovskaya 6) contain two types with differences in chromosome 6A. Octoploid triticale was homogenous for the emergency protein spectra.

Secondary triticales have been created via intercrossing of the primary hexaploid and octoploid triticale and intra- and intergenomic recombinations with the best cultivars. Combining traditional and tissue culture methods allows the production of hexaploid triticale with higher grain yields and other valuable agronomic characters.

Department of Genetics: Spring bread wheat cultivars from the Department of Genetics, ARISER, during 2004–07.

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

During 2004–07 in the Department of Genetics, two spring hard red bread wheats and one spring hard white bread wheat cultivars were produced. These cultivars were breed from wide crosses and show the effects and influence of alien chro-

mosomes and genes for resistance to disease, namely leaf rust and powdery mildew. Brief characteristics are described below.

Favorite, a hard red bread wheat derived from the cross 'L2033/Belyanka'; the pedigree of L2033 is 'L504*2/Krasnokutka 10'. L504 has the *Lr19*-translocation and Krasnokutka 10 is a spring durum wheat cultivar. Favorite is a medium maturing, medium-tall cultivar. The grain yield of Favorite is higher than that of the standard cultivar Yugovostochnaya 2 from 0.2 to 0.7 t/ha. This cultivar is resistant to lodging and to preharvest sprouting and has good bread-making qualities. Favorite is resistant to leaf rust, powdery mildew, and moderately resistant to loose smut.

Voevoda has the same pedigree as that of Favorite. The main difference between Voevoda and Favorite is resistance to stripe rust and moderately resistant to lodging.

Lebedushka is a hard white bread wheat derived from the cross 'Belyanka/Dobrynya'. Lebedushka is a medium maturing, medium-tall cultivar. The grain yield of Lebedushka is higher than that of the standard cultivar Yugovostochnaya 2, from 0.2 to 0.5 t/ha. This cultivar is resistant to lodging, leaf rust, powdery mildew, and has good bread-making qualities. The basic disadvantage for this cultivar is susceptibility to preharvest sprouting. Nevertheless, in the planting area where preharvest sprouting is not a problem, this cultivar may be used successfully.

The evaluation of spring bread wheat cultivars, NILs, and promising lines resistant to stem rust.

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Stem rust of bread wheat in the Saratov district of the Volga Region of Russia is seldom a problem and epidemics are not severe. Nevertheless, in the southwest part of the Saratov district, epidemics of leaf rust were observed during the last three years. The majority of spring bread wheat plantings in this zone were with cultivars L503, L505, Belyanka, Dobrynya, and Prohorovka. Only Prohorovka has an IT = 0 to stem rust. The cultivars L503, L505, Belyanka, and Dobrynya had ITs = 3 for stem rust. The severity for L503, L505, and Dobrynya was 15–20% and 50–60% for Belyanka. The former cultivars have the T7DS·7DL-7Ae#1- translocation with *Lr19*/*Sr25* genes. Obviously, the decrease in severity in these cultivars are caused by residual effect of *Sr25* gene. The NILs with ITs = 0 were promising lines with the Sr gene combination of *Sr24* + *Sr25* and *Sr25* + *Sr31*.

The identification of wheat–Thinopyrum elongatum chromosomes substitutions in leaf rust-resistant lines.

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During 1993–2000 at ARISER, *Th. elongatum* (2n=70) was crossed with the spring bread wheat cultivar Saratovskaya 55 and backcrossed four times with cultivar Saratovskaya 29. Among the wheat–*Th. elongatum* lines that were resistant to leaf rust and powdery mildew, four lines were highly resistant leaf rust, L1858/1, L1858/2, L1857, and L1178. C-banding of these lines showed *Th. elongatum* substitutions with chromosomes 6D (L1858/1 and L1858/2), 3B (L1857), and 7D (L1178). Two bread wheat–*Th. elongatum* translocations with Lr genes are noted in the Gene Catalog, T7DL-7DS-7Ae#1L (*Lr19)* and T3DS-3DL-3Ae#1L (*Lr24*). In the Saratov district of Volga Region of Russia, *Lr19* was overcome in 1994 year and presently ineffective. The test for allele identification in above-mentioned lines will concentrate on *Lr24*.

Genetic control of resistance of wheat to loose smut.

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Four cultivars and lines of spring bread wheat have shown a high level of resistance to a loose smut (race 23 = T18) after artificial inoculation. To determine the genetic control of resistance, these cultivars and lines crosses were made with the susceptible cultivar Saratovskaya 64 and line L528. We inoculated the F_2 and subsequently analyzed individual offspring

of each plant. The analysis of hybrid combinations in the F_2 has shown that cultivar Marroqui 588 and line PI 69282 probably contain two independent genes (Table 4). Line L2040 has two resistance genes for loose smut. The segregation for resistance in plants at the F_1BC_1 confirmed two resistant genes in line L2040.

Table 4. Segregation of a population of hybrids F_2 for resistance to 23 race of a loose smut. X^2 degrees of freedom = 1–3.48

		Segregation				
		Experimental		Theoretical		
Cultivar/Line/Hybrid	Generation	R	S	R	S	X^2
L528			98.8			
Saratovskaya 64			98.5			
L2040			7.4			
Preston		100				
Marroqui 588		100				
PI 69282		100				
L528/Marroqui 588	F_2	138	113	9	7	0.16
Marroqui 588/L528	F_2	146	98	9	7	1.28
Saratovskaya 64/Marroqui 588	F_2	77	56	9	7	0.15
Marroqui 588/L528//L528	F_1BC_1	79	20	3	1	1.22
L528/ PI 69282	F_2	156	111	9	7	0.51
PI 69282/L528	F_2	125	89	9	7	0.41
Saratovskaya 64/PI 69282	F_2	83	61	9	7	0.11
PI 69282/L528//L528	F_1BC_1	87	23	3	1	0.98
L528/Preston	F_2	168	138	9	7	0.23
L528/L2040	F_2	122	28	13	3	0.001
L2040/L528	F_2	114	29	13	3	0.22
Saratovskaya 64/L2040	F_2	74	19	13	3	0.17
L2040/L528//L528	F_1BC_1	109	28	3	1	1.52

The relationship between grain yield and grain protein content in spring bread wheat in the Volga region.

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Twenty-eight cultivars and experimental introgressive genotypes from the breeding program of ARISER, Russian Federation, were grown in a bare fallow, leached chernozem soil during four consecutive years, 2003, 2004, 2005, and 2006. The planting rate was $4x10^6$/ha and four replications were made for each trial. Plot size was 7.0 m^2. Fertilizers were not applied. For precipitation and temperature regimes, 2003 was optimal with a grain yield average of 4,433 kg/ha and a grain protein content 15.39%. In the 2004 and 2005, a leaf rust epidemic significantly lowered grain yield of susceptible genotypes. In 2004, the average yield of a susceptible genotype (n = 15) was 2,958 kg/ha with a grain protein of 15.82%. A resistant genotype with an *Lr* translocation yielded 3,289 kg/ha with a grain protein content of 16.05%. In 2005, the average grain yield of the susceptible genotypes (n = 15) was 2,302 kg/ha and the average grain protein content was 16.0%; a resistant genotype had 2,874 kg/ha and 17.0%, respectively. For 1,000-kernel weight, the difference between sibs was not significant. Correlation coefficients between grain yield and 1,000-kernel weight were positive, but weak to average. The correlation coefficients between the grain yield and protein were negative in 2003, r = –0.50**, in 2006 r = –0.39*. During the leaf rust epidemic in 2004, correlation coefficients between grain yield and protein content of the resistant genotypes was –0.85 ** (negative) and 0.34 (positive), for susceptible genotypes, but in 2005, resistant genotypes were r = –0.24 (negative) and susceptible 0.57** (positive). Correlation coefficients between 1,000-kernel weight and grain protein content were negative in all years.

The influence of EXTRASOL on economic valuable characteristics in winter triticale.

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Much recent attention in the agronomical practice has been given to the use of the various biostimulating preparations that influence efficiency, resistance to abiotic and biotic stress, and production quality. One such biostimulator with a complex action is the commercial preparation Extrasol. Extrasol improves feeding elements in a plant, increases seed germination, adjusts enzymatic activity in vegetative cells, accelerates plant development, and reduces infection of phytopathogenic microorganisms, which are reflected in plant productivity.

The action of Extrasol was studied in 2005–06 on the winter triticales Yubileynaya, Sargau, and Student. Experimental sowings were placed in fields of bare fallow in four replicates. We treated vegetative plants at tillering (the beginning of May), a 1% Extrasol solution. The analysis of structure element productivity was carried out using standard techniques. Plant height and spike length were measured. The number of plants, spike productivity, weight of grain from one square meter, and the 1,000-kernel weight were measured. The data were subjected to dispersive analysis.

The extrasol treatment tended to markedly increase the efficiency of productivity parameters, especially 1,000-kernel weight, however, the majority of studied characteristics did not significantly differ from the controls. In 2005–06, the influence of genotype on characteristic prevailed.

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Breeding and genetic analysis for height in spring wheat.

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In the Russian Far East, tall wheat cultivars lodge under the summer monsoon and when grain yield is greater than 2 t/ha. Dwarf cultivars from the U.S., Mexico, Canada, and India were hybridized to create lodging-resistant cultivars. In Khabarovsk, short stalk was inherited very well, but at the same time, negative traits such as wheat drought resistance, suscepibility to *Fusarium* and *Helminthosporium*, and unstable yields, were also inherited.

Materials and Methods. Four F_1–F_2 hybrids, 'ERO-4/Dalnevostochnaya' (ERO-4/DV), 'Opal/Okeanskaya 39' (OPAL/OK39), 'Molodyozhanaya/Primorskaya 1738' (MD/P1738), and 'Molodyozhnaya/Lutescens 47' (MD/L47) were used. The height difference between the cultivars was 12–25 cm. Each cultivar has one or more valuable features. ERO-4 (Brazil) is resistant to disease and drought. Dalnevostochnaya (Russia) is a strong wheat with high quality grain. Opal (Germany) is medium sized, resistant to lodging and disease, and has a large spike. Molodyozhnaya (Russian Federation) has a short stalk and is resistant to lodging. Lutescens 47 (Russian Federation) is productive and has medium resistance to lodging and disease. Okeanskaya 39 and Primorskaya 1783 (Russian Federation) have large spikes and 1,000-kernel weights.

Seed was sown in a field as follows: P_1 (mother) – F_1 – F_2 – P_2 (father). The cultivar Monakinka was used as the check. The height of the parentals and check were determined from 20–30 plants, 15–20 plants of the F_1, and 69–95 in the F_2. Variation within the rows was calculated according to Dospekhov (1973), predomination degree (hp) according to Griffing (1950), heterosis using Omarov (1975), transgression frequency according to Voskresenskaya and Shpot (1967), heritability (H^2) using Warner (1971), and the number of genes according to Rokitsky (1978). The degree of conformity with theoretically expected results was measured by a X^2 test.

Results and Discussion. The efficiency of gene transfer depends on the inheritance and degree of variability of the trait. Three F_1 hybrids inherited height from a dwarf parent; another hybrid (ERO-4/DV) from a tall parent (Table 1, p. 116). The 'MD/P1738' hybrid F_1 had a hp = –1.27, indicating superdominance of the dwarf parent. Plant height increased in

Table 1. Heritability of plant height in the parental lines and in the F_1–F_2 hybrid generations. CD+ is complete dominance of the high trait; ID– is incomplete dominance of the low trait; and ED– is extradominance of the low trait.

Hybrid combination	Mean (cm)				hp		Heritability in the F_1
	P_1	F_1	F_2	P_2	F_1	F_2	
DRO-4/Dalnevostochnaya	74.2±1.4	86.0±0.6	83.0±0.9	86.1±1.1	0.98	0.47	CD+
Opal/Okeanskaya 39	75.9±1.1	77.0±0.4	87.6±0.7	86.5±1.3	–0.79	1.21	ID–
Molodyozhanaya/Primorskaya 1738	67.9±1.1	65.4±0.6	84.0±0.8	86.3±0.9	–1.27	0.75	ED–
Molodyozhnaya/Lutescens 47	67.9±1.1	71.9±1.2	77.6±0.8	90.9±0.8	–0.65	–0.16	ID–
Monakinka (check)	90.0±1.2						

the F_2 compared to the F_1 except for the 'ERO-4/DV' cross. Plant height increased by 10.6 cm in the 'OPAL/OK39' F_2, by 18.6 cm in 'MD/P1738', and by 5.7 cm in 'MD/L47' (Table 2). Table 2 shows the height differences in the hybrid F_1s and F_2s. For the 'MD/P1738' cross, the height of the F_2 is greater than in the F_1. Three hybrids have an hp <1. The 'OPAL/O39' hybrid has an hp >1 indicating heterosis. The lack of heterosis proves the necessity of making selections in the early generations. The variability was greater in the hybrid F_2s (Table 3). Factors of genotypic variability, depending on the hybrid, make up 6.3–8.5% and 7.8–10.3% for phenotypic variability.

Table 2. Tall plant heterosis in parental lines and in the F_1–F_2 hybrid generations (* = p < 0.001).

Hybrid combination	Tall plant parental deviation (cm)		Heterosis		
	F_1	F_2	Check	F_1	F_2
DRO-4/Dalnevostochnaya	–0.1	–3.1	0.1	–0.1	–3.6
Opal/Okeanskaya 39	–9.5*	1.1	–10.4	–11.0	1.3
Molodyozhanaya/Primorskaya 1738	–20.9*	2.3	–23.9	–24.2	–2.7
Molodyozhnaya/Lutescens 47	–19.0*	–13.3*	–16.3	–20.9	–14.6

Table 3. Variability in plant height in parental cultivars and their hybrids. For the F2 coefficient of variation, the numerator is the phenotypic and the denominator is the genotypic variation.

Hybrid combination	Generation	Variability limit (cm)	Difference max–min (cm)	Variation coefficient (%)
DRO-4/Dalnevostochnaya	P_1	66–88	22	7.9
	P_2	78–94	16	5.8
	F_1	83–91	8	2.9
	F_2	56–95	39	10.3/8.4
Opal/Okeanskaya 39	P_1	65–82	17	6.5
	P_2	73–100	27	7.4
	F_1	73–80	7	2.7
	F_2	70–101	31	7.3/4.8
Molodyozhanaya/Primorskaya 1738	P_1	62–76	14	6.7
	P_2	79–94	15	4.9
	F_1	60–70	10	3.3
	F_2	65–95	30	7.8/6.3
Molodyozhnaya/Lutescens 47	P_1	62–76	14	6.7
	P_2	82–96	14	4.4
	F_1	60–87	27	7.3
	F_2	65–93	28	10.3/8.4

No transgressive segregation was observed in the F_2. The height of the hybrids was within the limit of variation of the paternal cultivars (Table 3) except for the 'ERO-4/DV' hybrid, which varied between 56–95 cm, and the ERO-4 parent was 66–88 cm and the DV parent was 78–94 cm. In this cross, most of the dwarf plants were 10–24 cm shorter than those of the check Monakinka, a difference of 20–35 cm compared to the mean height of the check. Depending on the hybrid combination, shorter plants varied from 10.6–55.6% (Table 4, p. 117). With respect to the check Monakinka, all the hybrids show signs of transgressive segregation (Table 4), which is why it is better to select shorter plants from the hybrid than from the standard check cultivar.

Table 4. Transgressive segregation parameters for plant height in the hybrid F_2s.

Hybrid combination	Minimum height (cm)		Trangression (%) toward Check		Trangression (%) toward < Parent	
	< Parent	Hybrid	Degree	Frequency	Degree	Frequency
DRO-4/Dalnevostochnaya	66.7	60.3	24.6	31.0	9.5	4.6
Opal/Okeanskaya 39	67.0	71.7	10.4	10.6	0.0	0.0
Molodyozhanaya/Primorskaya 1738	61.3	67.3	15.9	20.3	0.0	0.0
Molodyozhnaya/Lutescens 47	61.3	65.0	18.8	55.6	0.0	0.0

In the F_2 hybrids of 'ERO-4/DV' and 'OPAL/O39', the difference in plant height was not large (10–12 cm) and the phenotypic distribution was close to normal. Hybrids 'MD/P1738' and 'MD/L47' differed by as much as 25 cm. Plants that were two standard deviations less than the parental were considered undersized or tall. For the undersized plants, the interval was 58.8/77 cm (MD) and for the tall plants, it was 78.1/94/5 cm (P1738). The ratio was close to 13:3 for the 'MD/P1738' F_2 and 7:9 for the 'MD/L47' F_2 (Table 5).

Table 5. Plant height in the hybrid F_2.

Hybrid combination	Number of plants	Tall vs. short plants: actual	Tall vs. short plants: theoretical	X_2	Significance level (p)
Molodyozhanaya/Primorskaya 1738	64	55:9 13.75:2.25	52:12 13:3	0.92	0.50>p>0.25
Molodyozhnaya/Lutescens 47	80	33:47 6.6:9.4	33:45 7:9	0.22	0.75>p>0.50

The number of genes controlling plant height in the 'MD/P1738' hybrids was 2.0 and in the 'MD/L47' hybrids was 2.24 (Table 6), which should be two and three genes, respectively. The other two crosses have one gene and wheat phenotypic activity makes hybrid analysis difficult. The heritability coefficient H^2 is a sufficient indicator for the efficiency of breeding for a characteristic. The highest H^2 values were in the 'ERO-4/DV' hybrids (0.70), followed by 'MD/P1738' (0.67), and 'MD/L47' (0.66) (Table 6). Thus, the lack of heritability and the high degree of transgressive segregation and the coefficients of genotypic variation combined with high heritability need to be considered for breeding plants that are dwarf or resistant to lodging.

Table 6. Plant height heritability in the parental lines and the F_1–F_2 hybrid generations.

Hybrid combination	Cultivar and hybrid variation (σ^2) P_1	F_1	F_2	P_2	Heritability	Number of genes
DRO-4/Dalnevostochnaya	34.65	24.90	6.07	72.08	0.70	0.40
Opal/Okeanskaya 39	24.62	40.49	2.71	40.62	0.44	0.49
Molodyozhanaya/Primorskaya 1738	20.54	16.71	4.69	41.61	0.67	2.00
Molodyozhnaya/Lutescens 47	2.54	15.74	27.47	63.34	0.66	2.24

From our studies, the following lines were selected from the hybrid populations: 'ERO-4/DV' lines 131 and 132; 'OPAL/O39' lines 408, 721, 755, and 774; 'MD/P1738' lines 499, 502, and 523; and 'MD/L47' lines 402, 426, and 438. All these lines are 1.5–2 times more productive than the check Monakinka, resistant to lodging and disease, and have optimal height (75–80 cm) for the conditions of far-eastern Russia.

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Races of Puccinia graminis f. sp. tritici in Russian Federation in 2006.

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Monitoring the race composition of the wheat stem rust pathogen is done annually in the same fields of three regions of the Russian Federation; Central Russia (Moscow Region), the Northern Caucasus (Rostov Region), and Western Siberia (Tomsk Region). Development of disease may vary according to climatic conditions and the source of infection. Long-term observations indicated that infection on wheat and other grains generally appeared in the fields as separate groups of plants infected by stem rust. Under conditions unfavorable for development of the fungus, plants infected by rust were usually found on separate wheat cultivars with high susceptibility to pathogen. For example, the stem rust pathogen is found yearly in Rostov Region on wheat cultivars Albidum 28 and Albidum 43. However, considering the high infection potential of the pathogen, monitoring virulence and race composition of the fungus is extremely important to predict the appearance of new pathogen races in order to control development of stem rust epidemics.

The 2006 growing season was relatively favorable for development of wheat stem rust. Separate hotbeds of the pathogen were found on many wheat and barley cultivars in Central Russia and the Northern Caucasus. In Northern Siberia, only aeciospores were found on barberry. No large infection was observed, possibly explained by an insufficient amount of inoculum.

Races were determined by infecting 16 wheat lines with known resistance genes with monouredinial fungal isolates (Roelfs and Martens 1988). Fourteen races of *P. graminis* f.sp. *tritici* were identified in populations of the fungus from different regions of the Russian Federation. Races that occurred with a frequency of 8% or higher were referred to as dominant and those with lesser frequency as rare (Lekomtseva et al. 2007). Races TKNT (46%), TKNS (11%), and TKPT (8%) dominated in 2006. Races TKST and TTNT had occurrence frequencies of 7% (Table 1).

Table 1. Races of *Puccinia graminis* f. sp. *tritici* in the Russian Federation in 2006.

Race	Susceptibility of *Sr* genes	Number of isolates	%
KJNT	21, 9e, 7b, 6, 8a, 36, 30, , 9a, 9d, 10, Tmp	1	1
RKNT	5, 21, 7b, 6, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp	3	4
TKNT	**5, 21, 9e, 7b, 6, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp**	**34**	**46**
TKNS	**5, 21, 9e, 7b, 6, 8a, 9g, 36, 30, 9a, 9d, 10**	**8**	**11**
TKPT	**5, 21, 9e, 7b, 6, 8a, 9g, 36, 30, 13, 9a, 9d, 10, Tmp**	**6**	**8**
TKST	**5, 21, 9e, 7b, 6, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp**	**5**	**7**
TKKT	5, 21, 9e, 7b, 6, 8a, 9g, 36, 30,13, 9a, 9d, 10, Tmp	3	4
TFNT	5, 21, 9e, 7b, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp	1	1
TTNT	**5, 21, 9e, 7b, 11, 6, 8a, 9g, 36, 30, 9a, 9d, 10, Tmp**	**5**	**7**
TTPT	5, 21, 9e, 7b, 11, 6, 8a, 9g, 36, 30,13, 9a, 9d, 10, Tmp	4	5
RTPT	5, 21, 7b, 11, 6, 8a, 9g, 36, 30,13, 9a, 9d, 10, Tmp	1	1
PKQT	5, 9e, 7b, 6, 8a, 9g, 9a, 9d, 10, Tmp	2	3
TTST	5, 21, 9e, 7b, 11, 6, 8a, 9g, 36, 9b, 30, 9a, 9d, 10, Tmp	1	1
TJST	5, 21, 9e, 7b, 6, 8a, 36, 9b, 30, 9a, 9d, 10, Tmp	1	1
Total		75	100

The frequency of rare races in populations of the stem rust pathogen may indicate instability in the composition of the fungal population, connected with the different susceptibility of host plant cultivars, the different adaptation properties of various pathogen races to the environment, or the sensitivity of individual virulence genes to temperature or illumination.

Table 2. Dominant and rare races of *Puccinia graminis* f.sp. *tritici* in various regions of the Russia Federation in 2006.

Region	Host plant	Dominant races (%)	Rare races (%)
Central Russia	Barberry	77	23
	Wheat	78	22
	Barley	77	23
	Gramineous plants	66	34
Northern Caucasus	Wheat	43	57
	Gramineous plants	66	34
Western Siberia	Barberry	100	0

Composition analysis of races in different regions and on various host plants indicated that the percent of rare races was similar for barberry, wheat, and barley (22–23%) in Central Russia and in the Northern Caucasus in 2006; the frequency of dominant races was less than that of rare races (43% and 57%, respectively). The proportion of dominant and rare races was similar (66% in Central Russia and 34% in the Northern Caucasus) for Gramineous plants in these regions. Only dominant races were registered on barberry in Western Siberia (Table 2).

The high variability of race composition of wheat in Northern Caucasus also may indicate the presence of infective sources from places where barberry grows in the mountainous regions of this zone. Evaluating tolerance of wheat lines indicated that, in 2006, most were found susceptible to stem rust, with the exclusion of *Sr11*, *Sr9b*, and *Sr13* (Table 3).

Table 3. Number of monouredinial isolates virulent to wheat lines with *Sr* genes.

Sr gene	%
5	98
6	98
7b	100
8a	98
9a	75
9b	**12**
9d	97
9e	97
9g	97
10	98
11	**16**
13	20
21	97
30	98
36	100
Tmp	89

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RAPD distribution of Russian isolates of Puccinia graminis f.sp. tritici by the high-GC primers.

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To minimize wheat loss due to rust in the Russian Federation, annual control of the molecular and virulence variation in the *P. graminis* f.sp. *tritici* population is essential. Although the variation in virulence is under strong race selection, the molecular polymorphism of isolates could reflect any neutral trend in the current pathogen population (Roelfs et al. 1997; McCallum et al. 1999).

For the genetic analysis of fungal DNA polymorphism, we used RAPD–PCR improved by the high-GC 10-nt primers (Kubelik and Szabo 1995). These primers generated much higher numbers of both amplification products per primer and polymorphism among isolates in comparison with the 15-nt primers we used previously (Table 1).

Table 1. Comparison of 15-nt arbitrary primers with 10-nt high-GC primers from RAPD analysis of DNAs from 36 Russian isolates of *Puccinia graminis* f.sp. *tritici*.

Item	PR3 (GTG)5	Core GAGGGTGGXGGXTCT	CRL-11 CCACCGCGCC	CRL-9 CAGCCGCCCC	CRL-7 GCCCGCCGCC
Segment/primer	5.7	8.6	10.25	11.9	14.3
% Polymorphism detected/primer	42	50	82	75	65

The high-GC primers increased the efficiency of DNA-fingerprinting for genetic analysis of *P. graminis* f.sp. *tritici* (Pgt). We screened five arbitrary primers on DNAs from 36 Russian *Pgt*-isolates with different geographic and host-plant origin collected in 2005 (Table 2). All primers gave scorable DNA segments (strong bands on the gel), and the high-GC primers yielded an average of 12.15 amplification products per primer with an average of 74% of polymorphisms. To estimate genetic variation of *Pgt*-isolates, we used a clustered method to create phylogenetic trees (Treecon for Windows). All dendrograms were characterized by similar topologies but different levels of cluster stability. The higher indexes confirmed the RAPD-distribution of isolates by the high-GC primers (Fig. 1, p. 121). Because it had been already fixed by annual analysis since 2001 (Skolotneva et al. 2005, 2007), there was a clear host-plant grouping of *Pgt*-isolates in the barberry cluster, wheat, barley, and some cereal grasses.

Table 2. Isolates of *Puccinia graminis* f.sp.*tritici* in different regions of the Russian Federation in 2005.

Isolate No.	Region	Host plant
2.1/2.2	Central Russia, Moscow area	*Berberis vulgaris*
3.1/3.2	Central Russia, Moscow area	*Berberis vulgaris*
4.1/4.2	Central Russia, Moscow area	*Berberis vulgaris*
7.1/7.2	Central Russia, Moscow area	*Triticum aestivum*
8.1/8.2	Central Russia, Moscow area	*Triticum aestivum*
9.1	Central Russia, Moscow area	*Triticum aestivum*
10.1/10.2	Central Russia, Moscow area	*Triticum aestivum*
11.1/11.2	Central Russia, Moscow area	*Triticum aestivum*
14.1/14.2	Central Russia, Moscow area	*Hordeum distichum*
15.1/15.2	Central Russia, Moscow area	*Elytrigia repens*
16.1/16.2	Northern Caucasus, Rostov area	*Triticum aestivum*
18.1/18.2	Northern Caucasus, Rostov area	*Triticum aestivum*
19.1	Northern Caucasus, Rostov area	*Triticum aestivum*
22.1/22.2	Northern Caucasus, Rostov area	*Triticum aestivum*
23.1/23.2	Northern Caucasus, Rostov area	*Hordeum distichum*
25.1/25.2	Western Siberia, Tomsk area	*Berberis vulgaris*
26.1/26.2	Western Siberia, Tomsk area	*Elytrigia repens*
27.1/27.2	Western Siberia, Tomsk area	*Dactylis glomerata*
28.1/28.2	Western Siberia, Tomsk area	*Phleum pratense*

Isolate genotypes from wheat were constantly clustered (by index bootstrap up to 91%). Only traces of the geographical differences among them were found on the subcluster level. Therefore, we suggested the wheat cultivars provided the same pressure on the molecular polymorphism of the wheat stem rust pathogen throughout the European Russia.

Table 3. The index description of the separated clusters with Western Siberian isolates of *Puccinia graminis* f.sp. *tritici* created by RAPD-analysis with five arbitrary primers.

Item	PR3	Core	CRL-11	CRL-9	CRL-7
Average percentage of the dendrogramm groups	50.2%	54,25%	70.75%	71.44%	64%
Bootsrap values of cluster reliability	76%	36%	97%	100%	57%
Divergence of the cluster from other groups in genetic scale	0.31	0.28	0.63	0.62	0.18

The sexual process on barberry is the greatest source of the race variability in the pathogen population. However, we observed that the RAPD polymorphism of *Pgt*-isolates was independent of recombination forces, combining their genotypes into the stable cluster (by index bootstrap up to 86%). Having more information available about genotypes by this improved RAPD method suggested an important role of the host-plant type with a special set of the biochemical and physiological characters for the molecular variation of wheat stem rust pathogen. We also could describe a separate cluster of *Pgt*-isolates with geographical (from Western Siberia, Tomsk area) and molecular (on RAPD data) differences (Table 3, p. 120).

Comparable virulence analysis of the spore collections from European Russia and Western Siberia had not demonstrated their isolation (Lekomtseva et al. 2007). We predicted that new local population could be formed by the accumulation of the neutral DNA-polymorphisms in the distinct region.

We suggest a relatively stable RAPD distribution of *P. graminis* f.sp. *tritici* isolates in European Russia by host-plant origin during last 5 years and that the molecular outlines of the pathogen group from the Western Siberia obtained by using the high-GC primers.

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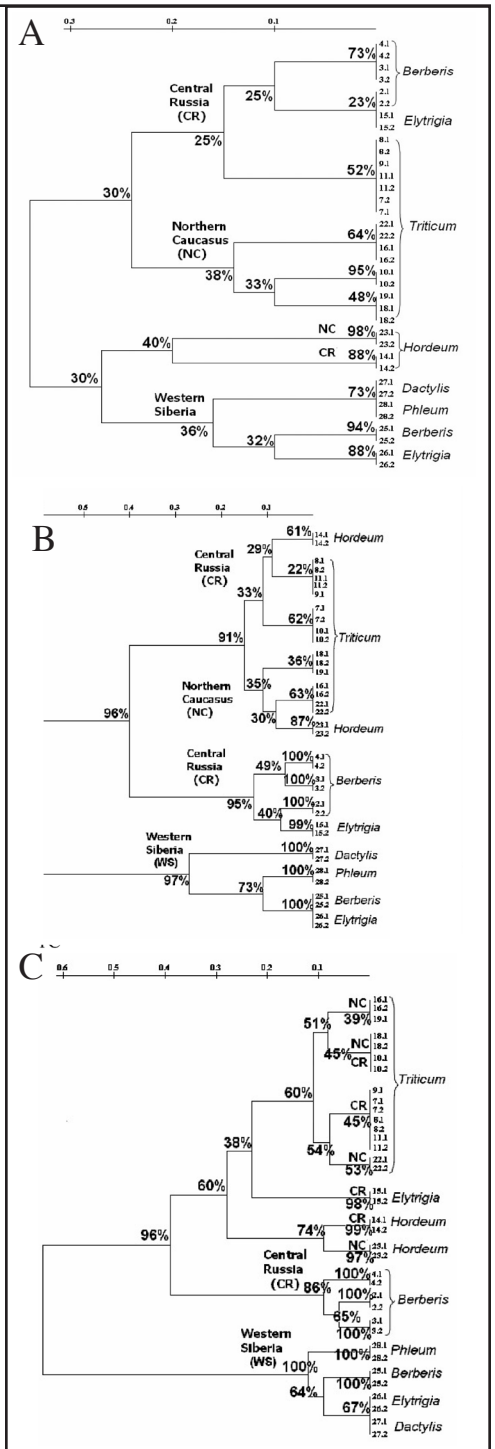

Fig. 1. RAPD-diversity of 36 Russian isolates of *Puccinia graminis* f.sp. *tritici*. A: by primer CORE; B: by the high-GC primer CRL-11; and C: by the high-GC primer CRL-9.

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Using isogenic analysis to study genotype effect in in vitro cell and tissue culture of wheat.

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Isogenic analysis using NILs that differ in alleles for only one gene is an exact tool, allowing the establishment of straight and pleiotropic effects of concrete genes for various characters. Using this method it is possible to search genes with a strong positive effect for interesting characters.

Isogenic analysis is seldom used to study morphogenetic processes in cell and tissue culture *in vitro*. Practical use of in vitro isogenic analysis is especially useful when the genes are known to have a precise phenotypic effect and economic value, such as genes for short stalk.

For a number of years, we have screened a set of NILs of soft and hard wheat that differ for the short stalk character in *in vitro* anther and somatic tissue culture.

We found that the *Rht*, *s1*, and *Q* genes in the soft wheat Saratovskaja 29 influence morphogenic anther and haploid formation and regeneration in *in vitro* anther culture, the formation of meristematic tissue in somatic calli, and regeneration ability during long-term callus cultivation.

We also compared the influence of the *Rht-B1b* gene on stages of *in vitro* anther and somatic tissues cultivation in three varieties of hard wheat. For all investigated genes, the greatest positive effect was on haploids in anther culture and morphogenesis in somatic calli in a line with the *Rht-B1c* gene. The *Q* gene increases the frequency of haploid formation and plant regenerants in anther culture.

A serious restriction in using isogenic analysis is the creation of the NILs. Nevertheless, studying the effects of genes will help answer the question of the genetic processes proceeding in vitro cell and tissue culture.

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Wheat plant growth in the presence of aluminum ions is an indication of tolerance to aluminum toxicity.

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Aluminum toxicity is one of the most important issues for poor soils. Wheat makes poor growth and productivity if Al ions are present in the soil. We have established that some wheats have a positive reaction Al ions. When the spring wheat cultivar Lada was grown in an aluminum solution (Ca (1 x 10^{-4} M) + Al (1 mg/l)), leaf length was greater than that of the control plants (Ca (1 x 10^{-4} M)) (Fig. 1). This result was unexpected. We later determined that the increase in yield in same variant in vegetation tests. However, not all wheat plants are capable of increased growth and yield in the presence Al ions.

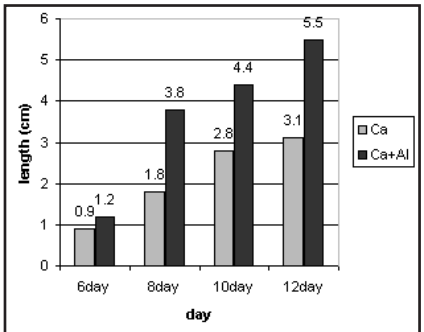

Fig. 1. Leaf length of the spring wheat cultivar Lada grown in an aluminum solution (Ca (1 x 10^{-4} M) + Al (1 mg/l)) and the control plants (Ca (1 x 10^{-4} M))

Materials and Methods. For vegetation tests, the spring wheat cultivars Voronegskaya, Yugo-vostochnaya 2, Kerba, and Omskaya 24 were grown in cells

filled with sod-podzol soil with medium macroelement availability, pH 5.2–5.6 (in different test years). The cultivars were grown in 6l plots. The procedure included a control (without aluminum), Al1 (6 mg/kg soil), Al2 (13 mg/kg soil), Al1+K (100 mg K/kg soil), and Al2 + K (100 mg K/kg soil).

Results and Discussion. We determined that productivity gains in Al1 and Al2, in the presence of aluminum ions, exceeded the control and the variants with potassium. These data do not confirm nor disprove the hypothesis that potassium ions in a soil solution would diminish aluminum toxicity; aluminum is toxic as it is. However, detailed analysis of the situation helped unveil the reason of such results. Initially, the test in distilled water was conducted to exclude irrelevant effects. Wheat seedlings were grown in distilled water with using a control, 1 mg/l Al, 3 mg/l Al, 12 mg/l Al, and 40 mg/l Al. The results did not show a strict dependence in root length in the test variants, but we explicitly established activate growth in the above-ground parts of the plant at very low concentrations of aluminum in the medium (1 and 3 mg/l). These plants were called aluminum sensitive (Table 1). Less sensitive cultivars would have above-ground growth at higher aluminum concentrations.

Table 1. Length of wheat lseedlings at the 10 day (cm) in solution containing aluminum ions.

Aluminum concentration	Cultivar				
	Voronegskaya	Irgina	Priokskaya	Omskaya	Kerba
Control	9.5	13.5	12.1	12.1	14.3
1 mg/l Al	11.0	14.8	12.1	8.7	14.2
3 mg/l Al	10.7	13.2	13.9	10.5	14.0
12 mg/l Al	10.5	13.5	12.7	12.5	10.7
40 mg/l Al	10.6	13.3	11.3	9.2	13.4

Exactly which cultivars are capable of active growth in the presence of aluminum at the lowest possible concentrations have yield ability exceeding that of the control (Fig. 2). These results show that those cultivars capable of steady growth on soils containing aluminum ions are also highly sensitivity to aluminum ions at the lowest possible concentrations at the earliest stages of development. The capability for sensing aluminum ions enabled plants to activate the mechanism to adapt and gain steady growth.

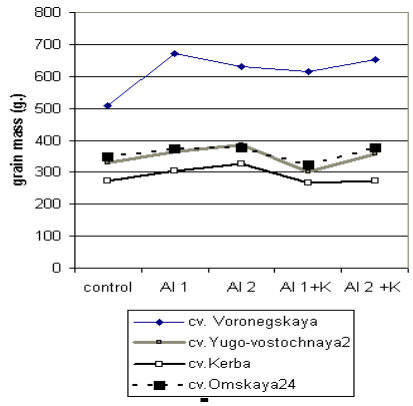

Fig 2. Grain yield (g/plant) for the cultivar Lada in the control (Ca) and in a solution of Ca + Al.

We know that potassium ions diminish the effects of aluminum toxicity and increase the general competition of ions in solution. However, in vegetative tests, the variants with added potassium ions showed low fertility, below that of control plants. Based on the activation of adaptation to aluminum ions by the reduction in the effects of aluminum toxicity by potassium ions, we believe that potassium ions are the reason for a plants inability to develop full tolerance against aluminum. The early growth phases, i.e., the period of adaptation against edaphic stress, on basis of aluminum ion sensitivity is vitally important for wheat cultivars capable of steady growth and adaptation to aluminum ions.

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The oxidation of saturated free fatty acids by winter wheat mitochondria.

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The most important catabolic pathway of free fatty acids (FFA) is β-oxidation with acyl-CoA formation, which is further fully oxidized in the Krebs cycle to CO_2 and H_2O. Animal β-oxidation is known to take place in mitochondria and peroxisomes (Schulz H 1991). Questions about the localization of plant mitochondrial β-oxidation was under discussion

for a long time (Masterson and Wood 2000a). Using FFA as a mitochondrial oxidation substrate was discovered only at early stages of germination of oil-containing seeds such as sunflower and lettuce (Raymond et al. 1992; Salon et al. 1988). In experiments with pea mitochondria, differences in contribution of peroxisomal and mitochondrial β-oxidation at different stages of growth and different organs were shown (Masterson and Wood 2000b, 2001). We suppose that mitochondrial β-oxidation in plants plays a key role in the response of lipid metabolism on changes in plant organism development. Data exists on the possibility of highly purified mitochondria from glucose-starved root tips of maize to oxidize octanoate and palmitate (Dieuaide et al. 1993). At the same time, no data exists about the possibility that the mitochondria of winter wheat shoots use saturated fatty acids as oxidation substrate.

Previously, we showed that unsaturated (linoleic, oleic, petrozelinic, and erucic) and saturated (lauric, palmitic, stearic and begenic) fatty acids cause uncoupling of oxidative phosphorylation in the mitochondria of winter wheat shoots (Grabelnych et al. 2003, 2004, 2005). We found that unsaturated FFA could be used as the sole oxidation substrate for winter wheat shoots mitochondria (Grabelnych et al. 2003, 2004). The present investigation studied the possibility of saturated fatty acids as the sole oxidation substrate for winter wheat shoots.

Materials and Methods. Three-day-old etiolated seedlings of the winter wheat cultivar Irkutskaya ozimaya were germinated on moist paper at 26°C. Mitochondria were extracted from winter wheat shoots by differential centrifugation and purified on Percoll gradient 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 activity was recorded polarographically at 26°C using a closed-type platinum electrode in a 1.4-ml cell (Estabrook 1967). The reaction mixture contained 125 mM KCl, 18 mM KH_2PO_4, 1 mM $MgCl_2$, and 5 mM EDTA, pH 7.4. Mitochondrial β-oxidation was initiated by addition to mitochondrial incubation medium of 0.5 mM L-carnitine, 0.2 mM ATP, 10 mkM CoA, 0.1 mM $MgCl_2$, and 10 mM malate. In our work, we used such saturated fatty acids as lauric (C12:0), palmitic (C16:0), stearic (C16:0), arachidic (C20:0), and lignoceric (C24:0) in concentrations from 1 mkM to 500 mkM. The concentrations of respiratory chain inhibitors used were 0.4 mM KCN and 1 mM benzhydroxamic acid (BHAM). The concentration of etomoxir (carnitine *O*-palmitoyltransferase I inhibitor) was 37.5 mkM. The concentration of mitochondrial protein was analysed by Lowry method (Lowry et al. 1951). All experiments were performed on 3–6 separate mitochondrial preparations. The data obtained were analyzed statistically and arithmetic means and standard deviations are presented.

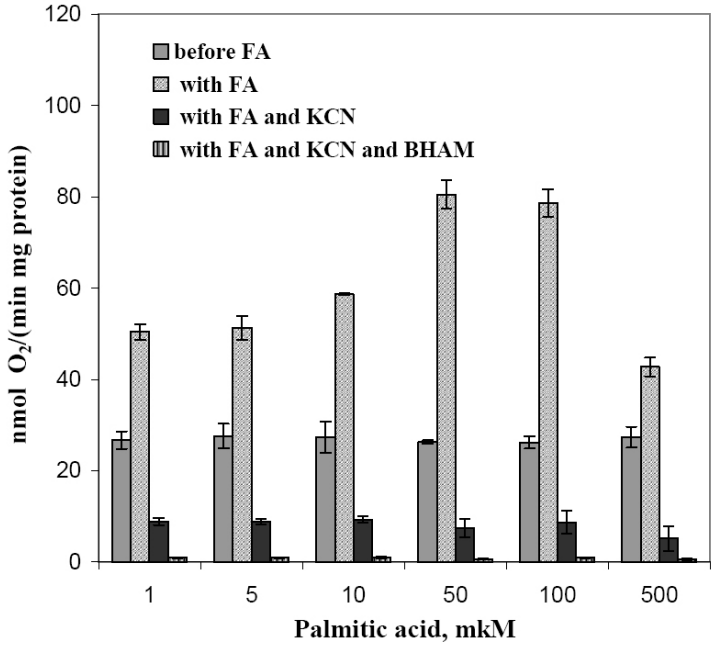

Fig. 1. The influence of palmitic acid on the consumption of oxygen in the mitochondria of winter wheat shoots. Winter wheat mitochondria (0.25 mg/ml) were suspended in reaction medium and respiration was initiated by fatty acid addition. Before FA, oxygen consumption rate of winter wheat mitochondria before fatty acid addition in presence of carnitine cycle and mitochondrial β-oxidation activators; with FA, oxygen consumption rate after fatty acid addition; with FA and KCN, oxygen consumption rate after addition KCN to mitochondria oxidizing fatty acid; and with FA and KCN and BHAM, oxygen consumption rate after subsequent BHAM addition. M±SD, *n=3-6*.

Results and Discussion. Previously, we found that the greatest uncoupling activity among studied saturated fatty acids had C12 and C16 acids. So it was interesting to study others roles of saturated acids in winter wheat mitochondria. We also found that unsaturated fatty acids, especially linoleic (18:2, n-9, 12) and α-linolenic (18:3, n-3) acids, could be used as a sole oxidation substrate for winter wheat shoots mitochondria. Here we show that saturated fatty acids could be used as a sole oxidation substrate for winter wheat mitochondria too.

All studied saturated fatty acids could not be used as oxidation substrate for winter wheat mitochondria without the addition of incubation medium substrates, which were necessary for mitochondrial β-oxidation and the carnitine cycle (Master-

son and Wood 2000a) and which was shown in the experiments when we did not add these substrates to the mitochondria incubation medium. In these experiments, no stimulation of respiration by winter wheat mitochondria occurred. But in experiments with the addition of L-carnitine, CoA, ATP, $MgCl_2$ and malate, mitochondria of the winter wheat shoots could use saturated acids as a sole oxidation substrate.

The possibility of using palmitic acid as an oxidation substrate for winter wheat mitochondria was shown in the presence of mitochondrial β-oxidation and carnitine cycle activators (Fig. 1. p. 124). The increasing rate of respiration depended on the palmitic acid concentration. The most significant increase in oxygen consumption by winter wheat mitochondria was observed after the addition of 50 and 100 mkM palmitic acid. The increase was 3-fold for both these concentrations. Higher concentrations of palmitic acid (500 mkM) did not cause significant increase in respiration rate. To determine how the cytochrome and alternative electron transport pathways participate during oxidation of saturated fatty acids, we studied the sensitivity of oxygen consumption induced by saturated fatty acid to such inhibitors of these pathways as KCN (that blocks electron transport through complex IV) and BHAM (that blocks electron transport through alternative CN-resistant oxidase). The palmitate-induced mitochondria respiration was sensitive to KCN and BHAM addition (Fig. 1, p. 124).

The use of stearic acid as an oxidation substrate for winter wheat mitochondria in presence of mitochondrial β-oxidation and carnitine cycle activators depended on concentration of this acid also (Fig. 2). The most significant increase in oxygen consumption by winter wheat mitochondria was observed after the addition of 50 and 100 mkM stearic acid. This increase was 3-fold and 3.6-fold for 50 and 100 mkM concentrations, respectively. Addition of KCN to winter wheat mitochondria oxidizing stearic acid caused full inhibition of respiration (Fig. 2).

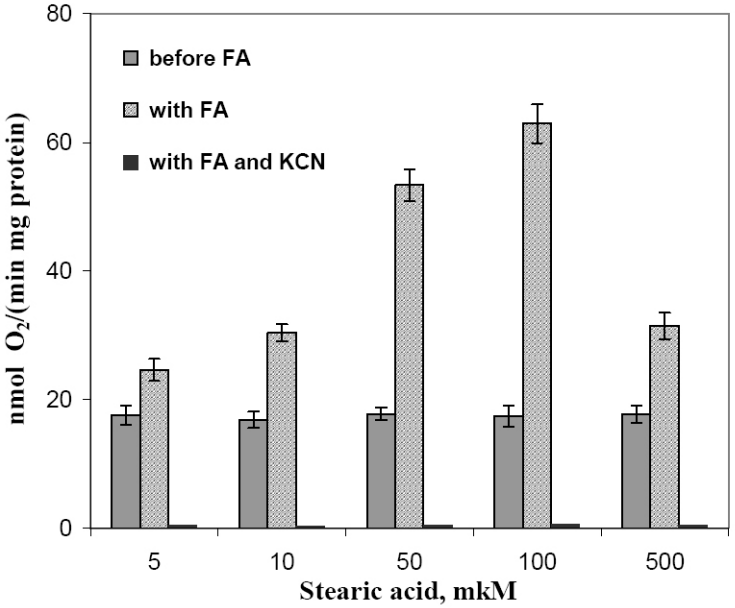

Fig. 2. Influence of stearic acid on the oxygen consumption of winter wheat shoots mitochondria. Winter wheat mitochondria (0.25 mg/ml) suspended in reaction medium and respiration was initiated by fatty acid addition. Before FA, oxygen consumption rate of winter wheat mitochondria before fatty acid addition in presence of carnitine cycle and mitochondrial β-oxidation activators; with FA, oxygen consumption rate after fatty acid addition; and with FA and KCN, oxygen consumption rate after addition KCN to mitochondria oxidizing fatty acid. M±SD, *n=3-6*.

We used etomoxir, which is irreversible inhibitor of carnitine *O*-palmitoyltransferase I (EC 2.3.1.21; CPT-I), the rate-limiting enzyme in the transport of long-chain fatty acids into mitochondrion, to prove that oxidation of saturated fatty acids associated with mitochondrial β-oxidation. The addition of etomoxir to winter wheat mitochondria oxidizing palmitic or stearic acid decreased the rate of oxidation caused by fatty acid addition (Fig. 3, p. 126). Sensitivity of mitochondrial respiration induced by palmitic or stearic acid oxidation to inhibitor of carnitine *O*-palmitoyltransferase I showed that oxidation of these acids was the result of classical β-oxidation process with carnitine cycle involvement. These data allow us to conclude that transport of palmitic and stearic acids into mitochondrial matrix involve carnitine shuttle system. Sensitivity of mitochondria respiration induced by palmitic or stearic acid oxidation to KCN and BHAM showed that during oxidation of these acids electrons could pass through cytochrome and cyanide-resistant pathways. We found that lauric (C12:0), arachidic (C20:0), and lignoceric (C24:0) acids could not be used as a sole oxidation substrate for winter wheat mitochondria even in presence of activators mitochondrial β-oxidation and carnitine cycle.

The data obtained allowed us to conclude that the mitochondria of winter wheat shoots could use saturated fatty acids as a sole oxidation substrate only in presence of mitochondrial β-oxidation and carnitine cycle activators. This means that oxidation of saturated fatty acids in winter wheat mitochondria is the result of classical mitochondrial β-oxidation with participation of carnitine shuttle systems. During mitochondrial β-oxidation of palmitic and stearic

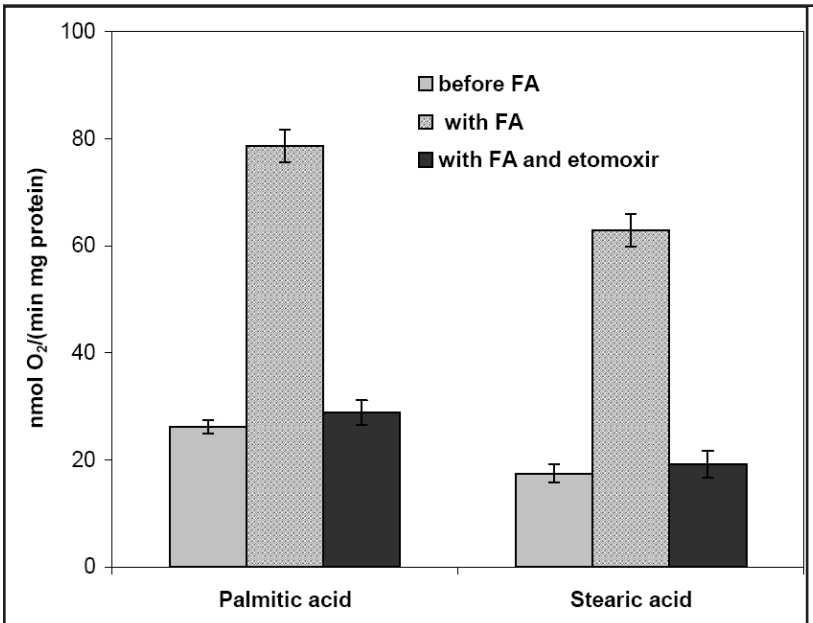

Fig. 3. Sensitivity of winter wheat mitochondria to oxygen consumption induced by palmitic acid or stearic acid oxidation to etomoxir. With FA, oxygen consumption rate after fatty acid addition; with FA and etomoxir, oxygen consumption rate after 37.5 mkM etomoxir addition to mitochondria oxidizing fatty acid. M±SD, *n=3-6*.

acids, electrons passed through the cytochrome and alternative pathways of mitochondrial electron transport chain.

Acknowledgements. This work was performed, in part, with the support of President Russian Federation grants for state support of leading scientific schools of Russian Federation (SS-4812.2006.4) and a young candidate of science of Russian Federation (YC-1876.2007.4), an interdisciplinary integration project of the Russian Academy of Sciences №47, and the Siberian Division of Russian Academy of Sciences Youth Grant (project 115).

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The sensitivity of winter wheat mitochondria swelling to inhibitors of ADP/ATP-antiporter and uncoupling proteins under stress conditions.

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The ADP/ATP-antiporter and uncoupling proteins (UCP) are integral proteins of inner mitochondrial membrane of plants and participate in induced by free fatty acid uncoupling of oxidative phosphorylation (Skulachev 1999; Bouillaud et al. 2001). 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). Moreover, the ADP/ATP-antiporter participates in formation of permeability transition pore (PTP) and in apoptotic processes of cell (Tsujimoto et al. 2006). PTP is opened by two modes: on the one hand, PTP is activated by Ca^{2+} ions and inhibited by cyclosporine A (CsA) and Mg^{2+} ions; on the other hand, PTP is a Ca^{2+} - independent and insensitive to CsA and Mg^{2+} ions (He and Lemasters 2002).

Our previous study showed that CsA-sensitive Ca^{2+}/palmitate-dependent mitochondrial PTP exists in mitochondria of the winter wheat seedlings (Pavlovskaya et al. 2007). Under conditions of cold stress and hardening, the mitochondrial pore functions as CsA-insensitive, whereas the oxidative stress followed short-term cold stress and cold hardening cause the appearance of mitochondria sensitivity to CsA (Pavlovskaya et al. 2007). Thus, different mechanisms seem to be responsible for the PTP function.

The aim of the present investigation was to study of swelling sensitivity from cold-stressed and cold-hardened winter wheat seedlings mitochondria to inhibitors of ADP/ATP-antiporter and uncoupling proteins and influence of oxidative stress on change of this sensitivity.

Materials and Methods. Three-day-old etiolated seedlings of the cold-resistant, winter wheat cultivar Zalarinka germinated on moist paper at 26°C were used. Seedlings were subjected to short-term (-1°C, 1 h) cold stress, cold hardening for 7 days at 4°C, oxidative stress, short-term (-4°C, 1 h) cold stress with subsequent oxidative stress or cold hardening for 7 days at 4°C with subsequent oxidative one. Oxidative stress was induced by immersing root tips of intact three days-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 seedlings shoots by differential centrifugation (Pobezhimova et al. 2001), and their swelling was 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 $MgCl_2$. Mitochondrial swelling was followed spectrophotometrically by the decrease in optical density (OD) of the mitochondrial suspension (0.25 mg/ml) under de-energized conditions at 26°C at 540 nm. We used the incubation medium including 200 mM KCl and 20 mM MOPS (pH 7.4). The following concentrations of test reagents were used: 0.1% bovine serum albumin (BSA) clear free fatty acids; 1 mkM carboxyatractyloside (Catr), an inhibitor of ADP/ATP-antiporter; and 1 мM GDP, an inhibitor of plant uncoupling mitochondrial proteins. The concentration of mitochondrial protein was analysed by Lowry method (Lowry et al. 1951). Results are represented as the mean of at least three determinations per experiment. The data obtained were analyzed statistically and arithmetic means and standard deviations are presented.

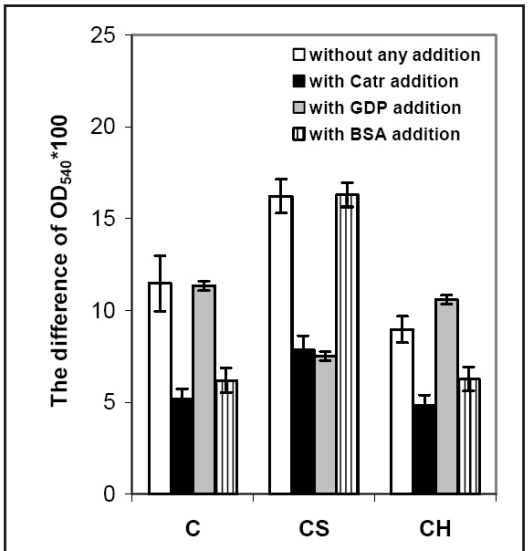

Fig. 4. The influence of inhibitors of ADP/ATP-antiporter and uncoupling proteins on the swelling of mitochondria from control (C), cold-stressed (-4°C, 1 h) (CS) and cold-hardened (4°C, 7 days) (CH) winter wheat shoots. The concentrations used were 1 mkM Catr, 1 mM GDP, and 0.1% BSA. The difference in optical density was calculated by formula $dOD=(OD_{t0} - OD_{t1})*100$, where OD_{t0} is the initial optical density and OD_{t1} the optical density after 5 min of incubation. M±SD, *n=3-6*.

Results and Discussion. In experiments with incubation of mitochondria isolated from control winter wheat seedlings with Catr, we detected the decrease in optical density of mitochondrial suspension in 5 min of incubation about 46.0% whereas GDP did not influence (Fig. 4). After BSA addition we observed the decrease of swelling extent mitochondria about 46.0% (Fig. 4).

The short-term cold treatment of seedlings was accompanied by increase of mitochondrial swelling extent and change of its sensitivity to studying inhibitors (Fig. 4, p. 127). The decrease of swelling after 5 min of incubation with Catr and GDP was 51.7% and 53.6%, respectively. After BSA addition to mitochondria incubation medium swelling extent of these organelles did not change (Fig. 4, p. 127). The extend of the decrease of mitochondrial swelling under the action of uncoupling proteins and ADP/ATP-antiporter inhibitors pointed to contribution of these proteins in response to short-term cold stress. If in mitochondria of control seedlings the action of GDP on swelling was absent, then its influence on mitochondrial swelling from seedlings subjected to cold stress pointed to important role of uncoupling proteins under conditions of cold stress. The absence of the influence of BSA on mitochondrial swelling was explained by increase of free fatty acid content during cold stress. We believe that used BSA concentration (0.1%) is not sufficient for binding these free fatty acids.

The cold hardening of seedlings led to a decrease in swelling isolated from mitochondria, however, the action of Catr, GDP, and BSA was similar to their actions in control mitochondria (Fig. 4, p. 127). These data indicated that only ADP/ATP-antiporter participated in swelling of winter wheat mitochondria caused by actions of free fatty acids during cold hardening as well as non-stressed conditions.

The oxidative stress caused by treatment of seedlings with a 0.5 mM solution of H_2O_2 did not accompany changes in mitochondrial volume. After the addition Catr to mitochondria incubation medium, seedlings subjected to oxidative stress we observed significant decrease of swelling (81.5%), whereas BSA caused only a 43.9% decrease in swelling; GDP did not influence (Fig. 5). These data indicated important role of ADP/ATP-antiporter during oxidative stress. Short-term cold stress and cold hardening of seedlings after subsequent oxidative stress was not accompanied by significant changes of volume isolated of them mitochondria (Fig. 5). The action of used inhibitors on mitochondrial swelling was similar to the action of these inhibitors on mitochondrial swelling from seedlings subjected to oxidative stress only. In both cases, the additions of Catr and BSA led to decrease of mitochondrial swelling extent whereas GDP did not have such influence (Fig. 5). These data prove that, under combined actions of two stress factors, the ADP/ATP-antiporter and uncoupling proteins contribution to mitochondrial swelling differed from one that of an individual stress factor.

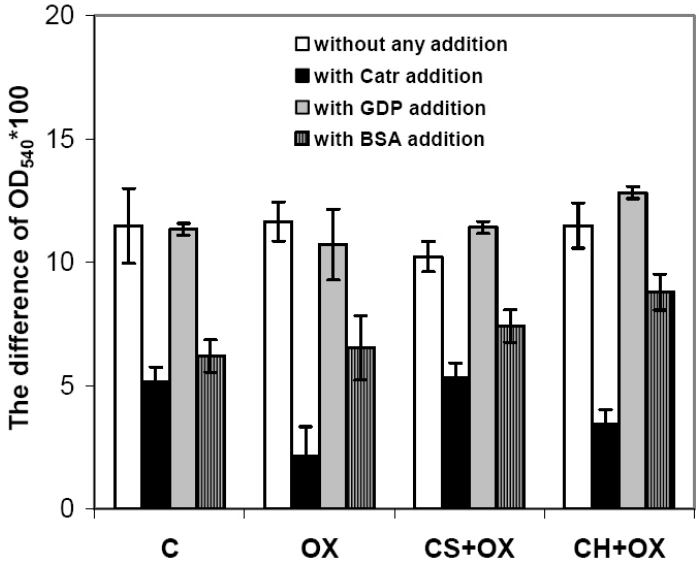

Fig. 5. The influence of inhibitors of ADP/ATP-antiporter and uncoupling proteins on the swelling of mitochondria from control (C), oxidative-stressed (0.5 mM H_2O_2, 4 h) (OX), cold-stressed (-4°C, 1 h) with subsequent oxidative stress (0.5 mM H_2O_2, 4 h) (CS+OX), and cold-hardened (4°C, 7 days) with subsequent oxidative stress (0.5 mM H_2O_2, 4 h) (CH+OX) winter wheat shoots. The concentrations used were 1 mkM Catr, 1 mM GDP, and 0.1% BSA. The difference in optical density was calculated by formula $dOD=(OD_{t0} - OD_{t1})*100$, where OD_{t0} is the initial optical density and OD_{t1} the optical density after 5 min of incubation. M±SD, *n=3-6*.

Our data indicate that ADP/ATP-antiporter participated in stimulated by free fatty acids swelling both in mitochondria from control winter wheat seedlings and in mitochondria from seedlings subjected to cold and oxidative stresses. The uncoupling proteins participated in mitochondria swelling process only during short-term cold stress when increase of free fatty acids occurred (Vojnikov et al. 1983). Because the CsA-sensitive pore functions in mitochondria of the winter wheat seedlings (Pavlovskaya et al. 2007), then ADP/ATP-antiporter contribution to mitochondrial swelling can suppose that this carrier can be involved to this pore formation.

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Defensins of Triticum urartu and T. monococcum subsp. aegilopoides seed.

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Plants have evolved diverse mechanisms to combat fungal and bacterial infections. The most important among them are the reinforcement of plant cell walls and the release of different components with antimicrobial properties. They comprise the reactive oxygen species, phytoalexins, and PR-proteins including antimicrobial peptides (AMPs) (Selitrennikoff 2001; Garcia-Olmedo et al. 2001).

Defensins are the most conserved cysteine-rich AMPs which were found in nearly all taxa of living organisms: invertebrates, vertebrates, plants and fungi (Thomma et al. 2002). Plant defensins are small (45–54 amino acid residues), basic peptides with four disulphide bridges. Despite a conserved scaffold, the amino acid sequences of defensins vary considerably with only eight cysteine residues being conserved. Variation in amino acid sequences most likely accounts for diverse biological functions displayed by different members of the family. By *in vitro* studies, defensins were shown to exhibit antifungal/antibacterial and insecticidal activities, some of them inhibit enzymes, others act as ion channel

blockers (Broekaert et al. 1995; Lay and Anderson 2005). Defensins were demonstrated to be associated with resistance to abiotic stress (Koeke et al. 2002; Mirouze et al. 2006). Some defensins are constitutive components of plant cells, while others are induced upon challenge with pathogens or stressful abiotic factors. Defensins show promise for creation of resistant plants and the development of new drugs in medicine as an alternative to conventionally used antibiotics and antimycotics.

In our previous studies, we studied defensins from seeds of *T. kiharae*, a synthetic allopolyploid produced by crossing *T. timopheevii* with *Ae. tauschii*, and related *Triticum* and *Aegilops* species (Egorov et al. 2005; Odintsova et al. 2006). We have focused our attention on defensins of *T. monococcum* subsp. *aegilopoides* and *T. urartu*, the presumable A-genome donors to polyploid wheats and compared their structure and complexity with defensins from *T. kiharae*.

Materials and Methods. The species used in this study were *T. monococcum* subsp. a*egilopoides* from Azerbaidzhan, *T. urartu* from Syria, and *T. kiharae*. Flour was extracted with a mixture of two acids (1 M HCl and 5% HCOOH) for 1 h at room temperature and desalted on an Aquapore RP300 column. Freeze-dried acidic extract was subjected to chromatography on Heparin Sepharose. Proteins and peptides were eluted with a stepwise NaCl gradient. The 100-mM NaCl fraction was collected, desalted as described above and separated on a Superdex Peptide HR 10/30 column (Amersham, Pharmacia, Biotech, Uppsala, Sweden). Proteins and peptides were eluted with 0.05% TFA, containing 5% acetonitrile at a flow rate of 250 µl/min, and monitored by absorbance at 214 nm. The peptide fraction was further separated by RP-HPLC on a Vydac C18 column (4.6 x 250 mm, particle size 5 µm) with a linear acetonitrile gradient (10–50%) for 1 h at a flow rate of 1 ml/min and 40°C. Peptides were detected at 214 nm. Mass spectra were acquired on a model Reflex III mass spectrometer (Bruker Daltonics, Bremen, Germany). N-terminal amino acid sequences were determined by automated Edman degradation on a model 492 Procise sequencer (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's protocol.

Results and Discussion. For the isolation of defensins from the diploid species, we followed the procedure earlier developed for the isolation of *T. kiharae* defensins (Egorov et al. 2005; Odintsova et al. 2006). Acidic extraction of flour was followed by subsequent separation of the protein-peptide extract by a combination of different types of HPLC (affinity, size-exclusion and reversed-phase). Defensins were identified on the basis of their retention time from the RP-HPLC column, mass-spectrometric analysis and, in some cases, N-terminal sequencing of the reduced and alkylated peptides. In *T. monococcum* subsp. *aegilopoides* seeds, the following defensins were found: D1.1, D1.2, D2, and a D3 homologue; its N-terminal amino acid sequence coincided with that of D3, although its molecular mass was different (Table 1).

Table 1. Defensins identified in *T. monococcum* subsp. *aegilopoides* seed.

RP-HPLC fraction number	N-terminal amino acid sequence	Molecular mass (Da)	Peptide
1	RDCESDSH	5130	Tk-AMP-D1.1
2	RTCQSQSH	5692	Tk-AMP-D1.2
3	RTCESQSHKF	5692	Tk-AMP-D2
4	RDCKSDSHKFHGACF	4859	Tk-AMP-D3 homologue

Table 2. Defensins identified in *T. urartu* seed.

RP-HPLC fraction number	N-terminal amino acid sequence	Molecular mass (Da)	Peptide
1	RDCESDSH	5130	Tk-AMP-D1.1
2	RTCQSQSH	5736	Tk-AMP-D1
3	RTCESQSHKF	4980	Tk-AMP-D4
4	RDCKSDSHKFHGACF	5151	Tk-AMP-D5

The molecular mass analysis of the main fractions obtained by size-exclusion chromatography of *T. urartu* samples from Syria revealed the molecular masses characteristic of D1, D1.1, D4, and D5. The identity of these peptides to the above-mentioned defensins was confirmed by sequencing (Table 2).

Analysis of the data obtained showed that *T. monococcum* subsp. *aegilopoides* defensins differed considerably both from those of *T. urartu* and *T. monococcum*. In this species, we discovered D1.1, D1.2, D2, and a D3 homologue. Defensin D3 and its homologues were not found in *T. monococcum* and *T. urartu*, they we identified earlier in the species of the *Aegilops, Ae. tauschi* and *Ae. speltoides*, respectively (Odintsova et al. 2007).

In summary, our data on the array and amino acid sequences of D defensins provide new evidence for the closer relationship between the polyploid wheat *T. kiharae* and *T. urartu* than with *T. monococcum* subsp. *aegilopoides*. Of particular interest are that the amino acid sequences of D defensins are highly conserved and persisted for about 10 thousand years that followed from the origin of polyploid forms. This observation provides strong evidence in favor of vital functions of this AMP family in plants.

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ITEMS FROM THE REPUBLIC OF SOUTH AFRICA

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Triticale breeding.

Widespread stem rust and leaf rust infections occurred during 2007. All our established commercial cultivars proved to be highly susceptible and are being phased out. However, the recently released cultivar US2007 remained completely resistant. Another advanced line (to be named AgBeacon) that also has complete resistance and excellent yield potential is being multiplied for release in 2009 and has the pedigree: Massa/Nimir 3/3/Yogui 1/Tarasca 87 3// Hare 212/4/Ibis/8/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.

New material developed in each phase of the program included approximately 60,000 new, potentially different F_1 genotypes. For the second year, an F_7 nursery consisting of 204 pure lines was distributed to local breeders (PANNAR, SGI, Monsanto, Cengen, and Afgri-Seed). The same material was evaluated in Uganda for resistance to the UG99 stem rust virulence. A genotyping system (microsatellite and AFLP loci) to distinguish F_6 inbred lines from one another and from released commercial cultivars was tested and found to discriminate among the majority of lines.

Genetic studies.

Chromosomal mapping of rust-resistance genes derived from wild *Triticum* species were continued, including the last two of a number of leaf and stripe rust-resistance genes transferred in the wide-crosses program: (i) linked leaf and stripe rust-resistance genes (*LrS20*/*YrS20*) from *Ae. neglecta* were mapped to chromosome 6A using microsatellites and monosomic and telosomic analyses and (ii), monosomic analyses to determine the location of a leaf rust resistance gene (*Lrmac*) derived from *Ae. biuncialis* are being completed.

Attempts to reduce the amount of foreign chromatin associated with genes that were transferred earlier, were continued. (i) Following allosyndetic pairing induction, resistant testcross F_1 involving the *Lr59* (*Ae. peregrina*), *Lr56*/*Yr38* (*Ae. sharonensis*) and *LrS20*/*YrS20* (*Ae. neglecta*) translocations are being screened with appropriate microsatellite markers to physically map each translocation and to identify the most useful recombinants. (ii) Crosses to shorten the *Lr54*/*Yr37* translocation (*Ae. kotschyi*) thus far yielded ten recombinants. The shortest of these, S14-74, appears to have retained both resistances but has lost an associated dwarfing (*Rht*) gene. An attempt is being made to find a suitable STS marker for S14-74. (iii) Four putative recombinants of a translocation (carrying resistance genes *LrS13*/*SrS13* as well as linked gametocidal genes) derived from *Ae. speltoides* were physically mapped. Recombinant 04M127-3A is the most useful and is, therefore, being tested for presence of gametocidal genes and to determine if it can be shortened further.

A strategy to transfer genes for salt tolerance from *Th. distichum* chromosomes $2J_1^d$, $3J_1^d$, $4J_1^d$, and $5J_1^d$ to wheat and triticale was continued. (i) Putative triticale translocations involving $3J_1^dS$ and $3J_1^dL$ were tested for their ability to complement addition chromosome $2J_1^d$ in salt-tolerance tests. The $3J_1^dS$ translocation may carry the salt tolerance gene(s) associated with chromosome $3J_1^d$. Testcross progeny are being screened in an attempt to also find translocations involving $2J_1^d$. (ii) Triticale addition lines of chromosomes $2J_1^d$, $3J_1^d$, $4J_1^d$, and $5J_1^d$ also are being used to identify further AFLP and SSR marker loci for these chromosomes.

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Effects of introgressed 4N^v Aegilops ventricosa chromosome on yield and yield components in bread wheat.

The wild grass *Ae ventricosa* is an allotetraploid (2n=28; genomes D^{v}D^{v}N^{v}N^v) and has attracted considerable attention as a source of genes for resistance (RG) to pathogens such as insect and fungi. Genetic material from *Ae. ventricosa* has been transferred to hexaploid wheat through an intermediate self-sterile hybrid between *T. turgidum* and *Ae. ventricosa*, which was backcrossed using pollen from hexaploid wheat. The progeny were repeatedly selfed to obtain 42-chromosome, stable lines. One line, H-93-33 (4D/4N^v substitution), carried the genes *Pm* and *H27*, which confer resistance to powdery mildew and Hessian fly, respectively (Mena et al. 1988; Delibes et al. 1997). Introduction of these RGs from line H-93-33 into the commercial wheat cultivars Adalid and Astral was by backcrossing. Marker-assisted selection used the isozyme *Acph-N^{v}1*, which is linked to genes *H27* and *Pm* on 4N^v chromosome (Delibes et al. 1987, 1997). $BC_{4-6}F_4$-$BC_{4-6}F_9$ lines were evaluated against Hessian fly in Azuaga (38º14'N, 5º40'W) from 2000 to 2006; and $BC_{4-6}F_6$ lines were evaluated against powdery mildew in 2002 in Gimenells (41º39'N, 0º25'E). Lines with the *Acph-N^{v}1* marker were resistant to both Hessian fly and powdery mildew.

These lines, with and without *Acph-N^{v}1* marker, also were evaluated from 2000 to 2007 for grain yield in several Spanish localities under irrigated and unirrigated conditions. Averaged across the different genetic backgrounds and 18 different environments, the 4N^v introgression decreased grain yield by 17%. The effect of 4N^v introgression on grain yield, yield components, (evaluated as described by Bell and Fisher 1994), and quality was studied over five growing seasons (2000–05) in Gimenells under irrigated conditions. Averaged across the different genetic backgrounds and years, the 4N^v introgression decreased the fertile spike number/m^2 by 12.8 %, and kernels/spike by 7.8 % but increased kernel weight by 9.3 % and protein content by 12.4%. Bread making (determined by alveograph parameters, W, P, L, and P/L) was not affected significantly by the introgression. The isolines also differed in heading date. Lines without the introgression were 1 to 2 days earlier than those without.

The effects of *H27* and insecticide treatment for the control of Hessian fly were compared. Three pairs of NILs differing at the *H*27 gene were evaluated with and without insecticide Diazinon. The field trial was conducted in the 2005–06 growing season in Azuaga. Hessian fly damage was estimated visually by incidence of broken tillers on the second spring generation. The effect of insecticide on lines with *H*27 gene was not significant. Moreover, lines carry-

ing *H*27 gene had a lower incidence of broken tillers (P<0.01) than respective isolines without RG, thus *H*27 was more effective on the control of flies than insecticide treatment.

The effects of *Pm* and fungicide treatment to control powdery mildew on yield, yield components, and quality also were compared. The same three pairs of NILs used above, which differ at the *Pm* gene, were evaluated with and without fungicide (Cyproconazole plus Tiophanate-methyl). Field trials were conducted in the 2005–06 and 2006–07 growing seasons in Gimenells. Grain yield was 35.8% greater in 2007 than in 2006. In both years, treated plots yielded more than untreated plots. The decrease in yield in plots untreated (in relation with treated) was lower (4.7%) in lines with the $4N^v$ introgresion than in lines without introgression (8.7%). As expected, the *Pm* gene had some effect in controlling disease. Protein content was not affected by fungicide treatment, but it was affected positively by the introgression. Bread making was not affected by the introgression or fungicide treatment.

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Peroxidase expression in a cereal cyst nematode (Heterodera avenae) resistant hexaploid wheat line.

The incompatible interaction between plant and pathogen is often determined by the hypersensitive reaction (HR). This response is associated with accumulation of reactive oxygen species (ROS), which results in adverse growth condi-

tions for pathogens. Two major mechanisms involving either NADPH oxidases or peroxidases have been proposed for generation of ROS. Peroxidases (PER, EC 1.11.1.7), present in all land plants, are members of a large multigenic family with high number of isoforms involved in a broad range of physiological processes.

PER genes, which are expressed in nematode feeding sites, have been identified in several plant species (Zacheo et al. 1997). A strong correlation between HR and PER activities at four and seven days post nematode infection, was detected in roots of wheat lines carrying *Cre2, Cre5* (from *Ae. ventricosa*) or *Cre7* (from *Ae. triuncialis*) *Heterodera avenae* resistance genes (Andrés et al. 2001; Montes et al. 2003, 2004).

We have studied changes in root of peroxidase mRNAs levels after infection by *H. avenae* of a wheat/*Ae. ventricosa* introgression line (H-93-8) carrying *Cre2* (Delibes et al. 1993). We also report and classify the predicted protein sequences derived from complete peroxidase transcripts.

Materials and Methods. Seedlings from the resistant line (H-93-8), obtained from the cross [(*T. turgidum* cv. Rubroatum, H-1-1/*Ae. ventricosa*, AP-1)//*T. aestivum* cv. Almatense, H-10-15] (Delibes et al. 1993) were inoculated with pathotype Ha71 of *H. avenae*. Root sections and leaves were harvested 4 and 7 days-after-infection; uninoculated tissues served as controls. Total RNA was extracted using the method of Båga et al. (1995). PER cDNAz were synthesized using 3´RACE a Superscript™ one-step RT-PCR kit (Invitrogen Life Technologies, San Diego, CA) and a 5´RACE SMART™ RACE cDNA Amplification Kit (Clontech Laboratories, Inc, Mountain View, CA) kit according to the manufacturer's recommendations. Primers from conserved regions of plant peroxidase genes were used for second cDNA synthesis and PCR. Preferential amplification of different PER sequences was obtained with primers designed from low-sequence-homology areas. Amino acid sequences were derived from the coding regions and aligned using MultAlign program (Corpet 1988). A distance-based tree was constructed by NEIGHBOR Joining with MEGA version 3.1 (Kumar et al. 2004).

The expression levels of each PER group in inoculated roots and uninoculated controls were determined by qRT-PCR. Primers for each peroxidase cluster were designed using Primer Express 2.0 software (PE Applied Biosystems, Foster City, CA). PCRs were performed using Power SYBR® Green PCR Master Mix (PE Applied Biosystems, Foster City, CA) according to the manufacturer's instructions in a ABIPRISM 7300 Detection System and software (PE Applied Biosystems, Foster City, CA).

Results and Conclusions. Comparative analysis of the amino acid sequences predicted from cDNAs revealed that they contain conserved structural features and activity sites of typical class III peroxidases. The distance tree of wheat line H-93-8 peroxidases was organized in five major clusters of homologous genes (*Pox1*, *Pox2*, *Pox3*, *Pox4,* and *Prec1*; Fig. 1), strongly supported by Bootstrap values. Interestingly, two members from rice peroxidase group IV (BAC79531.1, BAC83103.1, Passardi et al. 2004), which resulted equivalent to pathogen inducible proteins (Chittoor et al. 1997), were closely related to *Pox1*, *Pox2*, and *Pox3*.

Both with and without attack, all PER groups showed weak expression profiles in leaves. PER classified as *Pox1*, *Pox2*, and *Pox3* exhibited enhanced expression in infected roots when compared to noninoculated controls. Nematode infection apparently did not alter the expression pattern of *Pox4*, *Prec1*, and *Putper* in roots. The *Pox3* cluster showed the highest levels of transcription, independently of attack.

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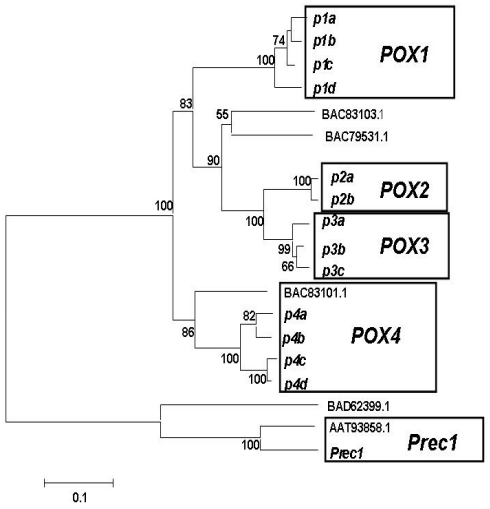

Fig. 1. Unrooted phylogenetic tree of wheat line H-93-8 PER based on predicted protein sequences and its relationships with representative rice peroxidases (GenBank accession numbers: AAT93858.1, BAD62399.1, BAC83101.1, BAC79531.1, BAC83103.1). The tree was constructed by the NEIGHBOR joining method. Values at nodes indicate Bootstrap supports greater than 50 %.

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Release of Mapeña spring bread wheat.

Mapeña is a spring bread cultivar released in 2007 carrying the *Cre*7 resistance gene to *H. avenae* transferred from *Ae. triuncialis* (Romero et al. 1998). The cultivar was developed from the cross 'TR-353/Betres//Alcotán/3/Rinconada/4/3*Betres' under the designation ID-2181. Mapeña is a high-yielding, medium maturing, semidwarf cultivar with moderate resistance to leaf rust, yellow rust, powdery mildew, and Septoria. This cultivar is better adapted to the southern and northeastern wheat growing regions of Spain. Mapeña has good quality properties for baking industry and is registered in the Spanish Catalogue of Commercial Plant Varieties (BOE, 2008).

Coöperation with other institutions.

We are coöperating with Agrosa Semillas Selectas SA.

Personnel.

Dr. Guillermo Briceño-Felix left the bread wheat program in the UdL-IRTA Center. Dra. María Dolores Romero has just retired from Consejo Superior de Investigaciones Cientificas.

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Karyotype characterization of wheat breeding lines carrying resistance genes from Aegilops ventricosa.

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We have used in situ hybridization combining genomic and repeated DNA fluorescent probes to determine the karyotype composition of two bread wheat introgression lines: H-93-33, which carries the gene *H27* for resistance to the Hessian fly *M. destructor* (Delibes et al. 1997); and H-93-8, carrying the gene *Cre2* which confers resistance to the cereal cyst nematode *H. avenae* (Delibes et al. 1993). Both introgression lines had been derived from an earlier cross between *T. aestivum* subsp. *aestivum* (2n=42; genome composition AABBDD) and a semi-fertile hybrid between *T. turgidum* subsp. *turgidum* (2n=28; genome composition AABB) and the wild grass *Ae. ventricosa* (2n=28; genome constitution $D^vD^vN^vN^v$). We also have examined several resistant advanced lines that were obtained from H-93-33 (lines ID-2151, ID-2193, Ma-1612-a and Ma-1612-b) or H-93-8 (line ID-2150) after 3 to 5 backcrosses with commercial wheats.

The ISH protocol was essentially as described in Sánchez-Morán et al. (2001). Three different DNA probe combinations were separately hybridized on mitotic slides from each of those breeding lines. The first mix contained differentially labelled A- and S-genome DNA probes, and D-genome DNA blocking. A second mix contained differentially labelled A- and D-genome DNA probes, and S-genome DNA blocking. These two probe combinations revealed the number of chromosomes belonging to the A and B genomes of wheat and to the D genome from either wheat or *Ae. ventricosa*. The third mix was primarily designed to reveal the suspected presence of N^v-genome chromosomes in those lines, which contained chromosome pairs that had been blocked by any of the two former probe combinations. This mix contained differentially labelled D- and N-genome DNA probes with durum wheat (AB) DNA was added as blocking. This mix also included the ribosomal DNA probe pTa71 and the repeated DNA probe pAs1 (Rayburn and Gill 1987). The latter probe provides a distinctive ISH pattern for individual D-genome chromosomes in wheat (Pedersen and Langridge 1997) and *Ae. ventricosa* (Badaeva et al. 2002). A summary of the karyotype findings in the lines examined is described here (Tables 1 and 2).

Table 1. Chromosome constitution of the bread wheat breeding lines. The D genomes of wheat and *Ae. ventricosa* are pooled in column D. An * indicates the genome includes a D-N translocation).

	Genome			
Line	A	B	D	N
H-93-33	14	14	12	2
ID-2151	14	14	14	0
ID-2193	14	14	14*	2*
Ma-1612-a	14	14	12	2
Ma-1612-b	14	14	14	0
H-93-8	12	14	12	4
ID-2150	14	14	14	0

Table 2. Identification of individual chromosomes in the breeding lines. A + indicates presence and a – indicates absence; T^1 is the translocation 4DS-4NS.4NL and T^2 is the translocation 5DS.5DL-$5D^vL$.

	Wheat							*Ae. ventricosa*	
Line	1D	2D	3D	4D	5D	6D	7D	D^v	N^v
H-93-33	+	+	+	-	-	+	-	$3D^v$, $5D^v$	$4N^v$
ID-2151	+	+	+	+	+	+	+	0	0
ID-2193	+	+	+	T^1	+	+	+	0	T^1
Ma-1612-a	+	+	+	-	+	+	+	0	$4N^v$
Ma-1612-b	+	+	+	+	+	+	+	0	0
H-93-8	+	+	-	-	T^2	+	-	$3D^v$, $4D^v$, T^2	$5N^v$, $7N^v$
ID-2150	+	+	+	+	+	+	+	0	0

H-93-33 and derived lines. The ISH analysis confirmed the existence of a $4N^v$(4D) substitution in H-93-33, which had been proposed from earlier biochemical and cytological analy-

ses (Mena et al. 1989). Comparison between the ISH patterns of pAs1 found in this line and those reported by Pedersen and Langridge (1997) and Badaeva et al. (2002) undoubtedly demonstrated the presence of additional *Ae. ventricosa* introgressed chromosomes, i. e., a 5D^{v}(5D) substitution and the replacement of wheat 7D by its nonhomoeologous 3D^{v}. None of these D^{v} genome introgressions is maintained in any of the Hessian fly resistant lines derived from H-93-33 that were checked. However, the 4N^{v}(4D) substitution has been transmitted to line Ma-1612-a, and a large part of the long arm of this alien chromosome is still present in a 4D-4N^{v} translocation detected in line ID-2193. These findings confirm former data indicating that gene *H27* is linked to Acph-N^{v}1, a molecular marker located on 4N^{v} (Delibes et al. 1997).

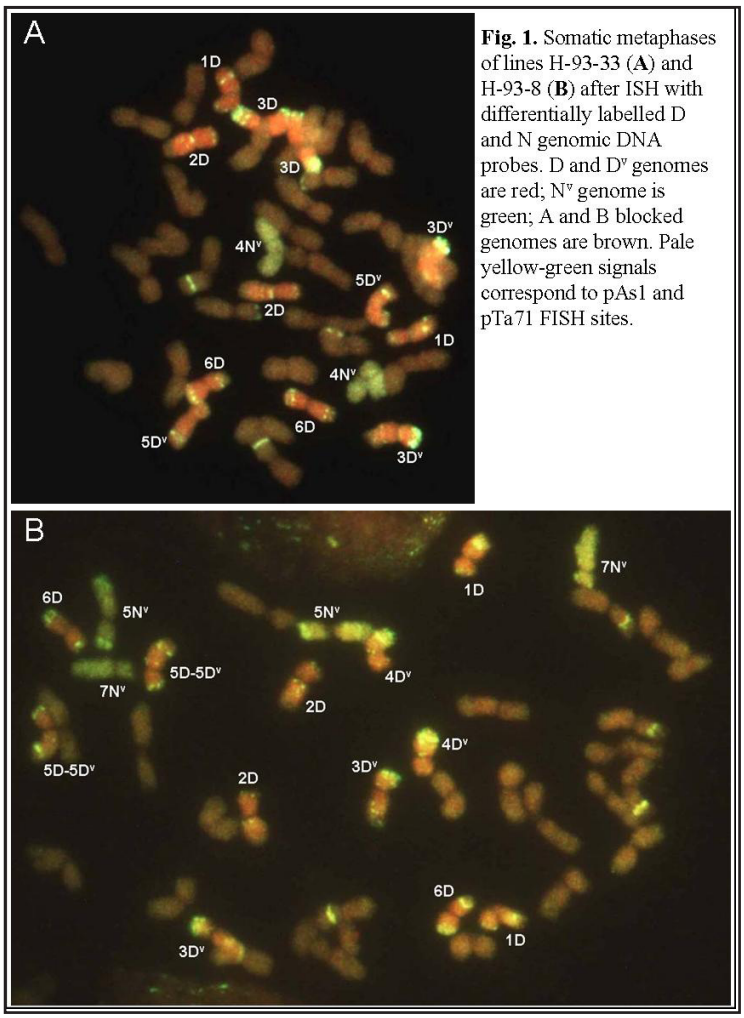

Fig. 1. Somatic metaphases of lines H-93-33 (**A**) and H-93-8 (**B**) after ISH with differentially labelled D and N genomic DNA probes. D and D^{v} genomes are red; N^{v} genome is green; A and B blocked genomes are brown. Pale yellow-green signals correspond to pAs1 and pTa71 FISH sites.

H-93-8 and derived lines. Previous results had proposed a double substitution in line H-93-8: 5N^{v}(5A) and 7N^{v}(7D) (Mena et al. 1993). The ISH analysis has demonstrate the presence of 5N^{v} and 7N^{v} and the absence of 7D in this introgression line, although it could not be confirmed that 5A is the A-genome pair absent in this line. Two additional substitutions (3D^{v}(3D) and 4D^{v}(4D)) and a 5D-5D^{v} translocation that were not previously detected by molecular marker approaches have been also cytologically evidenced (Fig. 1B). None of these alien chromosomes or translocations appears in the advanced line ID-2150, whose ISH karyotype is indistinguishable from that of bread wheat.

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Characterization of endosperm proteins and bread-making quality in wheat breeding lines carrying resistance genes for Mayetiola destructor and/or Heterodera avenae.

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The experimental material included thirteen bread wheat-breeding lines that carry genes for resistance to *M. destructor* and/or *H. avenae*. The sources of these resistances are the wild species *Ae. triuncialis* and *Ae. ventricosa* (lines TR and H-93, respectively) (Delibes et al. 1993, 1997; Romero et al. 1998). We have determined the composition in HMW-glutenin subunits (related with bread-making quality), puroindoline proteins (related with hardness of grain), and waxy proteins (related with starch viscosity). In addition to, we analysed the bread-making quality and some agronomic parameters of the lines. A previous analysis of prolamins by electrophoresis SDS-PAGE indicated the homogeneity of the lines.

Glutenins were extracted from crushed endosperm (Singh et al. 1991) and the extracts fractionated by SDS-PAGE electrophoresis (Payne et al. 1980). Waxy proteins were extracted from the flour, and electrophoresis was performed as described by Rodríguez-Quijano et al. (1998). Puroindoline allelic composition was obtained by DNA isolation (Dellaporta et al. 1983) and PCR amplification of pinA and pinB coding regions with specific primers (Giroux and Morris 1997).

Gluten strength was estimated by the SDS-sedimentation (SDSS) test (Mansur et al. 1990). Protein was measured with a NIR spectroscope (Infra-lyzer 300). Mixing time (MT), and resistance to breakdown (BDR) were determined using 10 g of flour and a National Manufacturing Co. Mixograph apparatus (Lincoln, NE), as described by Finney and Shogren (1972). Starch viscosity was analysed by a Rapid Visco Analyser (RVA-3D, Newport Scientific, Pty. Ltd.) and the viscosity peak (VP) parameter was derived from the RVA curve. All parameters were measured twice. Line Ma-99-75-5 (H93) was not tested because the amount of material was insufficient.

The results indicate variability for proteins in the breeding lines (Table 3). Regarding to bread-making quality, four lines stand out for their high dough strength: ID-2193, ID-2151, ID-2004 and Ma-99-93-1 (Table 3). Lines ID-2193 and Ma-99-93-1 are resistant for *M. destructor*, line T-2004 carries resistance genes for both *H. avenae* and *M. destructor* while line ID-2151 lacks resistance genes.

According to their composition in puroindoline proteins, the lines were identified as having a 'soft' or 'hard' endosperm (Table 3). This is an important classification to determine their final use since the hard wheat varieties are the most valuable in bread-making industry. Among the lines with good bread-making quality, three are hard and one is soft (Table 3).

Table 3. Genetic composition of the breeding lines.

Breeding line	Locus and HMW-glutenin subunits				Locus and alleles of waxy proteins		
	Glu-A1	*Glu-B1*	*Glu-D1*	Hardness	*Wx-A1*	*Wx-D1*	*Wx-B1*
ID-2181 (TR)	2*	17+18	5+10	Hard	*a*	*a*	*a*
T-2003 (TR)	1	7*+9	5+10	Hard	*a*	*a*	*a*
T-2004 (TR)	2*	6+8	5+10	Hard	*a*	*a*	*b*
T-2105 (TR)	2*	17+18	5+10	Hard	*a*	*a*	*b*
ID-2193 (H93)	1	7*+8	2+12	Hard	*a*	*a*	*a*
ID-2150 (H93)	1	7*+9	5+10	Hard	*a*	*a*	*a*
ID-2151 (H93)	1	7*+8	2+12	Soft	*a*	*a*	*a*
Ma-1612a (H93)	1	7*+8	2+12	Hard	*a*	*a*	*a*
Ma-1612b (H93)	1	7*+8	2+12	Hard	*a*	*a*	*a*
Ma-99-75-5 (H93)	1	7*+8	2+12	Hard	*a*	*a*	*a*
Ma-99-93-1 (H93)	1	7*+8	2+12	Hard	*a*	*a*	*a*
Ma-99-41-6 (H93)	Null	7*+8	2+12	Soft	*a*	*a*	*a*
Ma-99-104 (H93)	1	7*+8	2+12	Soft	*a*	*a*	*a*

The waxy protein analysis has revealed that two lines posses the null allele (*b*) for the *Wx-B1* locus. Yamamori et al. (1992) related the presence of null alleles with less amylose content on bread wheat starch. The ratio amylose/amylopectin is very important in relation to the end use of any variety. Oda et al. (1980) determined that the noodles made of flour that are low in amylose were the favourites of Japanese consumers. High viscosity peak from

RVA correlates with a lower content in amylose. The highest values for the VP parameter are found in the lines ID-2150, Ma-99-93-1, ID-2181, T-2004 and T-2105 (Table 4). These two latter lines are those having the null allele at the *Wx-B1* locus (Table 3, p. 140).

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Table 4. Quality parameters of the breeding lines.

Breeding lines	% Protein (14% Hum)	SDSS (mm)	Mixograph analysis		Starch viscosity VP (RVU)
			MT (s)	BDR (%)	
ID-2181 (TR)	9.9	71.0	156.0	15.4	306.6
T-2003 (TR)	10.5	67.0	120.0	27.7	275.6
T-2004 (TR)	11.4	86.5	165	13.3	301.9
T-2105 (TR)	9.9	79.0	90.0	17.2	313.9
ID-2193 (H93)	9.5	94.0	110.0	18.3	280.7
ID-2150 (H93)	8.9	65.5	150.0	15.4	313.9
ID-2151 (H93)	10.6	79.0	140.0	13.43	266.5
Ma-1612a (H93)	10.2	57.0	130.0	18.2	254.7
Ma-1612b (H93)	8.9	67.5	210.0	13.4	187.9

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ITEMS FROM TURKEY

ICWIP – ICARDA CIMMYT WHEAT IMPROVEMENT PROGRAM
CIMMYT International Wheat and Maize Improvement Center, Turkey Regional Office and Mexico.

The International breeding strategy for the identification of resistance in bread wheat against the soil borne pathogens dryland root tor and cyst and lesion cereal nematodes.

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Soil-borne pathogens (SBPs) including the dryland root rots and cereal nematodes are causing economic yield loss in many parts of the world where cereals dominate the cropping system and suboptimal growing conditions or cultural practices are common. One of the most effective control measures of these SBPs is the use of host resistance, whereby the inoculum level of these pathogens can be reduced to below economically damaging thresholds. CIMMYT International, in collaboration with The Turkish Ministry of Agriculture and Rural Affairs, has established an international field and laboratory-screening program for identifying spring and winter wheat accessions with resistance to SBPs. Several screening protocols for assessing resistance to both cereal root rots and nematodes have been modified and optimized. Known resistance sources to SBPs from other regions of the world have been tested against Turkish isolates of SBPs and several of these have been shown to be effective in the region. In addition, new sources of resistance with genetic variability have been identified against the prevalent SBPs. These diverse genes for resistance are being pyramided into both spring and winter bread wheat backgrounds using both conventional and molecular tools where feasible.

Introduction. Soil-borne pathogens, including dryland cereal root rots and cereal nematodes, are a major constraint to cereal production worldwide, particularly where cereals dominate rotations, and sub-optimal growing conditions and or cultural practices are common. Dryland root rots also commonly known as root, crown, or foot root rots include a complex of fungi with several species of crown root (CR) (*Fusarium* spp.) and common root rot (CRR) (*Bipolaris sorokiniana* (syns. *Helminthosporium sativum*, *H. sorokiniana*, teleomorph *Cochliobolus sativus* (Ito & Kurib.) Dresch.ex Dast.). The two most reported *Fusarium* species are *F. pseudograminearum* (formerly *F. graminearum* Group 1, teleomorph *Gibberella coronicola*) and *F. culmorum*. Furthermore, two groups of microscopic nematodes are commonly found on wheat roots and include several species of the cereal cyst nematode (CCN) *Heterodera* spp. and at least two important species of the root lesion nematode (RLN) *Pratylenchus thornei* and *P. neglectus*. Frequently, two or more SBPs can occur in the soil at one time, making a disease complex and hence a holistic approach in management principally based primarily on resistance but where possible integrated with rotational options is required.

Yield loss caused by these SBPs has been reviewed and documented in many regions of the world including Europe, America, and, in particular, the more marginal cereal production areas of West Asia, North Africa, Australia, and Canada, with losses reported between 3-50% (Diehl et al. 1983; Burgess et al. 2001; Singh et al. 2005; Nicol et al. 2001, 2004a; McDonald and Nicol 2005). Recent yield losses studies in Turkey have confirmed that cereal root rots and cereal nematodes are associated with yield losses of 42 and 45% in commonly cultivated winter wheats (Nicol et al. 2005; Hekimham et al. 2004). Considering the similarity in WANA (West Asia and North Africa), parts of South America, South Africa, and other parts of the world in relation to cropping patterns and climate, it is likely that soil-borne pathogens could cause similar economic losses in these regions.

Resistance, which is defined as a reduction in the multiplication of the pathogen, is one of the best methods to control these diseases. Although these nematodes and fungi have been considered important for several decades in certain countries, little advancement in breeding has been made. This is due to the difficulties of screening for these pathogens under field and greenhouse conditions. Currently, there are very few known effective sources of resistance against these pathogens available in commercially grown wheat cultivars, and many of the identified resistant sources are

Table 1. Sources of resistance against the soil-borne pathogens cereal cyst nematode (CCN) *Heterodera filipjevi*, root lesion nematode; *Pratylenchus thornei* (PT) and *P. neglectus* (PN); and crown rot (CR), *Fusarium culmorum*. R = resistant and MR = moderately resistant. Types of wheat are SW, spring wheat, and WW, winter wheat. Origins include MX, CIMMYT Mexico; AUS, Australia; AU UA, Australia, University of Adelaide; AU US, Australia, University of Sydney; TCI, Turkey, CIMMYT ICARDA Winter Wheat Improvement Program; TCI OR, Turkey, CIMMYT ICARDA Winter Wheat Improvement Program and Oregon State University, TK, Turkey, and TK E, Turkey, Eskisehir.

Type	Origin	Cross	Selection history	CCN	PT	PN	CR
AUS GS50AT34/SUNCO//CUNNINGHAM							
SW	MX	CMSS99Y05529T	-12M-6Y-010M-2SY-0B	R	MR		
AUS4930 5.3/Spear DH#41							
SW	MX			R			
CANADIAN/CUNNINGHAM//KENNEDY							
SW	MX	CMSS99M01564T	-040Y-0P0M-040SY-040M-040SY-17M			MR	
CROC_1/AE.SQUARROSA (224)//OPATA							
SW	MX	CMBW91Y00935S	-80Y-11KBY-1KBY-010M-1Y-2M-0Y-0SY				MR
KRICHAUFF							
SW	AUS UA				MR	MR	
MILAN							
SW	MX	CM75113	-B-5M-1Y-05M-2Y-3B-0Y-3SCM	R			
SILVERSTAR							
SW	AUS AU			R			
SLVS//BAU/MILAN							
SW	MX	CMSS99M02079S	-040M-040SY-040M-3CMME-1M		MR		
SUNCO/FRAME//PASTOR							
SW	MX	CMSS99M01589T	-040Y-0P0M-16SY-010M-010Y-8M	R			MR
SUNCO/PASTOR							
SW	MX						MR
SUNR11(GALA 2-49/(CN#133/SUNSTATE*4)//SUNSTATE)							
SW	AUS–US						MR
SUNR14 (GALA 2-49/(CN#133/SUNSTATE*4)//SUNSTATE)							
SW	AUS – US						MR
SUNR25 (GALA 2-49/(CN#133/SUNSTATE*4)//SUNSTATE)							
SW	AUS–US						MR
SUNR27 (GALA 2-49/(CN#133/SUNSTATE*4)//SUNSTATE)							
SW	AUS–US						MR
T.TAU.83.2.29/3/PRL/SARA//TSI/VEE#5/4/CROC_1/AE.SQUARROSA (224)//OPATA							
SW	MX	CMSS99M01789T	-040Y-0P0M-040SY-040M-1CMME-4M		MR	MR	
T.TAU.83.2.36/ATTILA							
SW	MX	CMSS99M02090S	-040M-8SY-010M-010Y-9M	R	MR		

Table 1 (continued). Sources of resistance against the soil-borne pathogens cereal cyst nematode (CCN) *Heterodera filipjevi*, root lesion nematode; *Pratylenchus thornei* (PT) and *P. neglectus* (PN); and crown rot (CR), *Fusarium culmorum*. R = resistant and MR = moderately resistant. Types of wheat are SW, spring wheat, and WW, winter wheat. Origins include MX, CIMMYT Mexico; AUS, Australia; AU UA, Australia, University of Adelaide; AU US, Australia, University of Sydney; TCI, Turkey, CIMMYT ICARDA Winter Wheat Improvement Program; TCI OR, Turkey, CIMMYT ICARDA Winter Wheat Improvement Program and Oregon State University, TK, Turkey, and TK E, Turkey, Eskisehir.

Type	Origin	Cross	Selection history	CCN	PT	PN	CR
VP1620 (VF304/TTAU.69.5-33//YANAC)							
SW	AUS				MR	MR	
338-K1-1//ANB/BUC/3/GS50A							
WW	TCI	TCI971351	-0SE-0YC-0YE-5YE-0YE-2YE-0YE		MR		
ALTAY 2000 ALTAY 2000							
WW	TK E		YE5470-0E-0E-0E-30E-0E	R			MR
BILINMIYEN96.7							
WW	TCI	F2.96.7	-0SE-4YA-4YC-0YC	R			MR
BILINMIYEN96.7							
WW	TCI	F2.96.7	SE-3YA-3YC-0YC			MR	MR
BURBOT-6							
WW	TCI OMM	WXD880137A	-9H-0YC-1YC-0YC-0YC-2YC-0YC-3YC-0YC				MR
ES84.24/GRK							
WW	TCI	CIT932135	-0SE-0YC-1YE-0YC-2YC-0YC				MR
ES84-24/DYNASTY							
WW	TK E	YE8224	-0E-0E-0E-1E-0E				MR
MVR27-82//LI7/LE2062							
WW	TK	AMJ20983	-6J-1YC-0YC	R			MR
SKP35/SAM2/4/55-1744/D101//MAYA.S/3/MUS.S/DRM.MAYA/ALD.S							
WW	TK E	YE8071	-0E-0E-0E-3E-0E				MR
TAM201/4/BL/AU/3/AGRI//HYS/7C/5/F134.71/NAC							
WW	TCI	CIT935155	-0SE-0YC-*-2YE-2YC-0YC				MR
TE2583A-11310/Obriy							
WW	TCI	TE4920	-1T-2T-1T-1T-2T-0T				MR
TURCAN #39							
WW	TCI						MR
4-22 WW	TK						MR
ES86-7							
WW	TK						MR
KUTLUK94							
WW	TK				MR		

Table 1 (continued). Sources of resistance against the soil-borne pathogens cereal cyst nematode (CCN) *Heterodera filipjevi*, root lesion nematode; *Pratylenchus thornei* (PT) and *P. neglectus* (PN); and crown rot (CR), *Fusarium culmorum*. R = resistant and MR = moderately resistant. Types of wheat are SW, spring wheat, and WW, winter wheat. Origins include MX, CIMMYT Mexico; AUS, Australia; AU UA, Australia, University of Adelaide; AU US, Australia, University of Sydney; TCI, Turkey, CIMMYT ICARDA Winter Wheat Improvement Program; TCI OR, Turkey, CIMMYT ICARDA Winter Wheat Improvement Program and Oregon State University, TK, Turkey, and TK E, Turkey, Eskisehir.

Type	Origin	Cross	Selection history	CCN	PT	PN	CR
SÖNMEZ2001							
WW	TK			R			
GÜN91							
WW	TK				MR		
YAKAR99							
WW	TK			R			MR
TOSUNBEY							
WW	TK			R			
BAĞCI2002							
WW	TK			R			
DOĞU88							
WW	TK						MR
LANCER							
WW	TK						MR
PALANDÖKEN97							
WW	TK						MR
FLAMURA85							
WW	TK						MR
KATE A-1							
WW	TK			R			
PEHLİVAN98							
WW	TK					MR	MR
PROSTOR99							
WW	TK						MR
SAROZ95							
WW	TK				MR		MR
ES05-KE21							
WW	TK				MR		
05BVD-1							

found in unadapted germ plasm which will require considerable breeding investment to produce commercial cultivars. Hence, a precise laboratory/field breeding strategy has been established by Turkish and CIMMYT scientists in Turkey with CIMMYT Mexico to identify and incorporate new sources of resistance, particularly those identified in well-adapted backgrounds.

Germ plasm screening for resistance to soil-borne pathogens. Over the last 4 years a clearly defined screening program has been established in Turkey in collaboration with Turkish NARs to screen against SBPs. The greenhouse resistance-screening program is at the Eskisehir ANADOLU station and the field crown rot screening program is conducted in Konya in collaboration with BDIARI (Bahri Dagdas International Agricultural Research Institute). The emphasis on screening has been with advanced lines or released cultivars and, due to the inherent variability of SBP data, at least 2 years of field or greenhouse data is deemed necessary before the line/cultivar is considered to be resistant.

Last year, more than 200 lines of germ plasm were screened for their resistances against a number of SBPs under greenhouse conditions. These germ plasm included TURKEY/CIMMYT/ICARDA (TCI) winter wheat, spring wheat from CIMMYT-Mexico, National Turkish materials, and sources obtained from international collaborators working with SBPs. Each line was screened against four SBPs including CCN (*H. filipjevi*), RLN (*P. thornei* and *P. neglectus*), and CR (*F. culmorum*), each with seven replicates, making the greenhouse throughput 5,600 plants.

As with previous years, a field-based screening program with more than 800 genotypes (making approximately 5,000 observation plots) of TCI, National, and CIMMYT Mexico for crown rot resistance was established in Konya for resistance under inoculated field conditions.

The methods used for the screening of SBP in both field and greenhouse are given in the reference Nicol et al. (2007). In all tests, commonly known check lines for both resistance and susceptibility are used for each SBP. Since the work has begun, more than 60 wheat lines have been identified with resistance or partial resistance against SBPs, which is equivalent or better than the currently known resistance. Many of the lines are high yielding adapted SW or WW and, in some cases, commercially released cultivars in both Australia and Turkey. In many cases, resistance has been found against more than one SBP, enabling the breeders to use this germ plasm against the SBP complex. The summary of the new greenhouse-screening program from 2007 are provided in Table 1 (pp. 143-145). CCN provides more complete resistance than the other three SBPs, due to major gene control of this pathogen, in comparison with both RLN and CR, which have reported quantitative inheritance controlled by several genes (Nicol and Rivoal 2008). These sources have been shared with both international and national breeding programs for both their validation and subsequent incorporation into germ plasm improvement.

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Experiments were on the grain from a 'black fallow after pea' rotation according using a split-plot design. First-order plots had the following fertilizer backgrounds: a) fertilizer omitted (using the natural fertility of soil and rotation of crops during 30 years); b) organic input (crop rotations plus 6.6 t of manure per hectare); c) intensive organic-mineral input (organic fertilizer plus applications of $N_{60}P_{60}K_{60}$ at primary plowing before planting, an N_{30} soil application at spring tillering, and an N_{30} outside root application with urea at flowering). The cultivars Kharus and Donetskaya 48 were planted in the third-order plots.

Planting was a SN-16M sower with rates in the 'forecrop–black fallow' rotation of 4.0×10^6 germinating seed/ha and 5.0×10^6 seed/ha in the 'after peas for grain' rotation. The plot area was 25 m^2. Experiments were replicated three times.

Harvest was by a pickup threshing method with a Sampo-130 combine. During harvest, grain samples were taken to determine cereal bug damage. Grain damage was measured in the laboratory, and the degree of damage estimated according to a 1–5 scale where 1 = least damage; 2 = one or two spots on a kernel that occupy one-fifth to a quarter of the surface; 3 = two or more spots on a kernel occupying not more than one-third of the surface; 4 = spots on more than one-third with strong deformation that turned black or caused a shrunken kernel; and 5 = the entire kernel is black and strongly deformed.

Grain quality analyses included test weight, crude gluten content in flour, protein content in grain, IDG, group, strength of flour, bread volume, general bread-making value, and grain class and were made in the laboratory of Grain Quality Technology. Experimental data was subjected to variance (two factorial experiment) and correlation analyses by using Excel software.

The meteorological data from June and July 2001-02 were similar. Data were recorded at the milk, waxy, and full maturity grain stages and included the harvest period when damage is caused generally by the 3rd-, 4th-, and 5th-stage larvae and, partly, young, winged insects. The average temperature and total precipitation exceeded normal by 11.3–12.1 % and 10.6–11.0 %, in June and July 2001-02, respectively. In 2004-05, the average temperature was near normal. Total precipitation in 2004 exceeded the norm by 15.0 % and in 2005 by 53.0 %.

Results. Maximum damage on winter wheat grain by cereal bug larvae was as high as 17.0 % in 2002, in 2004 and 2005 by 0.3 and 0.5 %, respectively. On average over the 2001-05 year period, grain damage to winter wheat by the cereal bug larvae on plots with organic-mineral fertilizer background by black fallow was 1.6 times less in comparison to the plots with a peas for grain rotation (Table 1, p. 148). The total grain damage according to the forecrop was 5.0 % for black fallow and 12.0 % after peas (LSD_{05} = 1.47%). In both instances, 79.6–83.3 % of the wheat grain had a score for the second gluten-quality group (74 units of IDG). Comparing black fallow peas-for-grain, we observed a marked increase in grain quality for crude gluten content of flour, from 28.8 to 30.9 (at LSD_{05} = 0.64 %); protein in grain, from 12.76 to13.31 %; flour strength, from 250 to 290 alveograph units; bread volume/100-g flour, from 550 to 573 ml; total bread-making estimate, from 3.6 to 4.2. The gluten quality of these variants was similar, at 74 units of IDG, matching the second group. On the whole, winter wheat grain with preceding black fallow corresponded to the second class and with peas-for-grain was in the third class. The 4-year average for grain yield in black fallow considerably exceeded that after peas by 0.59 t/ha or 9.1 %. Grain yield of winter wheat with the black fallow variant was 6.49 t/ha and after peas 5.90 t/ha (LSD_{05} = 0.30 t/ha).

Comparing winter wheat cultivars grown after black fallow with an organic-mineral fertilizer application, Kharus had, on average, 1.4 times more damage by bug larvae than Donetskaya 48, possibly because of the morphological characteristics of the cultivars. Between 2001-05, total damage to Donetskaya 48 was 3.9 % and Kharus was 5.3 % (LSD_{05} = 0.83 %). A damage score of 2 was assigned to 3.0 and 4.2 % of Donetskaya 48 and Kharus grain, respectively, which also corresponded to the second grain-quality group. Grain quality indices showed that Donetskaya 48 had a considerably higher content of crude gluten in the flour by 12.3 % and protein content by 9.6 %. Gluten quality of the flour in Donetskaya 48 was 15.7 % higher than that of Kharus. The grain of Donetskaya 48 corresponded to the second class and that of Kharus to the 3rd class. Despite a higher grain damage by the cereal bug in Kharus, strength of flour, bread volume, and total bread-making estimate slightly exceeded those of Donetskaya 48 by 13.3, 4.8, and 11.6 %, respectively. Mean estimates from 2001-05 for grain yield for Kharus were considerably higher than those for Donetskaya 48 by 1.25 t/ha (at LSD_{05} = 0.27 t/ha). Kharus has a higher genetic potential than Donetskaya 48. The productivity of Donetskaya 48 was 5.64 t/ha and Kharus was 6.89 t/ha.

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ITEMS FROM THE UKRAINE

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The impact of larvae of Eurygaster integriceps Put. on winter wheat grain.

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Winter wheat suffers from harmful organisms to a considerable extent. Among these pests, cereal insects are especially harmful not only on yield but also on grain quality of winter wheat. At present, with the reduction in the use of chemical protection, agronomical means of protection are important. Our aim is the search for zonal agnonomic methods that reduce the harmful impact of the cereal insect on the qualitative indices in winter wheat grain. We have made studies on a cultivar, forecrop, and fertilizer bases.

Material and Methods. Field experiments were at the Plant Breeding Laboratory of the Plant Production Institute NA. V.Ya. Yuriev of the UAAS (Eastern Forest-Steppe of Ukraine) in a fixed 9-course, fallow-crop rotation. The common, heavy chernozem soil has medium humus and is characterized by the following indices in the arable layer: humus, 5.25–5.38 %; pH of salt extract, 6.0–6.5; nitrogen content, 16.8–17.5, labile phosphorus, 11.2–14.8; and exchange potassium, 11.1–13.3 mg/100 g soil.

Table 1. Grain quality in winter wheat depending on cultivation conditions and seed damage by *Eurygaster integriceps* Put. (average over 2001–05, factor A).

Number of damaged seeds					Test weight (g/l)	Crude gluten content in flour (%)	Gluten IDG units	Quality group	Grain protein content, (%)	Flour strength alveograph units (w)	Bread volume/ 100-g flour (ml)	Total bread-making value	Grain glass	Grain yield (t/ha)
total	1	2	3	4										
Forecrop – black fallow (organic-mineral fertilizer background), factor B.														
5.4	0.2	4.3	0.8	0.1	773	30.9	74	II	13.31	290	573	4.2	2	6.49
Forecrop – peas for grain (organic-mineral fertilizer background), factor B.														
8.9	0.6	7.5	0.3	0.6	780	28.8	74	II	12.76	250	550	3.6	3	5.90
LSD_{05} for factors:														
A – 1.04														0.16
B – 0.74						0.64			0.73	42.19	88.35	1.33		0.12
AB – interaction – 1.47														0.30
Cultivar Donetskaya 48 (organic-mineral fertilizer background, forecrop – black fallow), factor B.														
3.9	0.2	3.0	0.8	0.0	783	34.1	83	II	14.10	241	555	3.8	2	5.64
Cultivar Kharus (organic-mineral fertilizer background, forecrop – black fallow), factor B.														
5.3	0.3	4.2	0.5	0.3	773	29.9	70	II	12.74	278	583	4.3	3	6.89
LSD_{05} for factors:														
A – 1.17														0.12
B – 0.83						1.49			1.41	67.55	122.75	1.44		0.15
AB – interaction –1,65														0.27
Fertilizer omitted in background, factor B.														
5.9	0.3	4.3	0.8	0.5	779	28.1	76	II	12.53	254	548	4.0	3	6,01
Organic fertilizer background – manure 30 t/ha, factor B.														
6.0	0.3	4.9	0.7	0.2	779	29.4	83	II	12.86	252	525	3.7	3	6.22
Organic-mineral fertilizer background – manure 30 t/ha + $(NPK)_{60}$, factor B.														
5.6	0.6	4.2	0.6	0.2	775	31.4	75	II	13.41	275	553	4.1	2	6.44
LSD_{05} for factors:														
A – 0.84														0.10
B – 0.73						1.15			0.65	36.70	30.75	0.80		0.16
AB – interaction – 1.45														0.23

The 4-year average for the different fertilizer backgrounds indicated that the least total grain damage by cereal bug larvae was in the block with organic-mineral fertilizer, 5.6 %. Damage in the blocks without fertilizer and with only organic fertilizer was 5.9 and 6.0 %, respectively. Total damage was 4.2–4.9 % in seed with a score of 2, which corresponded to 75–83 units of gluten quality (IDG, 2nd group). A reduction in grain damage, from 6.0 to 5.6 %, contributed to a reliable increase in crude gluten content in flour between 29.4 and 31.4 (LSD_{05} = 1.15 %), and protein content in the grain from 12.86 to 13.41 %, bread volume/100-g flour from 525 to 553 ml, and total bread-making estimate from 3.7 to 4.1 score. These analyses showed a negative correlation between the indices of grain quality and damage by the cereal bug (r = -0.8). However, higher gluten quality was found in grain from the organic fertilizer treatment, 83 alveograph units compared to 76 units for the block without fertilizer and 75 units for the block with organic-mineral fertilizer. Winter wheat grain grown without fertilizer and with organic fertilizers corresponded to the third class and that in the block with organic-mineral fertilizer to the 2nd class. On average, during 2001–05, the maximum grain yield was obtained in the organic-mineral fertilizer treatments, 6,44 t/ha, out-yielding the treatment without fertilizer by 0.43 t/ha (at LSD_{05} = 0.23 t/ha).

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Callus initiation and morphogenesis in in vitro culture of isogenic on gene type and rate of development in winter wheat lines.

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Methods of cultivating isolated cells, tissues, and organs for studying fundamental, plant physiology problems have found wide application in the development of unconventional approaches to various biological research areas and have a very wide spectrum of practical application (receiving of biologically active substances, transgeneration, selection, microcloning reproduction, and cryopreservation). The efficiency of cellular technology depends on many factors including the composition of nutrient medium, type of explant, age of a plant, and genotype (Machii et al. 1998; Stelmakh 1998; Tyankova and Zagorska 2001; Wang and Wei 2004). The search for genotypes with a high potential for callus formation and regeneration potential for the production of high-quality, fertile plant regenerants is a problem that depends on biotechnology (Tyankova and Zagorska 2001).

Systems of genetic monitoring of type (vernalization) and rates (photoperiod) developments determine a number of physiologico-biochemical processes of ability to vital activity of plants of wheat (Stelmakh 1998). These genetic systems also probably participate in the control of processes of callus initiation and morphogenesis *in vitro*.

Materials and Methods. Seven genotypes of soft winter wheat NILs for genes that control vernalization (*VRN1–VRN3*) and photoperiod *PPD1–PPD3*) were grown. The check cultivar Mironovskay 808 is completely recessive for all of these genes. Isogenic lines were produced by backcrossing with Mironovskay 808 by Stelmah (1998).

For production of callus and quality explants, we used the mature germ and apical meristems of aseptic roots. Seeds were sterilized in a 3% NaOCl solution for 15 min, washed for 5 min with sterile distilled water, and isolated germs transferred to a Petri dish with Murashige and Skoog medium (MS) with a full set of macro- and microsalts and containing 2,4 D (2 mg/l) as a growth regulator (Tyankova and Zagorska 2001). Explants were cultivated in the thermostat at 26°C in the dark. For apical root meristems, explants were grown for 4–5 days in on MS medium without phytohormone in the dark at 22°C. Isolated apical roots 1–1.5-cm long were transferred to MS medium with 2,4 D at 2 mg/l and cultivated in the dark at 26°C. At 14–21 days, explants isolated from apical meristems were sterilized with 3 % NaOCl solution for 15 min, washed 5 times in sterile distilled water, and placed on MS medium without phytohormone. Cultivation was at 22°C, with 3–4 lux of illumination and a 16-hour photoperiod at 70% humidity. For mature germ, seeds were sterilized and isolated germs were cultivated under the same conditions. The frequency callus induction and the efficiency of morphogenesis (%) was defined as the number of explants formed per callus or the number of plant regenerants to the initial number of explants. Results were from three independent experiments from not less than four Petri dishes or flasks (5–7 explants).

Results and Discussion. We investigated the influence of genotype on the efficiency of callus induction and morphogenesis *in vitro* on NILs for genes that control development (six lines and one cultivar that is recessive for all vernalization and photoperiod genes. We used mature germs and aseptic roots to produce primary callus. Mature germ is more effective at producing primary callus compared with apical meristems of aseptic roots.

All genotypes formed callus but with various frequencies (8–67%, Table 1). Using roots, the frequency of callus production was considerably below 20–30 %; line *PPD1* did not form callus in any experiment. Comparing the isolines for PPD and VRN, the PPD lines possess a greater potential for callus production. These lines differ in development; those with VRN are spring types and PPD and Mironovskay 808 (full recessive) are winter. Among the PPD lines, peak efficiency of callus production was found in line *PPD2* and the minimum in *PPD1*. Among the VRN lines, the minimum ability to generate callus was in line *VRN1* and the maximum in line *VRN3*.

Table 1. Callus initiation and morphogenesis in *in vitro* in NILs for the PPD and VRN genes of the wheat cultivar Mironovskay 808 (a cultivar fully recessive for genes PPD and VRN). Values expressed as frequency, % from number initial explants.

	Callus initiation		Morphogenesis *in vitro*	
Line	germ	roots	germ	apexes
Isogenic lines for PPD genes.				
PPD 1	8	0	75	31
PPD 2	67	30	50	13
PPD 3	58	20	100	50
Mironovskay 808	50	20	67	50
Isogenic lines for VRN genes.				
VRN 1	8	—	75	—
VRN 2	25	—	42	—
VRN 3	67	—	50	—
Mironovskay 808	50	—	67	—

Using various explants, we established differences between the types and rates of callus formation. Callus formation begins at apical sites in the roots 15–20 days earlier than in the mature germ. Differences were based on the degree of water and density to color of the callus. From aseptic roots, highly watery, friable, almost transparent, slightly whitish calli were obtained. From mature germ, the callus was more dense, less watery, and yellowish, which was characterized by differences confirmed by microscopic studies. Microscopically, callus tissue of the various isolines was shown to be typical for cereal callus cells; extended, with rounded ends, and not adjacent to each other. Cytological results showed that the various lines have calli that differ in sizes. The maximum length was in Mironovskay 808 and the minimum in cells of line PPD 3. Genotype influences the efficiency of callus formation and on the morphological features of cells of the callus tissues and also on their morphological potential.

Our results indicate that NILs for the *VRN* and *PPD* genes control the type and rate of development in wheat callus. More effective for growth *in vitro* are explants from mature germ, compared with those from apical meristems. Comparing the different isolines, those with *PPD* genes are easier to culture *in vitro* show higher morphogenetic potential than those with *VRN* genes. The maximum index of the efficiency of morphogenesis *in vitro* was for isoline PPD3 using mature germ and apical meristems. Among the VRN lines, peak regeneration efficiency *in vitro* was in line VRN1 and the minimum in isolines PPD2 and VRN2. Plants of line VRN2 have the longest period from shoot to heading. Plants of line PPD2 are the most sensitive to a short photoperiod and unfavorable day length conditions, followed by VRN2.

The efficiency of callus production and morphogenesis *in vitro* using mature germ to produce quality explants was shown. The processes of callus induction and morphogenesis depend on the genotype of the initial plant and are governed by different genetic systems. The maximum frequency of callus induction was in line PPD2 but also has the minimum indicators of efficiency of morphogenesis *in vitro*. Line VRN1 was shown to have maximum morphogenesis *in vitro* but the minimum frequency of callus generation. These results testify to the control of callus formation and morphogenesis by different, independent genetic systems. Genes that control type and rate of development, PPD and VRN, also help determine callus formation and morphogenesis *in vitro*.

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ITEMS FROM UNITED KINGDOM

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Genetic biodiversity for stripe and stem rust resistance in African wheat genotypes.

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A new program involves the genetic and phenotypic characterization of a large collection of African wheat genotypes for resistance to the new virulent stem rust *P. graminis* race Ug99. Stem rust resistance will be assessed in field trials in Kenya. The collection also will be assessed for resistance to stripe or yellow rust *P. striiformis* f.sp. *tritici* races in South Africa and the UK. DNA markers will be developed for useful sources of rust resistance and used as tools to determine the extent of biodiversity between the wheat genotypes. This program is a collaboration between Dr. L.A. Boyd at the JIC, UK, and Prof. Z.A. Pretorius and Dr. R. Prins at the University of the Free State, Bloemfontein, South Africa.

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ITEMS FROM THE UNITED STATES OF AMERICA

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Wheat breeding and genetics.

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Production conditions, test sites, and cultivar distribution. Total winter wheat production in 2007 was estimated at 94.0 x 10^6 bushels, a 135% increase from the 2006 crop and 37% higher than the 10-year average. Average grain yield at 41.0 bu/acre was the highest since 1999, 90% higher than in 2006 and 28% higher than the 10-year average. The area harvested for grain was estimated at 2.35 x 10^6 acres, up from 1.9 0 x 10^6 acres in 2006.

In 2006–07, 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 were much more favorable for high yields than what was experienced in 2005 and 2006. Above-average yields were achieved at most trial locations as a result of good autumn stand establishment, heavy winter snowfall, and adequate spring rains. Some drought stress was observed at most locations, however, due to lush autumn and spring growth and inadequate spring precipitation to sustain growth. The trials at Burlington were on the end of this spectrum, with drought stress limiting yields significantly in many entries (trial range 15-45 bu/acre). In general, relatively mild temperatures were observed throughout the growing season through to the end of grain filling. Most trial locations avoided significant disease or insect infestations, with the exception of stripe rust at the Lamar (most severe), Sheridan Lake, and Arapahoe locations. Leaf rust was observed at low levels at a few trial locations but did not cause any appreciable damage, despite severe localized infections and damage in nearby fields in southeast Colorado. A severe infection of WSMV was observed at the Dailey irrigated trial location and yields of susceptible entries were reduced significantly.

Planted acreage estimates for the 2007 crop were as follows: Jagalene – 14.2%; Prairie Red – 10.3%; Akron – 7.4%; Jagger – 7.4%; Hatcher – 6.5%; TAM 111 – 6.3%; TAM 107 – 5.6%; Ankor – 5.6%; Above – 5.0%; Trego – 3.7%; Prowers/Prowers99 – 2.9%; Yuma – 2.5%; Bond CL – 1.9%; Lamar – 1.9%; Avalanche – 1.6%; Other – 17.2%.

New cultivar release – Bill Brown hard red winter wheat. One new winter wheat cultivar was released in autumn 2007. The new cultivar, named **Bill Brown**, is a HRWW with very high dryland and irrigated yields, excellent drought stress tolerance, high test weight, resistance to both leaf and stripe rust, and excellent milling and baking quality characteristics. The name Bill Brown was chosen in honor of the memory of the former CSU Extension Plant Pathologist who devoted his career to the improvement and management of diseases of wheat and other grain crops. In three years of statewide testing in the dryland Colorado Uniform Variety Performance Trial (UVPT; 32 locations), Bill Brown had grain yields equivalent to those of the high-yielding wheat cultivar Hatcher, higher than all other entries in the trials, and 0.7 bu/acre (1.7%) higher than Bond CL, 0.9 bu/acre (2.2%) higher than Ripper, and 4.0 bu/acre (10.7%) higher than Jagalene. In three years of statewide testing in the Colorado Irrigated Variety Performance Trial (IVPT; 9 locations), Bill Brown was the highest yielding entry in the trials, approximately 3.4 bu/acre (3.9%) higher than Bond CL and 5.2 bu/acre (6.0%) higher than TAM 111, the next highest yielding entries in trials. Bill Brown will be an excellent replacement for wheat cultivars targeted specifically for high yield, irrigated production conditions and an excellent complement to both Hatcher and Ripper for dryland production conditions.

Detailed data on Bill Brown 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 increase. One new experimental line, designated as CO03W239, was advanced for Foundation Seed increase in autumn 2007. Pending further yield and quality evaluations in 2007-08, CO03W239 is targeted for re-

lease as a new cultivar in autumn 2008. CO03W239 is a HWW *Clearfield** line best adapted for dryland production conditions. In two years of testing in the UVPT (22 locations), CO03W239 has been slightly lower yielding than Hatcher and higher yielding than all other HWW cultivars except NuDakota. Relative to the available *Clearfield** wheats, CO03W239 has shown a yield equivalent to that of Infinity CL from Nebraska and a higher yield than both Bond CL and Above. CO03W239 has moderate resistance to stripe rust, moderate susceptibility to preharvest sprouting (similar to that of NuHills and NuDakota), and excellent milling and bread-baking quality characteristics. If released, CO03W239 would be the only dryland-adapted HWW *Clearfield** wheat available for production in the High Plains region.

Russian wheat aphid resistance.

Frank Peairs and Nora Lapitan collaborators.

Projects include:

– advancing a group of 70 biotype 2-resistant lines to replicated yield trials in 2008,
– screening a group of synthetic hexaploid wheats for RWA biotype-2 resistance,
– transfering RWA resistance from tetraploid wheat (Ben Beyer MS thesis project),
– characterizing triticale-derived, RWA-resistant wheat lines (collaboration with Dr. Kabwe Nkongolo, Laurentian University, Canada),
– developing several mapping populations with Iranian landrace selections for DNA marker identification,
– continuing to separate *Dn7* from the negative quality effects of the T1BL·1RS wheat:rye translocation (collaboration with Nora Lapitan, Junhua Peng, and Guihua Bai, USDA-ARS Genotyping Lab, Manhattan KS),
– evaluating elite RWA-susceptible lines for biomass loss from RWA, and
– exchanging RWA-resistant germ plasm with researchers in Australia and France for characterization of response to virulent biotypes from other areas of the world.

Clearfield wheat development.*

Projects in Clearfield* wheat development included:

– advanced a set of 7 single-gene *Clearfield** lines for a second year of testing in the 2008 CSU Elite nursery,
– advanced of a group of 45 double-gene *Clearfield** lines to replicated yield trials in 2008 (Advanced Yield Nursery), and
– implemented DNA markers for confirmation of the presence B-genome and D-genome *Clearfield** mutants in experimental wheat lines.

End-use quality evaluation and research (Brad Seabourn collaborator).

Evaluation and research included:

– expanding the CSU Wheat Quality Laboratory to isolate single kernel characterization system (SKCS) and milling equipment in a separate lab,
– implementing barcode readers for SKCS and Mixograph devices,
– developing a relational database system for storage and retrieval of routine screening data,
– analyzing over 2,950 grain and flour samples from the 2006 season, including 2,396 whole grain NIR tests, 1,737 flour NIR tests, 1,996 SKCS tests, 1,800 Mixographs, 540 Quad Senior mills, and 527 100-gram pup-loaf bakes,
– participating as a test collaborator in the Pacific Northwest Wheat Quality Council evaluation program,
– implementing a higher-throughput, modified Quadromat Senior milling system (with assistance from Doug Engle, USDA-ARS-PNWWQL, Pullman WA),
– characterizing the utility of whole-grain calibrations for SKCS kernel weight, diameter, and hardness for rapid selection (Josh Butler PhD dissertation research),
– characterizing the agronomic management effects on wheat end-use quality (project led by Jerry Johnson),
– documenting high and low molecular weight glutenin subunit composition of Great Plains winter wheat cultivars and experimental lines (project led by Pat Byrne), and

– documenting the influence of allelic variation *Glu-A1, Glu-B1, Glu-D1, Glu-A3, and Glu-B3* loci on Mixograph properties (project led by Pat Byrne).

USDA-CAPS project.

Pat Byrne, Nora Lapitan, Jorge Dubcovsky, and Guihua Bai (collaborators).

As part of this project, we have

– completed seed increase of our mapping population (Platte/CO940610) and planted a subset of this population at Fort Collins for phenotypic evaluation in 2006–07,
– planted 192 individuals from the CAP population at Fort Collins in fall 2007 under a linear move for side-by-side evaluation under full- and limited-irrigation,
– continued marker genotyping and mapping of CAP population (led by Pat Byrne and Nora Lapitan), and
– implemented marker assisted selection (MAS) for allele enrichment in segregating top-cross populations 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.

Preharvest sprouting tolerance.

Research in this area investigated

– using of the petri-dish germination test to characterize sprout tolerance of over 350 different hard red and hard white samples collected at Fort Collins and Akron,
– using of the intact-head sprout test for line reselection with over 1,200 individual heads sampled from hard white preliminary lines at Fort Collins, and
– assessing the utility of previously reported DNA markers to identify lines with improved sprout tolerance.

Graduate student research.

Three graduate student projects were on-going in 2006–07.

– Development and validation of near infrared reflectance (NIR) spectroscopy calibrations for whole-grain prediction of end-use quality characteristics (Joshua Butler). Josh is planning to submit and defend his PhD 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). Jennifer is planning to submit and defend her MS thesis in spring 2008.
– RWA biotype 2 resistance gene mapping and gene transfer from *Triticum turgidum* subsp. *dicoccoides* (Ben Beyer). Ben successfully defended his MS thesis in autumn 2007.

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GEORGIA / FLORIDA

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The 2007 Georgia winter wheat crop was grown on about 320,000 planted acres. Yields of wheat grown by top producers were around 6000 kg/ha on resistant cultivars to stripe rust. Average yield for the state was 3,200 kg/ha. The growing season was characterized by drought conditions in the autumn, which delayed planting, and in the spring by very dry conditions during the grain-filling period. A lack of vernalization was a problem for late maturing varieties. A late freeze in April with low temperatures of –4°C during boot stage resulted in very low yields for early and medium-maturing cultivars.

Breeding.

Three wheat cultivars, GA951231-4E25 (**Oglethrope**), GA951231-4E26 (**AGS 2026**), and GA96693-4E16 (**AGS 2020**), which are high-yielding, broadly adapted cultivars, were released by the University of Georgia in 2007 for growers in the Southeast. These three soft red winter wheat cultivars are high yielding with excellent test weight, disease and insect resistance, and will offer new sources of resistance to both pathogens and insects. Olgethrope and AGS 2026 have excellent Hessian fly (*H13*) and stripe and leaf rust resistance (*Lr37 Yr17*). Both cultivars are medium-maturing soft wheats. AGS 2020 is stripe and leaf rust resistant and is a medium maturing soft wheat with excellent milling and baking quality. All three cultivars have good resistance to wheat soil-borne mosaic virus.

GA 96693-4E16 (AGS 2020) is an early maturing, white chaffed, medium height line. AGS2020 was derived from the cross 'GA 88151/Hickory//AGS 2000'. The maturity is 3 days earlier than that of AGS 2000. AGS2020 is moderately resistant to current biotypes of Hessian fly in Georgia, resistant to races of leaf rust and stripe rust in the southeast U.S, and also resistant to soil-borne mosaic virus and powdery mildew.

GA 951231-4E25 (Virgoro Olgethorpe) is a medium-maturing, white chaffed, medium height line. The line was derived from the cross 'GA881130/Coker 9134'. The pedigree of GA 881130 is 'KSH8998/FR 81-10//Gore'. KSH8998 was developed from the cross of a hard wheat with *Ae. tauchii* to transfer Hessian fly resistance (*H13*). FR 81-10 was selected due to its resistance to leaf rust (*Lr37 Yr17*) from the cross 'Novisad 138/4/(4) *Ae. ventricosa*/*T. persicum*/2/Marve*3/3/Moisson'. Maturity is similar to that of AGS 2000. Virgoro Olgethopre is resistant to current biotypes of Hessian fly in Georgia including biotype L and is resistant to races of leaf rust and stripe rust due to adult-plant resistance, resistant to soil-borne mosaic virus, and susceptible to powdery mildew.

GA 951231-4E26 (AGS 2026) is a medium-maturing, white chaffed, medium height line. AGS2026 was derived from the cross 'GA881130/Coker 9134'. The pedigree of GA 881130 is 'KSH8998/FR 81-1//Gore'. KSH8998 was developed from the cross of a hard wheat with *Ae. tauchii* to transfer Hessian fly resistance (*H13*). FR 81-10 was selected due to its resistance to leaf rust (*Lr37 Yr17*) from the cross 'Novisad 138/4/(4) *Ae. ventricosa*/*T. persicum*/2/ Marve*3/3/Moisson'. AGS2026 is similar in maturity to AGS 2000. This cultivar is resistant to current biotypes of Hessian fly in Georgia including biotype L, is resistant to races of leaf rust and stripe rust due to adult-plant resistance, also is resistant to soil-borne mosaic virus, and susceptible to powdery mildew.

Leaf and stripe rust

Leaf rust was very severe in 2007. We identified effective genes such as *Lr37 Yr17* and derived lines from AGS 2000.

Stripe rust. Breeding lines and cultivars from universities and private companies (713 entries in 2006 and 380 entries in 2007) were evaluated in the field at Plains and Griffin, GA. Plots were inoculated with a local field culture of stripe rust. The races of stripe rust used for inoculation were collected in Georgia, identified and designated as PST 101 and 102 (Dr. X.M. Chen, Pullman, WA). Stripe rust infection type and percent severity data were assessed multiple times at each location. The results indicated that numerous cultivars and lines possess the resistant gene *Yr17* in SRWW. Other sources of seedling resistance were also identified in PIO26R61, Kinsco, and VA 270. A total of 102 lines from the field nursery were identified as having a level of resistance better than that of Pioneer 26R61. The first large-scale replicated screening of 591 breeding lines for stripe rust was undertaken early in 2007 using growth chambers. Eighty-nine lines were detected with some resistance. Again, the majority of the lines had the resistant gene *Yr17*. From field evaluations and a large seedling screening, a number of lines with adult-plant resistance were identified such as AGS 2031, AGS 2020, and PIO26R61. Additional evaluations are proposed to identify other sources of adult plant resistance.

Hessian Fly.

Wheat entries were evaluated at two locations, Griffin and Plains, GA. Several wheat cultivars showed good levels of Hessian fly resistance at Plains, GA, including aGS 2000, AGS 2010, AGS 2060, Jamestown, Pioneer 26R31, Pioneer 26R61, Coker 9152, SS 8641, AGS 2026, and Olgethorpe.

Scab.

Fusarium head blight is a potential devastating disease in the southeast region in the United States where low temperature and misted weather occurs frequently during SRWW flowering. Releasing new cultivars resistant to FHB is the most effective option to minimize the chance of FHB incidence and reducing DON contamination. Crosses were made since 2001 between AGS2000 or its derivatives and the FHB-resistant donor VA01-461 to introduce the exotic resistant genes into our widely local adaptive genetic background. Twelve advanced lines, 941523-E21, 991109-6E8, 991109-6A7, 991371-6E12, 991371-6E13, 031454-DH7, 031454-DH31, 031307-DH6, 031307-DH14, 031354-DH30, 981621-5E34, and 951306-2E13, derived from VA01W-461, which is a derivative of Sumai 3, were evaluated in scab nursery and field in 2006 and 2007 for FHB resistance and agronomy performances with Ernie and Coker 9835 as resistant and susceptible controls, respectively, under misted conditions in Griffin-Campus, GA. DNA markers, XGWM533, BARC133, XGWM493, and STS3B-256 for QTL on 3BS; BARC117, XGWM156, BARC186, and BARC56, for QTL on 5AS; BARC18, and BARC91 for QTL on 2BS were employed to genotype 12 new lines with the donor parent of VA01W-461.

Publications.

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Wheat production.

According to the USDA National Agricultural Statistics Service, Indiana farmers harvested 150,000 hectares (370,000 acres) of wheat in 2007, down 18% from 2006. Wheat yields in Indiana averaged 3,830 kg/ha (57 bu/acre) in 2007, 15 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. Unlike 2005 and 2006, growing conditions for winter wheat in 2007 were stressful; abnormally cool temperatures until late April, including a severe frost in mid-April that caused abandonment of some fields in southern Indiana. Beginning in early May, warm temperatures and increasingly dry soil with significant drought conditions developed by mid to late June, resulting in low grain yields and average to low test weight. Acreage prospects for 2007–08: preliminary reports are that 550,000 acres were seeded, and more acreage would have been seeded, but seed was limited. Wheat establishment was excellent and autumn growth was excellent prior to onset of winter.

Wheat disease summary.

Yellow dwarf, including BYDV and CYDV, were widespread and moderate to severe throughout the southern two-thirds of Indiana. Foliar diseases, including Fusarium head blight were present but not significant except in localized areas, likely due to unusually cool temperatures early in the spring growing season and dry conditions later in the growing season.

Performance of new cultivars.

Cultivar INW0731 yielded unusually well, ranking first or nearly first in multiple locations in Indiana and nearby regions, likely due to its demonstrated large root volume and moderate resistance to yellow dwarf. INW0731 has moderate resistance to Fusarium head blight from Freedom and Fundulea 201R, moderate resistance to leaf rust, resistance/tolerance to yellow dwarf, powdery mildew, Stagonospora nodorum blotch, Septoria leaf blotch, soil-borne wheat mosaic virus, and wheat spindle streak mosaic virus, and is susceptible to Hessian fly, stripe rust, and stem rust in Indiana.

INW0731 is adapted to southern Indiana and surrounding regions; it has survived winters very well in central and northern Indiana, but winters have been mild since 1996.

Cultivar INW0316, which has gene *Bdv3* introgressed from intermediate wheatgrass, a western U.S. range grass for grazing, continues to excel when yellow dwarf disease, caused by BYDV (PAV) and CYDV (RPV), is moderate to severe. INW0316 is especially well-suited to southern Indiana and adjacent areas because yellow dwarf is present many years, as in 2006 and 2007. In our multilocation performance tests in 2006 INW0316, Pioneer25R47, and Roane yielded, 103.2, 107.4, and 95.8 bu/a, respectively, $LSD_{0.05}$=7.7, averaged over four locations in mid to northern Indiana at which yellow dwarf was absent, and 89.0, 66.6, and 68.1 bu/a, respectively, $LSD_{0.05}$=6.5, at Evansville. Yellow dwarf severity on the three cultivars, respectively, at Evansville was 0, 3, and 4 (0=no symptoms to 9=severe leaf discoloration, plant stunting and little or no seed set). Infestation by viruliferous aphids, *Rhopalosiphum padi*, occurred in the sutumn of 2005. In 2007, INW0316, Pioneer25R47 and Roane yielded, 86.8, 86.2, and 78.2 bu/a, respectively, $LSD_{0.05}$=6.9, averaged over two locations in northern Indiana at which yellow dwarf was negligible. Grain yield averaged over three locations in central and southern Indiana at which yellow dwarf was moderately severe was, for the three cultivars 84.0, 78.6, and 73.8 bu/a, respectively, LSD=7.9. Yellow dwarf severity at these three locations averaged, respectively for the three cultivars, 0, 4 and 3.5, LSD=0.7. Infestation by viruliferous aphids occurred in autumn 2006 and in spring 2007 at Evansville.

Breeding/genetics. Combining multiple genes for resistance to foliar diseases, yellow dwarf, and Hessian fly in improved germ plasm and soft winter wheat cultivars adapted to Indiana.

Herb Ohm, Lingrang Kong, Xiaorong Shen, Judy Lindell, Stephen Baluch, Brett Ochs, and Kristen Rinehart.

Fusarium head blight. The chromosome segment 7EL from *Th. ponticum*, with resistance QTL, *Qfhs.pur-7EL*, was shortened to the distal one-third of T7DS·7DL7EL in wheat line P275-4 by crossing translocation line KS24-2 (T7DS·7EL) to the Chinese Spring wheat *Ph1b* deletion line. *Qfhs.pur-7EL* was mapped, by deletion bin mapping, to the distal portion of the introgressed 7EL segment. *Qfhs.pur-7EL* of P275-4 was combined with *Fhb1*, and in greenhouse tests using point inoculation (inoculation of a single floret at flowering with 500 *F. graminearum* macro spores in 10 μl dH_2O and placing a plastic bag over inoculated spikes for 3d) the disease severity averaged 0.75 diseased spikelets at 21 dai. We will carry out tests in the field under misted conditions in 2008.

Stem rust, yellow rust. We have identified and obtained germ plasm lines that have potentially new resistance to stem rust race TTKS (Ug99) and yellow rust. We have developed $F_{2:3}$ populations from crosses of the new resistant/susceptible lines. In collaboration with USDA–ARS laboratories at St Paul, MN; Pullman, WA; and Raleigh, NC; and at Purdue University for resistance to our local isolates of the causal fungal pathogens, the populations are being phenotyped for resistance. We will then screen the F_2 populations with SSR markers and map the resistance.

Marker-assisted selection. We have significantly expanded MAS as an integral part of the breeding program to combine a large number of desired QTL/genes for various important plant traits. MAS is a necessary technology to genotype parent lines for various desired traits and to plan parental combinations for efficiently combining a large number of desired plant traits.

Lab members. Lingrang Kong and Xiaorong Shen are Research Associates, Judy Lindell is a Research Molecular Biologist, and Stephen Baluch, Brett Ochs and Kristen Rinehart are doctoral students.

Interactions of wheat with virulent and avirulent Hessian fly larvae.

Christie Williams, Jill Nemacheck, Subhashree Subramanyam, Kurt Saltzmann, Marcelo Giovanini, and Stephen Baluch.

Wheat lectin deters insect feeding. During incompatible interactions, avirulent Hessian fly larvae are recognized by resistant wheat plants, resulting in the triggering a diverse set of plant defense responses. One component of this defense is the production of the HFR-1 protein. The ability of this protein to agglutinate red blood cells along with binding mannose-containing glycans demonstrates that this induced protein functions as a lectin. Because Hessian fly larvae are obligate parasites and cannot be grown in culture, feeding deterrent properties of HFR-1 were tested with *Drosophila*

melanogaster reared on artificial medium containing the protein. At low concentrations, the HFR-1 protein delayed larval development. At intermediate concentrations, larval development was arrested before pupation. At high concentrations, larvae crawled out of the medium and slowly starved to death on the side of the glass vial. These outcomes are consistent with HFR-1 lectin functioning as a feeding deterrent rather than an acute toxin.

Larvae manipulate wheat nutrient content. Virulent Hessian fly larvae manipulate their host plants to provide a good environment for their development. One plant component that is altered by these larvae is the production of certain amino acids. The increased production of methionine, histidine and phenylalanine is important because these essential amino acids must be obtained by the insect in its diet. Phenylalanine and tyrosine are necessary for the production of insect cuticle. Other amino acids that increase in abundance may contribute to energy production and other processes that benefit the larvae.

Lab members. Subhashree Subramanyam is a Purdue University postdoctoral researcher. Kurt Saltzmann is a USDA-ARS postdoctoral researcher. Jill Nemacheck is a research technician. Stephen Baluch is a joint Ph.D. student with Herb Ohm. Marcelo Giovanini, currently a corn breeder for Monsanto in his home country of Brazil, was a joint student with Herb Ohm.

Molecular interactions between Hessian fly and wheat.

Richard Shukle, Alisha Johnson, Kristin Saltzmann, Weilin Sun, and Jacob Shreve.

The objective of our research is to gain insight into the molecular interactions between Hessian fly and wheat. In this regard, previous research in our laboratory was directed toward transcriptional profiling of genes expressed in the larval Hessian fly during interactions with susceptible and resistant wheat. Results indicated that on susceptible wheat genes involved in establishing a feeding site, manipulation of host-plant cells, feeding and growth/development were up-regulated, while on resistant wheat genes involved in responding to stress and disruption of homeostasis (DAD–defender against apoptotic cell death, heat shock, detoxification, antioxidant defense, and excretion) were up-regulated. This supports the assumption that larvae on resistant plants encounter either toxic plant compounds, feeding deterrents, or cannot manipulate host-plant cells to develop a nutritive tissue to feed on. Of particular interest from this work was the transcriptional profile of one family of secreted salivary gland proteins (SSGPs). Results indicated the transcript levels for the SSGPs were equal in larvae at 6 hours on susceptible and resistant wheat. However, the transcript level in larvae on resistant wheat did not increase and showed a downward trend, whereas on susceptible wheat, the transcript level continued to increase peaking at 24 hours, suggesting that a rapid defense response in resistant wheat precludes the up-regulation of the genes encoding this family of SSGPs. Current research to further dissect Hessian fly/wheat interactions at the molecular level and identify novel approaches to genetically engineered resistance are focused toward (1) RNAi as a function genomics tool for genes expressed during Hessian fly/wheat interactions; (2) comparative salivary gland transcriptomics between divergent Hessian fly populations that differ in virulence to genes for resistance to reveal unique SSGPs involved in host-plant/tissue adaptation; and (3) electron microscopy studies of the larval midgut during compatible and incompatible interactions with wheat to reveal if the midgut is a target for toxic plant compounds in larvae on resistant plants and if so the possible mode of action.

Lab members. Alisha Johnson, USDA–ARS Research Technician and Ph.D. student; Kristin Saltzmann, USDA–ARS Research Technician; Weilin Sun, collaborating postdoctoral associate; and Jacob Shreve, undergraduate technician.

Population genetics of Hessian fly.

Brandon Schemerhorn, Yan M. Crane, Richard Smith, Philip Morton and Jennifer Sanders.

The objective of our research is to investigate the effects of genotype interaction between wheat and the Hessian fly on the genetic stability of the pest populations and risks to deployment of new resistance resources. In order to answer these questions, we have developed a microsatellite library and genetically mapped a set or markers to assess the population dynamics of the Hessian fly. We are currently using these markers to investigate geographic distance and biotype forms as barriers to gene flow. At this point, we have determined that in the southeastern United States, the barriers to gene flow between populations are not limited by distance, but rather geographical and climactic similarities in the

areas where populations were collected. Currently, this research has expanded into the Midwest, including Indiana, to determine if this trend will hold true. We currently are assessing E-chromosome makeup by AFLPs, the creation of a subtractive hybridization library and by in situ analysis of BAC clones from available libraries to investigate geographic distance and biotype forms as barriers to gene flow. We also have been working towards the elucidation of the processes of metabolic resistance to insecticides in the Hessian fly. The current data suggest that oxidative burst patterns are suggesting a complex cascade pathway whose function is yet to be determined.

Lab Members. Dr. Yan M. Crane, USDA–ARS Research Technician; Richard Smith, USDA–ARS Research Technician; Philip M. Morton, Ph.D. student; and Jennifer Sanders, undergraduate technician.

Fusarium graminearum: Regulatory genes for DON.

Jin-Rong Xu.

The whole-genome microarray of *F. graminearum* and targeted deletion mutants are being used to identify regulatory genes controlling DON accumulation in infested grains.

Septoria tritici blotch.

Disease resistance (Stephen Goodwin, Jessica Cavaletto, Ian Thompson, Emily Helliwell, and Alisa Ponomarenko). Additional screening was done to find molecular markers closely linked to Septoria tritici blotch resistance gene *Stb2* on chromosome 3BS. Approximately 350 lines of an F_3 recombinant-inbred population, derived from a cross between the Swiss cultivar Arina and the doubled-haploid DH115, were screened for resistance to *M. graminicola*, and 20 SSR markers showing polymorphism between the parents were tested on the progeny. Linkage and QTL analyses identified five markers closely linked to *Stb2*, including two markers not previously identified as mapping to this region. Of these, marker *Xwmc754* was found to be closely linked to *Stb2*, and may be useful in future applications of marker-assisted selection.

Differences among susceptible and resistant interactions of *M. graminicola* on wheat and the non-host barley were compared to reciprocal interactions of the barley pathogen *Septoria passerinii* on barley and wheat. Trypan blue staining showed that *M. graminicola* germinates on barley leaves and enters via the stomata similarly to wheat, but fungal growth stagnates shortly after penetration. Staining with 3,3-diaminobenzidine showed an accumulation of H_2O_2 around stomatal cells and, later, epidermal cells, indicating a possible hypersensitive response. Quantitative real-time PCR showed differences in fungal biomass among the interactions. These data show that *M. graminicola* penetrates cells and triggers production of reactive oxygen species, providing further evidence for an active defense response of barley to this wheat pathogen.

Large-scale, cDNA-AFLP profiling previously identified numerous genes with increased expression during the resistance response of wheat to the Septoria tritici blotch fungus, *M. graminicola*. To test whether these genes were associated with resistance responses, their levels of expression were measured at 12 time points from 0 to 27 days after inoculation (DAI) in two resistant and two susceptible cultivars of wheat by real-time quantitative PCR. None of these genes was expressed constitutively in the resistant wheat cultivars. Instead, infection of wheat by *M. graminicola* induced changes in expression of each gene in both resistant and susceptible cultivars over time. Four genes were induced from about 10 to 60 fold only at early stages (3 h-1 DAI) during the incompatible interactions. Nine other genes had bimodal patterns with both early (1-3 DAI) and late (12-24 DAI) peaks of expression. The remaining gene had a trimodal pattern of expression in the resistant cultivar Tadinia. Therefore, the resistance response of wheat to *M. graminicola* is not completed during the first 24 hours after contact with the pathogen, as thought previously, but can extend into the period from 18 to 24 DAI when fungal biomass increases dramatically in susceptible interactions. Significant differential expression of the defense-related genes between the resistant and susceptible wheat cultivars and RILs after inoculation with *M. graminicola* suggests that these genes may play a major role in the resistance mechanisms of wheat.

Fungal genomics (Goodwin lab). The trigger for the switch from biotrophic to nectrotrophic growth of *M. graminicola* in wheat and the mechanisms of resistance in the host are not known. To better understand the biology of this pathosystem, the genome of the pathogen was sequenced completely at the Joint Genome Institute by filling in the gaps in an 8.9×

draft sequence. The essentially finished sequence contains 18 chromosomes from telomere to telomere, plus five fragments. Four of the five fragments contain telomeres so they presumably make up two additional chromosomes for a total of 20. A comparative bioinformatics analysis of *M. graminicola* with seven other sequenced fungal genomes revealed that *M. graminicola* possessed fewer enzymes than expected for degrading plant cell walls. Analyses of grass-infecting pathogens versus those from other hosts indicated that the suites of cell wall-degrading enzymes were tailored to break down the cell wall compositions of their particular hosts. The frequency of transposable elements in the genome of *M. graminicola* was intermediate between those of other sequenced fungi. Many long (> 10 kb) retrotransposons were identified in the finished genome compared to the draft sequence, indicating the need for finishing of other fungal genomes. Availability of the finished genome for *M. graminicola* should greatly aid research on this organism and will help to understand its interaction with wheat.

To aid in comparative genomics, the sequence of the related banana pathogen *M. fijiensis* was obtained and released as a 7.1× draft during August of 2007. This genome was almost twice the size (73 Mb) of *M. graminicola* but had about the same number of genes. Much of the increased genome size seems to be due to higher numbers of families and higher copy numbers of retrotransposons in the genome of *M. fijiensis* compared to that of *M. graminicola*. The mitochondrial genomes of both species were obtained and also differed in size, with that of *M. fijiensis* about twice that of *M. graminicola*. Numbers of tRNA genes and unknown ORFs were higher in *M. fijiensis*. The set of structural genes within the two genomes were similar, but two genes in *M. fijiensis* contained introns that were absent from their homologs in *M. graminicola*. The reason for the increased genome size of *M. fijiensis* relative to that of *M. graminicola* is not known.

Lab members. Jessica Cavaletto and Dr. Ian Thompson are USDA–ARS Biological Science Research Technicians. Braham Dhillon is a Ph.D. student working on bioinformatics. Emily Helliwell completed her M.S. degree during the summer of 2007 and is now in a Ph.D. program at Pennsylvania State University. Alisa Ponomarenko also completed her M.S. during the summer of 2007 and is now in a Ph.D. program in bioinformatics at Purdue University.

Wheat viruses.

Epidemiology of wheat viruses (J.M. Anderson and B. Portwood). In this study, a multiplex reverse transcription polymerase chain reaction (M-RT-PCR) method was used to identify which viruses are present in field samples from 22 counties in Indiana. These samples were initially identified because they appeared to have viral disease symptoms. The multi-plex PCR can simultaneous detection and discrimination of eight viruses including five strains of barley/cereal yellow dwarf virus (B/CYDV), wheat spindle streak mosaic virus (wssmv), soil-borne wheat mosaic virus (SBWMV), and Wheat streak mosaic virus (WSMV). Analysis of these samples indicated that all 22 samples contained virus and all had mixed infections. BYDV-RMV was the least abundant virus as it was detected in five of the samples and generally appeared to present in very low levels. When the sample had B/CYDV typically they contained BYDV-PAV, -SGV, -MAV, and CYDV-RPV. WSSMV and SBWMV were present in 50% and 41% of the samples, respectively. Perhaps the most surprising result was the high percentage of samples (41%) that contained WSMV. This disease is transmitted by a mite that prefers a drier climate than that found in Indiana and, therefore, has not been considered to be a problem in Indiana or the Eastern U.S. These data suggest that this disease is more prevalent than previously thought. Although this is a very limited sample set collected just in the 2007 spring/summer these results demonstrate the utility of this method as a virus detection method and a tool for epidemiological studies.

Wheat-*Thinopyrum* mosaic chromosomes (K. Card and J.M. Anderson). A large number of *Thinopyrum*-wheat translocation recombinants in which the translocation chromosomes consist of an array of wheat and *Th. intermedium* chromatin segments were previously identified. These recombinants have been further characterized using additional DNA markers and are proving to be an excellent set of materials for identifying wheatgrass chromatin DNA markers.

Lab members. Brian Portwood is a USDA–ARS Biological Science Research Technician. Katie Card is currently a USDA–ARS Biological Science Research Technician at NCAUR in Peoria Illinois. Mahua Deb is currently a Research Associate with Chembiotek Research International, India.

Research personnel.

Paul Werner, an M.S. student with Herb Ohm, thesis research on characterizing and mapping yellow dwarf and crown rust resistance in oat, completed degree requirements in August 2007 and has joined his family's seed production business in Minnesota. Xiaorong Shen is the lab manager with a private pharmaceutical firm in Princeton, NJ.

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KANSAS

KANSAS AGRICULTURAL STATISTICS
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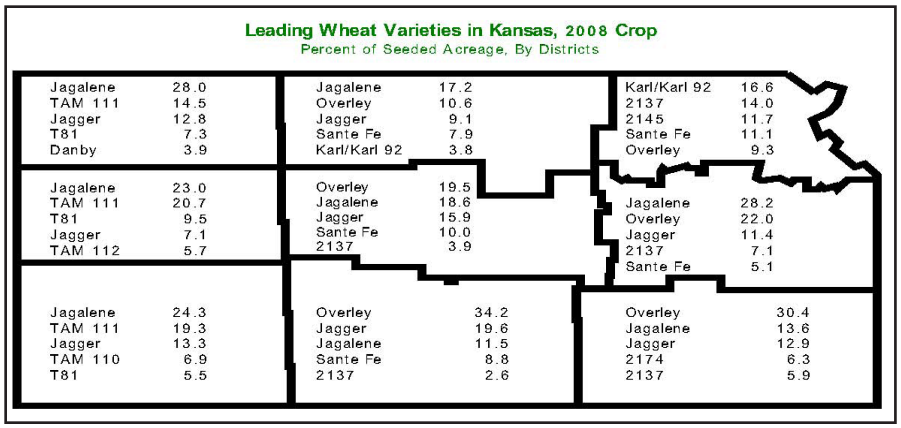
Jagalene recaptures number one.

Jagalene became the leading cultivar of wheat seeded in Kansas for the 2008 crop. Overley held this position last year. Accounting for 18.0 percent of the state's wheat, Jagalene was the most popular cultivar in five of the nine districts. Overley moved down to second place, with 17.3 percent of the acreage. Overley decreased 6 points but was the most popular cltivar in three of the nine districts. Jagger came in third at 14.7 percent, down 2.4 points. TAM 111 remained in fourth place, with 7.3 percent of the acreage. Sante Fe moved up to fifth place with 5.8 percent of the state's acreage. T81 moved up to sixth place at 2.8 percent while the KSU-maintained cultivar 2137 moved down to seventh place at 2.8 percent. TAM 112 moved up to eighth place with 1.6 percent of the acreage. TAM 110 moved down to ninth place with 1.4 percent of the acreage. Danby, a hard white cultivar, rounded out the top ten at 1.2 percent. Acres planted with blended cultivars were not included in the rankings by cultivar. Blends accounted for 10.4 percent of the state's planted acres and were used more extensively in the north-central, northeast, and central areas of the state. Out of the total acres planted w ith blends, 51.3 percent included Jagalene in the blend, 45.4 percent had Overley in the blend, and 44.7 included Jagger. Hard white cultivars accounted for 1.9 percent of the state's acreage. Danby was the leading hard white cultivar, accounting for 59 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 2008 crop and percent of seeded acreage.

1. Jagalene	18.0	6. T81	2.8
2. Overley	17.3	2137	2.8
3. Jagger	14.7	8. TAM 112	1.6
4. TAM 111	7.3	9. TAM 110	1.4
5. Santa Fe	5.8	10. Danby	1.2



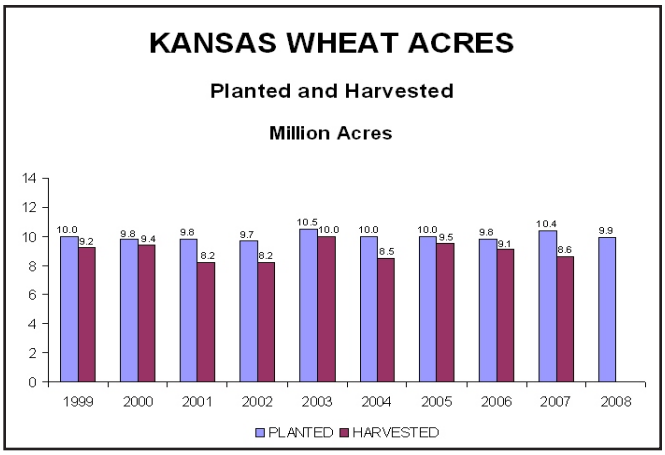


Table 2. Distribution of Kansas winter wheat cultivars, 2008 crop (— = cultivar not reported in this district; 0 = < 1%).

	Agricultural Statistics Districts									
Cultivar	NW	WC	SW	NC	C	SC	NE	EC	SE	State
	percent of seeded acreage									
Jagalene	28.0	23.0	24.3	17.2	18.6	11.5	5.0	28.2	13.6	18.0
Overley	0.6	0.8	0.6	10.6	19.5	34.2	9.3	22.0	30.4	17.3
Jagger	12.8	7.1	13.3	9.1	15.9	19.6	4.0	11.4	12.9	14.7
TAM 111	14.5	20.7	19.3	1.9	3.6	0.7	—	—	—	7.3
Santa Fe	0.0	0.0	—	7.9	10.0	8.8	11.1	5.1	5.1	5.8
T81	7.3	9.5	5.5	0.5	0.2	0.7	—	—	—	2.8
2137	1.0	3.6	1.7	2.6	3.9	2.6	14.0	7.1	5.9	2.8
TAM 112	2.8	5.7	4.1	0.3	0.3	0.3	—	—	—	1.6
TAM 110	0.4	4.2	6.9	—	—	—	—	—	—	1.4
Danby–HWWW	3.9	1.8	3.1	0.2	0.8	—	—	0.0	—	1.2
Cutter	0.1	0.2	0.1	1.1	0.5	2.0	0.2	0.2	0.2	0.9
Postrock	0.9	0.1	0.6	1.4	1.0	1.1	0.2	3.2	0.5	0.9
2174	—	0.1	—	0.0	0.5	1.8	—	1.9	6.3	0.9
Thunderbolt	3.4	2.3	0.7	0.4	0.6	0.1	—	—	—	0.9
Karl/Karl 92	0.1	0.4	—	3.8	0.6	0.2	16.6	2.8	1.2	0.8
2145	1.0	—	—	2.6	0.9	0.1	11.7	0.8	0.8	0.6
Ike	0.6	1.2	1.1	—	0.7	0.2	—	—	0.0	0.5
Protection	—	—	0.0	0.0	0.8	0.7	0.0	—	—	0.4
Stanton	2.0	0.1	0.7	—	—	0.1	—	—	—	0.3
Wesley	1.4	0.2	—	1.3	—	—	3.5	1.2	0.2	0.3
T136	—	0.0	0.9	0.2	0.1	0.4	—	—	0.1	0.3
Hatcher	1.4	0.8	—	—	—	0.1	—	—	—	0.3
Fuller	—	0.0	—	0.1	0.8	0.3	0.7	0.1	0.1	0.3
Keota	1.7	0.3	—	—	0.2	—	—	—	—	0.2
NuHills–HWWW	0.5	0.5	0.6	—	—	0.0	—	—	—	0.2
Larned	—	0.0	0.8	—	0.1	0.2	—	—	—	0.2
Above	1.2	0.3	0.3	—	—	—	—	—	—	0.2
Dumas	0.5	—	1.1	—	—	—	—	—	—	0.2
TAM 107	0.4	0.7	0.3	—	0.2	0.0	—	—	—	0.2
Dominator	0.1	—	—	0.3	0.8	—	0.1	0.9	—	0.2
Shocker	—	—	0.1	0.0	0.7	0.1	0.0	—	0.2	0.2
Millennium	1.3	0.2	—	0.2	—	—	0.1	0.8	0.0	0.2
Ankor	—	1.3	0.3	—	—	—	—	—	—	0.2
Trego–HWWW	0.4	0.4	0.3	0.4	—	—	—	—	—	0.2
2163	—	—	—	—	0.4	0.2	1.0	1.8	0.1	0.2
Blends	4.6	5.6	6.0	34.2	11.9	7.2	18.2	2.7	3.8	10.4
Other HWWW Cultivars	0.2	0.2	2.2	0.1	0.1	0.1	—	0.0	0.0	0.3
Other HRWW Cultivars	6.9	8.7	5.1	3.5	6.3	6.7	4.3	9.6	14.8	6.5
All Soft Red Cultivars	—	—	—	0.1	0.0	0.0	—	0.2	3.8	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, 1999–2008.

Cultivar	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008
	percent of seeded acreage									
Jagalene	—	—	—	—	—	3.0	21.2	27.2	23.1	18.0
Overley	—	—	—	—	—	0.1	2.2	16.3	23.3	17.3
Jagger	29.2	34.0	35.8	42.8	45.2	40.9	28.2	19.7	17.1	14.7
TAM 111	—	—	—	—	—	—	1.5	2.2	4.0	7.3
Santa Fe	—	—	—	—	—	—	—	0.2	1.3	5.8
T81	—	0.2	0.2	0.8	0.6	1.8	1.6	2.6	2.0	2.8
2137	22.0	23.1	22.3	15.5	13.3	8.6	5.7	3.1	2.9	2.8
TAM 112	—	—	—	—	—	—	—	—	0.4	1.6
TAM 110	0.5	1.3	2.8	3.0	3.8	4.2	3.3	2.2	1.5	1.4
Danby–HWWW	—	—	—	—	—	—	—	—	0.7	1.2
Cutter	—	—	—	—	—	0.7	1.7	1.8	2.1	0.9
Postrock	—	—	—	—	—	—	—	—	—	0.9
2174	—	1.1	3.0	3.1	3.1	2.8	3.0	1.2	1.1	0.9
Thunderbolt	—	—	0.2	0.6	0.8	1.4	1.7	1.1	0.4	0.9
Karl/Karl 92	5.9	3.5	3.3	3.6	3.2	2.3	1.5	1.1	1.0	0.8
2145	—	—	—	—	—	—	1.5	2.2	0.8	0.5
Ike	5.5	4.1	3.6	2.6	2.1	2.0	1.4	1.1	1.2	0.5
Protection	—	—	—	—	—	—	—	0.2	0.3	0.4
Stanton	—	—	—	0.1	0.6	1.4	1.4	0.8	0.2	0.3
Wesley	—	—	—	—	0.1	0.1	0.1	0.3	0.4	0.3
T136	—	—	—	—	—	—	—	—	—	0.3
Hatcher	—	—	—	—	—	—	—	—	—	0.3
Fuller	—	—	—	—	—	—	—	—	—	0.3
Keota	—	—	—	—	—	—	—	—	—	0.2
NuHills–HWWW	—	—	—	—	—	—	0.3	0.2	0.2	0.2
Larned	1.9	1.2	1.0	0.9	0.8	0.4	0.3	0.2	0.3	0.2
Above	—	—	—	—	—	0.2	0.1	0.1	—	0.2
Dumas	—	—	—	—	—	0.1	0.2	—	—	0.2
TAM 107	8.3	6.3	5.3	2.9	2.3	1.3	1.0	0.4	0.1	0.2
Dominator	0.8	1.4	1.5	2.0	2.2	1.5	1.1	0.8	0.4	0.2
Shocker	—	—	—	—	—	—	—	—	—	0.2
Millennium	—	—	—	—	—	—	—	0.1	0.1	0.2
Ankor	—	—	—	—	—	—	—	—	—	0.2
Trego–HWWW	—	—	0.3	0.8	1.8	3.5	2.9	0.4	0.5	0.2
2163	3.4	2.3	2.0	1.3	0.8	0.3	0.2	0.2	0.2	0.2
Blends	6.1	7.5	7.0	11.4	12.8	15.2	11.3	10.0	10.4	10.4
Other HWWW Cultivars	—	0.2	0.5	0.3	0.9	1.4	0.7	0.7	0.3	0.3
Other HRWW Cultivars	16.4	13.8	11.2	8.1	5.5	5.3	6.5	5.7	3.9	6.5
All Soft Red Cultivars	0.0	0.0	0.0	0.1	0.1	0.0	0.1	0.1	0.1	0.1
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

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Root growth of a drought-resistant and drought-sensitive wheat under compaction.

M.B. Kirkham.

The four soil physical factors that affect plant growth are water, temperature, aeration, and mechanical resistance (compaction). The first three are well studied (Kirkham, 2005), but relatively little information exists concerning the effect of compaction on root growth. One way to achieve different compactions is to grow plants in glass tubes of different diameters, which regulate the rigidity of the pore structure (Wiersum 1957). The objective of this experiment was to determine if roots of a drought-resistant winter wheat cultivar KanKing and a drought-sensitive winter wheat cultivar Ponca varied in their ability to penetrate soil in glass test tubes of two different diameters.

Materials and Methods. The wheat seeds were germinated in soil, and 11 days after planting were transplanted into 24 test tubes of two different diameters (8 or 10 mm internal diameter; all test tubes were 200 mm long), one plant per test tube. The day of transplanting was designated "Day 0" of the experiment. The test tubes were filled with a commercial potting soil. The test tubes were placed in a growth room. The experiment was a completely randomized one with two cultivars, two compactions, and six replications. Root length was monitored at noon daily between 5 and 26 days after transplanting. (Days 6, 8, and 20-22 were not monitored, because I as out of town.) Temperature at time of measurement averaged 20°C. The flux density of incident light, provided by cool-white fluorescent lamps, was 260 μmol m^{-2} s^{-1} from 06:00 to 20:00 h. The plants were kept well watered during the experiment by adding a few milliliters of water (usually daily) to the tubes. The exact amounts were not recorded, but they were less than 5 ml. Shoots were harvested (cut) 26 days after transplanting, and roots were extracted by wet sieving the soil. Dry weights of roots and shoots were determined.

Table 1. Root length (cm) of a drought-resistant (KanKing) and a drought-sensitive (Ponca) winter wheat grown in test tubes of two different diameters (8 or 10 mm). Mean and standard error are shown (n=6).

Days after transplanting into test tubes	KanKing, 8 mm	Ponca, 8 mm	KanKing, 10 mm	Ponca, 10 mm
5	0.33±0.16	1.67±1.11	1.17±0.65	0.50±0.25
7	1.17±0.54	4.50±1.85	3.67±1.33	5.42±1.53
9	2.00±0.66	4.92±1.80	5.42±1.87	7.33±1.78
10	3.08±1.12	5.92±1.90	6.58±1.44	7.33±1.78
11	3.92±1.46	7.50±2.41	8.42±1.72	11.92±2.18
12	6.08±2.61	8.50±2.56	10.42±2.16	15.08±1.45
13	7.00±3.05	11.33±3.29	10.67±2.04	14.67±1.29
14	7.17±3.07	10.25±3.56	11.33±2.00	15.67±0.46
15	8.08±3.52	11.67±2.98	13.75±2.35	15.83±0.46
16	8.42±3.54	11.25±3.03	13.75±2.78	16.58±0.52
17	8.42±3.83	12.00±2.91	14.58±2.51	17.58±0.45
18	10.08±3.45	12.42±3.09	14.50±2.39	18.00±0.49
19	9.17±3.96	11.75±3.30	14.42±2.46	17.83±0.66
23	9.25±4.13	12.58±3.07	15.08±1.80	18.50±0
24	9.25±4.13	12.00±3.67	15.25±1.78	18.50±0
25	9.33±4.09	12.33±3.16	15.25±1.78	18.50±0
26	9.25±4.13	14.92±3.02	15.25±1.78	18.50±0

Results and Discussion. Results for root length are shown in Table 1. After the first day of measurement, Ponca had a longer root length than KanKing in both the 8- and 10-mm diameter test tubes. By the end of the experiment, the roots of Ponca had reached the bottom of the test tubes with the 10-mm diameter and they were still growing in the test tubes with the 8-mm diameter, but those of KanKing had stopped growing under both treatments. The better growth of Ponca compared to KanKing under well watered conditions agrees with earlier results (Kirkham, 1989).

The dry weights of the roots at harvest in the 8- and 10-mm diameter test tubes were as follows: KanKing (mean ± SE): 0.625±0.025 g and 0.639±0.037 g, respectively; Ponca: 0.601±0.015 g and 0.644±0.012 g, respectively. The dry weights of the shoots in the 8- and 10-mm diameter test tubes were as fol-

lows: KanKing (mean ± SE): 0.586±0.004 g and 0.597±0.003 g, respectively; Ponca: 0.588±0.003 g and 0.601±0.002 g, respectively. The differences in growth, observed in root length, were not observed in the dry-weight data. The dry weights of roots and shoots of KanKing and Ponca were similar under the two treatments, except for the roots of KanKing, which had a higher dry weight in the 8-mm diameter tubes than the roots of Ponca. This suggests that KanKing may have a wider root than Ponca, which makes penetration of its roots into a compacted soil more difficult. It also suggests that the drought resistance of KanKing may be due, in part, to a heavier, more slowly growing root compared to Ponca.

In conclusion, the data showed that a drought-sensitive cultivar of winter wheat, Ponca, was better able to penetrate soil in a restricted root volume than a drought-resistant cultivar, KanKing. The results suggested that Ponca may have a thinner root than KanKing, which allows its roots to penetrate more easily into the pore space between solid particles in a compacted soil compared to KanKing.

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Wiersum LK. 1957. The relationship of the size and structural rigidity of pores to their penetration by roots. Plant Soil 9:75-85.

News.

A new graduate student, Nicole A. Rud (nrud@ksu.edu), has joined the laboratory. She is getting her master's degree jointly under Professor Kimberly A. Williams (kwilliam@ksu.edu) in the Department of Horticulture, Forestry, and Recreational Resources and M.B. Kirkham (mbk@ksu.edu). Nicole is studying the causes of the physiological disorder, edema.

Mr. Prasanna Ayyaru Thevar (prasan@ksu.edu), a Master's degree student, continues his studies. He is determining the transpiration efficiency of different lines of sorghum.

Mr. Intkhab Hazoor Wahla, the Ph.D. student from the University of Agriculture, Faisalabad, Pakistan, who spent six months in the laboratory last year, has returned to Pakistan. The results of his study have been published (Wahla and Kirkham, 2007).

Publications.

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Wahla IH and Kirkham MB. 2007. Heavy metal displacement in salt-water-irrigated soil during phytoremediation. Env Pollution (In press).

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Notice of release of KS08WGGRC50 wheat streak mosaic virus- and Triticum mosaic virus-resistant hard red winter wheat germ plasm.

B.S. Gill, B. Friebe, L.L. Qi, D.L. Wilson, W.J. Raupp, A.K. Fritz, D.L. Seifers, T.J. Martin, and M.O. Pumphrey.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS08WGGRC50 hard red winter wheat germ plasm with resistance to wheat streak mosaic virus and *Triticum* mosaic virus for breeding and experimental purposes. Scientists participating in this development were B.S. Gill, B. Friebe, L.L. Qi, D.L. Wilson, and W.J. Raupp, Department of Plant Pathology, Kansas State University, Manhattan, Kansas; A.K. Fritz, Department of Agronomy, Kansas State University, Manhattan, Kansas; D.L. Seifers and T.J. Martin, Kansas State University, Agricultural Research Center, Hays, Kansas; and M.O. Pumphrey, USDA-ARS Plant Science and Entomology Research Unit, Department of Agronomy, Kansas State University, Manhattan, Kansas.

KS08WGGRC50 is an improved derivative of KS93WGRC27 with the resistance gene *Wsm1* in the form of a wheat–*Th. intermedium* recombinant chromosome T4DL·4DS-4Ai#1S (rec213). The recombinant chromosome consists of the long arm of wheat chromosome 4D, most of the short arm of 4D, and a shortened distal segment derived from the short arm of the *Th. intermedium* chromosome 4Ai#1 harboring *Wsm1*. *Wsm1* is temperature sensitive and confers resistance to wheat streak mosaic virus and *Triticum* mosaic virus at low temperature around 18°C, whereas at higher temperatures around 24°C *Wsm1* breaks down and is no longer effective. KS08WGGRC50 is derived from the cross KS93WGRC27/2*TA3809(CSph1b)//Wichita/3/2*Overley. The F_2-derived families are homozygous for *Wsm1* but are segregating for other traits.

Small quantities (3 grams) of seed of KS08WGGRC50 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506. Genetic material of this release will be deposited in the National Plant Germplasm System where it will be available for research purposes, including the development of new cultivars.

Development and characterization of wheat–Leymus racemosus translocation lines with resistance to Fusarium head blight.

B. Friebe, L.L. Qi, B.S. Gill, and P.D. Chen.

Working with scientists at Nanjing Agricultural University in China, we have identified a new source of resistance from the perennial grass relative *L. racemosus* (Lr). A chromosome segment (designated as 7Lr#1S) from this grass specifying resistance to FHB was transferred to a chromosome arm 7AL of wheat in the form of a translocation T7AL·7Lr#1S. This translocation stock was crossed twice with *ph1b* mutant stock. We screened 154 BC_1 plants from the cross 'T7AL·7Lr#1S / *ph1b*' using molecular markers to assay for *ph1b* and T7AL·7Lr#1S. Sixty-one plants were homozygous ph1b/ph1b and heterozygous for the translocation chromosome T7AL·7Lr#1S/7A. These plants were either backcrossed with Overley and Danby or selfed. We have developed a large, recombinant population of 1,400 BC_2 and more than 8,000 BC_1F_2 seeds. In homozygous *ph1b* genotypes, the alien 7Lr#1S arm with the gene(s) for FHB resistance is expected to recombine with homoeologous wheat arm 7AS. Meiotic pairing analysis in plants homozygous for *ph1b* and heterozygous for T7AL·7Lr#1S/7A failed to detect any metaphase I association in more than 500 PMCs, suggesting that the recovery of recombinants will be very difficult. Recently, a total of 1,150 BC_2 plants were screened using molecular markers, and three plants were found to be recombinants. Rec.124 is a proximal recombinant with the proximal 80% from 7Lr#1S and the distal 20% from 7AS. Two other recombinants, rec. 679 and rec.989, are distal recombinants with the proximal 80% from 7AS and the distal 20% from 7Lr#1S. These recombinants were confirmed by GISH indicating that the recovery of recombinants is possible, although at a very low frequency. These recombinants will be screened for scab resistance in the greenhouse. Our previous data indicated that a scab-resistance gene from *Ley-*

mus most likely resides in the distal region of the short arm of chromosome 7Lr#1. Three different recombinants provide a good opportunity to further map the FHB resistance gene to a specific chromosome region of 7Lr#1S. The FHB resistant recombinants will then be transferred to adapted wheat cultivars.

Stripe rust and leaf rust resistance from Ae. geniculata.

V. Kuraparthy, P. Chhuneja, H.S. Dhaliwal, S. Kaur, 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 probe showed three different kinds of introgressions. All three types of introgression lines showed complete and similar resistance to the most prevalent races of leaf (PRTUS25, PRTUS35, PNMQ, MCDL, and PRTUS6) 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, Overley, and NewHills adapted to the Southern Great Plains (SGP), specifically to Kansas, and to advanced breeding lines (KCB35, KCB36, and KCB37) of the KSU wheat-breeding program by standard backcrossing. Cleaved Amplified Polymorphic Sequence markers were developed as diagnostic PCR-based markers for MAS of *Lr57* and *Yr40* genes into hard winter wheats. Two different CAPS markers were developed based on EST marker (XBF200555) diagnostically detecting the alien introgressed segment in T5DL·5DS-5MgS(0.95). BC_3F_2 plants segregating for rust resistance are being evaluated in the field at two locations in Manhattan. Homozygous $BC_3F_{2:3}$ and BC_3F_4 plants with rust resistant genes will be further evaluated in the field for subsequent germ plasm release.

Because most of the wheats grown in Kansas and SGP are hard winter wheats, the quality of the germ plasm lines with *Lr57* and *Yr40* genes were analyzed by molecular characterization of the Hardness (Ha) locus. Southern hybridization indicated that the *Pina-D1* and *Pinb-D1* genes were deleted in the rust-resistant introgressions, including the translocation (T5DL·5DS-5MgS(0.95)) line used for marker-assisted selection. Because the mutations and/or deletion of *Pina-D1* and *Pinb-D1* in wheat confers hard grain texture, deletion of these genes in T5DL·5DS-5MgS(0.95) suggested that germ plasm lines containing the *Ae. geniculata* segment with the *Lr57* and *Yr40* genes will give hardness to wheat. This further implied that transfer of the alien segment with *Lr57* and *Yr40* to Kansas winter wheats does not impair their quality requirements. Using genetic analysis and molecular characterization of the EMS mutants, one additional leaf rust resistance gene *LrGen* was identified in T5DL·5DS-5MgS(0.95). This suggested that the alien introgressed segment in act like a natural gene pyramid with multiple disease resistance genes for wheat improvement.

Leaf rust resistance from Ae. triuncialis.

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

One agronomically desirable, rust-resistant introgression line T2BS·2BL-2tL(0.95) was selected and advanced to BC3F11 from a cross of hexaploid wheat and *Ae. triuncialis*. The small wheat-*Ae. triuncialis* translocation T2BS·2BL-2tL(0.95) with leaf rust resistance gene *Lr58* provides a seedling resistance. The translocation line was resistant to the most prevalent races of leaf rust in Kansas. Molecular characterization suggested that the alien introgressed *Ae. triuncilais* segment with *Lr58* was less that 3.5% of the chromosome arm 2BL of wheat. Molecular markers (*XksuH16*, *XksuF11*, and *Xbg123*) diagnostically detected the alien introgressed segment in T2BS·2BL-2tL(0.95).

The rust-resistance gene *Lr58* was transferred to the HRWW cultivars Jagger and Overley by standard backcrossing. Molecular markers and/or phenotypic selection at the seedling stage for rust resistance were used to select the backcross F_1 and homozygous F_2 plants with rust resistance. Three backcrosses were made to develop BC_3F_1 plants and homozygous BC_3F_2 plants are selected based on the diagnostic DNA-marker-based assays using the SSR marker *Xcfd50* and/or RFLP marker *XksuH16*. Homozygous $BC_3F_{2:3}$ and BC_3F_4 plants with rust-resistance genes will be evaluated in the field for subsequent germ plasm release. CAPS based diagnostic markers are being developed for marker assisted transfer of *Lr58* for wheat improvement.

Chromosome specific BAC libraries, new markers for marker-assisted breeding and wheat physical mapping.

S.K. Sehgal, W.L. Li, P. Rabinowicz, and B.S. Gill.

We are working with Dr. J. Dolezel, Czech Republic, on making chromosome-specific libraries for physically mapping the wheat genome. We grew all the double–ditelosomic stocks of Chinese Spring wheat and sent 20,000 seeds of several ditelosomic stocks (3A, 1A, 1D, 3D, and 4A) to the Dolezel laboratory. A 55,584 BAC-clone library from chromosome arm 3AS was constructed using the restriction enzyme *Hind*III and fingerprinted with the SNaPshot-based high-throughput technique. After removing clones with very small insert sizes and cross-contamination, 47,063 BAC fingerprints were used for contig assembly with FPC computer program. There are currently 1,677 contigs and 11,939 singletons. On average, there are 21 BAC clones per contig with ~235 Kb in length. The largest contig has 417 BAC clones and is ~ 2.7 Mb in length. The BAC clones in the assembly provide 75% coverage of the chromosome arm 3AS (Gill et al. 2008).

To anchor the BAC contig to genetic and deletion-bin maps, the 68 plates of the BAC library were pooled in six dimensions, 190 BAC pools distributed to the mapping labs, and 408 EST-STS primer pairs designed. A total of 145 EST–STS markers have been mapped to 3AS and 80 mapped to individual BACs using the BAC pooling strategy. Over 100 contigs have been anchored using this approach. From the BAC end sequences, we also designed primer pairs for 234 SSR and 240 genic STS markers. Polymorphisms were screened for the markers developed by this project and those previously mapped to 3AS, between the parental lines *T. monococcum* subsp. *aegilopoides* and subsp. *monococcum*, from which a mapping population of 94 recombinant inbred lines was derived. Currently, 41 (30 SSR, 5 EST-STS, and 8 genic STS) markers are polymorphic and 18 placed in a linkage map. The map is collinear with the 3A map of hexaploid wheat.

We have sequenced the ends of 9,984 BAC clones and obtained 16,795 high-quality BESs with an average read-length of 500 bp and a total length 8.3 Mb of genomic sequences. About 6.2% of the BESs are genic and 74% are repeated sequences, similar to the BES composition of the 3B library. All the BESs are submitted to GenBank. From the BESs, we identified 1,057 microsatellite markers for the 3AS arm and designed primer pairs for 234 SSR and 240 genic STS markers. We have established collaboration with Dr. Gina Brown-Guedira, USDA–ARS, for testing these markers for their utility in wheat breeding.

Personnel.

Three new students joined the WGGRC laboratories in 2008, Bhanu Kalia and Shankar Rao, working toward their Ph.D. degrees, and Nolan Rothe, working toward an M.S. degree. Two new Research Associates, Calli Bi and Jia Li, are both Research Associates from the Peoples Republic of China.

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M. Tilley, F.E. Dowell, B.W. Seabourn, T.C. Pearson, J.D. Wilson, E.B. Maghirang, S.H. Park, S.R. Bean, T.J. Herald, F. Xie, Y.R. Chen, D.L. Brabec, J.E. Throne, O.K. Chung, F.H. Arthur, M.S. Caley, and J.F. Campbell.

A rapid, small-scale method to evaluate dough viscoelastic properties

F. Xie and B.W. Seabourn

The viscoelastic properties of dough (i.e., extensibility and resistance to extension) influence each step of the baking process, as well as the quality of the final product, and thus are important quality factors to consider in the selection of suitable lines for advancement in wheat-breeding programs. The objective of this study was to develop a rapid small-scale method to evaluate dough extensibility and resistance to extension properties. A total of 20 HRWW flour samples varying in protein content and rheological properties were studied. The standard extensigraph method and a small-scale texture analyzer (TA) method utilizing a Kieffer rig were compared and used as reference methods for a new near infrared spectroscopy (NIRS) method. Spearman rank correlation coefficient (r) between extensibility measured

by Extensigraph and by TA was 0.85, whereas that of resistance to extension was 0.71. The coefficient of determination (R^2) between resistance to extension measured by the NIRS and by extensigraph was 0.90 with a relative predictive determinate (RPD) of 3.4; that of extensibility was 0.86 with an RPD of 3.4. The high correlation between the NIRS and standard extensigraph measurements showed that the NIRS technique had excellent potential as a rapid small-scale method to predict both dough extensibility and resistance to extension.

Adaptation of polyphenol oxidase measuring methods (AACCI Method 22-85) for wheat meal and flour and their relationship to alkaline noodle color.

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

Noodle darkening is catalyzed by polyphenol oxidase (PPO) activity, and a method for measuring PPO activity of wheat kernels has been approved by the AACCI. Here we modified that PPO method (AACCI Method 22-85) for whole wheat meal and refined flour and measured PPO on 76 samples including 72 HRWW samples from the Southern Regional Performance Nursery (SRPN, n=46) and the Wheat Quality Council (WQC, n=26) harvested in 2002, and four hard white wheats grown (2003) in Kansas. The modified method was less time consuming (10 min vs. 60 min for reaction time) and less laborious. Its repeatability for wheat meal was the best (coefficient of variance, CV = 3.0%), followed by flour (CV = 9.8%), and kernel (CV = 12.4%). The correlations (r, n = 76) between kernel and meal, kernel and flour, and meal and flour PPO levels were 0.75, 0.56, and 0.55 ($P<0.0001$), respectively. The meal PPO showed the highest negative correlation (r = -0.73****) with noodle brightness (L*), followed by kernel (r = -0.63****) and flour (r = -0.44**, $P<0.05$) for SRPN samples and Lakin (n = 47).

Applying single-kernel sorting technology to developing scab-resistant lines.

F.E. Dowell and E.B. Maghirang.

We are using automated, single-kernel near-infrared (SKNIR) spectroscopy instrumentation to sort Fusarium head blight infected kernels from healthy kernels and to sort segregating populations by hardness to enhance the development of scab-resistant hard and soft wheat cultivars. We sorted three replicates of 192 samples into a damaged fraction yielding an average of 61.3 ppm DON and a healthy fraction yielding an average of 0.73 ppm DON. This collaborative work with Dr. Gene Milus and Peter Horevaj investigated the resistance of SRWW lines to DON and NIV chemotypes of *F. graminearum*. In another study, we also sorted the soft portion of a 'hard x soft' cross into FHB-infected and healthy fractions, and likewise sorted the hard portion into FHB-infected and healthy fractions. The 'hard x soft' crosses were separated into the hard and soft portions in 2006 where the respective portions were inoculated and planted. The 2007 scabby and healthy fractions of the hard and soft lines will be planted this autumn to determine if our sorting will result in populations with FHB resistance. This work is in coöperation with Dr. Anne McKendry and Dr. Stephen Baenziger. Other work in coöperation with Dr. Stephen Wegulo, Julie Breathnach, and Dr. Stephen Baenziger used the automated SKNIR system to rapidly assess lines for FHB resistance by running multiple samples and obtaining a count of infected and healthy kernels. We have done this for about 300 lines and the information is being used to select resistant lines for further testing.

Characterization of chemically modified waxy, partially waxy, and wild type tetraploid wheat starch.

L.E. Hansen, D.S. Jackson, R.A. Graybosch, J.D. Wilson, and R.L. Wehling.

Durum wheats contain two granule-bound starch synthase (GBSS) genes (*wx-A1*and *wx-B1*) controlling amylose synthesis; the other major starch polymer in durum wheat is amylopectin. Starches with little or no amylose are waxy. A GBSS null (nonproducing) gene results in a starch granule with reduced amylose content, or a partial waxy character. Sets of wild type, partial waxy (wx-A1 null or wx-B1 null), and waxy (wx-A1 and wx-B1 double null) durum wheat lines were developed in several genetic backgrounds. Seed from the individual genotypes, wild type to full waxy, were composited across genetic backgrounds with the intent of removing confounding genetic background effects. The starches from each genotype from two crop years were isolated using dough ball washing followed by flow table separa-

tion. Protein (0.1% to 0.4% dwb), lipid (0.0% to 0.3% dwb), and amylose (0% to 30% dwb dependent upon genotype) contents in the isolated starches were determined. These isolated starches had mostly large granules with a size distribution profile similar to commercially prepared waxy or wild type starches. Hydroxypropylation using propylene oxide was performed three times on each sample, resulting in an average molar substitution of 0.040 (± 0.010). Rapid-visco analyses were performed and profile changes, defined as the average of the mathematical difference of substituted minus native results in cp of the pasting curves for waxy (peak viscosity, 176; breakdown, 329; final viscosity, -206; setback, -53.5; and pasting time, -0.8) and wild type (peak viscosity, 510; breakdown, 677; final viscosity, 646; setback, 813; and pasting time, -2.2) were observed. Substituted fully waxy starches had increased peak viscosities, breakdowns, reduced final viscosities, setbacks, and pasting times. Regular (full wild type) substituted starches had increased peak viscosities, breakdowns, final viscosities, setbacks, and decreased pasting times. These modified forms of starches are used as thickeners in foods and frozen preparations such as pie fillings, sauces, gravies, and salad dressings. Rapid-visco analyses results for the partial waxy genotypes and a phosphorus di-ester cross-linking reaction will also be presented.

Digital image analysis of cereals.

J.D. Wilson.

Image analysis is the extraction of meaningful information from images, mainly digital images by means of digital-processing techniques. The field was established in the 1950s and coincides with the advent of computer technology, as image analysis is profoundly reliant on computer processing. As computer sciences has expanded with respect to data storage and processing speed, the applications of digital image analysis also has expanded into all areas of science and industry. The cereal sciences industry also has expanded the use of image analysis to include classification and morphological identification of cereal grains, phytopathological identification of diseases, milling yield and quality of various cereals, starch size distribution as related to quality, bread volume and crumb grain scores, noodle quality and numerous other aspects of cereal processing and research. 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, distribution, and shape have long been recognized as an important variable in the efficiency of a range of processes including predicting rheology and flow behavior. Digital image analysis coupled to light microscopy offers the ability to have physical parameters recorded for each individual particle and to distinguish among individual granules, agglomerated granules, and nonstarch particles.

Discrimination of soft and hard white wheat kernels using the single-kernel characterization system parameters and kernel imaging.

T.C. Pearson, D.L. Brabec, and H. Dogan.

Natural variation in the hardness of wheat kernels often results in an overlap between hard and soft classes in the distribution of hardness indices (HI) as measured with the single-kernel characterization system (SKCS) and is a major contributor to classification errors. This is particularly true for the case of the hard white and soft white wheat classes. To address this problem, a color camera was incorporated into the SKCS system so that color and kernel size data could be combined with SKCS measurements for classification purposes. Samples of hard red, soft red, hard white, and soft white wheat were classified using the SKCS system with and without the camera and results compared. Using the camera system, errors for separating hard from soft white classes were reduced to less than 5%, compared to 17.1% using SKCS alone. Furthermore, improved data processing applied to the low-level data currently produced by the SKCS system led to greater than 50% reduction in classification errors between soft white and hard red as compared to using HI data alone. Similar improvements in classification accuracies for 300-kernel mixtures of soft and hard white also were achieved, which should aid grain inspectors in properly identifying mixtures of these two classes. Unfortunately, for the soft and hard red classes, incorporating the camera data decreased classification accuracy while increasing the complexity of the system.

Effect of high molecular weight glutenin subunits (HMW-GS) on tortilla quality.

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

Tortillas are the most popular non-bread wheat based product. Flour used in tortilla production has been typically optimized for bread making. The flour properties that determine good quality bread do not necessarily provide good quality tortillas. In this study, the influence of HMW-GS was investigated on tortilla quality. Two biotypes derived from the HRWW cultivar Centurk were used, which contained the following HMW-GS: 2*, 7+9, 2+12 and 2*, 7+9, 5+10. The flours were paired according to protein content of 10.02% (2+12) and 9.92% (5+10) in Group 1 and 10.30% (2+12) and 10.42% (5+10) in Group 2. Tortillas were prepared in a laboratory scale and analysis was carried out at days 0, 2, 4, 7, and 14. Diameter, rollability, and textural properties using the TA-TX2 Texture Analyzer were determined. Tortilla diameter was statistically larger in tortillas made from low protein flour containing HMW-GS 2+12 ($p > 0.05$) among the four conditions. Independently of the protein content used, flour with subunits 5+10 showed a better overall rollability than flour with subunits 2+12. Texture analysis revealed no difference in tortilla stretchability among the flours. However, the rupture force (Fr) of tortillas was affected by flour protein content. When lower protein content was used, Fr was greater for tortillas made with HMW-GS 2+12, conversely, when higher protein content was used, Fr was greater for tortillas made with HMW-GS 5+10. These results indicated better tortillas were obtained with higher protein content flours containing HMW-GS 5+10.

Improving grain-breeding programs through NIR-based, single-kernel sorting.

F.E. Dowell, E.B. Maghirang, and P.S. Baenziger.

We developed automated visible and near-infrared (NIR) spetroscopy procedures and instrumentation to select kernels with specific hardness, protein, and color traits to enhance the development of FHB-resistant, hard and soft wheat cultivars. The system also shows potential to sort for other characteristics such as FHB damage, vomitoxin levels, ergosterol levels, vitraeousness, sprout damage as measured by α-amylase content or falling number, moisture content, selenium content, Karnal bunt-infected kernels, and waxy character. Our single-kernel, NIR system can sort single kernels based on specified properties at a rate of about one kernel/2 s (500–1000 g/day). We also have high-speed sorting technology that can sort visible defects at rates as much as 80,000 kernels/s (300 bu/hr). This technology is now used routinely for such applications as purifying red or white breeding lines, removing Karnal but-infected kernels during routine inspection for the APHIS national surveys, and selecting waxy seeds from segregating populations. Although most of our work has been with wheat, we also have shown applications for proso millet, barley, rice, and sorghum.

Objective image analysis for bread quality characteristics using a C-Cell instrument.

Y.R. Chen, F. Xie, B.W. Seabourn, and M.S. Caley.

Bread volume, crumb grain, crumb texture, and crumb color are the most important quality factors evaluated in wheat-based bread products. Each of these factors can be estimated by using separate instruments or by experienced baking experts. The objective of this study was to investigate the potential of a C-Cell instrument in evaluating all these bread factors concurrently. Based on C-Cell image data collected from pup loaves of a set of 53 HRWW breeding lines, correlation coefficient of loaf volume obtained by rapeseed displacement with data obtained by C-Cell images was 0.90. After all data from C-Cell images and crumb grain scores were categorized into seven levels based on number of cells, the average data of each category were then correlated with the average sample crumb grain score. The correlation coefficient of the average crumb grain scores (0-6 scales) subjectively determined by an expert baker with the average cell number, the average cell wall thickness, the average coarse/fine cluster, and the average crumb fineness (number of cells/mm^2) was 0.97, -0.93, 0.89, and 0.91, respectively. The results indicated that the C-Cell instrument had the capability potential to determine all of the important bread attributes simultaneously.

Precooked, fiber-enriched wheat flour obtained by extrusion: rheological and functional properties.

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

Functional and rheological properties of different process conditions of extruded wheat flour with 0%, 10%, 20%, and 30% fiber levels were studied in the production of cookies and tortillas. Functional and rheological properties were evaluated using Rapid Visco Analyzer and mixograph equipment. Results showed that peak viscosity increased for the 20% fiber level of extruded wheat flour (123.1 cP) and nonsignificant difference was shown for all other fiber-level extruded wheat flour for lower process conditions and to nonextruded wheat flours. The pasting properties for the high processing treatment (treatments are explained above) were decreased from 98.2 cP to 52 cP with increasing fiber level content. Mixograph peak time was observed similar for all fiber levels in high processing extruded wheat flour and nonextruded wheat flour and decreased in low processing extruded wheat flour. Peak height (66.6 cm) was higher in high processing extruded wheat flour as compared to low processing extruded wheat flour (26.8 cm) and nonextruded wheat flour (44.6 cm). Quality parameters including weight, height, width, width/thickness, spread factor, rollability, and extensibility were evaluated for cookies and tortillas made from precooked wheat flour and compared with those of nonextruded wheat flour. As the percent fiber content was increased, the quality parameters deteriorated for both nonextruded and extruded wheat flour cookies. The deterioration was more significant in the high processing tortillas. No significant difference ($p < 0.05$) was observed in rollability of nonextruded wheat flour tortillas whereas a significant difference ($p < 0.05$) was observed in extensibility values for extruded wheat flour tortillas.

Rapid assessment of insect fragments in flour milled from wheat infested with known densities of immature and adult Sitophilus oryzae (L.) (Coleoptera: Curculionidae).

M.D. Toews, J. Perez-Mendoza, J.E. Throne, F.E. Dowell, E.B. Maghirang, F.H. Arthur, and J.F. Campbell.

Milling wheat infested with low densities of internal feeding insects can result in flour containing insect fragments. The Food and Drug Administration (FDA) enforces a standard or defect action level stating that a maximum of 75 insect fragments per 50 g flour is allowed. However, the relationship between level of infestation and number of resulting fragments is not well documented, and a more rapid method for enumerating insect fragments is needed. We characterized the number of insect fragments produced from milling small lots of wheat spiked with known densities and life stages of *S. oryzae*. Insect fragments were enumerated with near-infrared spectroscopy (NIRS), a quick nondestructive procedure, and with the industry standard flotation method. Results showed that an individual small larva, large larva, pupa, or adult produced 0.4, 0.7, 1.5, and 27.0 fragments, respectively. NIRS-predicted counts of less than 51 (from small larvae), less than 53 (from large larvae), less than 43 (from pupae), or 0 (from adults) indicated that there were less than 75 actual fragments in that sample because the upper bound of associated 95% inverse prediction confidence intervals was less than the standard; NIRS-predicted counts of greater than 98, greater than 117, greater than 108, or greater than 225 fragments (same life stages as above) signaled that these flour samples contained more than 75 actual fragments. These data suggest that NIRS could be adopted for rapid assessment of insect fragments resulting from relatively low levels of infestation with immature life states, but was not accurate enough for enumerating fragments resulting from adults at densities relevant to FDA standards.

Registration of Guymon wheat.

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

Guymon (Reg. No. CV- 1018, PI 643133) is a HWWW cultivar developed and released coöperatively by the Oklahoma Agricultural Experiment Station and the USDA–ARS in 2005. Guymon is recommended for grain-only and dual-purpose production systems in an area of the southern High Plains centered by the city serving as its namesake, Guymon, OK. Guymon is an F_2-derived line selected from the cross 'OK95G701/WI89-163W' performed in 1995. OK95G701 was eventually released by the Oklahoma AES and the USDA–ARS as Intrada, whereas WI89-163W was subsequently named and released by AgriPro-Coker as Platte. Single heads were collected from a F_2 bulk population grown at Stillwater, OK, in 1997. In the following year, selection was imposed in Stillwater, OK, on the $F_{2:3}$ head rows based

on late-spring freeze tolerance, stem extension, spike density and size, kernel size, uniformity of phenotype at harvest maturity, and consistent kernel color. The head-row progeny was evaluated in 1999 at Stillwater and Lahoma, OK, and selected on the basis of forage accumulation, autumn vegetative growth habit, simulated-grazing tolerance, spring green-up, heading date, test weight, grain yield, wheat protein content, kernel hardness, and kernel size. Subsequent generations were advanced by bulk-selfing in the field. Minimal roguing of slightly taller variants was performed each year until 2004 despite this line being F_2 derived. With an initial frequency of 1.5% red kernels, seed from the 2003 harvest were passed through a single-kernel sorter to reduce the frequency of red kernels to <0.3% (Engineering Research Unit, USDA–ARS–GMPRC, Manhattan, KS). From a final breeder-seed increase in 2004, we detected 0.0 to 0.2% red kernels based on the NaOH-bleach test of multiple samples. As of the 2006–07 crop year, Guymon is a F_2-derived line in the F_{12} generation.

Registration of Okfield wheat.

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

Okfield (Reg. No. CV-1019, PI 643087) is a HRWW cultivar developed and released coöperatively by the Oklahoma Agricultural Experiment Station and the USDA–ARS in 2005. Okfield is recommended for dryland wheat production using either grain-only and dual-purpose management systems in the west-central Great Plains. Reasons for its release were tolerance to imazamox herbicide, improved winter dormancy retention relative to other imazamox-tolerant cultivars, and good stay-green capacity of the flag leaf. Okfield resulted from a single cross between an imazamox-tolerant BC_3F_2 plant with the pedigree 'TXGH12588-120*4/FS4' and the HRWW experimental line HBZ374C, eventually released as 2174 by the Oklahoma AES and the USDA–ARS in 1997. 2174 has the pedigree 'IL71-5662/PL145 (PI 600840)//2165'. TXGH12588-120 is an unreleased sister line of the HRWW cultivar TAM 110, and FS4 was derived by sodium azide-induced mutagenesis of the cultivar Fidel. The BC_3F_2 population was provided by American Cyanamid Co. Ownership of the gene mutation was subsequently transferred to BASF Corporation. The F_1 plant generation was produced in the greenhouse in 1998, and the F_2 generation was advanced at Stillwater the following year. Single heads were collected from plants which survived a single application of imazamox (36 gai/ha) in February 1999.

Separating waxy from wild-type kernels using an automated NIR sorting system.

F.E. Dowell, R.A. Graybosch, W.A. Berzonsky, and S.R. Delwiche.

Waxy (amylose-free) wheat is gaining interest because it converts to ethanol faster than other wheat, is a possible low-fat replacement for vegetable shortening, is used to produce modified food starches, and has unique absorption and pasting characteristics. Several breeding programs are developing waxy lines in an attempt to take advantage of these potential new markets. After crosses between waxy and nonwaxy breeding lines, the frequency of waxy progeny may be as low as 1/64. The ability to segregate waxy seed from segregating populations can provide breeding materials enriched in the number of individuals with this desired trait. We have shown that near-infrared spectroscopy can separate the waxy kernels (all null alleles) from partial waxy kernels (at least one null allele and one functional allele) or wild-type kernels (all functional alleles). Our automated system can separate waxy from nonwaxy kernels at a rate of about 1 kernel/2 s, which is a rate sufficient to select waxy kernels from breeding lines or to purify contaminated samples. Testing on hundreds of samples over several years shows that waxy kernels can be selected from segregating lines with about 100% accuracy. We have applied this technology to sorting hard red winter, hard red spring, and durum wheat, in addition to sorting waxy proso millet. Prior to our research, the only ways to distinguish between full and partial waxy were iodine staining and the use of molecular markers. These techniques are too slow and tedious for purifying large seed samples, thus our technology offers significant advantages to breeding programs working on the waxy characteristic.

Starch granule size distribution of hard red winter and hard red spring wheat: Their relationship to wheat, flour, and bread-making quality.

S.H. Park, J.D. Wilson, and B.W. Seabourn.

Starch was isolated from 98 HRWW and 99 HRSW lines. Granule size/volume distributions of the isolated starches were analyzed using a laser diffraction particle size analyzer. Significant differences were observed in the size distribution between the HRWW and HRSW. The B-type granules (< 10 μm in diameter) occupied volumes in the range 28.5–49.1% (mean 39.9%) for HRWW whereas HRSW B-type granules occupied volumes in the range of 37.1–56.2% (mean 47.3%). The mean granule sizes of the distribution peaks less than 10 μm in diameter also showed a significant difference (HRWW, 4.32 vs. HRSW, 4.49 μm), but the mean sizes of the distribution peaks larger than 10 μm were not significantly different (21.54 vs. 21.47 μm). Numerous wheat and flour quality traits also showed significant correlation to starch granule size distributions. Most notably, protein content was inversely correlated with parameters of B-type granules. Crumb grain score seemed to be affected by starch granule size distribution, showing significant inverse correlations with B-type granules. Furthermore, the linear correlations were improved when the ratio of B-type granules to protein content was used, and in addition, polynomial relation was applied. There seemed to an optimum range of B-type granules for different protein content flour to produce bread with better crumb grain.

The relationship of bread quality to kernel, flour, and dough properties.

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

We measured the relationship between bread quality and 49 HRSW) or 48 HRWW grain, flour, and dough quality characteristics. The estimated bread quality attributes included loaf volume, bake mix time, bake water absorption, and crumb grain score. The best-fit models for loaf volume, bake mix time, and water absorption had R^2 values of 0.78 to 0.93 with five to eight variables. Crumb grain score was not well estimated, and had R^2 values around 0.60. For loaf volume models, grain or flour protein content was the most important parameter included. Bake water absorption was best estimated when using mixograph water absorption and flour- or grain-protein content. Bake water absorption models could generally be improved by including farinograph, mixograph, or alveograph measurements. Bake mix time was estimated best when using mixograph mix time, and models could be improved by including glutenin data. When the data set was divided into calibration and prediction sets, the loaf volume and bake mix time models still looked promising for screening samples. When including only variables that could be rapidly measured (protein content, test weight, single kernel moisture content, single kernel diameter, single kernel hardness, and bulk moisture content, and dark hard and vitreous kernels), only loaf volume could be predicted with accuracies adequate for screening samples.

The relationship between different biotypes and protein composition of HRWW flours and their affect on alkaline noodle color and texture.

S.H. Park, M. Tilley, S.R. Bean, B.W. Seabourn, and R.A. Graybosch.

Twenty-five samples of biotypes derived from two HRWW) cultivars, Centurk and OK102, were grown in a randomized complete block design at Mead, NE. The biotypes varied in their (HMW-GS composition with five different HMW-GS allelic combinations present across the samples (2*, 7+8, 2+12; 2*, 7+9, 2+12; 2*, 6*+8*, 3+12; 2*, 6*+8*, 5+10; and 2*, 7+9, 5+10). These lines were selected to determine the relationship between HMW-GS and protein composition on color and texture of alkaline noodles. Protein composition, including insoluble polymeric protein (IPP), soluble polymeric protein (SPP), gliadin, and albumin and globulin (AG) was found to vary significantly between the various HMW-GS combinations. Flour protein content was not significantly different between the various sets. For mixograph mixing time, 83.6% of the variation among the samples was explained by HMW-GS composition, whereas 89.0% of the mixing tolerance variation was. Most noodle color traits were not significantly affected by HMW-GS groups except for a and b values at 24 hr after production. For cooked noodle texture, water uptake was significantly affected by HMW-GS groups but cooking loss was not. Noodle texture profiles including hardness, springiness, chewiness, resilience, cohesiveness, and adhesiveness were significantly affected by HMW-GS types. Overall protein composition was significantly

correlated with noodle texture: SPP % was positively correlated with hardness ($r = 0.83$, $P<0.0001$) and negatively with springiness ($r = -0.77$, $P<0.0001$), resilience ($r = -0.76$, $P<0.0001$), and adhesiveness ($r = -0.44$, $P<0.05$), whereas IPP% was negatively correlated with hardness ($r = -0.74$, $P<0.0001$). Protein composition was also significantly correlated with cooking water uptake and noodle color.

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.R. Bean.

The Perten Single Kernel Characterization System (SKCS) is the current reference method to determine single wheat kernel texture. However, the SKCS calibration method is based on bulk samples, and there is no method to determine the measurement error on single kernel hardness. The objective of this research was to develop a single-kernel hardness reference based on single-kernel particle size distributions (PSD). A total of 473 kernels drawn from eight different classes were studied. Material from single kernels crushed on the SKCS was collected and milled in a fabricated mill, which simulates the last two rolls of a Quadrumat Jr. The PSD of each single kernel was then measured using a laser particle counter. Calibrations using data from the PSD and SKCS were then used to estimate single kernel PSD and classify kernels into their genetic classes. Wheat kernels from soft and hard classes having SKCS hardness indices (HI) between 40 and 60 typically had a PSD that is expected from their genetic class, even though their HI overlapped. That is, soft kernels tend to have more particles below 21 micrometers than hard kernels do after milling. As such, a combination of HI and PSD gives better discrimination between genetically hard and soft classes than either parameter measured independently. Additionally, use of SKCS predicted PSD combined with other low level SKCS parameters appears to reduce classification errors into genetic hardness classes by about 50% over what can currently be accomplished with HI alone.

Use of NILs to determine glutenin composition and functionality in flour.

S. Mondal, M. Tilley, J.N. Alviola, R.D. Waniska, S.R. Bean, K.D. Glover and D.B. Hays.

Tortillas were prepared from each deletion line and the parent lines. The elimination of certain HMW-GS alleles alter distinct, but critical aspects of tortilla quality such as diameter, shelf stability and overall quality. Two deletion lines possessing HMW-GS 17+18 at *Glu-B1* and deletions in *Glu-A1* and *Glu-D1* had significantly larger tortilla diameters, yet tortilla shelf life was compromised or unchanged from the parent lines used to develop the deletion lines or the commercial tortilla flour used as a control. Alternatively, a deletion line possessing *Glu-A1* and *Glu-D1* (HMW-GS 1, 5+10) and a deletion in *Glu-B1* also significantly improved tortilla diameters. Although the increase in diameter was less than the line possessing only HMW-GS 17+18 at *Glu-B1*, the stability of the tortillas were however maintained and improved compared to the parent lines containing a full compliment of HMW-GS. Thus, presence of subunits 5+10 at *Glu-D1* alone or in combination with subunit 1 at *Glu-A1* appears to provide a compromise of improvement in dough extensibility for improved tortilla diameters while also providing sufficient gluten strength to maintain ideal shelf stability.

Personnel news.

GMPRC welcomes Dr. Thomas Herald as the new Research Leader for the Grain Quality and Structure Research Unit. Dr. Herald joins us from Kansas State University where he served as a professor in the Food Science Institute.

Dr. Herald was raised in Michigan. He earned his B.S. degree in Food Science from Michigan State University, East Lansing MI in 1980. He served as a Peace Corps Volunteer from 1980-1983 in Swaziland, Southern Africa. Dr. Herald completed his M.S. and Ph.D. degrees in Food Science at Michigan State University in the area of food chemistry. Dr. Herald worked in the food industrial sector with Yoplait USA and Kellogg's. He recently completed a 16 + year career at Kansas State University holding the rank of professor in the Food Science Program. Dr. Herald's research focus was on the

chemical and physical properties of food and food ingredients. He has 58 peer-reviewed publications and numerous invited presentations at national and international meetings. As Research Leader for the GQSRU, Dr. Herald will integrate his technical background into the identification and utilization of wheat cultivars and sorghum hybrids for use in value-added systems that will include both food and non-food applications.

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MINNESOTA

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Wheat rusts in the United States in 2007.

MINNESOTA

Wheat stem rust (*Puccinia graminis f. sp. tritici*). The first reports of wheat stem rust in 2007 were in soft red wheat winter varietal plots in south central Louisiana at Crowley and in southwest Louisiana at Jeanerette on 23 April. Stem rust was severe in some plots, but the distribution of infections was not uniform throughout the nursery. Hot, dry weather accelerated the crop to maturity in these plots.

On 23 April, traces of stem rust were found in two wheat plots in southern Texas at Castroville. On 8 May, a hot spot of wheat stem rust was found in a SRWW plot in central Texas at McGregor. On 10 May, stem rust severities ranged from 5–75% with 50% of the plants infected on the susceptible cultivar Winmaster in plots at Castroville and Uvalde in southern Texas.

On 23 May, low levels of wheat stem rust were found in the susceptible McNair 701 plot at Stillwater, in north-central Oklahoma.

In the spring of 2007, stem rust was found in susceptible plots of soft and red winter wheat in the southern U.S., but stem rust was not found in any commercial fields.

The next reports of wheat stem rust in 2007 were in late June when an infection site was observed in a plot of the susceptible winter wheat cultivar McNair 701 at the Rosemount experiment station in Minnesota and low levels were found on susceptible lines in spreader rows at Brookings, South Dakota. In early July, low levels of stem rust were found in plots of the susceptible spring wheat cultivar Baart at Waseca and Lamberton, Minnesota. During the second week in July, low levels of stem rust were found in a Baart plot at the west central experiment station at Morris, Minnesota.

In mid-July, trace levels of stem rust were observed in a plot of Radiant winter wheat at Lisbon, North Dakota. Moderate levels of stem rust were observed on a triticale line on July 23 at the Fargo, ND Experiment Station. In late July, trace levels of stem rust were found in the susceptible spring wheat cultivars Baart and Max at the Carrington and Langdon experiment stations in North Dakota. In summary, during the month of July, trace levels of wheat stem rust were found in susceptible winter wheat and spring wheat plots from southeastern Minnesota to east-central South Dakota and onto northeastern North Dakota. Stem rust was not observed on any current wheat cultivars in research plots or in commercial fields in this area.

In mid-July, stem rust was found in winter wheat breeding plots near Pullman, Washington.

In late July, stem rust was not observed in Manitoba and eastern Saskatchewan, Canada, commercial wheat fields, but was found on the susceptible line Little Club at Indianhead, Saskatchewan.

The wheat stem rust observation maps are available on the CDL website (http://www.ars.usda.gov/SP2UserFiles/ad_hoc/36400500Cerealrustbulletins/2007wsr.pdf).

Virulence of wheat stem rust. From collections made from the above locations (including samples from the Triticales) race QFCS was identified as the predominant race (Table 1). This is a common race that has been found in the U.S. the past several years. This race is relatively avirulent; the majority of the U.S. cultivars are resistant to QFCS. Race RCRS was found in a collection from Brookings, South Dakota. Viable isolates were not recovered from samples collected in Oklahoma and Washington.

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	36	LA, TX, MN, SD, ND
RCRS	1	SD

Stem rust on barberry (alternate host for stem rust). On 22 May, aecial development was light on susceptible barberry (*Berberis vulgaris*) bushes growing in southeastern Minnesota. In early June, no aecial development was found on susceptible barberry bushes growing in south central Wisconsin. Infections on the common barberry from southeast Minnesota were *P. graminis f. sp. secalis*. *Puccinia graminis f. sp. tritici* and *P. graminis f. sp. avenae* were not isolated from barberry samples.

Wheat leaf rust (*Puccinia triticina*). Southern Plains – Texas. In early February, low levels of leaf rust were reported in central Texas wheat plots and by late February, high levels of rust were found in the plots. In mid-March, low amounts of leaf rust were found on lower wheat leaves in the irrigated nursery at Castroville, Texas. Moisture was limited from late January to mid-March in much of the state of Texas. In plots at College Station, leaf rust was at low levels except for high severities in Jagelene (*Lr24* resistance). By the second week of April, susceptible cultivars such as Jagalene and Jagger (*Lr17* resistance) in nurseries at Castroville and College Station, Texas, had 80% leaf rust severities on lower leaves. On highly resistant cultivars such as Fannin and Endurance, no infections were found. Low to moderate levels of rust were reported in Texas fields. In early June, high severity (100%) levels of leaf rust were reported in irrigated nursery plots of susceptible winter wheat cultivars at Bushland, Texas (Fig. 1). At the same time leaf rust was not present in the dryland nurseries.

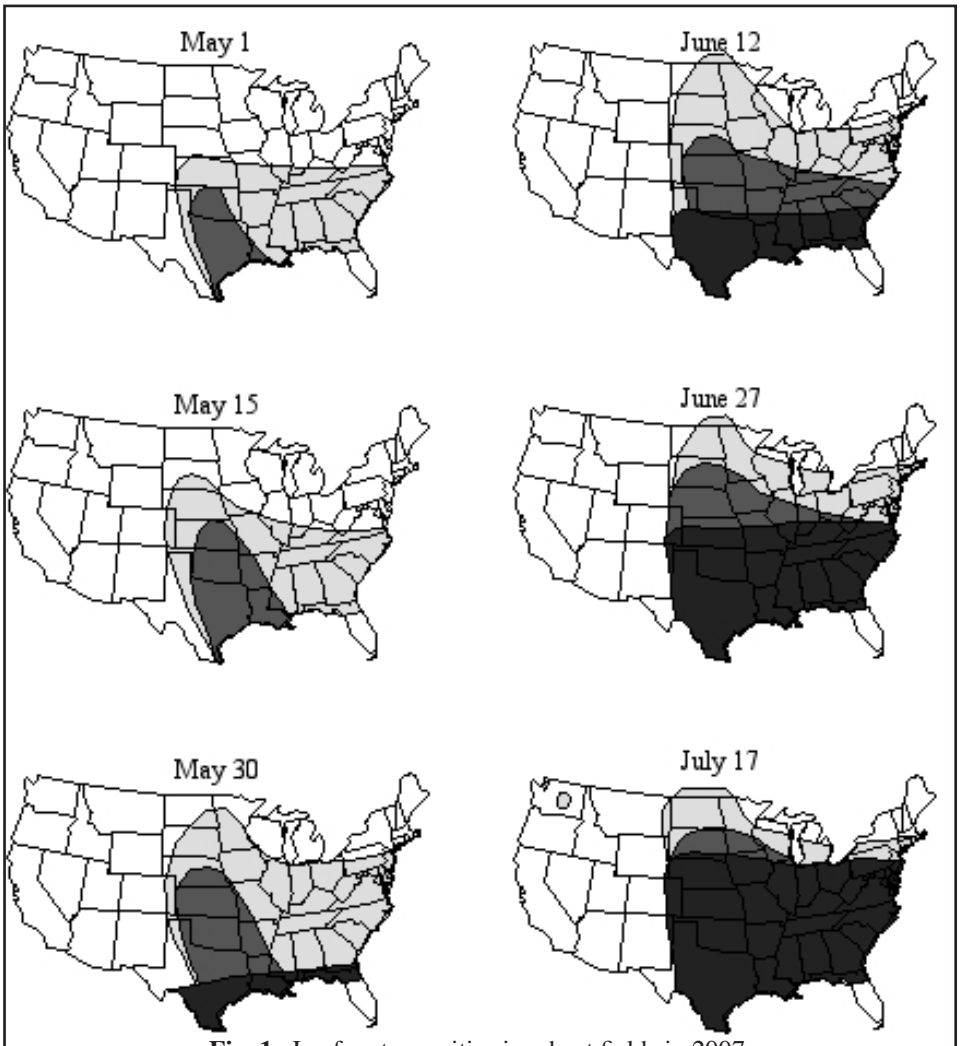

Fig. 1. Leaf rust severities in wheat fields in 2007.

Oklahoma. In early February, traces of leaf rust were found on susceptible varieties in the plots at Stillwater, Oklahoma. In late February, leaf rust was light in southwest Oklahoma fields. By mid-March leaf rust still was light in plots and fields in Oklahoma. In mid-April, severe levels of leaf rust had been reported on susceptible cultivars in north-central Oklahoma plots. And by late April, high severity levels of leaf rust had been reported on susceptible cultivars in north-central Oklahoma plots. During the first two weeks in May, high levels of leaf rust were observed in central Oklahoma on susceptible cultivars. In late May, high severity (80%) levels of

wheat leaf rust were found in fields throughout the state of Oklahoma (Fig. 1, p. 183). With adequate moisture for rust development, leaf rust increased throughout Oklahoma and Texas and provided inoculum for the northern wheat growing areas.

Central Plains – Kansas, Nebraska, Colorado. In mid-March, traces of leaf rust were found in Manhattan, Kansas plots. The leaf rust appeared to have over wintered, because it was limited to the lower leaves. In early April, low levels of rust were found in the lower and middle canopy of susceptible wheat in plots at Manhattan. In mid-April, 5% severities were reported on the lower leaves of Jagger and Jagalene in south-central Kansas. Leaf rust was scattered and at high levels in locations where moisture was sufficient for rust infections.

During the first two weeks of May, wheat leaf rust was found in plots and fields from southeastern Colorado to south-central Nebraska. High levels of leaf rust were observed from central Oklahoma to central Kansas on susceptible varieties. With adequate moisture for rust development, leaf rust increased throughout this area.

In late May, high severity (80%) levels of wheat leaf rust were found in fields throughout Kansas and Nebraska. Many fields were sprayed for rust control and some fields of susceptible cultivars were almost a total loss due to leaf rust. Commonly grown cultivars such as Jagalene and Jagger were susceptible.

During the first week in June in northwestern Kansas, high severity levels of leaf rust were found in susceptible cultivars of hard red and white winter wheat. By the first week in June, high levels of wheat leaf rust were found in south-central and southeastern Nebraska winter wheat fields.

In 2007, the overall estimated loss due to leaf rust in Kansas was 13.9 % (roughly 50 million bushels) (Table 4, p. 190), which is well above the 20-year average of 3.8%. The 13.9% loss was the highest for leaf rust or any disease in Kansas since 1976 when disease loss estimates were initiated. Yield losses were estimated from fungicide plot data, cultivar surveys, cultivar disease ratings and disease surveys.

Northern Plains – Minnesota, South Dakota, North Dakota, Montana. During the first two weeks of May, wheat leaf rust was found in plots and fields in south-central South Dakota. On 23 May, traces of wheat leaf rust were found on susceptible winter wheat cultivars in the Rosemount, Minnesota, nursery and on 25 May, low levels of leaf rust were found on winter wheat in southeastern North Dakota fields. On 1 June, traces of wheat leaf rust were found on susceptible spring wheat cultivars in the St. Paul, Minnesota, nursery. In early June, leaf rust was increasing in southern South Dakota winter wheat fields and plots.

During the third week in June, plots of susceptible winter wheat cultivars such as Jagalene, in east-central Minnesota, east-central South Dakota and southwestern Nebraska had 60% rust severities, whereas resistant cultivars had only trace levels of infection on the flag leaves. Throughout this area fungicide usage on winter wheat was very common this year with many fields receiving multiple applications. By late June, spring wheat had leaf rust severities of trace to 5% on lower leaves in southern Minnesota and South Dakota fields (Fig. 1, p. 183). Susceptible spring wheat cultivars in southern Minnesota plots had 20% rust severities with most infections on the lower leaves.

This year there was more leaf rust than normal in the upper Midwest on both spring and winter wheat. Increased amounts of rust inoculum than in previous years arrived from the winter wheat region because of ideal conditions for infection in the Southern Plains, which increased the rust severities on the winter wheat. Regular rainfall in May and June in many areas of the northern Great Plains further increased rust development. Over 50% of the wheat fields in the spring wheat region were treated with fungicide, which prevented losses due to leaf rust and FHB (Table 4, p. 190).

During the last week in June, high levels of leaf rust were found in spring wheat plots at Lamberton in southwest Minnesota. Leaf rust was found at high severity levels on cultivars Knudson and Ada that had been previously rated as resistant to moderately resistant. In mid- July, trace to 80% leaf rust severities were observed on flag leaves of spring wheat cultivars in fields and plots from south-central Minnesota (Fig. 1, p. 183) to east central South Dakota and east central North Dakota. Hot dry weather combined with severe leaf rust infections killed the flag leaves of spring wheat.

During the fourth week in July, wheat leaf rust was widespread and at high severity levels on susceptible and moderately resistant spring wheat cultivars in research plots in North Dakota and northwestern Minnesota. The cultivars

Knudson and Briggs with *Lr16* and *Lr34* had low to moderate levels of leaf rust infection, a significant increase from previous years. Cultivars postulated to have *Lr21* (RB07, Glenn, Steele, Faller, and Howard) were highly resistant. In western North Dakota and eastern Montana high temperatures and leaf rust defoliated leaves in susceptible wheat lines in research plots. No leaf rust was observed on durum wheat cultivars. In fields throughout North Dakota trace to moderate levels of leaf rust were observed in a small number of fields due to highly resistant cultivars and common use of fungicide sprays. Many fields that had been sprayed had no rust infections.

In early July, low levels of leaf rust were found in spring wheat plots at Sidney in northeastern Montana.

Louisiana. In late February, leaf rust was found on susceptible cultivars in statewide variety trails in southwest Louisiana. During the second week in April, plots in southern Louisiana had high levels of leaf rust, whereas levels were light in fields. Many of these southern areas provided rust inoculum for areas further north.

Arkansas. In early April, leaf rust was light throughout Arkansas. In mid-April, freezing temperatures slowed further leaf rust development.

Southeast - Mississippi, Georgia, Alabama, South Carolina. In late April, plots of susceptible wheat cultivars in southern Alabama and southwestern Georgia had leaf rust severities up to 20% on lower leaves. Leaf rust was either absent or at trace levels in commercial fields in Georgia and Alabama. Dry conditions in March and April slowed rust development throughout much of the southeastern U.S. SRWW area.

Mid-Atlantic – North Carolina, Virginia. Trace amounts of leaf rust were found in plots in the Coastal Plain area of North Carolina in early April (Fig. 1, p. 183). In the last week in April, 10% leaf rust severities were observed on lower leaves of wheat in southeastern and eastern North Carolina plots.

In late April, high levels of leaf rust were found on the lower leaves of susceptible lines in a nursery at Warsaw, Virginia. The rust was found on the closest leaves to the ground level, indicating that leaf rust may have over wintered at this location. During the first two weeks in May, light levels of leaf rust were found in plots and fields in the coastal plains of Virginia.

In late May, wheat leaf rust was increasing in fields and plots in the coastal plains of Virginia. High leaf rust severity levels were observed in nurseries in northeastern South Carolina and eastern Virginia.

This year wheat leaf rust development was greater than normal in the Mid-Atlantic states and losses occurred in a few areas (Table 4, p. 190).

New York. In mid-June, low levels of wheat leaf rust were found in plots in Cayuga County, New York.

Midwest. In early June, wheat leaf rust was found in fields from northeastern Missouri to southern Illinois at 60% severity on flag leaves. There were yield losses to leaf rust in the soft red winter cultivars in this area. In early June, trace levels of leaf rust were found on flag leaves in wheat fields from northwestern Ohio, northwestern Indiana, to south-central Wisconsin. In plots in west-central and northeastern Indiana, 20% severities were found on lower leaves. In early June, leaf rust was found on several breeding lines in a nursery at Wooster, in north-central Ohio. In early July, low levels of leaf rust were found in winter wheat fields in eastern Wisconsin. Lack of moisture limited rust development in some locations in the northern SRWW area.

Western U.S. In mid-May, no leaf rust was detected in nurseries throughout the San Joaquin Valley in California. In the Pacific Northwest, wheat leaf rust was found at low levels in northwestern Washington and in irrigated fields in central Washington.

Canada. In early June, light levels of wheat leaf rust were found in winter wheat cultivars at the University of Manitoba, Canada, and other locations in southern Manitoba and on susceptible spring wheat cultivars at Homewood, Manitoba. On 23 and 24 July, wheat fields were surveyed in Manitoba and eastern Saskatchewan. Leaf rust was widespread and severe in Manitoba fields that were not sprayed with fungicide. Severities of 80% were observed on the flag leaves in some fields, although the average level of infection was approximately 20%. Highest severities in Saskatchewan were near the Manitoba border and declined to trace levels near Regina.

Wheat leaf rust virulence. In 2007, 52 races of wheat leaf rust were found in the U.S. (Table 2, pp. 186-187). Races with virulence to *Lr24* increased in frequency throughout all wheat growing regions of the U.S. (Table 3, p. 188). Virulence to *Lr24* was highest throughout the Great Plains region, where a number of winter wheat cultivars have *Lr24*. Virulence to *Lr9* and *Lr41* was high throughout the Great Plains region. Virulence to *Lr26* occurred in all regions of the U.S., and was highest in the eastern region. Virulence to *Lr16* was highest in the spring wheat region of Minnesota and North and South Dakota, where a number of the spring wheats have this gene. Virulence to *Lr17* was found equally in all regions of the U.S. Virulence to *Lr18* occurred in the southeast and northeast, where a number of SRWWs have this

Table 2. Races of *Puccinia triticina* in the U.S. in 2007 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 %. SE includes the states of LA, AR, MS, AL, GA, FL, TN, SC and NC; NE includes states of VA, WV, MD, PA, DE, NJ, NY, MA, CT, RI, VT, NH, and ME; and OH Valley includes states of MO, IL, KY, OH, IN, MI and WI.

Race	Virulence combination (ineffective *Lr* genes)	SE		NE		OH Valley		TX OK–NM		KS–NE IA–CO		MN SD–ND MT–WY		WA		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBDB	14a	2	2.2	0	0	0	0	0	0	0	0	4	1.2	0	0	6	0.7
CCPSB	3,26,3ka,17,30,B,10,14a	0	0	2	2.9	0	0	0	0	0	0	0	0	0	0	2	0.2
LCDSB	1,26,17,B,10,14a	2	2.2	0	0	0	0	0	0	0	0	0	0	0	0	2	0.2
MBDSB	1,3,17,B,10,14a	0	0	0	0	0	0	2	1	1	0.8	0	0	0	0	3	0.3
MBDTG	1,3,17,B,10,14a,18,28	0	0	2	2.9	0	0	0	0	0	0	0	0	0	0	2	0.2
MBGJG	1,3,11,10,14a,28	0	0	0	0	1	2.3	0	0	0	0	0	0	1	100	5	0.6
MBPSB	1,3,3ka,17,30,B,10,14a	0	0	0	0	0	0	0	0	0	0	6	1.8	0	0	6	0.7
MBRJG	1,3,3ka,11,30,10,14a,28	1	1.1	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
MBTSB	1,3,3ka,11,17,30,B,10,14a	2	2.2	0	0	0	0	0	0	0	0	0	0	0	0	2	0.2
MCDSB	1,3,26,17,B,10,14a	6	6.5	11	15.7	1	2.3	5	2.5	1	0.8	2	0.6	0	0	26	3.1
MCGJG	1,3,26,11,10,14a,28	4	4.3	0	0	0	0	0	0	0	0	0	0	0	0	4	0.5
MCRKG	1,3,26,3ka,11,30,10,14a,18,28	4	4.3	1	1.4	0	0	0	0	0	0	0	0	0	0	5	0.6
MCTSB	1,3,26,3ka,11,17,30,B,10,14a	0	0	3	4.3	0	0	0	0	0	0	0	0	0	0	3	0.3
MDGJG	1,3,24,11,10,14a,28	0	0	2	2.9	0	0	0	0	0	0	0	0	0	0	2	0.2
MDPSC	1,3,24,3ka,17,30,B,10,14a,42	0	0	0	0	1	2.3	0	0	2	1.6	1	0.3	0	0	4	0.5
MDSPC	1,3,24,3ka,11,17,B,14a,18,42	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0.2
MFBJG	1,3,24,26,10,14a,28	5	5.4	0	0	0	0	0	0	0	0	0	0	0	0	5	0.6
MFGJH	1,3,24,26,11,10,14a,28,42	6	6.5	26	37.1	0	0	0	0	0	0	0	0	0	0	32	3.7
MFPSC	1,3,24,26,3ka,17,30,B,10,14a,42	15	16.1	7	10	8	18.2	28	14.2	18	14.4	45	13.4	0	0	121	13.9
MGBJG	1,3,16,10,14a,28	0	0	0	0	0	0	0	0	0	0	3	0.9	0	0	3	0.3
MJDSC	1,3,16,24,17,B,10,14a,42	0	0	0	0	0	0	2	1	2	1.6	0	0	0	0	4	0.5
MLDSD	1,3,9,17,B,10,14a,41	0	0	0	0	0	0	34	17.3	14	11.2	58	17.3	0	0	106	12.2
NBBFG	1,2c,14a,18,28	0	0	5	7.1	0	0	0	0	0	0	0	0	0	0	5	0.6
NBBKG	1,2c,10,14a,18,28	0	0	6	8.6	0	0	0	0	0	0	0	0	0	0	6	0.7
PBBGG	1,2c,3,10,28	0	0	0	0	0	0	0	0	2	1.6	0	0	0	0	2	0.2
PBDGG	1,2c,3,17,10,28	0	0	0	0	0	0	0	0	1	0.8	0	0	0	0	1	0.1
PCDSG	1,2c,3,26,17,B,10,14a,28	2	2.2	0	0	0	0	0	0	0	0	2	0.6	0	0	4	0.5
SBDGG	1,2a,2c,17,10,28	0	0	0	0	0	0	0	0	0	0	2	0.6	0	0	2	0.2
SBDSB	1,2a,2c,17,B,10,14a	0	0	0	0	0	0	0	0	0	0	1	0.3	0	0	1	0.1

gene. Virulence to *Lr21* was not found in any region. Virulence to *Lr41* was found in all regions except the southeast and Ohio Valley, California, and Washington. Virulence to *Lr42* was found in all regions except California and Washington.

In the Southeast, the most common race, MFPSC (16.1%), had virulence to *Lr17, Lr24,* and *Lr26* (Table 3, p. 188*)*. In the Northeast, the most common race, MFGJH (37.1%) had virulence to *Lr11, Lr24,* and *Lr26*. In the Midwest, TDBGH (22.7%) had virulence to *Lr2a*, *Lr24,* and *Lr42*. This also was the most common race identified in the U.S. In

Table 2 (continued). Races of *Puccinia triticina* in the U.S. in 2007 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 %. SE includes the states of LA, AR, MS, AL, GA, FL, TN, SC and NC; NE includes states of VA, WV, MD, PA, DE, NJ, NY, MA, CT, RI, VT, NH, and ME; and OH Valley includes states of MO, IL, KY, OH, IN, MI and WI.

Race	Virulence combination (ineffective *Lr* genes)	SE		NE		OH Valley		TX OK–NM		KS–NE IA–CO		MN SD–ND MT–WY		WA		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
SBJDG	1,2a,2c,11,17,14a,28	0	0	0	0	0	0	0	0	1	0.8	0	0	0	0	1	0.1
TBBJG	1,2a,2c,3,10,14a,28	6	6.5	0	0	0	0	0	0	0	0	1	0.3	0	0	7	0.8
TBRKG	1,2a,2c,3,3ka,11,30,10,14a,18,28	2	2.2	0	0	0	0	0	0	0	0	0	0	0	0	2	0.2
TCBJG	1,2a,2c,3,26,10,14a,28	0	0	0	0	0	0	0	0	2	1.6	0	0	0	0	2	0.2
TCDSB	1,2a,2c,3,26,17,B,10,14a	0	0	0	0	2	4.5	0	0	0	0	1	0.3	0	0	3	0.3
TCMJG	1,2a,2c,3,26,3ka,30,10,14a,28	5	5.4	0	0	0	0	0	0	0	0	0	0	0	0	5	0.6
TCRJG	1,2a,2c,3,26,3ka,11,30,10,14a,28	0	0	0	0	2	4.5	0	0	0	0	0	0	0	0	2	0.2
TCRKG	1,2a,2c,3,26,3ka,11,30,10,14a,18,28	8	8.6	0	0	0	0	0	0	1	0.8	1	0.3	0	0	10	1.2
TCSJG	1,2a,2c,3,26,3ka,11,17,10,14a,28	0	0	1	1.4	0	0	0	0	0	0	0	0	0	0	1	0.1
TDBBG	1,2a,2c,3,24,28	0	0	0	0	2	4.5	0	0	0	0	0	0	0	0	2	0.2
TDBGG	1,2a,2c,3,24,10,28	4	4.3	2	2.9	2	4.5	10	5.1	2	1.6	21	6.3	0	0	41	4.7
TDBGH	1,2a,2c,3,24,10,28,42	0	0	0	0	10	22.7	16	8.1	43	34.4	88	26.3	0	0	157	18.1
TDBJG	1,2a,2c,3,24,10,14a,28	6	6.5	0	0	6	13.6	57	28.9	6	4.8	18	5.4	0	0	93	10.7
TDBJH	1,2a,2c,3,24,10,14a,28,42	4	4.3	0	0	7	15.9	14	7.1	6	4.8	11	3.3	0	0	42	4.8
TDDGH	1,2a,2c,3,24,17,10,28,42	0	0	0	0	0	0	0	0	2	1.6	6	1.8	0	0	8	0.9
TFBGH	1,2a,2c,3,24,26,10,28,42	0	0	0	0	0	0	4	2	7	5.6	5	1.5	0	0	16	1.8
TFBJG	1,2a,2c,3,24,26,10,14a,28	8	8.6	0	0	0	0	12	6.1	4	3.2	6	1.8	0	0	30	3.5
TGBJG	1,2a,2c,3,16,10,14a,28	1	1.1	0	0	0	0	6	3	0	0	0	0	0	0	7	0.8
TJBGH	1,2a,2c,3,16,24,10,28,42	0	0	0	0	1	2.3	2	1	3	2.4	30	9	0	0	36	4.1
TJBJG	1,2a,2c,3,16,24,10,14a,28	0	0	0	0	1	2.3	2	1	5	4	22	6.6	0	0	30	3.5
TLBJG	1,2a,2c,3,9,10,14a,28	0	0	0	0	0	0	0	0	2	1.6	0	0	0	0	2	0.2
TLGJG	1,2a,2c,3,9,11,10,14a,28	0	0	0	0	0	0	1	0.5	0	0	0	0	0	0	1	0.1
TNRJK	1,2a,2c,3,9,24,3ka,11,30,10, 14a,28, 41,42	0	0	2	2.9	0	0	0	0	0	0	1	0.3	0	0	3	0.3
TOTAL		93		70		44		197		125		355		4		868	

Table 3. Virulence frequencies (%) of *Puccinia triticina* in the U.S. in 2007 to 20 differential lines of Thatcher wheat with leaf rust-resistance genes. SE includes the states of LA, AR, MS, AL, GA, FL, TN, SC and NC; NE includes states of VA, WV, MD, PA, DE, NJ, NY, MA, CT, RI, VT, NH, and ME; and OH Valley includes states of MO, IL, KY, OH, IN, MI and WI.

Resistance gene	SE		NE		OH Valley		TX OK–NM		KS–NE IA–CO		MN ND–SD MT–WY		WA		U.S. Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
Lr1	91	97.8	68	97.1	44	100.0	197	100.0	125	100.0	331	98.8	4	100.0	860	99.1
Lr2a	44	47.3	5	7.1	33	75.0	124	62.9	84	67.2	214	63.9	0	0.0	504	58.1
Lr2c	46	49.5	16	22.9	33	75.0	124	62.9	87	69.6	216	64.5	0	0.0	522	60.1
Lr3	89	95.7	59	84.3	44	100.0	197	100.0	124	99.2	328	97.9	4	100.0	845	97.4
Lr9	0	0.0	2	2.9	0	0.0	35	17.8	16	12.8	59	17.6	0	0.0	112	12.9
Lr16	1	1.1	0	0.0	2	4.5	12	6.1	10	8.0	55	16.4	0	0.0	80	9.2
Lr24	48	51.6	39	55.7	38	86.4	149	75.6	100	80.0	254	75.8	0	0.0	628	72.4
Lr26	65	69.9	51	72.9	13	29.5	49	24.9	33	26.4	62	18.5	0	0.0	273	31.5
Lr3ka	37	39.8	16	22.9	11	25.0	30	15.2	21	16.8	54	16.1	0	0.0	169	19.5
Lr11	27	29.0	35	50.0	3	6.8	3	1.5	2	1.6	2	0.6	4	100.0	76	8.8
Lr17	27	29.0	26	37.1	12	27.3	73	37.1	42	33.6	124	37.0	0	0.0	304	35.0
Lr30	37	39.8	15	21.4	11	25.0	28	14.2	21	16.8	54	16.1	0	0.0	166	19.1
LrB	27	29.0	25	35.7	12	27.3	73	37.1	38	30.4	116	34.6	0	0.0	291	33.5
Lr10	91	97.8	65	92.9	42	95.5	195	99.0	124	99.2	331	98.8	4	100.0	852	98.2
Lr14a	89	95.7	68	97.1	29	65.9	165	83.8	65	52.0	183	54.6	4	100.0	603	69.5
Lr18	14	15.1	14	20.0	0	0.0	2	1.0	1	0.8	1	0.3	0	0.0	32	3.7
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
Lr28	66	71.0	47	67.1	32	72.7	124	62.9	87	69.6	217	64.8	4	100.0	577	66.5
Lr41	0	0.0	2	2.9	0	0.0	34	17.3	14	11.2	59	17.6	0	0.0	109	12.6
Lr42	25	26.9	35	50.0	27	61.4	68	34.5	83	66.4	187	55.8	0	0.0	425	49.0
Total	93		70		44		197		125		335		4		868	

Texas and Oklahoma, the most common race TDBJG (28.9%) had virulence to *Lr2a* and *Lr24*. In Kansas and Nebraska, the most common race TDBGH (34.4%) had virulence to *Lr2a, Lr24*, and *Lr42*. In Minnesota, South Dakota, and North Dakota, TDBGH (26.3%)was the most common race, which also was the most common race in the U.S.

Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*). Southern Plains. In early February, wheat stripe rust was found at low severities in plots at College Station and McGregor in central Texas. Dry conditions were not favorable for rust development in February and early March. By late March, stripe rust development in Texas was equal to last year. In mid-April, only low levels of stripe rust were found in plots in southern, central, and north-central Texas. In late April, in north-central Texas fields, trace levels of active sporulating stripe rust infections were found and, at the same locations, leaf rust was increasing rapidly in the fields and plots (Fig. 2, p. 189). During the first two weeks of May, traces of wheat stripe rust were reported in north central Oklahoma plots. Most of these infections were found on the F-1 or flag leaves. In late May, severe levels of stripe rust were reported in irrigated plots in the Oklahoma panhandle (Fig. 2, p. 189). However, little stripe rust was found in dryland plots and fields. In comparison, leaf rust was heavy in both irrigated and dryland plots in the same area. In early June, high severity (100%) levels of stripe rust were observed in irrigated nursery plots of susceptible winter wheat cultivars at Bushland, Texas. No stripe rust was found in the dryland nurseries. The southern plains infection sites provided a reduced amount of inoculum for the northern regions of the U.S.

Central Plains. During the first two weeks of May, traces of wheat stripe rust were reported in southeastern Colorado plots, east central Nebraska plots, central and north central Kansas plots and fields. Most of these infections were found on the F-1 or flag leaves. In late May, stripe rust was present at many Kansas locations but appeared to be a heavier in western Kansas. Leaf rust was the predominant disease in western Kansas and many growers in this area responded to the disease threat with timely fungicide applications. Stripe rust was found at many locations in central Kansas, but the disease appeared to be held in check by the widespread use of resistant cultivars. In early June, in an irrigated nursery in

northwestern Kansas, 70% stripe rust severities were observed in susceptible cultivars. Low levels were found on previously resistant cultivars. In 2007, the overall estimated loss due to wheat stripe rust in Kansas was 0.2%, which is below the 20-year average of 1.31% (Table 4).

In early June, stripe rust was found in wheat plots in southern Nebraska and in northeastern Colorado fields.

By the third week in June, light levels of stripe rust (1-10% severities) were found in winter wheat in northwestern Nebraska fields and southwestern South Dakota plots (Fig. 2). In the roadside ditch near one of the fields, 40% severities were observed on jointed goatgrass *Ae. cylindrica*.

Northern Plains. By late June, hot and dry conditions brought stripe rust infections to almost a complete remission in the Great Plains states. In late July, no stripe rust was detected in spring wheat in northwest Minnesota or northern North Dakota.

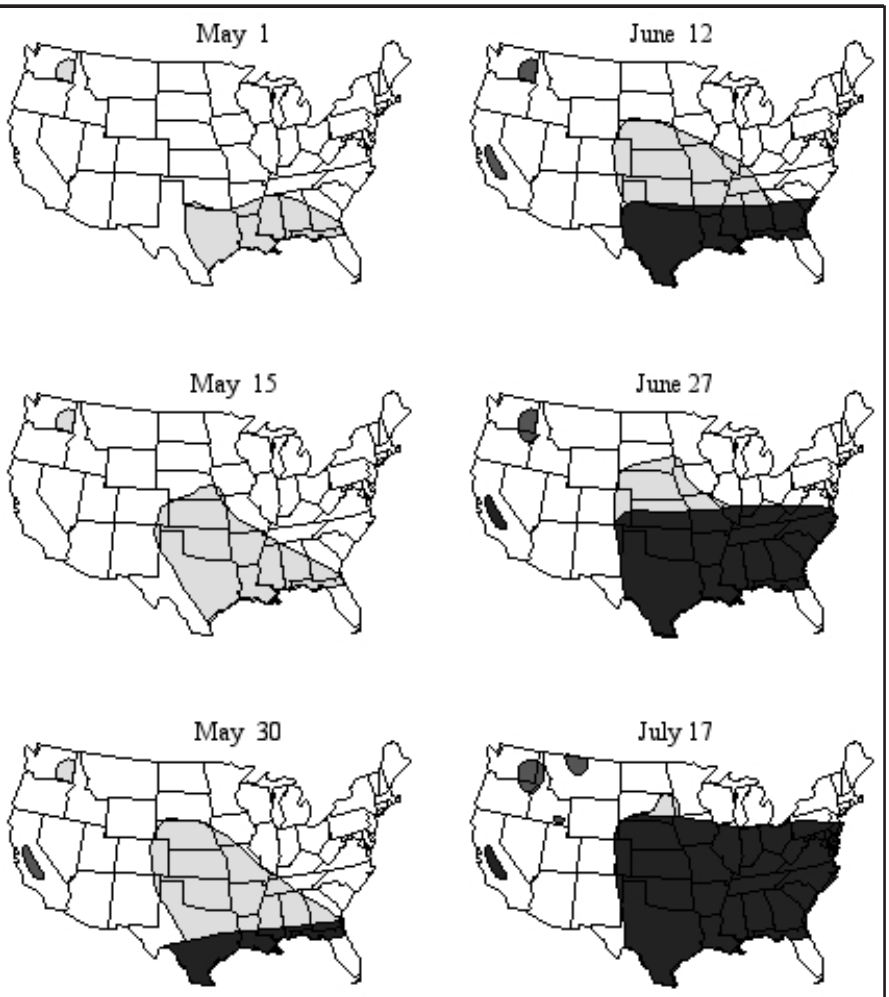

Fig. 2. Stripe rust severities in wheat fields in 2007.

In late May, heavy wheat stripe rust was found in Bozeman, Montana plots, but was spotty throughout the rest of the state. Susceptible winter wheat varieties were more affected than spring wheat varieties. Some growers in the golden triangle of north central Montana sprayed for stripe rust control in winter wheat. Hot dry conditions throughout June prevented stripe rust from becoming a problem.

Louisiana. In late February, light levels of stripe rust were found in wheat fields and plots in southern Louisiana. One crop consultant suggested spraying for stripe rust. In early April, traces of stripe rust were found in wheat plots in Louisiana. In late April, dry and warm conditions slowed stripe rust development in plots and fields in Louisiana.

Arkansas. In early March, wheat stripe rust was reported in southeast and southwest Arkansas fields. Hot spots were seen from the road in a few fields by 13 March. Fungicides were recommended for all fields with stripe rust and several fields were sprayed. By early April, stripe rust was increasing throughout Arkansas, but freezing temperatures in mid-April affected further stripe rust development.

Southeast. In late April, dry and warm conditions slowed stripe rust development in plots and fields throughout the southeastern U.S. For example, in southern Alabama and southwestern Georgia traces of wheat stripe rust were found in a few plots. In these locations most of the stripe rust infections had occurred earlier, in mid to late winter, when temperatures were cooler.

This year there were few stripe rust inoculum sources in the southern U.S. Then as day and nighttime temperatures continued to increase, they surpassed the optimum for stripe rust development and this lead to a reduced amount of rust for the northern wheat growing regions of the U.S.

Table 4. Estimated losses in winter wheat due to rust in 2007 (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	80	43.0	3,440	0.0	0.0	T	T	0.0	0.0
AR	700	41.0	28,700	0.0	0.0	T	T	T	T
CA	240	80.0	19,200	0.0	0.0	0.0	0.0	2.0	391.8
CO	2,350	40.0	94,000	0.0	0.0	1.0	949.5	T	T
DE	55	68.0	2,740	0.0	0.0	0.0	0.0	0.0	0.0
FL	9	57.0	513	0.0	0.0	T	T	0.0	0.0
GA	230	40.0	9,200	0.0	0.0	T	T	0.0	0.0
ID	710	73.0	51,830	0.0	0.0	T	T	0.5	260.5
IL	890	57.0	50,730	0.0	0.0	0.5	254.9	T	T
IN	370	57.0	21,090	0.0	0.0	1.0	213.0	0.0	0.0
IA	28	50.0	1,400	0.0	0.0	T	T	0.0	0.0
KS	8,600	33.0	283,800	0.0	0.0	13.9	45,923.4	0.2	660.8
KY	250	49.0	12,250	0.0	0.0	0.1	12.3	0.0	0.0
LA	220	54.0	11,880	0.0	0.0	1.0	121.2	1.0	121.2
MD	170	68.0	11,560	0.0	0.0	0.0	0.0	0.0	0.0
MI	540	65.0	35,100	0.0	0.0	T	T	T	T
MN	60	48.0	2,880	0.0	0.0	3.0	89.1	0.0	0.0
MS	330	56.0	18,480	0.0	0.0	0.5	92.9	0.0	0.0
MO	880	43.0	37,840	0.0	0.0	2.0	772.2	T	T
MT	2,190	38.0	83,220	0.0	0.0	T	T	0.2	166.8
NE	1,960	43.0	84,280	0.0	0.0	7.0	6,357.3	0.2	181.6
NJ	28	51.0	1,428	0.0	0.0	0.0	0.0	0.0	0.0
NM	300	26.0	7,800	0.0	0.0	0.0	0.0	0.0	0.0
NY	85	52.0	4,420	0.0	0.0	0.5	223.2	0.0	0.0
NC	500	40.0	20,000	0.0	0.0	0.5	100.5	0.0	0.0
ND	445	50.0	22,250	0.0	0.0	5.0	1,171.1	0.0	0.0
OH	730	63.0	45,990	0.0	0.0	1.0	464.5	0.0	0.0
OK	3,500	28.0	98,000	0.0	0.0	4.0	4,126.3	1.0	1,031.6
OR	735	55.0	40,425	0.0	0.0	T	T	0.5	203.1
PA	155	58.0	8,990	0.0	0.0	1.0	90.8	0.0	0.0
SC	135	31.0	4,185	0.0	0.0	0.5	21.0	0.0	0.0
SD	1,980	48.0	95,040	0.0	0.0	4.0	3,960.0	T	T
TN	260	41.0	10,660	0.0	0.0	T	T	0.0	0.0
TX	3,800	37.0	140,600	T	T	6.7	10,608.3	4.5	7,125.0
UT	125	48.0	6,000	0.0	0.0	0.0	0.0	T	T
VA	205	64.0	13,120	0.0	0.0	T	T	0.0	0.0
WA	1,690	64.0	108,160	0.0	0.0	T	T	0.5	543.5
WV	6	58.0	348	0.0	0.0	T	T	0.0	0.0
WI	270	69.0	18,630	0.0	0.0	1.0	188.2	0.0	0.0
WY	125	26.0	3,250	0.0	0.0	T	T	0.0	0.0
Total	35,936	42.1	1,514,429		T		75,739.7		10,685.9
U.S.% Loss				4.73		0.67		0.29	
U.S. Total	35,952	42.2	1,515,989						

Table 5. Estimated losses in spring wheat due to rust in 2007 (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	80.0	1,520	0.0	0.0	T	T	0.0	0.0
ID	450	68.0	30,600	0.0	0.0	T	T	T	T
MN	1,650	47.0	77,550	0.0	0.0	5.0	4,081.6	0.0	0.0
MT	2,400	23.0	55,200	0.0	0.0	T	T	T	T
NV	1	100.0	100	0.0	0.0	0.0	0.0	0.0	0.0
ND	6,500	36.0	234,000	0.0	0.0	2.0	4,775.5	0.0	0.0
OR	120	53.0	6,360	0.0	0.0	0.0	0.0	0.5	31.9
SD	1,340	39.0	52,260	0.0	0.0	2.0	1,066.5	0.0	0.0
UT	7	60.0	420	0.0	0.0	0.0	0.0	T	T
WA	447	46.0	20,562	0.0	0.0	T	T	1.0	207.7
WI	8	35.0	280	0.0	0.0	1.0	2.8	0.0	0.0
WY	5	39.0	195	0.0	0.0	0.0	0.0	0.0	0.0
Total from above	12,947	37.0	479,047		0.0		9,926.0		239.6
U.S. % loss				0.0		2.03		0.05	
U.S. total	13,878	37.0	479,047						

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	79	100.0	7,900	0.0	0.0	0.0	0.0	0.0	0.0
CA	75	95.0	7,125	0.0	0.0	0.0	0.0	0.0	0.0
ID	15	83.0	1,245	0.0	0.0	0.0	0.0	0.0	0.0
MT	475	24.0	11,400	0.0	0.0	0.0	0.0	0.0	0.0
ND	1,460	30.0	43,800	0.0	0.0	0.0	0.0	0.0	0.0
SD	8	27.0	216	0.0	0.0	0.0	0.0	0.0	0.0
Total from above	2,112	33.9	71,686		0.0		0.0		0.0
U.S. % loss				0.0		0.0		0.0	
U.S. Total	2,112	33.9	71,686						

Midwest. In early June, foci of stripe rust were noted in plots at Saint Jacob, Illinois (near St. Louis, MO), and traces were found in plots at Owensboro in western Kentucky. These are the only two locations in the northern SRWW area where stripe rust was reported this year.

California. The growing season in California was extremely dry this year. The overall disease impact, even on susceptible varieties, was less than in 2006. However, rain showers and cool temperatures in mid-late April in the Sacramento Valley, allowed stripe rust to reach very high severity levels on susceptible cultivars not treated with fungicide. In early May, only trace levels of wheat stripe rust developed in the drier San Joaquin Valley. By mid-May, despite the very dry

conditions, severe levels of rust developed in small areas of fields of susceptible varieties in the San Joaquin Valley. Because of the late development and limited spread of the disease, yield losses were minimal (Table 5, p. 191).

In mid July, stripe rust developed up to 40–100% severities on susceptible winter and spring wheat entries in the monitoring nurseries at Tule Lake, a high elevation area in northeastern California. The rust level was relatively low compared to those in the past several years.

Pacific Northwest. As usual, stripe rust reached 50% severity by the first week in April and 60% severity during the third week in April on susceptible entries in winter wheat nurseries at Mount Vernon in northwestern Washington. By the end of May in northwestern Washington, 100% stripe rust severities were observed on susceptible winter wheat entries and 40% severities on susceptible spring wheat entries.

In mid-April, early-planted HRWW fields had up to 10% stripe rust severity in south-central Washington. Timely application of fungicides prevented further development of stripe rust in this region and prevented further spread of the disease to other regions. The dry weather conditions from late April to late May and reduced rust inoculum, made rust development slow and light in the major wheat growing regions in the Pacific Northwest. In mid-May, low levels of stripe rust were found in nurseries in the Palouse region with some hot spots of severities up to 40%. In early June, stripe rust severities ranged from 10% to 40% in eastern Washington winter and spring wheat plots.

By the end of May, wheat stripe rust was reported in experimental fields in Pendleton, Oregon, and Moscow, Idaho. In mid June, wheat stripe rust developed in eastern and central Washington fields and in dryland and irrigated fields in northeastern Oregon. In mid June, stripe rust severities reached 100% on susceptible entries around Pullman and Walla Walla and 60-80% at Lind, Pendleton and Hermiston on winter wheat and 40–60% on susceptible entries at these locations on spring wheat. However, stripe rust was light in commercial wheat fields due to resistance of cultivars, low inoculum, and dry weather conditions from late April to late June.

Hot and dry weather conditions during the first two weeks of July stopped the stripe rust season in most of the Pacific Northwest. Similar to 2006, stripe rust of wheat was light in commercial fields and therefore, yield losses caused by stripe rust were low. However, stripe rust did develop to 100% severity on susceptible entries in unirrigated experimental plots of both winter and spring wheat under natural infection in Washington, and 60-80% severities in wheat nurseries in northeastern Oregon and northern Idaho.

Canada. In late July, isolated pustules of stripe rust were observed in some fields in Saskatchewan, Canada, but the severity was very low.

NEBRASKA

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Nebraska wheat crop.

In 2007, 2,050,000 acres (830,00 ha) of wheat were planted in Nebraska and 1,960,000 acres (790,000 ha) were harvested with an average yield of 43 bu/acre (2,890 kg/ha) for a total production of 84,280,000 bu (2,304,504,000 kg). The 2006 Nebraska wheat crop was estimated at 61,200,000 bu (1,667,088,000 kg), which represented a 36 bu/acre state (2,420 kg/ha) average yield on 1,700,000 harvested acres (688,500 ha). The autumn was generally conducive to good emergence

across the state. The winter was relatively mild with more snow than normal in western NE. Winterkilling was minor, however, a late spring frost was damaging (surprisingly so) to early lines in areas of Nebraska where the wheat was advanced. Most of the wheat was in the rosette stage when the frost came, so it was assumed the damage would be minor, however, some lines seemed to be weakened and became more susceptible to the onset of later diseases and stresses. The spring growing season began and stayed on the dry side in parts of western NE, thus reducing diseases other than viruses. However, much of eastern NE had ample moisture during flowering and grain-fill leading to high yields, leaf diseases, and FHB. At harvest, much of the rains stopped, and the harvest seed quality was good.

Waxy wheat development and characterization.

R. Graybosch.

Approximately 25 waxy winter wheats were evaluated for agronomic performance in Nebraska. As part of coöperative projects with Kansas State and Oklahoma State Universities, the study also was seeded at two Kansas locations and at Pendleton, OR. Eight lines evaluated were deemed promising enough to continue testing in 2008. Disease susceptibility was an issue with many lines, and these were discontinued. Two waxy winter wheats (NX03Y2489 and NX04Y2107) were entered in the 2008 Northern Regional Performance Nursery. Experiments to identify new uses for partial waxy (reduced amylose) and waxy (amylose-free) starches of bread and durum wheats were continued. Durum starches were modified via hydroxypropylation. Substituted fully waxy starches had increased peak viscosities, breakdowns, reduced final viscosities, setbacks, and pasting times. These modified forms of starches are used as thickeners in foods and frozen preparations such as pie fillings, sauces, gravies, and salad dressings. Coöperative experiments with scientists at Kansas State University and the USDA–ARS–GMRPL at Manhattan established the following: a) replacement of wild-type bread flour by 10–20% waxy wheat flour can improve both loaf volume and shelf-life stability, perhaps reducing the need for artificial shelf-life extenders in commercial bakeries and b) automated seed sorting technology, coupled with near-infrared spectroscopy, can separate waxy kernels (all null alleles) from partial waxy kernels (at least one null allele and one functional allele) or wild-type kernels (all functional alleles). This rate is sufficient to select waxy kernels from breeding lines or to purify contaminated samples.

Hard red winter wheat development.

P. S. Baenziger, R. Graybosch, Lan Xu, S. Wegulo, and G. Hein.

Camelot is a HRWW cultivar developed coöperatively by the Nebraska Agricultural Experiment Station and the USDA–ARS and released in 2008 by the developing institutions. Camelot was released primarily for its superior adaptation to rain-fed wheat-production systems in Nebraska and adjacent areas in the northern Great Plains. Camelot will be exclusively marketed by the NuPride Genetics Network in keeping with their marketing plans. Camelot was tested under the experimental designation NE01604.

NH03614 CL is a HRWW cultivar developed cooperatively by the Nebraska Agricultural Experiment Station and the USDA–ARS and released in 2008 by the developing institutions and the South Dakota Agricultural Experiment Station and the Wyoming Agricultural Experiment Station. NH03614 CL contains a patented gene owned by BASF. BASF retains ownership of the gene. NH03614 CL was released primarily for its herbicide resistance and superior adaptation to rain-fed, wheat-production systems in Nebraska, Wyoming, and South Dakota, and wheat-producing counties in adjacent states. NH03614 CL is a Clearfield™ wheat that will be used with Beyond® herbicide (active ingredient imazamox (2-[4,5-dihydro-4-methyl-4-(1-methylethyl)-5-oxo-1*H*-imidazol-2-yl]-5-(methoxymethyl)-3-pyridinecarboxylic acid) BASF Corp., Triangle Park, NC). NH03614 CL will be marketed as Husker Genetics Brand 'Compass'. NH03614 CL was tested under the experimental designation NNH03614.

Hard white winter wheat development.

R. Graybosch and P.S. Baenziger.

Anton HWWW was coöperatively developed and released in 2007 by the USDA–ARS and Nebraska Agricultural Experiment Station. Anton was released primarily for its low levels of grain and flour polyphenol oxidase (PPO). Low levels of grain PPO correlate with enhanced end-use quality, including final product color in noodle applications. Low PPO also is desirable for the establishment of a viable Great Plains hard white wheat production industry. Anton was tested under the experimental designation NW98S097.

Development of WSMV-resistant winter wheat.

R. Graybosch, G. Hein, P.S. Baenziger, and L. Divis.

Mace is a HRWW cultivar coöperatively developed and released in 2007 by the USDA–ARS and Nebraska Agricultural Experiment Station. Mace was released primarily for its resistance to WSMV, and its adaptation to rain-fed and irrigated wheat production systems in Nebraska and adjacent areas in the northern Great Plains. Resistance to WSMV is conditioned by the *Wsm1* gene, present on an introgressed chromosome arm from *Th. intermedium*. Mace was tested under the experimental designation N02Y5117.

Organic wheat breeding efforts.

P.S. Baenziger, R. Little, L. Xu, C. Shapiro, D. Lyon, S. Knezevic, K. Russell, G. Hein, S. Wegulo, R. Flores, V. Schlegel, R. Wehling, and L. Sarno.

The long-term goal of this effort is to develop small grains cultivars and cropping systems incorporating small grains that will improve the profitability and competitiveness of organic producers. The specific objectives of our research are to: 1. determine if current advanced experimental wheat lines and released cultivars have potential for organic wheat production and 2. based upon what we learn in the organic wheat trials, augment our wheat-breeding program to develop wheat cultivars ideally suited to organic production. Others will attempt to 3. develop an integrated organic soil fertility management program to increase grain protein content and 4. reduce tillage or increase organic matter in organic systems by the use of small grains cover crops to suppress weeds, or to suppress weeds by flaming. Our outreach efforts will include the development of workshops and web-based materials to explain the wheat breeding process and variety selection, prioritizing the desirable traits for organic production and marketing, involving organic producers in the planning and on-farm evaluation (using on-farm demonstration plots) of an integrated organic farm package involving the best cultivar(s) grown using the best fertility regime and cover crops. This project should be very complementary to our conventional wheat breeding effort in that organic producers emphasize the need for excellent end-use quality and disease resistance, but can accept lower yields. Conventional wheat producers emphasize the need for higher yield and can accept average disease resistance and end-use quality. Hence, each set of lines can be used as parents to develop improved lines or the complementary program.

Winter triticale nursery.

P.S. Baenziger.

In 2007, no new triticale lines were recommended for release; however, we selected ten lines for increase (five small and five large increases) as possible replacements or to complement NE426GT and NE422T, which continue to perform well. With the interest in maize for ethanol, we believe that the future is very bright for triticale in that it can be grown over the winter as forage or grain crop in areas where maize cannot be grown successfully. The grain will substitute for maize in animal rations and the forage can be used as forage, cellulosic ethanol feed stocks, or as a ground cover. Coöperation with Iowa State University continues to provide excellent efforts in the grain and, we believe, in the future bioenergy uses of triticale. Forage data for the 2007 triticale variety trial was provided by Dr. Ken Vogel and the USDA–ARS. Germ plasm exchange for this minor crop remains a concern and we are willing to exchange our triticale germ plasm (as well as our wheat germ plasm) with other programs.

Additional information on Dr. P.S. Baenziger's projects in 2007 can be found at http://agronomy.unl.ecu/ grain/ WHTANN0732708.PDF.

Personnel.

Satyanarayana Tatineni joined the USDA–ARS group as a molecular virologist. Mr. Javed Sidiqi successfully completed his M.S. degree. Mr. Zakaria Aj-Alouni successfully completed his Ph.D. degree. Dr. Liakat Ali completed his postdoctoral assignment and accepted a position with the University of Arkansas. We welcome Mr. Richard Little to his new position as Organic Wheat Breeding Project Coordinator. We also welcome Ms. Somrudee Onto and Mr. Ali Bakhsh as new graduate students to our program.

Publications.

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2007 Wheat Production in the Commonwealth of Virginia.

W.E. Thomason, C.A. Griffey, and J. E. Seago

Growing Conditions. Planting conditions for the 2006–07 small grain crop ranged from acceptable soil moisture to excessively wet in some southeastern counties. Forty-two percent of the small grain crop was planted by 29 October, which was exactly the five year mean. Rain and unseasonable warm temperatures in early winter favored small grain development, especially helping later planted stands. Average temperatures in January were more than seven degrees above the long- term average for that time of year and resulted in a boost in small grain growth (Fig 1). Late winter brought unseasonable cool temperatures and dry weather with February and March rainfall at 70 percent of normal (Fig. 2). Cold damage and the dry spring resulted in the wheat crop being rated 54 percent good and 27 percent fair.

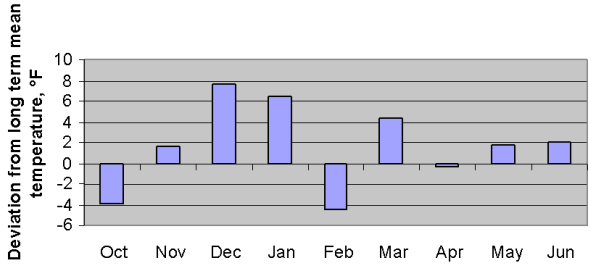

Fig. 1. Temperature deviation from long-term mean.

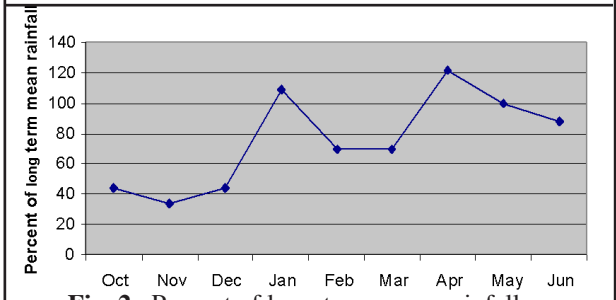

Fig. 2. Percent of long-term mean rainfall.

The 'Easter Freeze' resulted in some damage to wheat and especially barley fields, but the Virginia crop overall fared much better than many of our neighbors. More damage was reported in early heading cultivars and location, even within the field, seemed to have a major impact. Dry conditions at harvest time facilitated a timely harvest with USDA reporting wheat harvest 12 percent ahead of normal on 1 July. These warm and dry conditions resulted in slightly smaller kernels in most instances. Overall quality of the 2007 crop was good. Test weight averaged 0.27 lb/bu more than the 2006 crop, largely because dry conditions allowed continued harvest without weathering. Grain protein was 0.11 percent higher in 2007 compared to 2006, also due to warm and dry conditions during grain fill.

Disease and insect incidence and severity. Stripe rust, was only found at one of the seven Official Variety Test sites in 2007. Initial infection foci were observed at Orange, VA in plots of 'Sisson' wheat, carrying resistance gene *Yr*9, indicating that the race likely was PST100. Powdery mildew incidence again was lower than usual for the fourth consecutive year in the Eastern Shore and Coastal Plain region. Leaf rust infection was moderate on susceptible cultivars grown in research yield trials at Holland, VA, and high at Warsaw and Painter, VA. Cultivars such as Sisson and USG3209 having gene *Lr*26 and McCormick having gene *Lr*24 were susceptible to leaf rust. Race surveys conducted USDA–ARS Cereal Disease Lab on 18 samples from six regions in Virginia indicate that race MFGJH (virulence for genes *Lr1*, *3*, *10*, *11*, *14a*, *24*, *26*, *28*, *42*) was most common at Warsaw (northeast), Holland (southeast) and Painter (eastern shore) VA. Race TNRJK (virulence for genes *Lr1*, *2a*, *2c*, *3*, *3ka*, *9*, *10*, *11*, *14a*, *24*, *28*, *30*, *41*, *42*) also was present at Painter, VA. Race TDBGG (virulence for genes *Lr1*, *2a*, *2c*, *3*, *10*, *24*, *28*) was present at Blacksburg (southwestern) VA. Race MCDSB (virulence for genes *Lr1*, *3*, *10*, *14a*, *17*, *26*, *B*) was present at Blackstone (southern Piedmont) and race MCTSB (virulence for genes *Lr1*, *3*, *3ka*, *10*, *11*, *14a*, *17*, *26*, *30*, *B*) was common at Orange (northern Piedmont) VA. The incidence of FHB was low in 2007 and DON toxin levels were predominantly below 1 ppm. Barley yellow dwarf virus infection was low to moderate at two test sites (Warsaw and Blacksburg, VA) and moderate to high at two other sites (Orange and Blackstone, VA).

Production. Virginia wheat producers planted on 230,000 acres (93,150 ha) in 2006–07, up 40,000 acres (16,200 ha) from the previous year and 22,000 acres (8,910 ha) more than the 2000–06 mean. Harvested area in 2006–07 was estimated at 205,000 acres (83,025 ha), up 30 percent over the previous two seasons. Statewide average yield was 64 bu/ac (4,300 kg/ha), four bu/acre (269 kg/ha) higher than the 5-year average yield of 60 bu/acre (4,031 kg/ha). Overall wheat production was 13.1 x 10^6 bushels. Wheat acreage is estimated to have increased an additional 50,000 acres in 2007–08 due to stronger prices.

State cultivar tests. A total of 90 entries were evaluated in 6 trials at six locations across the Commonwealth in 2007. No-till tests planted into corn stubble also were conducted at Warsaw and Holland, VA. Included in this total were 35 released cultivars and 55 experimental lines (42 developed at Virginia Tech). Average grain yields ranged from 70 to 92 bu/acre (4,703 to 6,182 kg/ha) with an over location test average of 81 bu/acre (5,442 kg/ha). Wheat cultivars with yields ranging from 84 to 92 bu/acre (5,644 to 6,182 kg/ha) and significantly above the test average included USG 3665, Branson, USG 3555, Tribute, and USG 3209. Twenty experimental lines also produced yields within a similar range that was significantly higher than the eight-location test average. Average test weights of wheat lines ranged from 57.5 lb/bu (740 kg/m^3) to 62.6 lb/bu (806 kg/m^3) with a test average of 60.0 lb/bu (772 kg/m^3).

2007 Virginia Small Grain Yield Contest results. There were six entries grown in four counties in the 2007 Virginia wheat yield contests. Five of the entries were grown no-till and one conventional till. The three highest yields came from producers in different counties and were obtained with different cultivars. Results are presented in Table 1.

Table 1. 2007 Virginia Small Grain Yield Contest results.

Place	Farm	Yield County	Planting (bu/acre)	date	Cultivar
1	John N Mills & Sons	Hanover Co.	107.41	10/12/2006	Vigoro 9510
2	Hampstead Farm	Middlesex Co.	106.49	10/25/2006	SS MVP 57
3	Flaggy Run Farms, LLC	So. Hampton Co.	98.36	10/16/2006	SS 520
Additional entries:					
	Grainfield Farm	Hanover Co.	97.86	10/14/2006	Roane
	Corbin Hall Farm	Middlesex Co.	93.247	11/3/1006	Pioneer 26R31
	Laurel Springs Farm	Westmoreland Co.	80.30	10/22/2006	Tribute

Three unusual arthropods in small grains in 2007–08

Ames Herbert, Extension Entomologist.

The 2007–08 small grain season brought three unusual insect/arthropod problems to wheat in Virginia and northeast North Carolina. Winter grain mite, *Penthaleus major* (Dugès), began showing up in large numbers in wheat fields on our Eastern Shore counties in December. Populations were large enough, for the first time that we know of, to damage and even kill plants in large areas. After some hustling, we were able to connect growers with relevant educational materials and management got underway. Very soon after the first reports from the 'Shore', we started receiving calls from northeast North Carolina, then counties to our west, then north of us from the Middle Peninsula region, and eventually from our Northern Neck region. By March, these mites were infesting fields throughout the majority of our small grain production area. Interestingly, I also got calls from central North Carolina and from as far away as Alabama. We are currently surveying to determine the extent of the mite infestation, but based on what we have been hearing, several thousands of acres were infested, and many hundreds were treated. There is very little information about this mite in terms of thresholds and management in wheat, and even less to help explain the widespread problem we encountered this season.

The second unusual insect problem was what I termed 'spring-only' aphid infestations. Although it is not uncommon to see a few aphids in wheat in the spring months (a few per row foot), this year infestations were large, sometimes exceeding 200 to 300 per row foot, and mostly comprised of the species, bird cherry-oat aphid. The location of these infestations was also unusual, being mostly in the southeastern part of the state, rather than in the Middle Peninsula and northeast counties. Our research from the late 1980s and early 1990s showed that even large populations of these 'Spring-only' aphid infestations did not present a threat to grain yields, as they were not associated with the transmission of barley yellow dwarf, the primary aphid-related agent responsible for decreasing grain quality and yield. But because they were not used to seeing them, and because of the high wheat prices, many growers took the opportunity to tank-mix insecticides with spring fungicide applications. Again, like with the mites, we do not know what combination of factors lead to this unusual 'spring-only' aphid outbreak.

The third, and maybe related unusual wheat insect problem was Hessian fly. I say 'maybe related' because indeed, all of these pest problems may somehow be related to the generally warmer winters, drier summers, and increase in crop and cover-crop residue in fields because of the increase in reduced tillage practices. This year Hessian fly populations have been very large and long lasting in some fields, and have been giving headaches to growers and crop consultants, especially in northeast North Carolina. Because Hessian fly is so unusual in our area of the country, we have not had the opportunity to develop good data-based management recommendations, which of course opens the door to speculation, desperation treatments and seat-of-the-pants recommendations.

Are these pest problems going to recur, or were they flukes, not to seen for another bunch of years? Now that we have seen them, we will be on the lookout next season and, hopefully, be in a better position to react with some timely field research efforts. It will take coördination across state lines and disciplines, and even so, at least a few seasons to develop good management strategies.

On the positive side, cereal leaf beetle populations were extremely low this year, with almost no fields even coming close to developing economic thresholds. Was this weather related too? Or have we gradually reduced cereal leaf beetle numbers with annual pyrethroid sprays in wheat? The latter could be possible since cereal leaf beetle undergoes a single generation each year, and only infests small grains. Killing that one generation in wheat (they are very susceptible to pyrethroid insecticides) greatly limits the number that are carried over to the next season. Incidence of barley yellow dwarf was also very low. We have three field trials across the eastern side of the state evaluating various aphid/BYD control treatments and virus incidence, even in the untreated controls, never exceeded 2% of the total area (compared with 30% in heavy pressure years). This does fit a known pattern, in that incidence of BYD is typically low in years following dry summers, which we certainly had in 2007. Dry summers limit the number and growth of the summer weed aphid hosts, which reduces summer build up and the number of aphids that move into grain fields in the fall.

Maybe the story behind the story is that weather is a critical factor in influencing pest populations. If weather patterns are changing, pest problems may also make some shifts in terms of both the species we find, and the infestation levels. Only time will tell.

Release of 'Jamestown' soft red winter wheat.

The SRWW cultivar **Jamestown** was derived from the cross 'Roane/Pioneer Brand 2691'. The cultivar was approved for release by the Virginia Agricultural Experiment Station in spring 2007, and certified seed will be available beginning in autumn 2009. Jamestown is a distinctly early heading, high yielding, short stature, awned, SRWW cultivar. Jamestown is widely adapted and provides producers in the mid-South, Deep South, and throughout the mid-Atlantic region with a distinctly early maturing, disease and pest resistant cultivar. Jamestown is notably resistant to Hessian fly, leaf rust, stripe rust, powdery mildew, and fusarium head blight.

On the basis of milling and baking quality evaluations over four crop years (2003–06), Jamestown tends to have higher break flour yields (30.5% versus 28.3%) and slightly softer texture (higher softness equivalent score 57.4% versus 54.1%) than those of USG 3209. Straight grade flour yields of Jamestown (71.7%) have been slightly higher than those of USG 3209 (71.1%). On average, Jamestown has higher flour protein concentration (8.92% versus 8.66%) and gluten strength (lactic acid retention value of 113% versus 107%) than those of USG 3209 and, therefore, may be suitable for use in making crackers and other products requiring moderate gluten strength. Overall, Jamestown has better baking quality than that of USG 3209 on the basis of lower values for sucrose retention capacity (93.8% versus 104%) and larger cookie diameters (17.0 cm versus 16.8 cm).

Release of 'USG 3555' soft red winter wheat.

USG 3555 is a high yielding, moderately-early heading, short stature, awnleted, SRWW. Derived from the cross 'VA94-52-60/Pioneer Brand 2643//USG 3209', it was released by the Virginia Agricultural Experiment Station in spring 2007, and certified seed will be available beginning in autumn 2008. USG 3555 is widely adapted and has potential for production in the mid-South, Deep South, and throughout the mid-Atlantic region. USG 3555 notably possesses a high level of resistance to powdery mildew, stripe rust, and stem rust, but is susceptible to Hessian fly.

On the basis of milling and baking quality data for four crop years (2003–06), USG 3555 tends to have higher break flour yields and slightly softer texture than those of USG 3209. Flour yields of USG 3555 have been similar to those of USG 3209. On average, USG 3555 has higher grain protein concentration and stronger gluten strength than USG 3209. Overall, USG 3555 has better pastry baking quality on the basis of lower values for sucrose retention capacity and larger cookie diameters than those of USG 3209 and also has good cake baking qualities.

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The mission of the lab is two-fold: conduct milling, baking, and end-use quality evaluations on wheat breeding lines, and conduct research on wheat grain quality and utilization. Our web site: http://www.wsu.edu/~wwql/php/index.php provides great access to our research, including a database of wheat varieties relating kernel hardness and puroindoline alleles. Our research publications are available on our web site.

We are serving as curator of the grain hardness, puroindoline, and *GSP-1* gene sections of the Catalogue of Gene Symbols in Wheat. Several new alleles have been documented in *Ae. tauschii*, synthetic hexaploids from CIMMYT, and other diploid taxa. Morris and Engle lead the Pacific Northwest Wheat Quality Council, a consortium of collaborators who evaluate the quality of new cultivars and advanced breeding lines. 'Waxy-Pen', a soft white spring waxy wheat, was released in 2006 and is the first waxy wheat to be registered in the United States. Seven puroindoline allele near-isogenic line (NIL) hexaploid wheat genetics stocks were developed and released by the USDA–ARS in 2007. Our current activities and projects include grain hardness and puroindolines, waxy wheat, polyphenol oxidase (PPO), arabinoxylans, SDS sedimentation test, and soft durums. Beecher and Luna are currently researching the genetic control of polyphenol oxidase activity and arabinoxylan content in wheat. Bettge is currently researching wheat biochemistry and its contribution to oxidative gelation, and the impact on batter viscosity and end-use quality.

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V. 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 (February 2008).

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	1987–07	Aberdeen, ID	54,803
Lysine Content	1966–69	Lincoln, NE	10,367
Awn Color	1983–97, 2007	Aberdeen, ID & Maricopa, AZ	24,572
Awn Type	1983–97, 2007	Aberdeen, ID & Maricopa, AZ	27,709
Glume Color	1983–97, 2007	Aberdeen, ID & Maricopa, AZ	24,764
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, 2005–07	Aberdeen, ID & Maricopa, AZ	28,641
Kernels/Spike	1983–94	Aberdeen, ID & Maricopa, AZ	3,666
Kernel Weight	1983–94, 2005–07	Aberdeen, ID & Maricopa, AZ	17,201
Leaf Pubescence	1983–94	Aberdeen, ID & Maricopa, AZ	20,888
Plant Height	1983–97	Aberdeen, ID & Maricopa, AZ	21,841
Plant Height – related to check	1999–2004	Maricopa, AZ	46,841
Rachis Length	1995	Maricopa, AZ	2,512
Shattering	1983–94	Aberdeen, ID & Maricopa, AZ	10,637
Spike Density	1983–98, 2007	Aberdeen, ID & Maricopa, AZ	19,609
Spikelets/Spike	1995	Maricopa, AZ	2,502
Spike Type	1983–97, 2007	Aberdeen, ID & Maricopa, AZ	19,374
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, Aegilops, 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. Accessions registered in the *Journal of Plant Registrations* or *Crop Science* are available by contacting the developers.

Table 2. PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2006–February 2007. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
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	North Dakota
646184	*Triticum aestivum*	Smoky Hill	United States	Kansas
646185	*Triticum aestivum*	Shocker	United States	Kansas
646196	*Triticum aestivum*	Cabernet	United States	California
647959	*Triticum aestivum* subsp. *aestivum*	NE01643	United States	Nebraska
648007	*Triticum aestivum* subsp. *aestivum*	Keota	United States	Kansas
648010	*Triticum aestivum* subsp. *aestivum*	Danby	United States	Kansas
648020	*Triticum aestivum* subsp. *aestivum*	RonL	United States	Kansas
648021	*Triticum aestivum* subsp. *aestivum*	Kuntz	United States	Kansas
648022	*Triticum aestivum* subsp. *aestivum*	AP604 CL	United States	Kansas
648023	*Triticum aestivum* subsp. *aestivum*	Palomino	United States	Kansas
648024	*Triticum aestivum* subsp. *aestivum*	Magnolia	United States	Missouri
648027	*Triticum aestivum* subsp. *aestivum*	Agawam	United States	Montana
648028	*Triticum aestivum* subsp. *aestivum*	Corbin	United States	Montana
648029	*Triticum aestivum* subsp. *aestivum*	Waikea	United States	Montana
648034	*Triticum aestivum* subsp. *aestivum*	ND 756	United States	North Dakota
648350	*Triticum aestivum*	Faller	United States	North Dakota
648390	*Triticum aestivum* subsp. *aestivum*	Arjun	India	Punjab
648391	*Triticum aestivum* subsp. *aestivum*	HD 2329	India	Delhi
648392	*Triticum aestivum* subsp. *aestivum*	Kundan	India	Delhi
648393	*Triticum aestivum* subsp. *aestivum*	DL 802-3	India	Delhi
648394	*Triticum aestivum* subsp. *aestivum*	DL 803-2	India	Delhi
648395	*X Triticosecale* sp.	TL 1210	India	Punjab
648396	*Triticum aestivum* subsp. *aestivum*	Azar	Iran	East Azerbaijan
648397	*Triticum aestivum* subsp. *aestivum*	Lanish	Iran	East Azerbaijan
648398	*Triticum aestivum* subsp. *aestivum*	Rashid	Iran	East Azerbaijan
648399	*Triticum aestivum* subsp. *aestivum*	Sardari	Iran	East Azerbaijan
648400	*Triticum aestivum* subsp. *aestivum*	Yavarez	Iran	East Azerbaijan
648401	*Triticum aestivum* subsp. *aestivum*	2440	Iran	East Azerbaijan
648402	*Triticum aestivum* subsp. *aestivum*	2455	Iran	East Azerbaijan
648403	*Triticum aestivum* subsp. *aestivum*	2461	Iran	East Azerbaijan
648404	*Triticum aestivum* subsp. *aestivum*	2462	Iran	East Azerbaijan
648405	*Triticum aestivum* subsp. *aestivum*	2467	Iran	East Azerbaijan
648406	*Triticum aestivum* subsp. *aestivum*	2470	Iran	East Azerbaijan
648407	*Triticum aestivum* subsp. *aestivum*	2476	Iran	East Azerbaijan

Table 2 (continued). PI assignments in *Triticum*, *Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
648408	*Triticum aestivum* subsp. *aestivum*	2477	Iran	East Azerbaijan
648409	*Triticum aestivum* subsp. *aestivum*	2492	Iran	East Azerbaijan
648410	*Triticum aestivum* subsp. *aestivum*	2493	Iran	East Azerbaijan
648411	*Triticum aestivum* subsp. *aestivum*	2500	Iran	East Azerbaijan
648412	*Triticum aestivum* subsp. *aestivum*	2501	Iran	East Azerbaijan
648413	*Triticum aestivum* subsp. *aestivum*	Ghanam	Pakistan	North-West Frontier
648414	*Triticum aestivum* subsp. *aestivum*	Gum	Pakistan	North-West Frontier
648415	*Triticum aestivum* subsp. *aestivum*	Gum	Pakistan	North-West Frontier
648416	*Triticum aestivum* subsp. *aestivum*	2828-3	Pakistan	North-West Frontier
648417	*Triticum aestivum* subsp. *aestivum*	98M71	South Africa	Cape Province
648418	*Triticum aestivum* subsp. *aestivum*	S14 Translocation	South Africa	Cape Province
648419	*Triticum aestivum* subsp. *aestivum*	0352-4	South Africa	Cape Province
648420	*Triticum aestivum* subsp. *aestivum*	92RL28	South Africa	Cape Province
648448	*Triticum aestivum* subsp. *aestivum*	Sinope	Netherlands	
648449	*Triticum aestivum* subsp. *aestivum*	Ilias	Netherlands	
648468	*Triticum aestivum* subsp. *aestivum*	Art	United States	Kansas
648469	*Triticum aestivum* subsp. *aestivum*	Hawken	United States	Kansas
648870	*Triticum turgidum* subsp. *durum*	Ribeiro	Portugal	Lisboa
648871	*Triticum turgidum* subsp. *durum*	Sahman	Turkey	Ankara
648872	*Triticum turgidum* subsp. *durum*	Sahman	Turkey	Nevsehir
648873	*Triticum turgidum* subsp. *durum*	Bolvadin	Turkey	Konya
648874	*Triticum turgidum* subsp. *durum*	Kirmizi	Turkey	Malatya
648875	*Triticum turgidum* subsp. *durum*	Menceki	Turkey	Elazig
648876	*Triticum turgidum* subsp. *durum*	Kurt	Turkey	Bursa
648877	*Triticum turgidum* subsp. *durum*	Bijela Brkulja	Bosnia and Herzegovina	
648878	*Triticum turgidum* subsp. *durum*	9309	Ethiopia	Gonder
648879	*Triticum turgidum* subsp. *durum*	9347	Ethiopia	Gonder
648880	*Triticum turgidum* subsp. *durum*	9603	Ethiopia	
648881	*Triticum turgidum* subsp. *durum*	9861	Ethiopia	Welo
648882	*Triticum turgidum* subsp. *durum*	9863	Ethiopia	Welo
648883	*Triticum turgidum* subsp. *durum*	9648	Ethiopia	Welo
648884	*Triticum turgidum* subsp. *durum*	9656	Ethiopia	Welo
648885	*Triticum turgidum* subsp. *durum*	NSGC 18398	Jordan	
648886	*Triticum turgidum* subsp. *durum*	K876	Iran	Khuzestan
648887	*Triticum turgidum* subsp. *durum*	55	Greece	Central Greece
648888	*Triticum turgidum* subsp. *durum*	Veneny 3787	Hungary	Pest
648889	*Triticum turgidum* subsp. *durum*	ELS 6304-37	Ethiopia	Shewa
648890	*Triticum turgidum* subsp. *durum*	IAR/W/14-1	Ethiopia	
648891	*Triticum aestivum* subsp. *aestivum*	341	Ethiopia	Shewa
648892	*Triticum aestivum* subsp. *aestivum*	Kokana	Turkey	Ankara
648893	*Triticum aestivum* subsp. *aestivum*	143/4	Turkey	Erzurum
648894	*Triticum aestivum* subsp. *aestivum*	Dickson's No. 444	Argentina	Buenos Aires
648895	*Triticum aestivum* subsp. *aestivum*	ELS 6404-45	Ethiopia	Kefa
648896	*Triticum aestivum* subsp. *aestivum*	NSGC 18416	Turkey	Isparta
648897	*Triticum aestivum* subsp. *aestivum*	Menceki	Turkey	Elazig
648898	*Triticum aestivum* subsp. *aestivum*	Som	Turkey	Tokat
648899	*Triticum aestivum* subsp. *aestivum*	Kunduru	Turkey	Malatya
648900	*Triticum aestivum* subsp. *aestivum*	Sari	Turkey	Konya
648901	*Triticum aestivum* subsp. *aestivum*	Bugday	Turkey	Urfa
648902	*Triticum aestivum* subsp. *aestivum*	10-1	Ethiopia	Gonder
648903	*Triticum aestivum* subsp. *aestivum*	PLT 76-1955	Peru	Ancash

Table 2 (continued). PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
648904	*Triticum aestivum* subsp. *aestivum*	MG 31108	Ethiopia	Shewa
648905	*Triticum aestivum* subsp. *aestivum*	MG 31318	Ethiopia	
648906	*Triticum aestivum* subsp. *aestivum*	MG 31488	Ethiopia	
648907	*Triticum aestivum* subsp. *aestivum*	MG 31497	Ethiopia	
648908	*Triticum aestivum* subsp. *aestivum*	MG 31513	Ethiopia	
648909	*Triticum aestivum* subsp. *aestivum*	MG 31655	Ethiopia	Shewa
648910	*Triticum aestivum* subsp. *aestivum*	MG 31713	Ethiopia	Shewa
648911	*Triticum aestivum* subsp. *aestivum*	MG 07710	Ethiopia	Shewa
648912	*Triticum aestivum* subsp. *aestivum*	MG 18185	Algeria	
650113	*Triticum aestivum*	XW05K	United States	Indiana
650114	*Triticum aestivum*	XW05G	United States	Indiana
650115	*Triticum aestivum*	XW05J	United States	Indiana
650845	*Triticum turgidum* subsp. *durum*	DT676	Canada	Saskatchewan
650855	*Triticum aestivum*	W1377	United States	Colorado
651012	*Triticum aestivum* subsp. *aestivum*	T5AmS-5AS.5AL R#45	United States	California
651021	*Triticum aestivum*	LA482	United States	Louisiana
651023	*Triticum aestivum* subsp. *aestivum*	TUBBS 06	United States	Oregon
651026	*Triticum aestivum* subsp. *aestivum*	CDC BUTEO	United States	
651031	*Triticum turgidum* subsp. *durum*	FORTISSIMO	United States	California
651032	*Triticum aestivum* subsp. *aestivum*	CAL ROJO	United States	California
651033	*Triticum aestivum* subsp. *aestivum*	ULTRA	United States	California
651043	*Triticum aestivum* subsp. *aestivum*	MACE	United States	Nebraska
651044	*Triticum aestivum* subsp. *aestivum*	ANTON	United States	Nebraska
651045	*Triticum aestivum* subsp. *aestivum*	N04Y2244	United States	Nebraska
651046	*Triticum aestivum* subsp. *aestivum*	N04Y2245	United States	Nebraska
651047	*Triticum aestivum* subsp. *aestivum*	N04Y2246	United States	Nebraska
651048	*Triticum aestivum* subsp. *aestivum*	N04Y2247	United States	Nebraska
651049	*Triticum aestivum* subsp. *aestivum*	N04Y2248	United States	Nebraska
651050	*Triticum aestivum* subsp. *aestivum*	N04Y2249	United States	Nebraska
651051	*Triticum aestivum* subsp. *aestivum*	N04Y2254	United States	Nebraska
651052	*Triticum aestivum* subsp. *aestivum*	N04Y2255	United States	Nebraska
651053	*Triticum aestivum* subsp. *aestivum*	N04Y2256	United States	Nebraska
651054	*Triticum aestivum* subsp. *aestivum*	N04Y2257	United States	Nebraska
651055	*Triticum aestivum* subsp. *aestivum*	N04Y2258	United States	Nebraska
651056	*Triticum aestivum* subsp. *aestivum*	N04Y2259	United States	Nebraska
651057	*Triticum aestivum* subsp. *aestivum*	N04Y2264	United States	Nebraska
651058	*Triticum aestivum* subsp. *aestivum*	N04Y2265	United States	Nebraska
651059	*Triticum aestivum* subsp. *aestivum*	N04Y2266	United States	Nebraska
651060	*Triticum aestivum* subsp. *aestivum*	N04Y2267	United States	Nebraska
651061	*Triticum aestivum* subsp. *aestivum*	N04Y2268	United States	Nebraska
651062	*Triticum aestivum* subsp. *aestivum*	N04Y2269	United States	Nebraska
651063	*Triticum aestivum* subsp. *aestivum*	N04Y2270	United States	Nebraska
651064	*Triticum aestivum* subsp. *aestivum*	N04Y2272	United States	Nebraska
651065	*Triticum aestivum* subsp. *aestivum*	N04Y2274	United States	Nebraska
651066	*Triticum aestivum* subsp. *aestivum*	N04Y2275	United States	Nebraska
651067	*Triticum aestivum* subsp. *aestivum*	N04Y2276	United States	Nebraska
651068	*Triticum aestivum* subsp. *aestivum*	N04Y2277	United States	Nebraska
651069	*Triticum aestivum* subsp. *aestivum*	N04Y2279	United States	Nebraska
651070	*Triticum aestivum* subsp. *aestivum*	N04Y2281	United States	Nebraska
651071	*Triticum aestivum* subsp. *aestivum*	N04Y2282	United States	Nebraska
651072	*Triticum aestivum* subsp. *aestivum*	N04Y2283	United States	Nebraska

Table 2 (continued). PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
651073	*Triticum aestivum* subsp. *aestivum*	N04Y2284	United States	Nebraska
651074	*Triticum aestivum* subsp. *aestivum*	N04Y2285	United States	Nebraska
651075	*Triticum aestivum* subsp. *aestivum*	N04Y2286	United States	Nebraska
651076	*Triticum aestivum* subsp. *aestivum*	N04Y2287	United States	Nebraska
651077	*Triticum aestivum* subsp. *aestivum*	N04Y2288	United States	Nebraska
651078	*Triticum aestivum* subsp. *aestivum*	N04Y2289	United States	Nebraska
651079	*Triticum aestivum* subsp. *aestivum*	N04Y2290	United States	Nebraska
651080	*Triticum aestivum* subsp. *aestivum*	N04Y2291	United States	Nebraska
651081	*Triticum aestivum* subsp. *aestivum*	N04Y2292	United States	Nebraska
651082	*Triticum aestivum* subsp. *aestivum*	N04Y2293	United States	Nebraska
651083	*Triticum aestivum* subsp. *aestivum*	N04Y2294	United States	Nebraska
651084	*Triticum aestivum* subsp. *aestivum*	N04Y2295	United States	Nebraska
651085	*Triticum aestivum* subsp. *aestivum*	N04Y2296	United States	Nebraska
651086	*Triticum aestivum* subsp. *aestivum*	N04Y2297	United States	Nebraska
651087	*Triticum aestivum* subsp. *aestivum*	N04Y2298	United States	Nebraska
651088	*Triticum aestivum* subsp. *aestivum*	N04Y2301	United States	Nebraska
651089	*Triticum aestivum* subsp. *aestivum*	N04Y2302	United States	Nebraska
651090	*Triticum aestivum* subsp. *aestivum*	N04Y2303	United States	Nebraska
651091	*Triticum aestivum* subsp. *aestivum*	N04Y2304	United States	Nebraska
651249	*Triticum aestivum* subsp. *aestivum*	2002-488	United States	Idaho
651250	*Triticum aestivum* subsp. *aestivum*	Increase 74	United States	Idaho
651251	*Triticum aestivum* subsp. *aestivum*	2002-63	United States	Idaho
651252	*Triticum aestivum* subsp. *aestivum*	2003-5	United States	Idaho
651253	*Triticum aestivum* subsp. *aestivum*	2003-28	United States	Idaho
651254	*Triticum aestivum* subsp. *aestivum*	2003-289	United States	Idaho
651255	*Triticum aestivum* subsp. *aestivum*	AWA 82096-1	United States	Idaho
651256	*Triticum aestivum* subsp. *aestivum*	AWA 82097-1	United States	Idaho
651257	*Triticum aestivum* subsp. *aestivum*	2002-36	United States	Idaho
651258	*Triticum aestivum* subsp. *aestivum*	Bare 5	United States	Idaho
651259	*Triticum aestivum* subsp. *aestivum*	Increase 12	United States	Idaho
651260	*Triticum aestivum* subsp. *aestivum*	Increase 12 Winter-hardy selection	United States	Idaho
651261	*Triticum aestivum* subsp. *aestivum*	2003-7	United States	Idaho
651262	*Triticum aestivum* subsp. *aestivum*	2003-1	United States	Idaho
651263	*Triticum aestivum* subsp. *aestivum*	2003-10	United States	Idaho
651264	*Triticum aestivum* subsp. *aestivum*	2003-3	United States	Idaho
651265	*Triticum aestivum* subsp. *aestivum*	2003-22	United States	Idaho
651266	*Triticum aestivum* subsp. *aestivum*	Increase 25-1	United States	Idaho
651267	*Triticum aestivum* subsp. *aestivum*	Increase 25-2	United States	Idaho
651268	*Triticum aestivum* subsp. *aestivum*	Increase 6	United States	Idaho
651269	*Triticum aestivum* subsp. *aestivum*	2003-248	United States	Idaho
651270	*Triticum aestivum* subsp. *aestivum*	2003-245	United States	Idaho
651271	*Triticum aestivum* subsp. *aestivum*	2003-242	United States	Idaho
651272	*Triticum aestivum* subsp. *aestivum*	Increase 9	United States	Idaho
651273	*Triticum aestivum* subsp. *aestivum*	Increase 77	United States	Idaho
651274	*Triticum aestivum* subsp. *aestivum*	2003-250	United States	Idaho
651275	*Triticum aestivum* subsp. *aestivum*	2003-253	United States	Idaho
651276	*Triticum aestivum* subsp. *aestivum*	2002-65	United States	Idaho
651277	*Triticum aestivum* subsp. *aestivum*	2003-8	United States	Idaho
651278	*Triticum aestivum* subsp. *aestivum*	2004-51	United States	Idaho
651279	*Triticum aestivum* subsp. *aestivum*	Pope 301R	United States	Idaho

Table 2 (continued). PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
651280	*Triticum aestivum* subsp. *aestivum*	Pope 302R	United States	Idaho
651281	*Triticum aestivum* subsp. *aestivum*	Pope 303R	United States	Idaho
651282	*Triticum aestivum* subsp. *aestivum*	Pope 304R	United States	Idaho
651283	*Triticum aestivum* subsp. *aestivum*	Pope 305R	United States	Idaho
651284	*Triticum aestivum* subsp. *aestivum*	Pope 306R	United States	Idaho
651285	*Triticum aestivum* subsp. *aestivum*	Pope 307R	United States	Idaho
651286	*Triticum aestivum* subsp. *aestivum*	Pope 308R	United States	Idaho
651287	*Triticum aestivum* subsp. *aestivum*	Pope 309R	United States	Idaho
651288	*Triticum aestivum* subsp. *aestivum*	Pope 310R	United States	Idaho
651289	*Triticum aestivum* subsp. *aestivum*	Pope 311R	United States	Idaho
651290	*Triticum aestivum* subsp. *aestivum*	Pope 312R	United States	Idaho
651291	*Triticum aestivum* subsp. *aestivum*	Pope 313R	United States	Idaho
651292	*Triticum aestivum* subsp. *aestivum*	Pope 314R	United States	Idaho
651293	*Triticum aestivum* subsp. *aestivum*	Pope 315R	United States	Idaho
651294	*Triticum aestivum* subsp. *aestivum*	Pope 316R	United States	Idaho
651295	*Triticum aestivum* subsp. *aestivum*	Pope 5R	United States	Idaho
651296	*Triticum aestivum* subsp. *aestivum*	2003-42	United States	Idaho
651297	*Triticum aestivum* subsp. *aestivum*	Selection 1	United States	Idaho
651298	*Triticum aestivum* subsp. *aestivum*	2002-76	United States	Idaho
651299	*Triticum aestivum* subsp. *aestivum*	2002-152	United States	Idaho
651300	*Triticum aestivum* subsp. *aestivum*	2002-73	United States	Idaho
651301	*Triticum aestivum* subsp. *aestivum*	2002-547	United States	Idaho
651302	*Triticum aestivum* subsp. *aestivum*	Weston Erect	United States	Idaho
651303	*Triticum aestivum* subsp. *aestivum*	2003-215	United States	Idaho
651304	*Triticum aestivum* subsp. *aestivum*	2003-212	United States	Idaho
651305	*Triticum aestivum* subsp. *aestivum*	2003-6	United States	Idaho
651306	*Triticum aestivum* subsp. *aestivum*	2002-2	United States	Idaho
651307	*Triticum aestivum* subsp. *aestivum*	2003-159	United States	Idaho
651308	*Triticum aestivum* subsp. *aestivum*	2003-160	United States	Idaho
651502	*Triticum aestivum* subsp. *aestivum*	06IFAFS2	United States	Montana
651503	*Triticum aestivum* subsp. *aestivum*	06IFAFS3	United States	Montana
651504	*Triticum aestivum* subsp. *aestivum*	06IFAFS16	United States	Montana
651505	*Triticum aestivum* subsp. *aestivum*	06IFAFS17	United States	Montana
651506	*Triticum aestivum* subsp. *aestivum*	06IFAFS26	United States	Montana
651507	*Triticum aestivum* subsp. *aestivum*	06IFAFS27	United States	Montana
651508	*Triticum aestivum* subsp. *aestivum*	06IFAFS36	United States	Montana
651509	*Triticum aestivum* subsp. *aestivum*	06IFAFS37	United States	Montana
651510	*Triticum aestivum* subsp. *aestivum*	06IFAFS44	United States	Montana
651511	*Triticum aestivum* subsp. *aestivum*	06IFAFS45	United States	Montana
651512	*Triticum aestivum* subsp. *aestivum*	06IFAFS48	United States	Montana
651513	*Triticum aestivum* subsp. *aestivum*	06IFAFS49	United States	Montana
651514	*Triticum aestivum* subsp. *aestivum*	06IFAFS223	United States	Montana
651515	*Triticum aestivum* subsp. *aestivum*	06IFAFS227	United States	Montana
651516	*Triticum aestivum* subsp. *aestivum*	06IFAFS225	United States	Montana
651517	*Triticum aestivum* subsp. *aestivum*	06IFAFS233	United States	Montana
651612	*Triticum aestivum* subsp. *aestivum*	Sounder	United States	Idaho
651616	*Triticum aestivum* subsp. *aestivum*	Expresso	United States	Montana
652450	*Triticum aestivum* subsp. *aestivum*	8641	United States	Georgia
652451	*Triticum aestivum* subsp. *aestivum*	USG 3295	United States	Georgia
652452	*Triticum aestivum* subsp. *aestivum*	AGS 2031	United States	Georgia
652453	*Triticum aestivum* subsp. *aestivum*	S-24	Pakistan	

Table 2 (continued). PI assignments in *Triticum, Secale*, *Aegilops*, and *X Triticosecale* from January 2007–February 2008. There were no PI assignments in *Aegilops* and *Secale* during this period.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
652923	*Triticum aestivum* subsp. *aestivum*	Samson	United States	
652924	*Triticum aestivum* subsp. *aestivum*	Blade	United States	
652926	*Triticum aestivum* subsp. *aestivum*	Aspen	United States	
652927	*Triticum aestivum* subsp. *aestivum*	Winterhawk	United States	
652930	*Triticum aestivum* subsp. *aestivum*	RB07	United States	Minnesota

VI. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2008 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, 2007, and 2008 Supplement are displayed on the GrainGenes Website: http://wheat.pw.usda.gov.

INTRODUCTION

9. Laboratory Designators

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Gene Symbol

Add to gene symbols list:

Vil. VIN3-like genes similar to Arabidopsis VIN3.

1. Gross Morphology: Spike characteristics

1.1. Squarehead/spelt

Q. **v:** Iranian spelts {0140}. **tv:** *T. turgidum* ssp. *carthlicum, durum* and *polonicum* {10457}.
ma: *Q* was cloned and shown to have similarity to *AtAP2* (APETALA 2) transcription factors {10457}, the *Q* allele was more abundantly transcribed than the *q* allele {10457}.

q. **v:** Insert 'European' in front of 'spelt' and add reference {10457}, i.e., 'European spelts {10457}'.
tv: *T. turgidum* ssp. *dicoccum, dicoccoides* {10457}.

4. Aluminium Tolerance

Insert before the QTL section:

Allelic variation at the promoter of *Almt-D1* is associated with differences in Al tolerance. Molecular and pedigree analysis suggest that Al resistance in modern wheat germ plasm is derived from several independent sources {10532}.

Add to QTL:

'Atlas 66 (insensitive)/Chisholm (sensitive)' RILs. One QTL, located in chromosome 4DL, corresponded to ALMT1 and accounted for 50% of the phenotypic variation {10483}. A second QTL was located on 3BL ($R^2 = 0.11$); nearest marker *Xbarc164-3B* {10483}. Both QTL were verified in 'Atlas/Century' {10483}.

5. Anthocyanin Pigmentation

5.3. Red/purple coleoptiles.

Rc-A1. Rc {10451}[3]. 7AS[3] {10451}. **dv:** PAU14087 {10451 }.
ma: *Xcfa2174-7AS* – 11.1 cM – *Rc-A1* – 4.3 cM – *Xgwm573-7AL/Xwmc17-7AL* { 10451}[3].

8. Blue Aleurone

Ba2. *Ba* {10451}. **dv:** PAU5088 = G2610 = PI 427389 {10451}.
ma: *Xcfd71-4A* – 10.3 cM – *Ba* – 16.5 cM – *Xcfa2173-4A* {0802}[3].

10. Boron Tolerance

Bo1. Add: 7BL {10460}. **v:** Carnamah {10460}**;** Frame {10460}; Krichauff {10460}; Yitpi {10460}.
ma: *Bo1* co-segregated with several STS-PCR markers, including *Xaww11-7BL*, falling within a 1.8 cM interval {10460}. The AWW7L7 (*Xaww11*) PCR marker allele was a good predictor of boron tolerance {10460}.

17. Dormancy (Seed)

Seed dormancy in wheat has several components, including factors associated with vivipary and red grain colour. Dormancy is an important component of resistance/tolerance to preharvest sprouting (PHS).

Vivipary: Othologues of maize viviparous 1 (*Vp-1*) are located in chromosomes 3AL, 3BL, and 3DL {9961} approximately 30 cM distal to the *R* loci. Variability at one or more of these loci may be related to germination index and hence to PHS {10468).

Three sequence variants of ***Vp-B1*** identified in {10468} were used to develop STS marker VpiB3 whose amplified products showed a significant, but not complete, association with germination index used as one measure of PHS.

Pre-harvest sprouting:

Phs1 {10500}. *Phs* {9960}. **i:** Haruyokoi*6 / Leader {10500}; Haruyokoi*6 / Os21-5 {10500}.
v: Leader {10500}; Os21-5 {10500}.
ma: *Xhbe03-4AL* – 0.5cM – *Phs1* – 2.1 cM – *Xbarc170-4AL* {10500}.

phs1. **v:** Haruyokoi {10500}.

QTL: As currently listed.

20. Flowering Time

Winter wheat cross 'Ernie (early)/MO94-317 (late)', days to anthesis (dta):
Qdta.umc-2D, linked to *Xbarc95-2D*, $R^2 = 0.74$ {10456}.

26. Glaucousness (Wasiness/Glossiness)

26.2. Epistatic inhibitors of glaucousness

Iw2. *Iw3672* {10510}. **v:** Synthetic hexaploid line 3672 {10510}.
ma: *Xbarc124-2D* – 0.9 cM – *Iw2* – 1.4 cM – *Xwe6* (*AL731727*) {10510}.

29. Grain Quality Parameters

29.2. Flour, semolina and pasta colour

Add at end of section:

QTL: Analysis of yellow flour pigment in an RIL population of 'PH82-2 (low)/Neixiang (high)' revealed major QTL on chromosomes 7A co-segegating with marker *YP7A* ($R^2 = 0.2 – 0.28$) (see Phytoene synthase 1), and 1B ($R^2 = 0.31 – 0.54$) probably contributed by 1RS {10501}.

29.8. Loaf volume

Add:

QTL: Loaf volume score consistent across three environments was scored in an RIL population 'Renan/Recital' and revealed major QTL on chromosomes 3A (flanking markers *Xfbb250-3A*, *Xgwm666-3A*, positive effect from Renan) and 7A (flanking markers *Xcfa2049-7A*, *Xbcd1930-7A*, positive effect from Recital) {10536}.

32. Hairy Leaf

Add note: A QTL analysis of the ITMI population identified loci determining hairiness of leaf margins and auricles in regions of chromosomes 4B and 4D orthologous to *Hl1*{10516}.

***Hl1*.** **ma:** *Xgwm375-4B* - 12.1 cM - *Hl1* - 2.1 cM {10516}.

***Hl2*.**

Add note following this entry:

The hairy leaf gene (Hl^{Aesp}) in *Ae. speltoides* introgression line 102/00^{I} was allelic with *Hl2* {10516}.

39. Height

39.1. Reduced Height: GA-insensitive

39.2. Reduced Height: GA-sensitive

***Rht8c*.v:** Add: Chuanmai 18 {10512}.

To the note following *Rht8c* add:

Although the 'diagnostic' association of *Rht8c* and $Xgwm261_{192}$ applied in many Strampelli derivatives and European wheats, there was no association between reduced height and this allele in Norin 10 and its derivatives {10512}. The pedigrees of a number of Chinese wheats postulated to have *Rht8c* on the basis of the marker trace to Italian sources {10515}.

41. Hybrid Weakness

41.4. Apical lethality

Apical lethality is caused by complementary recessive genes and is characterized by stunting and tiller death at the 4–5 leaf stage. The lethal genotype was designated *apd1 apd1 apd2 apd2* {10492}.

Apd1 {10492}. **v:** WR95 = Kalyansona / Gigas // HD1999 / Sonalika /3/ *T. turgidum* subsp. *carthlicum* {10492}.

apd2 {10492}. **v:** HD2009 {10492}; HW2041 {10492}; Lok-1 {10492}; others {10492}.

***Apd1 Apd2*.** **v:** Atila {10492}; Kalyansona {10492}; others {10492}.

apd1apd2 Lethal genotype.

Uniculm plants occurred as heterozygous segregates among progenies, but homozygous uniculm lines could not be established {10492}.

57. Polyphenol Oxidase (PPO) Activity

QTL: Chara (medium high PPO) / WW2449 (low PPO): one QTL was located on chromosome 2A. Two markers (one SNP, one CAPS) based on BQ161439 were polymorphic between the parents and showed linkage or allelism with PPO loci *Xtc1* and *XPPO-LDOPA*.

Xtc1 – 0.6 cM – *XPPO-LDOPA/XPPO18/BQ161439* {10484}.

59. Reaction to Black-Point of Grain

QTL: Add to the paragraph starting with 'Sunco/Tasman': Markers *Xgwm319-2B* and *Xgwm048-4AS* were confirmed in a 'Batavia/Pelsart (resistant)' DH population {10494}.

60. Response to Photoperiod

Insert following the current *Ppd-B1* entry:

Ppd-D1. Comparative mapping showed that *Ppd-D1* was co-linear with barley *Ppd-H1* – a member of the pseudo-response regulator (PRR) gene family {10466}. Stocks with *Ppd-D1a* had a 2,089bp deletion upstream of the coding region leading to misexpression of the 2D PRR gene {10466}.

Ppd-D1a. **v:** Add: Festival {10466}; Kavkaz {0917}; Orqual {10466}; Recital {10466}; Saitama 27 {10466}; Sideral {10466}; Soissons {10466}; Talent {10466}; Texel {10466}.
ma: Stocks with *Ppd-D1a* had a 2,089-bp deletion upstream of the coding region leading to mis-expression of the 2D PRR gene {10466}.

61. Response to Salinity

61.1. K+/Na+ discrimination

Kna1.

Add note: *Kna1* is a possible othologue of *Nax2* and is the Na^+ transporter *TaHKT1;5-D* {10455}.

6.1.2 Sodium exclusion

Nax1 {10452}. 2AL {10452}. **i:** Tamaroi*6/Line 149 = P06306 {10453}.
tv: Line 149 *Nax2* = 126775b {10452}.
dv: AUS 90382 *Nax2* = C68.101{10455} = JIC *T. aegilopoides* no. 3.

ma: *Nax1* was mapped as a QTL in the region *Xpsr102-2A* – 5.4 cM – *Xwmc170 -2A* – 0.9 cM – *Xksud22-2A/Xksu16-2A* – 0.8 cM – *Xgwm312-2A* with $R^2 = 0.38$ in 'Tamaroi/Line 149' {10452}. *TmHKT7-A2* was identified as a putative candidate Na^+ transporter{10454}.
Nax1 promotes withdrawal of Na^+ from xylem in leaf bases and roots {10453}.

Nax2 {10453}. 5AL {10455}. **i:** Tamaroi*6/Line 149 = P05603 {10453}.
tv: Line 149 *Nax1* = 126775b {10452, 10453}.
dv: AUS 90382 *Nax1* = C68.101{10455} = JIC *T. aegilopoides* no. 3.

ma: Co-segregation with *Xgwm291-5A/Xgwm140-5A/Xgpw2181-5A* {10455}. *TmHKT1;5-A* was identified as a candidate for *Nax2* {10455}.
Nax2 is a likely orthologue of *Kna1* {10455}.

63. Response to Vernalization

Add to the comment following *Vrn3* entries:
…… to Arabidopsis *FLOWERING LOCUS T* (*FT*) {10421}. Polymorphisms in the A and D genome copies of *TaFT* are associated with variation of earliness components in hexaploid wheat {10533}.

Add as a comment at the end of the section:
Three genes up-regulated by vernalization were cloned from *T. monococcum* subsp. *monococcum* {10531}. These were VIN3-like genes similar to Arabidopsis VIN3.

Vil-1{10531}. GenBank DQ886919 {10531}. **ma:** *T. monococcum* subsp. *monococcum* chromosome $5A^m$ {10531}.
Vil-2{10531}. GenBank DQ886917 {10531}. **ma:** *T. monococcum* subsp. *monococcum* chromosome $6A^m$ {10531}.
Vil-3{10531}. GenBank DQ886918 {10531}. **ma:** *T. monococcum* subsp. *monococcum* chromosome $1A^m$ {10531}.

71. Tenacious Glumes

Tg1. **ma:** Placed in a 12 cM interval between *Xwmc112-2D* and *Xbarc168-2D* {10497}.
Add below *Tg2*:
A QTL analysis of the relationship of glume tenacity (*Gt*) with threshability (*Ft*) and the size of the glume base scar (*Gba*) after glume detachment in two crosses, viz. the ITMI population and CS* /CS (*Ae. tauschii* 2D), was undertaken {10497}. In the first cross *QFt.orst-2D.1* and *QGt.orst-2D.1* were closely associated with *Xgwm261-2D*, and *XFt.orst-2D.2* and *XGt.orst-2D* were associated with *Xgwm455-2D*; in the second population only the first pair along with *XGba. orst-2D* were detected; these appeared to correspond with *Tg1* {10497}.

75.9. Grain yield

Add:

Grain yield under drought stress

QTL: 'Dharwar Dry (drought tolerant)/Sitta': SSR locus *Xwmc89-4AL* was the marker most closely associated with with QTL for grain yield, grain fill rate, spike density, grains/m^2, biomass, and drought susceptibility index covering a genetic distance of 7.7 cM {10488}.

Proteins

77. Proteins

77.2.6. Endopeptidase

***Ep-D1b*.**

Add comment after the present entry: Assuming that *Ep-D1* encoded an oligopeptidase G, comarative genetics were applied to develop a STS marker for identifying resistance gene *Pch1*{10513} (see Reaction to *Tapesia yallundae*).

77.2.29. Starch branching enzyme

Insert headings:

Starch Branching Enzyme I

Present entries are in this section.

Starch Branching Enzyme II

SbeII

Suppression of SBEIIb expression alone had no effect on amylose content; however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose {10534}.

77.2.32.1 Phytoene synthase 1

Add introduction: Phytoene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Flour colour and Grain quality parameters: Flour, semolina and pasta colour). The gene *Psy-A1* was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents {10501}. Most hexaploid wheat culitvars have a 676-bp insertion in intron four that is absent in Australian cultivars Dundee, Raven, and Aroona with high yellow pigment. The *Psy-B1b* allele from tetraploid wheat Kofa is the result of a B–A intergenomic conversion event that probably occurred in Cappelli *ph1c* mutant l {10530}. An EMS mutation in the *Psy-E1* gene is associated with whiter endosperm in lines carrying the *Th. elongatum* 7EL translocation.

Psy-A1

Psy-A1a {10501}. GenBankEF600063 {10501}. No 37-bp insertion in intron 2 (194-bp fragment for marker *Yp7A*) {10501}. 676-bp insertion in intron 4 {10530}.
v: Chinese common wheats with high pigment content: CA9648 {10501}; Neixiang 188 {10501}.
ma: *Xwmc809* – 5.8 cM – *Yp7A* {10501}.

Psy-A1b {10501}. GenBank EF6000644 {10501}. 37-bp insertion intron 2 (231 bp fragment for marker *Yp7A*) {10501}. 676-bp insertion in intron 4 {10530}.
v: Chinese common wheats with low yellow pigment content {10501}. Ph82-2 {10501}; Xinong 336 {10501}.

Psy-A1c {10530}. Hexaploid wheats with no 37-bp insertion in intron 2 and no 676-bp insertion in intron 4 {10530}.
v: High yellow pigment cultivars: Aroona (PI 464647) {10530}; Dundee (PI 89424, PI106125) {10530}; Raven (PI 303633, PI 330959) {10530}.

Psy-A1d {10530}. GenBank EU096090 {10530}.
tv: Kofa {10530}; UC1113 {10530}.

Psy-B1

Psy-B1a {10530}. GenBank EU096093 {10530}.
tv: UC1113 {10530}.

Psy-B1b {10530}. GenBank EU096092 {10530}.
tv: Kofa {10530}.

Psy-E1

Psy-E1a {10530}. GenBank EU096095 {10530}.
v: Agatha (7EL translocation) {10530}.

Psy-E1b {10530}. = EU096095 with P to L mutation at amino acid 422 {10530}.
v: EMS mutant Agatha-28-4 (10530); Wheatear {10530}.

7.2.34. Polyphenol oxidase

Add as intoductory statement: High PPO activity in kernels and flour leads to a time-dependent discolouration of end products such as noodles, pasta and breads.

Primers different from those in {10386) were developed in {10504}, but their ability to distinguish phenotypic groupings (alleles) were similar. A null allele of *Ppo-D1* was identified for this locus using primer pair WP3-2 {10504}.

Ppo-A1.

Ppo-A1a. **v:** Add reference ‘,10504’ to existing reference panels, i.e., {10385, 10386, 10504} and {10386, 10504}.

Ppo-A1b. **v:** Nongda 183 {10504}. Add reference ‘,10504’ to ‘others’.

Ppo-D1.

Ppo-D1a. **v:** Add reference ‘,10504’ to existing reference panels.

Ppo-D1b. **v:** Nongda 183 {10504}. Add reference ‘,10504’ to others.

Ppo-D1c [{10504}]. *Ppo-D1null* {10504}. **v:** Gaiyuerui {10504}; Xiaobingmai {10504}; Zm2851 {10504}; XM 2855 {10504}; 9114 {10504}.
ma: Wheats with this allele tend to have lower PPO activity {10504}.

Endosperm Storage Proteins

77.3.1. Glutenins

77.3.1.1. Glu-1

Glu-A1

Add:

Glu-A1y [{10535}]. 2·· {10535}. **v:** 211.12014 {10535}.

Glu-A1-1

In the following entries that appear in the 2006 Supplement:

Glu-A1v {10327}. 2.1* {10327}. **v:** KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.

Glu-A1w [{10327}]. 2’ {10327}. **v:** TRI14165/91 {10327}.

replace ‘***Glu-A1v***’ and ‘***Glu-A1w***’ with ‘***Glu-A1-1v***’ and ‘***Glu-A1-1w***’, respectively.

Add:

Glu-A1-1x [{10535}]. 2·· {10535}. **v:** 211.12014 {10535}.

77.5.8. Puroindolines and grain softness protein

Under the preamble, add:

Recent reviews {10522, 10523} provide comprehensive descriptions of the molecular genetics and regulation of puroindolines. Morris and Bhave {10524} reconciled the D-genome puroindoline alleles with DNA sequence data. Bonafede et al. {10525, 10526} developed a CS line (PI 651012) carrying a T5A^{m}S·5AS translocation from *T. monococcum* subsp. *monococcum*; the translocated chromatin carries A-genome *Pina, Pinb*, and *Gsp-1* alleles that confer softer kernel texture.

Pina-D1b

i: Add: Near-isogenic pairs were developed in McNeal, Outlook, Hank, Scholar, and Explorer {10527}.
v: add: This BAC clone also contains *Pinb-D1a* {10431}.

Pina-D1m. Add: **v:** Hongheshang, (GenBank EF620907) {10208}.

Pina-D1n. Add: **v:** Xianmai GenBank EF620908) {10208}.

Correct:

Pinb-D1p {10121}. **v:** Nongda 3213 {10121}; Nongda 3395 {10121}.

Pinb-D1u. **v:** Tiekmai, add: (GenBank EF620911) {10427}.

Delete existing information and relace with:

Pinb-D1x {10528}. **v:** Kashibaipi (GenBank AM909618) {10528}.

Pinb-D1ab **v:** Add: Tuokexunyihao {10528}.

Pathogenic Disease/Pest Reaction

78. Reaction to Barley Yellow Dwarf Virus

Bdv2. 7D = T7DS-7Ai#1S7Ai#1L group: **v:** Glover (with TC6) {10491}.

79. Reaction to *Blumeria tritici*

79.1. Designated genes for resistance

Pm12. **ma:** Add: Secondary recombination analysis indicated that *Pm12* was located in the long arm of 6S between *Xwmc105* and *Xcau127* {10517}.

Pm21. **ma:** Add: Marker NAU/Xibao15, developed from a serine/threonine gene upregulated by powdery mildew infection, acts as a co-dominant marker for lines carrying *Pm21* {10519}.

Pm37. **v:** List as: PI 615588 = NC99BgTAG11 = Saluda*3/PI 615588 {10372}.
ma: Add: *Xgwm332-7A* – 0.5 cM – *Pm37* – 0.5 cM – *Xwmc790-7A* – 15.5 cM – *Pm1* {10372}.

Pm39 {10481}. Adult-plant resistance. 1BL {10480, 10481}.
i: Avocet-R+*Lr46*/*Yr29* = Avocet-R*3//Lalb mono 1B*4/Pavon 76 {10480}. Genotypes with *Lr46*/*Yr29*; see Reaction to *Puccinia triticina*, Reaction to *P. striiformis*.
v: Saar (CID: 160299, SID: 188) *Pm38* {10481}.
ma: *Xwmc719-1BL* – 4.3 cM – *Lr46*/*Yr29*/*Pm39* – 2.5 cM – *Xhbe248-1BL* {10481}.

To the paragraph following the last named *Pm* gene and beginning; 'Single resistance genes……' add: A further gene derived from *T. monococcum* PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3 / PI427772 {10479}.

79.2. Suppressors of *Pm*

79.3. Temporary designated genes for resistance to *Blumeria graminis*

PmLK906 {10476}. Resistance is recessive (10476, 0928}. 2AL {10476,10477}.
v: Lankao 90(6)21-12 {10476}; Zhengzhou 9754 {10476}.
ma: *TacsAetPR5-2A*/*Pm4* – 3.9 cM – *Xgwm265-2A* – 3.72 cM – *Pm39* – 6.15 cM – *Xgdm93-2A* {10476, 10477}. *TacsAetPR5-2A* was converted to a STS marker {10477}.

79.4. QTL for resistance to *Blumeria graminis*

At the end of the paragraph ending with ' ….. Becker / Massey {0284}.' Add: These QTL were confirmed by the addition of extra markers to the 'Becker/Massey' map and in a separate analysis of 'USG 3209 (A Massey derivative)/Jaypee (susceptible)' {10505}. USG 3209 possessed *Pm8* (T1BL·1RS) and an unknown specific resistance factor and their combination had a positive effect on APR even though neither was effective against the races used to identify the QTL {10505}.

81. Reaction to *Diuraphis noxia*

Dn7. *Dn2414* {10478}. **v:** ST-ARS 02RWA2414-11 {10474}.
ma: *Xhor2-1R* – 1.7 cM – *Dn7* – 1.0 cM – *Xscb241-1R* {10474}. Marker $Xrems1303_{320}$ was amplified only in genotypes resistant to biotype 3 and presumably possessing *Dn7* {10474}.

82. Change to: **Reaction to *Fusarium* spp.**

82.1. Disease: Fusarium head scab, scab

Insert as an introductory statement before listing the first gene:
Whereas much of the recent genetic work involved FHB caused by *F. graminearum*, according to {10514} *F. culmorum* is more damaging than *F. graminearum* in terms of FHB severity, kernel damage, yield reduction, and DON/NIV contamination.

Fhb3 {10529}. 7D = T7AL·7Lr#1S {10529}. **v:** TA 5608 (10529}.
al: *Leymus racemosus* {10529}.
The level of type-2 resistance conferred by *Fhb3* was similar to that of Sumai 3 {10529}.

***QFhs.ndsu-3AS*.ma:** Add: *Qfhs.ndsu-3AS* was placed within a 11.5-cM region flanked by TRAP marker loci *Xfcp401-3A* and *Xfcp397.2-3A* {10482}. This gene is unlikely to be a homoeologue of *Qfhs.ndsu-3BS* = *Fhb1* {10482}.

QFhs.pur-7El {10489}. $7el_2$ {10489}, T7DS·7DL-$7el_2$ {10489}. **su:** K2630 {10489}.
v: K11695 = T7DS·7DL-$7el_2$ {10489}; KS10-2 = T$7el_2$S·$7el_2$L-7DL {10489}; KS24-1 and KS24-2 = T7DS·$7el_2$ {10489}.
ma: *Qfhs.pur-*$7el_2$ was flanked by *BE445653* and *Xcfa2270-7D* {10489}. These markers also were present in KS10-2 {10489}.

QTL: Add after 'Chokwang/Clark':
'Ernie (Resistant)/MO94-317 (Susceptible)': 243 F_8 RIL population. Four QTL from Ernie detected as follows:
Qfhs.umc-2B, linked to *Xgwm278-2BS*, $R^2 = 0.04$ {10456}.
Qfhs.umc-3B, linked to *Xgwm285-3BS*, $R^2 = 0.13$ {10456}.
Qfhs.umc-4B, linked to *Xgwm495-4BL*, $R^2 = 0.09$ {10456}.
Qfhs.umc-5A, Linked to *Xgwm165-5A*, $R^2 = 0.17$ {10456}.
Evidence was provided to suggest the QTL acted additively {10456}.

Add after 'Arina/Forno':
'Arina/Riband' DH lines: QTL affecting AUDPC were identified in 1BL (2), 2B, 4DS, 6BL, and 7AL (Arina), and 7AL and 7BL (Riband). The most effective was the 4DS QTL that appeared to be an effect of *Rht-D1a* rather than height *per se* {10464}.

'Cansas (moderately resistant)/Ritmo (susceptible)' : Map-based analysis across environments revealed seven QTL, *QFhs.whs-1BS* (1RS), *QFfhs.whs-3B* (not *Fhb1*), *QFhs.whs-3DL, QFhs.whs-5BL, QFhs.whs-7AL*, and *QFhs.whs-7BL* (cumultatively, $R^2 = 0.56$). The chromosome 1D gene was primarily involved in resistance to fungal penetration and the others in resistance to spread {10503}. There were significant correlations of FHB response with height and heading date {10503}.

Add above 'Frontana/Remus' entry:
'Veery (susceptible)/CJ 9306 (resistant)': Four QTL, *QFhs.ndsu-3BS* (*Xgwm533b* – Xgwm493), *QFhs.nau-2DL* (*Xgwm157 – Xwmc-041*), *QFhs.nau-1AS* (*Xwmc024 – Xbarc148*), and *QFhs.nau-7BS* (*Xgwm400 – gwm573*) accounted for 31, 16, 10, and 7%, respectively, of the average phenotypic variation over three years {10490}.

Continue under 'Dream/Lynx': 'Dream*4/Lynx' lines were developed by selection of QTL on chromosomes 6AL, 7BS, and 2BL. Lines carrying *QFhs.lfl-6AL* and *QFhs.lfl-7BS* were more resistant than lines lacking them; the 2BL QTL effect was not verified {10470}.

Change the heading 'DON accumulation' to 'Resistance to DON accumulation'
Add:
'Veery/CJ 9306 (resistant)': Four QTL contributed to resistance; *QFhs.ndsu-3BS*, nearest marker *Xgwm533b* ($R^2 = 0.23$), *QFhs.nau-2DL, Xgwm539* ($R^2 = 0.2$), *QFhs.nau-1AS, Xbarc148* ($R^2 = 0.05$) and *QFhs.nau-5AS, Xgwm425* ($R^2 = 0.05$) {10496}.

82.2. Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* species.

83.Reaction to *Heterodera avenae* Woll.
CreX {10486}. Derived from *Ae. variabilis*. 2AS or 2DS {10486}. **ad:** Line M {10487}.
v: Line D {10486}.
ma: RAPD markers $OP02_{1000}$, $OpR4_{1600}$, $OpV3_{450}$ {10486}.
CreY {10486}. Derived from *Ae. variabilis*. 3BL {590}. **v:** Line X {10487}.
ma: Co-segregation with RAPD $OpY16_{1065}$ {0103} which was converted to SCAR16 {10486}.
May be the same gene as *Rkn-mn1* (see reaction to *Meloidogyne naasi*).

84. Reaction to *Magnaporthe grisea* (Herbert) Barr

Rmg1 {10462}.	1D {10462}.	**s:** CS (Cheyenne 1D) {10462}.
		v: Cheyenne (10462}; Norin 26 {10462}; Shin-chunaga {10462}.
Rmg2 {10461}.	7A {10461}.	**i:** CS (Thatcher 7A) {10461}.
		v2: Thatcher *Rmg3* {10461}.
Rmg3 {10461}.	6B {10461}.	**i:** CS (Thatcher 6B) {10461}.
		v2: Thatcher *Rmg2* {10461}.

86. Reaction to *Meloidogyne* spp.

***Rkn-mn1*.** **ma:** After RAPD Op_{1065} insert: (converted to SCAR Y16 {10486}). May be the same as *CreY* (see reaction to *Heterodera avenae*).

87. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

***Stb6*.** **v:** Add: Bezostaya 1 {10495}.

89. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

Disease: Septoria nodorum blotch, Stagonospra nodorum blotch.
This entire section has been revised

89.1. Genes for resistance

Snb1 {856}.	3AL {856}.	**v:** Red Chief {856}.
		v2: EE8 *Snb2* {856}.
Snb2 {856}.	2AL {856}.	**v2:** EE8 *Snb1* {856}.
Snb3 {1594}.	5DL {1594}.	**s:** CS*/Synthetic 5D {1594}.
		v: Synthetic {1594}.
		dv: *Ae. tauschii* {1594}.
SnbTM {856, 857}.	3A {857}, 3AL {856}.	**v:** Coker {10210}; Hadden {10210}; Missouri {10210}; Red Chief {10210}; 811WWMN 2095 {10210}; 86ISMN 2137 {10210}. **tv:** *T. timopheevii* subsp. *timopeevii*/2*Wakooma {856}; *T. timopheevii* subsp. *timopeevii* PI 290518. *T. timopheevii* subsp. *timopeevii* derivatives: S3-6 {857}; S9-10 {857}; S12-1 {857}. **ma:** $UBC521_{650}$ - 15 cM - *SnbTM* - 13.1 cM - $RC37_{510}${0212}. $UBC521_{650}$ was converted to a SCAR marker {0212}.

Allelism of the hexaploid wheat gene and the *T. timopheevii SnbTM* was suspected. but not confirmed.

QTL

A QTL analysis of SNB response in the ITMI population found significant effects associated with chromosome 1B (probably *Snn1*) and 4BL, with an interactive effect involving the 1BS region and a marker on chromosome 2B {10009}. An additional QTL on 7BL was effective at a later stage of disease development {10009}.

Four QTL, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B. and 5D, were mapped in a 'Liwilla/Begra' DH population. Longer incubation period and lower disease intensity were contributed by Liwilla {10045}.

Two QTL for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in 'Arina/Forno' RILs {10065}. The 3BL QTL, designated *QSng.sfr-3BS*, was associated with marker *Xgwm389-3B* and explained 31.2% of the variation. The resistance was contributed by Arina {10065}. The 4BL QTL, *QSng.sfr-4BL*, was associated with *Xgwm251-4B* and explained 19.1% of the variation. Resistance was contributed by Forno {10065}. A QTL on 5BL, *QSng.sfr-5BL*, overlapped with QTL for plant height and heading time {10065}. *QSng.sfr-3BS* peaked 0.6 cm proximal to *Xsun2-3B* {10465}. Association mapping involving 44 modern European cultivars indicated that the association was retained in a significant proportion of genotypes {10465}.

A QTL, *QSnl.ihar-6AL*, identified in DH lines of 'Alba (resistant)/Begra (susceptible)' accounted for 36% of the phenotypic variance in disease severity and 14% of the variance in incubation period {10143}.

'Forno (susceptible)/Oberkulmer spelt (resistant)'. Among 204 RILs, leaf and glume responses were genetically different but correlated ($R^2 = 0.52$). Ten QTL for glume blotch (SNG) resistance were detected, six from Forno. A major QTL ($R^2 = 35.8\%$) was associated with q. Eleven QTL (four from Forno) affected leaf blotch; three of these (chromosomes 3D, 4B, and 7B) with $R^2 > 13\%$ were considered potential candidates for MAS {10250}.

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).

'Br34/Grandin': Three QTL with resistance effects from BR34; *Qsnb.fcu-5BL.1* (*Tsn1*), $R^2 = 0.63$, *Qsnb.fcu-5BL.2*, $R^2 = 0.06$, and *Qsnb.fcu-1BS* (vicinity of *Snn1*) $R^2 = 0.10$ (10458). QTL analysis of the RIL population with Culture *Sn6* revealed four QTL, *Qsnb.fcu-2DS* ($R^2 = 0.3 – 0.49$) associated with *Snn2*, *Qsnb.fcu-5BL* ($R^2 = 0.14 – 0.2$) associated with *Tsn1*, *Qsnb.fcu-5AL* ($R^2 = 0 – 0.13$) associated with *Xfcp13-5A*, and *Qsnb.fcu-1BS* ($R^2 = 0$ - 0.11) associated with *Xgdm125-1BS* {10507}.

'P91193D1 (partially resistant)/P92201D5 (partially resistant)' RIL populations were tested in India and Western Australia for glume resistance. Two QTL were idientified: *Qng.pur-2DL.1* from P91193D1 ($R^2 = 12.3$ in Indiana and 38.1% in WA, respectively; *Xgwm526.1-2D – Xcfd50.2-2D*) and *QSng.pur-2DL.2* from P99201D5 ($R^2 = 6.9\%$ and 11.2%, respectively; *Xcfd50.3-2D – wPT9848*) {10471}.

89.2. Sensitivity to SNB toxins

Tsn1 {10458, 346, 10207}. Sensitive to SnToxA which is functionally identical to Ptr ToxA {10459}.
v: See reaction to *Pyrenophora tritici repentis* {10458}. Cheyenne {0007}; Hope {0007}; Jagger {0007}; Kulm {346,10030, 10458}; ND495 {0007}; Timstein {0007}; Trenton {0315}.
tv: Langdon {10458}.

tsn1 {346,10207}. Insensitivity (disease resistance) is recessive {346}. 5BL {346}.
v: AC Barrie {10153}; AC Cadillac {10153}; AC Elsa {10153}; BR34 {0007}; CEP17 {0007}; Chinese Spring {0007}; Erik {0007,10030}; Hadden {10155}; Laura {10153}; Line 6B-365 {10155}; Red Chief {10155}; 1A807 {0007}; 1A905 {0007}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122.
tv: Altar 84 {0007}; D87450 {0007}; *T. turgidum* subsp. *dicoccoides* Israel A {10506}.
ma: *Xbcd1030-5B* – 5.7 cM – *tsn1* – 16.5 cM – *Xwg583-5B* {346}; *tsn1* – 3.7 cM – *Xbcd1030-5B* {0007}; *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}.

snn1 tsn1. Atlas 66 {10458}; BR34 {10458}; Erik {10458}; Opata 85 {10458}; ND688 {10458}.

Snn1 {10008}. Sensitivity to 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}.

snn2. **v:** Br34 {10507}.

Snn2 {10507}. Sensitivity to SnTox2 is dominant {10507}. 2DS {10507}.
v: BG223 {10507}. **v2:** Grandin *Tsn1Tsn* {10507}.
ma: *Xgwm614-2D* – 7.6 cM – *Snn2* – 5.9 cM – *Xbarc95-2D* {10507}.

90. Reaction to *Puccinia graminis*

Sr9a. **ma:** *Xbarc101-2B/Xgwm12-2B* – 2.7 cM – *Xgwm47-2B* – 0.9 cM – *Sr9a/Xwmc175-2B* {10472}.

Sr8b. **tv:** According to Luig {841} one of the genes in Leeds is *Sr8b*. This could be the gene located on chromosome 6A in ST464-A1 {10473} and one of the genes present in ST464, a parent of Leeds.

Sr9e. **tv:** ST464-A2 {10473}. **tv2:** ST464 *Sr13* {10473}.

Sr13. **tv:** ST464-C1 {10473}. **tv2:** ST-464 *Sr9e* {10473}.

Genotype lists: add: {10511}.

Sr46 {10538}. 2DS {10538}. **v:** L-18913 / Meering selections R9.3 {10538}; R11.4 {10538}; R14.2 {10538}.
v2: L-18913 = Synthetic, Langdon / *Ae. tauschii* var. *meyeri* AUS 18913 *Sr9e* {10538}.
ma: Co-segregation with RFLP *Xpsr649-2DS* at both the diploid and hexaploid levels {10538}. A PCR-based marker, *csSC46*, was developed from a BAC clone containing *Xpsr649* {10538}.

91. Reaction to *Puccinia striiformis*

91.1. Designated genes for resistance to stripe rust

Yr21. After 1B add reference: {',10450'}.
A closely linked gene, also in Lemhi, conferred resistance to *P. s. hordei* {10450}. Both genes were mapped relative to RGAP markers. *Yr21 – YrRpsLem,* 0.3 cM {10450}.

Yr41 {10502}. ***YrCN19***{10228}. 2BS {10228, 10502}. **v:** AIM {10228}; AIM6 {10228}; Chuannong 19 {10228, 10502}.
ma: Complete linkage to a 391-bp allele of *Xgwm410-2BS* {10228}. *Xgwm410-2B* – 0.3 cM – *Yr41* {10502}.

91.2. Temporarily designated genes for resistance to stripe rust

YrCN19. This listing can be deleted.

91.3. Stripe rust QTL

Add at end of section: *T. monococcum* subsp. *monococcum* PAU14087 (resistant) / *T. monococcum* subsp. *aegilopoides* PAU5088 (resistant): RIL population: One adult-plant resistance QTL identified in each parent and named *QYrtm.pau-2A* (in a 3.6 cM interval between *Xwmc407-2A* and *Xwmc170-2A*; $R^2 = 0.14$) and *QYrtb.pau-5A* (in a 8.9 cM interval between *Xbarc151-5A* and *Xcfd12-5A*; $R^2 = 0.24$) {10518}.

92. Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr3.
At the end of the section add note: Durum cv. Storlom likely carries *Lr3a* or *Lr3b* {10469}. Cv. Camayo was considered to have a closely linked gene, or *Lr3* allele {10469}. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B* {10469}. All three Thatcher NILs with named *Lr3* alleles carried the STS marker {10469}.

Lr13. **ma:** *Lr13* – 10.7 and 10.3 cM – *Xgwm630-2BS* {10463}.
Lr14a. Add: *LrLla* {10520}. **tv:** Lloreta INIA {10520}; Somateria {10520}.
ma: *Xwmc273-7B* – 13 cM – *Lr14a* – 10 cM – *Xgwm344-7B* {10520}.
Lr22a. **i:** Neepawa*6/RL5404, RL4495 {10467}; Thatcher*7//Tetra-Canthatch/RL5271, RL6044 {10467}.
ma: *Xgwm455-2D* - 1.5 cM - *Lr22a* - 2.9 cM - *Xgwm296-2D* {10467}.
Lr34. **v2:** Mentana *Lr3b* {10493}.
ma: After the entry …csLV34a ……*Lr34* {10387}. Add: STS marker csLV34 was used to confirm or postulate the presence of *Lr34* in Australian culitvars {10493}.
Lr58. **ma:** After the third RFLP add: '..... and SSR marker *Xcfd50* …..'.
Lr61 {10485}. 6BS {10485}. **tv:** Guayacan 2 {10485}; Guayacan INIA {10485}.
ma: Closely linked and distal to 3 AFLP markers about 22 cM distal to SSR marker *Xwmc487-6B* {10485}.

93. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

This entire section has been revised. Disease: Tan spot, yellow leaf spot.
Virulence in the pathogen is mediated by host-specific toxins and host resistance is characterized at least in part by insensitivity to those toxins. Three toxins, Ptr ToxA, Ptr ToxB, and Ptr ToxC, have been identified (see {10153}). Toxin sensitivity determined by use of toxins extracted from pathogen strains and resistance determined by infection experiments are treated as different traits, although common genes may be involved.

93.1. Insensitivity to tan spot toxin (necrosis)

tsn1 {346, 10207}.	Insensitivity (disease resistance) is recessive {346}.	*Tsr1* {10508}, see Resistance to tanspot	5BL {346}.

v: AC Barrie {10153}; AC Cadillac{10153}; AC Elsa {10153}; Atlas 66 {10458}; BR34 {0007,10458}; CEP17 {0007}; Chinese Spring {0007,10458}; Erik{0007,10030,10458}; Laura {10153}; IA807 {0007}; IA905 {0007}; ND688 {10458}; Opata 85 {10458}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. tauschii* C122 {346,10207,10458}; Synthetic W-7984 = Altar 84/*Ae. tauschii* CI 18 {0007,10458}.

tv: Altar 84 {0007}; D87450 {0007}. *T. turgidum* subsp. *dicoccoides* Israel A {10506}.

ma: *Xbcd1030-5B* – 5.7 cM – *tsn1* – 16.5 cM – *Xwg583-5B* {346}; *tsn1* – 3.7 cM – *Xbcd1030-5B* {0007}; *Xfcg7-5B* – 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/Xfcc1/XBE443610* {10413}.

Tsn1. Sensitive to Ptr ToxA.

v: Grandin {10458}; Bobwhite {10458}; Cheyenne {0007, 10458}; Glenlea {10458}; Hope {0007, 10458}; Jagger {0007}; Katepwa {10458}; ND2709 {10458}; ND495 {0007}; Sumai 3 {10458}; Timstein {0007, 10458}.

tv: Langdon {10458}.

v2: Kulm *Tsc1* {346,10030,10458}; Trenton *Tsc1* {0315}.

In Kulm/Erik, toxin response accounted for 24% of the variation in disease response, which was affected by 4–5 genes {10030}.

Ptr ToxA is functionally identical to *S. nodorum* ToxA but has two predicted amino acid differences {10459}. See Reaction to *Phaeosphaeria nodorum*.

93.2. Insensitivity to tan spot toxin (chlorosis)

tsc1 {344}. Insensitivity is recessive. *QTsc.ndsu-1A* {9924}.

v: Katepwa {0315}; Opata 85 {344}; Synthetic W-7984 {0315}.

Tsc1 {344}. Sensitivity to Ptr ToxC {344}. 1AS {344}.

v: 6B365 {0315}; Opata 85 {344}.

v2: Kulm *Tsn1* {0315}; Trenton *Tsn1* {0315}.

ma: *Gli-A1* – 5.7 cM – *Tsc1* – 11.7 cM *XksuD14-1A* {0315}.

According to {10376} the same allele, presumably *tsc1*, 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.

tsc2. Insensitivity allele {10015}. **v:** Opata 85 {0315,10015}.

Tsc2. Sensitive to Ptr ToxB {10015}. 2BS {10015}.

v: Synthetic W-7984 {10015}.

93.3 Resistance to tanspot

Tsr1. [*tsn1* See: Insensitivity to tanspot toxin]. Resistance is recessive.

5BL **v:** Genetic stocks that do not have *Tsn1* and other genes that respond to toxins produced by the pathogen.

Tsr2. [*tsn2* {10344}]. Resistance is recessive. Confers resistance to race 3 {10344}. 3BL {10344}.

sutv: LDN (DIC-3B) {10344}.

tv: *T. turgidum* subsp. *dicoccoides* Israel-A {10344}.

tv2: *T. turgidum* subsp. *turgidum* no. 283, PI 352519 *Tsr5* {10344}.

ma: Identified as a QTL in region *Xgwm285-3B – Xwmc366.2-3B* (R^2 = 91%) {10344}, also classified as a single gene: *Xgwm285-3B* – 2.1 cM – *tsn2* – 15.2 cM – *Xwmc366.2-3B* {10344}.

Tsr3. [*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.

Tsr4. Resistance is recessive. [*tsn4* (10350)]. Resistance to race 1 (culture ASC1a) {10350}. 3A {10350}.

v: Salamouni {10350}.

Tsr5. *tsn* {10509} . 3BL {10509}.

tv2: *T. turgidum* subsp. *turgidum* no. 283, PI 352519 *Tsr2* {10509}.
ma: *Tsr5* – 8.3 cM – *Xgwm285-3B* – 2.7 cM – *Tsr2* {10509}.

QTL:

QTsc.ndsu-1A {9924}. Resistance is likely recessive {344}. [*Tsc1* {344}]. 1AS {344}. **v:** Synthetic W7984 {344}.**ma:** Association with *Gli-A1* {344, 0040, 0264}. *QTsc.ndsu-1A*, or a closely associated gene, confers insensitivity to Ptr ToxC, see {0315}. Inoculation with purified toxin Ptr ToxC was used to map this locus. *QTsc.ndsu-1A* confers resistance in both seedlings and adult plants.

QTsc.ndsu-4A. 4AL {0090}. **v:** Opata 85 / W-7984 (ITMI) RI mapping population; resistance was contributed by W-7984 {0090}; In W-7976 / Trenton resistance was contributed by W-7976 {0264}. **ma:** Association with *Xksu916(Oxo2)* - 4A and *Xksu915(14-3-3a)-4A* {0090}; In W-7976 / Trenton there was association with *Xwg622-4A* {0264}; Minor QTL in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants {0264}.

QTL: ITMI population: In addition to *tsc2* which accounted for 69% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL (*Xksu916(Oxo)-4AS*, W-7948) accounted for 20% of the phenotypic variation {10015}. 'Grandin (susceptible)/BR34 (resistant)' RILs: QTL in 1BS, *QTs.fcu-1BS*, (13-29% of variation depending on race) and 3BL, *QTs.fcu-3BL*, (13-41%) were involved in resistance to 4 races. Five other QTL showed race specific responses {10248}.

Introgressions of genes for insensitivity to Ptr ToxA and Ptr ToxB are outlined in {10153}.

96. Reaction to Soil-Borne Cereal Mosaic

Add: **QTL:** *QSbv.ksu.5D* in interval *Xcfd86-5D – Xcfd10-5D* in 'TA 4152-4/Karl 92'. TA 4152-4 = '*T. turgidum* subps. durum Altar 84/*Ae. tauschii* WX193 {10521}'.

97. Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides*

Pch1. **v:** Add: Coda {10513}. **ma:** Add: Leonard et al. {10513} predicted that *Ep-D1* might encode an oligopeptidase B, and by comparative genetics, developed primers to a wheat oligopeptidase B-encoding wheat EST BU1003257. Complete linkage occurred for a derived STS marker *Xorw1* and *Pch1* in a Coda / Brundage RIL population and the marker identied the presence or absence of *Pch1* 44 among wheat accessions {10513}.

98. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Bt10. **i:** BW553 = Neepawa*6 // Red Bobs / PI178383 (10475}.

99. Reaction to *Tilletia indica* Mitra

QTL:

Qkb.ksu-4BL.1. 'WL711/HD29 (resistant)' RILs: $R^2 = 0.25$, associated with *Xgwm538-4B* {10498}. 'WH542/W485 (resistant)' RILs: $R^2 = 0.15$, *Xgwm6-4BL – Xwmc349-4BL* interval {10499}.

Xkb.ksu-5BL.1. 'WH542/HD29 (resistant)' RILs: $R^2 = 0.19$, *Xgdm116-5BL – Xwmc235-5BL* {10499}.

Xkb.ksu-6BS.1. 'WH542/HD29 (resistant)' RILs: $R^2 = 0.13$, *Xwmc105-6BS – Xgwm88-6BS* {10499}.

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VII. ABBREVIATIONS USED IN THIS VOLUME.

PLANT DISEASES, PESTS, AND PATHOGENS:

BYDV = barley yellow dwarf virus
BMV = barley mosaic virus
CCN = cereal cyst nematode, *Heterodera avenae*
FHB = Fusarium head blight
RWA = Russian wheat aphid
SBMV = soilborne mosaic virus
SLB = Septoria leaf blotch
TMV = *Triticum* mosaic virus
WDF = wheat dwarf mosaic
WSBMV = wheat soilborne mosaic virus
WSMV = wheat streak mosaic virus
WSSMV = wheat spindle streak mosaci virus
WYMV = wheat yellow mosaic virus
E. graminis* f.sp. *tritici = *Erysiphe graminis* f.sp. *tritici* = the powdery mildew fungus
F. graminearum = *Fusarium graminearum* = head scab fungus
F. nivale = **Fusarium nivale** = snow mold fungus
H. avenae = *Heterodera avenae* = cereal cyst nematode
P. graminis = *Polymyxa graminis* = wheat soilborne mosaic virus vector
P. striiformis* f.sp. *tritici = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus
P. triticina = *Puccinia triticina* = *P. recondita* f.sp. *tritici* = leaf rust fungus
R. cerealis = *Rhizoctonia cerealis* = sharp eyespot
R. solani = *Rhizoctonia solani* = Rhizoctonia root rot
R. padi = *Rhonpalosiphum padi* = bird cherry-oat aphid
S. tritici = *Septorai tritici* = Septoria leaf spot fungus
S. graminearum = *Schizaphus graminearum* = greenbug
St. nodorum = *Stagonospora nodorum* = Stagonospora glume blotch
T. indica = *Tilletia indica* = Karnal bunt fungus

SCIENTIFIC NAMES AND SYNONYMS OF GRASS SPECIES (NOTE: CLASSIFICATION ACCORDING TO VAN SLAGEREN, 1994):

A. strigosa = *Avena strigosa*
Ae. cylindrica = *Aegilops cylindrica* = *Triticum cylindricum*
Ae. geniculata = *Aegilops geniculata* = *Aegilops ovata* = *Triticum ovatum*
Ae. markgrafii = *Aegilops markgrafii* = *Aegilops caudata* = *Triticum caudatum*
Ae. speltoides = *Aegilops speltoides* = *Triticum speltoides*
Ae. tauschii = *Aegilops tauschii* = *Aegilops squarrosa* = *Triticum tauschii*
Ae. triuncialis = *Aegilops triuncialis* = *Triticum triunciale*
Ae. umbellulata = *Aegilops umbellulata* = *Triticum umbellulatum*
Ae. peregrina = *Aegilops peregrina* = *Aegilops variabilis* = *Triticum peregrinum*
Ae. ventricosa = *Aegilops ventricosa* = *Triticum ventricosum*
S. cereale = *Secale cereale* = rye
T. aestivum* subsp. *aestivum = *Triticum aestivum* = hexaploid, bread, or common wheat
T. monococcum* subsp. *aegilopoides = *Triticum boeoticum*
T. turgidum subsp. dicoccum = *T. dicoccon* = *Triticum dicoccon* = *T. dicoccom*
T. turgidum* subsp. *durum = *Triticum durum* = durum, pasta, or macaroni wheat
T. aestivum* subsp. *macha = *Triticum macha*
T. militinae = *Triticum militinae*
T. aestivum* subsp. *spelta = *Triticum spelta*
T. timopheevii* subsp. *timopheevii = *Triticum timopheevii*
T. timopheevii* subsp. *armeniacum = *Triticum araraticum* = *T. araraticum*
T. turgidum* subsp. *dicoccoides = *Triticum dicoccoides* = wild emmer wheat
T. turgidum* subsp. *dicoccum = *Triticum dicoccum*
T. urartu = *Triticum urartu*

Th. bessarabicum = *Thinopyrum bassarabicum*
Th. elongatum = *Thinopyrum elongatum* = *Agropyron elongatum*
Th. intermedium = *Thinopyrum intermedium* = *Agropyron intermedium*

Scientific journals and publications:

Agron Abstr = Agronomy Abstracts
Ann Wheat Newslet = *Annual Wheat Newsletter*
Aus J Agric Res = *Australian Journal of Agricultural Research*
Cereal Res Commun = *Cereal Research Communications*
Curr Biol = *Current Biology*
Eur J Plant Path = *European Journal of Plant Pathology*
Funct Integ Genomics = *Functional Integrative Genomics*
Int J Plant Sci = *International Journal of Plant Science*
J Cereal Sci = *Journal of Cereal Science*
J Hered = *Journal of Heredity*
J Phytopath = *Journal of Phytopathology*
J Plant Phys = *Journal of Plant Physiology*
Mol Gen Genet = *Molecular and General Genetics*
Nat Genet = *Nature Genetics*
PAG = Plant and Animal Genome (abstracts from meetings)
Phytopath = *Phytopathology*
Plant Breed = *Plant Breeding*
Plant, Cell and Envir = *Plant, Cell and Environment*
Plant Cell Rep = *Plant Cell Reporter*
Plant Dis = *Plant Disease*
Plant Physiol = *Plant Physiology*
Sci Agric Sinica = *Scientia Agricultura Sinica*
Theor Appl Genet = *Theoretical and Applied Genetics*
Wheat Inf Serv = *Wheat Information Service*

Units of measurement:

bp = base pairs
bu = bushels
cM = centimorgan
ha = hectares
kDa = kiloDaltons
m^2 = square meters
m^3 = cubic meters
μ = micron
me = milli-equivalents
mmt = million metric tons
mt = metric tons
Q = quintals
T = tons

Miscellaneous terms:

Al = aluminum
AFLP = amplified fragment length polymorphism
ANOVA = analysis of variance
A-PAGE = acid polyacrylamide gel electrophoresis
AUDPC = area under the disease progress curve
BW = bread wheat
CHA = chemical hybridizing agent
CMS = cytoplasmic male sterile

CPS = Canadian Prairie spring wheat
DH = doubled haploid
DON = deoxynivalenol
ELISA = enzyme-linked immunosorbent assay
EMS = ethyl methanesulfonate
EST = expressed sequence tag
FAWWON = Facultative and Winter Wheat Observation Nursery
GA = gibberellic acid
GIS = geographic-information system
GM = genetically modified
GRIN = Germplasm Resources Information Network
HPLC = high pressure liquid chromatography
HMW = high-molecular weight (glutenins)
HRSW = hard red spring wheat
HRRW = hard red winter wheat
HWSW = hard white spring wheat
HWWW = hard white winter wheat
ISSR = inter-simple sequence repeat
kD = kilodalton
LMW = low molecular weight (glutenins)
MAS = marker-assisted selection
NSF = National Science Foundation
NILs = near-isogenic lines
NIR = near infrared
NSW = New South Wales, region of Australia
PAGE = polyacrylamide gel electrophoresis
PCR = polymerase chain reaction
PFGE = pulsed-field gel electrophoresis
PMCs = pollen mother cells
PNW = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada)
PPO = polyphenol oxidase
QTL = quantative trait loci
RAPD = random amplified polymorphic DNA
RCB = randomized-complete block
RFLP = restriction fragment length polymorphism
RILs = recombinant inbred lines
RT-PCR = real-time polymerase-chain reaction
SAMPL = selective amplification of microsatellite polymorphic loci
SAUDPC = standardized area under the disease progress curve
SCAR = sequence-characterized amplified region
SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis
SE-HPLE = size-exclusion high-performance liquid chromatography
SH = synthetic hexaploid
SNP = single nucleotide polymorphism
SRPN = Southern Regional Performance Nursery
SRWW = soft red winter wheat
SRSW = soft red spring wheat
STMA = sequence tagges microsatellite site
SWWW = soft white winter wheat
SSD = single-seed descent
SSR = simple-sequence repeat
STS = sequence-tagged site
TKW = 1,000-kernel weight
UESRWWN = Uniform Experimental Soft Red Winter Wheat Nursery
VIGS = virus-induced gene silencing

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XI. VOLUME 55 MANUSCRIPT GUIDELINES.

Manuscript guidelines for the *Annual Wheat Newsletter*, volume 55. The required format for Volume 55 of the *Annual Wheat Newsletter* will be similar to previous editions edited from Kansas State University.

CONTRIBUTIONS MAY INCLUDE:

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

FORMATTING & SUBMITTING MANUSCRIPTS:

Follow the format in volume 44–54 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 55 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, 2009, and will cost $40.

The *Annual Wheat Newsletter* will continue to be available (Vol. 37–55) 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/ggpages/awn/.

COST:

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In the interest of remaining solvent, the NWIC has approved future distribution primarily by computer diskette. We are asking that you renew your contribution or, if you have not contributed in the past, to join the list of contributors. Contributions from individuals in the range of $25 to $50 play a significant role in financing the *Newsletter*. An increase in the number of individual contributors is very important and, with continued support, we hope to meet our financial obligations in 2008. The address for contibutions is Dr. Brett Carver, Department of Agronomy, Oklahoma State University, Stillwater, OK 74078, U.S.A.